De Novo Transcriptome Assembly of *Isatis indigotica* at Reproductive Stages and Identification of Candidate Genes Associated with Flowering Pathways

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ABSTRACT. The appropriate timing of bolting and flowering is one of the keys to the reproductive success of *Isatis indigotica*. Several flowering regulatory pathways have been reported in plant species, but we know little about flowering regulatory in *I. indigotica*. In the present study, we performed RNA-seq and annotated *I. indigotica* transcriptome using RNA from five tissues (leaves, roots, flowers, fruit, and stems). Illumina sequencing generated 149,907,857 high-quality clean reads and 124,508 unigenes were assembled from the sequenced reads. Of these unigenes, 88,064 were functionally annotated by BLAST searches against the public protein databases. Functional classification and annotation assigned 55,991 and 23,072 unigenes to 52 gene ontology (GO) terms and 25 clusters of orthologous group (COG) categories, respectively. A total of 19,927 unigenes were assigned to 124 Kyoto Encyclopedia of Genes and Genomes (KEGG) pathways, and 80 candidate genes related to plant circadian rhythm were identified. We also identified a number of differentially expressed genes (DEG) and 91 potential bolting and flowering-related genes from the RNA-seq data. This study is the first to identify bolting and flowering-related genes based on transcriptome sequencing and assembly in *I. indigotica*. The results provide foundations for the exploration of flowering pathways in *I. indigotica* and investigations of the molecular mechanisms of bolting and flowering in Brassicaceae plants.

Isatis indigotica, a biennial herbaceous plant belonging to the Brassicaceae family, is distributed widely across the Chinese mainland. The dried leaves and roots of the plant, which are also known as “Ban-Lan-Gen” and “Da-Qing-Ye” in China, have commonly been used as medicines for hundreds of years to treat mumps, febrile diseases, eruptive diseases, sore throat, and inflammatory diseases (National Pharmacopoeia Committee, 2015). Bolting and flowering are crucial developmental stages in the life cycle of *I. indigotica*. Premature bolting limits vegetative growth and reduces yield and quality of medicinal products of *I. indigotica*.

The formation of bolting and flowering is of great importance in plant life cycle and marks the transition from vegetative growth to reproductive development. A proper bolting and flowering time is crucial for reproductive success and high productivity (Amasino and Michaels, 2010; Srikanth and Schmid, 2011). The interplays of central flowering genes regulate the transition from vegetative growth to reproductive development (Moon et al., 2005; Parcy, 2005). The genes involved in flowering control have been characterized in *Arabidopsis thaliana* and have been integrated into multiple flowering pathways, including vernalization, aging, photoperiod,

the gibberellin (GA), and autonomous pathways (Amasino and Michaels, 2010; Srikanth and Schmid, 2011; Wang, 2014). In recent years, functional genes and regulatory pathways related to flowering time have also been investigated in many crops, including maize [*Zea mays* (Dong et al., 2012)], rice [*Oryza sativa* (Shrestha et al., 2014; Tsuji et al., 2011)], strawberry [*Fragaria ×ananassa* (Sánchez-Sevilla et al., 2014)], and soybean [*Glycine max* (Jung et al., 2012)].

RNA-seq is an important tool for obtaining transcripts from certain plant tissues under specific physiological conditions or at specific developmental stages (Strickler et al., 2012; Wang et al., 2009). Illumina (San Diego, CA) sequencing techniques have increased gene discoveries in the life sciences in recent years (Zhang et al., 2013). RNA-seq technology has been extensively used in transcriptome analyses of model plant species, such as *A. thaliana* (Zhu et al., 2013), maize (Dukowicz-Schulze et al., 2014; Thakare et al., 2014), soybean (Stamm et al., 2014), rice (Huang et al., 2014), and non-model plant species, such as wild strawberry [*Fragaria vesca* (Mouhu et al., 2009)] and radish [*Raphanus sativus* (Nie et al., 2016)]. Tang et al. (2014) conducted transcriptome sequencing of *I. indigotica* by using Illumina technology to determine the genes involved in the biosynthesis of the active ingredient and its derivatives at the vegetative growth stage. There is still a lack of studies of the molecular mechanisms of bolting and flowering regulation of *I. indigotica*, and further transcriptome sequencing studies of *I. indigotica* at reproductive stages are needed.

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In this study, Illumina technology was used to sequence mRNAs of *I. indigotica* from various tissues (flowers, leaves, stems, roots, and fruit) to investigate the molecular mechanisms of bolting and flowering regulation of *I. indigotica*. On the basis of unigene assembly and analysis of DEGs, several candidate genes related to the flowering pathway were analyzed by quantitative real time polymerase chain reaction (qRT-PCR). The results of this study will enhance our understanding of the bolting and flowering-time regulatory networks in *I. indigotica* and provide clues for further investigations on the molecular genetic mechanisms underlying bolting and flowering regulation in the Brassicaceae plants.

Materials and Methods

PLANT MATERIALS AND RNA ISOLATION. The experiment was carried out at the greenhouse of Nanjing Agricultural University (Nanjing, China). The seeds of *I. indigotica* cultivar Bozhou was sown in plastic pots (29.6-cm diameter, 19.7-cm height) containing a compost of humus and vermiculite at a ratio of 1:1 on 8 Sept. 2015. Plants were grown under a natural light condition at 25 °C maximum and -2 °C minimum with 60% to 75% air humidity. The plants were irrigated with distilled water once in every 5 d until they were sampled. The plants were sampled when some fruit appeared and flowering was still lasting. A total of 500 mg of different tissues of *I. indigotica*, including roots, stems, leaves, fruit, and flowers were collected on 7 Apr. 2016 and then stored at -80 °C until analyzed. Three biological replicates from distinct plants were harvested for each tissue. Total RNA was extracted from each tissue using the Trizol plus kit (Biouniquer, Nanjing, China) and treated with DNase I to remove contaminated DNA. We used the 2100 Bioanalyzer to analyze the quality and integrity of the DNase I-treated RNA (Agilent Technologies, San Francisco, CA).

RNA-SEQ LIBRARY CONSTRUCTION AND SEQUENCING. mRNAs were purified from total RNA using the Oligotex mRNA Midi Kit (Qiagen, Dusseldorf, Germany) and quantified using a spectrophotometer (Nano-Drop 2000; Thermo Scientific, Waltham, MA) and used to generate the cDNA library according to the Illumina manufacturer's instructions. Briefly, fragmentation buffer was added to interrupt mRNA to short fragments. Random hexamer primers were added to these short fragments to synthesize the first-strand cDNA. The second-strand cDNA was synthesized using the Super-Script double-stranded cDNA synthesis kit (Invitrogen, Carlsbad, CA) and purified with a QiaQuick PCR extraction kit (Qiagen).

DE NOVO ASSEMBLY OF TRANSCRIPTOME. Transcriptome de novo assembly was conducted using the Trinity program based on the de Bruijn graph algorithm (Grabherr et al., 2011). Clean reads were first assembled to form longer fragments named contigs. Based on the paired-end reads, different contigs from the same transcript sequences and the distance among them were detected and calculated. These contigs were then further assembled by the Trinity to generate unigenes which have no extension on either end. To quantify gene expression abundance, fragments per kilobase per transcript per million mapped reads (FPKM) was used (Mortazavi et al., 2008). The expression level of each unigene was calculated with the formula: $FPKM = (10^6 \times C \times 10^3) / NL$, where C is the number of reads that uniquely aligned to a certain unigene, N is the total number of reads that uniquely aligned to all unigenes, and L is the number of bases on this unigene.

FUNCTIONAL ANNOTATION AND CLASSIFICATION. Unigenes were annotated against the publicly available protein databases NCBI nonredundant protein [NR (Polashock et al., 2010)], Swiss-Prot (Sato et al., 2006), COG (Natale et al., 2000), GO (Boyle et al., 2004), protein family [Pfam (Bateman et al., 2002)], euKaryotic ortholog groups [KOG (Li et al., 2003)], and KEGG (Wixon and Kell, 2000) using BLASTx with an E -value cutoff of $1.0E-05$. Based on the BLAST results, the coding sequence of unigenes were determined based on their orthologous proteins. If a unigene did not have a hit in any database, ESTScan software was used to find potential coding regions (Iseli et al., 1999), including the nucleotide (5'-3') and amino acid sequences of the coding regions. Based on the NR annotations, the Blast2GO program was used to gain GO annotations for the unigenes using a cutoff value of $1.0E-05$ at the second level according to molecular functions, cellular components, and biological processes (Conesa et al., 2005). GO functional classification and distribution of gene functions of each assembled unigene were performed using WEGO software at the macro level (Ye et al., 2006).

DIFFERENTIAL EXPRESSION ANALYSIS. RNA-seq by expectation maximization, which allows for the assessment of transcript abundances based on the mapping of RNA-seq reads to the assembled transcriptome, was used for transcript abundance estimation of the de novo-assembled transcripts (Li and Dewey, 2011). Differential expression analysis of two groups was performed using the DEGseq R package (1.10.1) (Wang et al., 2010). The false discovery rate (FDR) method was used to determine the threshold probability value in multiple tests. The probability values were adjusted using the Benjamini-Hochberg procedure (Benjamini and Hochberg, 1995). If the FDR was smaller than 0.05 ($FDR \leq 0.01$) and the absolute value of the log2 fold change was ≥ 2 , the unigene was considered to be a significant DEG. The Pearson correlation coefficient was calculated among the five samples according to the gene expression profiles.

GO enrichment analysis of the DEGs was implemented by the Goseq R packages based on the Wallenius noncentral

Table 1. Summary of the sequencing data from the five tissues of *Isatis indigotica*.

Samples	Clean reads (no.) ^z	Clean data (no.) ^y	GC content (%) ^x
Flower	33,718,037	10,115,411,110	47.37
Fruit	31,951,066	9,585,319,800	47.51
Leaf	28,623,805	8,587,141,500	47.57
Root	26,789,893	8,036,967,900	47.05
Stem	28,825,056	8,647,516,800	46.91

^zNumber of pair-end reads in clean data.

^yNumber of nucleotides in clean data.

^xRatio of guanine (G) and cytosine (C) to total nucleotides.

Table 2. Summary of the transcriptome assembly of *Isatis indigotica*.

	Transcript	Unigene
Total no.	176,074	124,508
Total length (nt) ^z	165,549,067	99,942,890
N50 (nt) ^z	1,338	1,027
Mean length (nt)	940.22	802.70
Number of length $\geq$ 500 nt	105,783	64,954
Number of length $\geq$ 2,000 nt	17,740	8,644

^znt = nucleotide; N50 = the median size of transcript/unigene.

Fig. 1. The length distribution of assembled transcripts and unigenes in *Isatis indigotica*.

Table 3. Summary of functional annotation for *Isatis indigotica* unigenes.

Database ^z	Unigenes (no.)	Percentage (%)
COG	23,072	18.53
GO	55,991	44.97
KEGG	19,927	16.00
KOG	55,409	44.50
Pfam	50,154	40.28
Swissprot	55,189	44.33
NR	80,287	64.48
Total	88,064	70.73

^zCOG = clusters of orthologous groups (Natale et al., 2000); GO = gene ontology (Boyle et al., 2004); KEGG = Kyoto Encyclopedia of Genes and Genomes (Wixon and Kell, 2000); KOG = euKaryotic ortholog groups (Li et al., 2003); Pfam = protein family (Bateman et al., 2002); NR = NCBI nonredundant protein (Polashock et al., 2010).

Fig. 2. Species distribution of the top BLAST hits against the NCBI nonredundant protein (Polashock et al., 2010) database.

hypergeometric distribution (Young et al., 2010). The numbers of all DEGs (upregulated and downregulated) were calculated for each GO term. In addition, KOBAS software was used to test the statistical enrichment of DEGs in KEGG pathways. The enrichment factor, which means the ratio of the DEGs number

and the number of genes that have been annotated in this pathway was used to represent enrichment intensiveness (Mao et al., 2005).

RT-PCR ANALYSIS. qRT-PCR was performed to validate the relative expression levels of several flowering genes in different *I. indigotica* tissues. Total RNA from various tissue samples was isolated and reverse transcribed into cDNA using the SuperScript III First-Strand Synthesis System (18080400; Invitrogen) following the manufacturer's protocol. The unigene specific primers for qRT-PCR were designed using Primer Premier 5 (PREMIER Biosoft Intl., Palo Alto, CA). Three biological replicates were subjected to the qRT-PCR assay, which was carried out using the SYBR green methodology and the ABI 7500 real-time PCR system (Applied Biosystems, Carlsbad, CA) with Actin as the reference gene. The relative fold expression changes were calculated using the $2^{-\Delta\Delta CT}$ method (Livak and Schmittgen, 2001).

Results

TRANSCRIPTOME SEQUENCING AND DE NOVO TRANSCRIPTOME ASSEMBLY. RNA-seq was performed using mRNA isolated from leaves, roots, flowers, fruit, and stems of *I. indigotica* in the reproductive stage to obtain a complete set of *I. indigotica* transcripts. A total of 149,907,857 high-quality clean reads consisting of 44.97 Gbp of sequences were obtained after removing adapter sequences, low-quality reads, and ambiguous reads. Flowers and roots had the largest (33,718,037) and the fewest (26,789,893) number of clean reads, respectively (Table 1). The numbers of the reads for leaf and stem were close and were 28,623,805 and 28,825,056, respectively. There were 31,951,066 reads for fruit. These reads were used to assemble transcripts by using Trinity (Platel and Jain, 2012). A total of 176,074 transcripts with a median size (N50) of 1338 bp and an average length of 940.22 bp were generated (Table 2); 124,508 unigenes were obtained with an N50 of 1027 bp and an average length of 802.70 bp. Length distributions of assembled transcripts and unigenes were presented in Fig. 1. About 52% of the 124,508 unigenes were longer than 500 bp, and 8644 unigenes (6.94%) were longer than 2 kb (Table 2).

FUNCTIONAL ANNOTATION OF *I. INDIGOTICA* TRANSCRIPTOME. To assign functional annotations of all the assembled unigenes, the sequence similarity search was performed against the NR, Swiss-Prot, COG, GO, Pfam, KOG, and KEGG public protein databases using a cutoff *E*-value of $1.0E-5$. Consequently, a total of 88,064 unigenes (70.73% of all unigenes) found matches in at least one of the public databases (Table 3; Supplemental Table 1). Further blast searches showed that 23,072, 55,991, 50,154, 55,409, 19,927, 55,189, and 80,287 unigenes had a match in the COG, GO, Pfam, KOG, KEGG, Swissprot, and NR databases, respectively.

Fig. 3. Gene ontology (Boyle et al., 2004) classification of the *Isatis indigotica* unigenes.

Fig. 4. Clusters of orthologous groups (Natale et al., 2000) functional classification of the *Isatis indigotica* unigenes.

Sequence similarity search against the NCBI NR database detected 80,287 annotated sequences (91.17% of all unigenes) that shared significant identity with known proteins (Table 3). The homologous species distribution is shown in Fig. 2. A

total of 19.06% of the annotated sequences had matches to genes from *Eutrema salsugineum*, followed by *Brassica napus* (14.97%), *Brassica rapa* (12.89%), and *Camelina sativa* (6.28%) (Fig. 2). The top hits were mostly Brassicaceae species, which indicated that the assembly and annotation of *I. indigotica* transcriptome are reliable.

GO AND COG CLASSIFICATION.

To further explore the functions of the *I. indigotica* unigenes, GO analyses were performed and 55,991 unigenes were categorized into 52 GO classes including 16 cellular components, 17 molecular functions, and 19 biological processes (Fig. 3). Under the cellular components, the three largest percentages of genes were “cell part” (42,536), “cell” (42,415), and “organelle” (33,702). Within the molecular function category, “binding” (29,463), “catalytic activity” (26,105), and “transporter activity” (3377) were the most highly represented categories. For the biological process category, the largest proportions of genes were clustered into “metabolic process” (35,975), “cellular process” (35,105 sequences), and “single-organism process” (30,137). However, only a few sequences came from the terms of “extracellular matrix part,”

Fig. 5. The correlation dendrogram of expression patterns among the leaves, flowers, fruit, stems, and roots of *Isatis indigotica*.

Fig. 6. Venn diagram of differentially expressed unigenes numbers among pairwise comparisons of flower, fruit, leaf, and stem with root.

“metallochaperone activity,” and “translation regulator activity.”

In the COG classification, 23,072 unigenes were assigned to 25 COG categories (Table 3; Fig. 4). Of these, “general function prediction only” was dominant (6178 sequences), followed by

“replication, recombination, and repair” (3175), “transcription” (2768), “translation, ribosomal structure and biogenesis” (2715), and “signal transduction mechanisms” (2390). Only a few genes matched the terms “extracellular structures” (1) and “nuclear structure” (9).

TISSUE-SPECIFIC TRANSCRIPTOME ANALYSIS AND IDENTIFICATION OF DEG IN *I. INDIGOTICA*. The Pearson’s distance correlation matrix, statistics of DEGs numbers, GO classification, and enriched KEGG pathways were used for comparative analysis. The RNA-Seq data were used to assess differences in the expression of genes in different tissues of *I. indigotica*, including leaves, flowers, fruit, stems, and roots. The FPKM values representing the expression levels of unigenes were calculated and compared among leaves, flowers, fruit, stems, and roots. The Pearson’s distance correlation matrix was generated to compare the transcriptomes from each sample. The correlation dendrogram showed the relative relationships among the five tissues visually (Fig. 5). The results suggest that leaves were most similar to fruit, and roots were significantly different from other tissues (Fig. 5).

We compared the expression levels of unigenes from different tissues of *I. indigotica* (Fig. 6). A unigene was regarded as a DEG when the fold change was ≥ 2 and the FDR was < 0.01 . There were 3690 DEGs between the flower and root, of which 3282 were downregulated, and 408 were upregulated (Table 4). In addition, there were 928 DEGs between the fruit and root, of which 784 were downregulated and 144 were upregulated. Moreover, we identified 717 DEGs between the leaf and root, 550 of which were downregulated and 167 of which were upregulated. Between the root and stem, 318 DEGs were downregulated whereas 570 DEGs were upregulated. Overall, we identified 272 common DEGs from the four comparison groups.

GO analysis of the DEGs in Flower_vs._Root showed that they were enriched in 52 categories, with cell part (1792 unigenes) representing the most abundant category, followed by cell (1783 unigenes), metabolic process (1607 unigenes), and cellular process (1579 unigenes) (Fig. 7). In Fruit_vs._Root, cell (640 unigenes) and cell part (639 unigenes) were the most abundant categories, followed by metabolic process (576 unigenes) and single-organism process (550 unigenes) (Supplemental Fig. 1). The most abundant categories in Leaf_vs._Root were similar to the categories in Fruit_vs._Root (Supplemental Fig. 2). The unigenes involved in cell (626 unigenes), cell part (626 unigenes), metabolic process (542 unigenes), cellular process (527 unigenes), organelle (519 unigenes), and single-organism process (498 unigenes) were enriched between root and stem (Supplemental Fig. 3).

Table 4. Summary of the differentially expressed genes (DEGs) numbers among pairwise comparisons of flower, fruit, leaf, and stem with root.

Comparison	DEG (no.)	Upregulated (no.)	Downregulated (no.)
Flower_vs._Root	3,690	408	3,282
Fruit_vs._Root	928	144	784
Leaf_vs._Root	717	167	550
Root_vs._Stem	888	570	318

KEGG pathway analysis showed that the DEGs in fruit, flowers, leaves, and stems were significantly enriched when compared with roots in several pathways, including photosynthesis, stilbenoid, diarylheptanoid, and gingerol biosynthesis, photosynthesis-antenna proteins, carbon fixation in photosynthetic organisms, pentose and glucuronate interconversions, and glucosinolate biosynthesis (Table 5). Some pathways, particularly the pathways of energy metabolism and biosynthesis of other secondary metabolites, were highly overlapping

Fig. 7. Gene ontology (Boyle et al., 2004) classification of differentially expressed unigenes in Flower_vs._Root.

Table 5. Top four enriched Kyoto Encyclopedia of Genes and Genomes (Wixon and Kell, 2000) pathways among pairwise comparisons of flower, fruit, leaf, and stem with root.

Comparison	Pathway terms	Enrichment factor ^z	<i>q</i> -value ^y	Unigenes (no.) ^x
Flower_vs._Root	Photosynthesis	0.27	3.27E-8	30
	Stilbenoid, diarylheptanoid and gingerol biosynthesis	0.31	0.00018	21
	Pentose and glucuronate interconversions	0.43	0.0098	24
	Limonene and pinene degradation	0.40	0.019	20
Fruit_vs._Root	Photosynthesis	0.072	0	27
	Photosynthesis-antenna proteins	0.081	8.47E-8	11
	Carbon fixation in photosynthetic organisms	0.22	2.26E-6	19
	Glucosinolate biosynthesis	0.094	0.0013	6
Leaf_vs._Root	Photosynthesis	0.068	0	28
	Carbon fixation in photosynthetic organisms	0.23	9.52E-6	18
	Photosynthesis-antenna proteins	0.096	1.52E-5	9
	Monoterpenoid biosynthesis	0.058	0.0051	4
Root_vs._Stem	Photosynthesis	0.075	0	27
	Photosynthesis-antenna proteins	0.12	0.0003	8
	Carbon fixation in photosynthetic organisms	0.29	0.0022	15
	Glyoxylate and dicarboxylate metabolism	0.23	0.017	9

^zEnrichment factor = ratio of differentially expressed genes number and the number of genes have been annotated in this pathway.

^yCorrected probability value. A lower *q*-value means greater intensiveness.

^xNumber of unigenes in each pathway.

Fig. 8. The pathway of circadian rhythm in *Isatis indigotica*. CCA1 = circadian clock associated 1; CHS = chalcone synthase; CO = constant; CRY1 = cryptochrome 1; CRY2 = cryptochrome 2; ELF3 = early flowering 3; FKF1 = flavin-binding kelch domain F box 1; GI = gigantea; LHY = late elongated hypocotyl; LKP2 = lov kelch protein 2; PHY A = phytochrome A; PHY B = phytochrome B; PHY D = phytochrome D; PHY E = phytochrome E; PIF3 = phytochrome interacting factor 3; TOC1 = timing of cab expression 1; WNK1 = with no lysine kinase 1; ZTL = zeitlupe; SCF = Skp1-cullin-F-box complex; APR3 = adenosine 5'-phosphosulfate reductase 3; APR5 = adenosine 5'-phosphosulfate reductase 5; APR7 = adenosine 5'-phosphosulfate reductase 7; APR9 = adenosine 5'-phosphosulfate reductase 9; CK2α = Casein Kinase2 α-subunit; CK2β = Casein Kinase2 β-subunit; PAP1 = production of anthocyanin pigment 1; LKP2 = Lov Kelch Protein2; UV-B = ultraviolet-B; Pfr = far-red light absorption Phytochrome.

in all comparisons. For example, ≈ 30 unigenes associated with photosynthesis were significantly enriched in flowers (Table 5). These results suggested that these genes were of great importance in the growth and development of *I. indigotica*.

KEGG PATHWAY ANALYSIS AND FUNCTIONAL GENES INVOLVED IN CIRCADIAN RHYTHM. To further analyze the transcriptome of *I. indigotica*, all unigenes were compared in the KEGG pathway database. In total, 19,927 unigenes were matched to the database and assigned to 124 KEGG pathways (Table 3; Supplemental Table 1). "Metabolic pathways" (ko01100: 5551 unigenes) had the largest number of unigenes, followed by "biosynthesis of secondary metabolites" (ko01110: 2552 unigenes), "ribosome" (ko03010: 1333 unigenes), "oxidative phosphorylation" (ko00190: 713 unigenes), and "spliceosome" (ko03040: 709 unigenes).

According to the pathway-based analysis, a total of 80 candidate genes were identified for the "circadian rhythm-plant" pathway (ko04712) (Fig. 8; Supplemental Tables 1 and 2). These rhythm-related genes, including circadian clock associated 1 (CCA1, K12134), gigantea (GI, K12124), late elongated hypocotyl (LHY, K12133), flavin-binding kelch domain F box 1 (FKF1, K12116), phytochrome D (PHYD, K12122), cryptochrome 1 (CRY1, K12118), phytochrome A (PHYA, K12120), phytochrome B (PHYB, K12121), phytochrome E (PHYE, K12123), with no lysine

kinase 1 (WNK1, K12132), phytochrome interacting factor 3 (PIF3, K12126), early flowering 3 (ELF3, K12125), lov kelch protein 2 (LKP2, K12117), and cryptochrome 2 (CRY2, K12119), were involved in many rhythmic processes such as photoperiodic flowering, cell elongation, and ultraviolet-B protection (Fig. 8). Besides, several genes, including constant (CO, K12135), zeitlupe (ZTL, K12115), timing of cab expression 1 (TOC1, K12127), and chalcone synthase (CHS, K00660), were implicated in plant light signaling pathways. Studying the roles of circadian-regulated genes responsible for controlling flowering could facilitate elucidation of interplays between photoperiod and the circadian clock.

IDENTIFICATION OF FLOWERING-ASSOCIATED GENES IN *I. INDIGOTICA*. The complex genetic network which controls the development transition of flowering comprised several co-ordinate flowering pathways (Srikanth and Schmid, 2011). More than 200 flowering-related genes have been identified and characterized in the model plant *A. thaliana* (Amasino and Michaels, 2010; Srikanth and Schmid, 2011). To identify the genes responsible for bolting and flowering regulation in *I. indigotica*, a local BLASTx similarity search against *A. thaliana* flowering genes was performed. A total of 91 unigenes that showed high homology to the known bolting and flowering-related genes in *A. thaliana* were identified, and these

Table 6. The identified candidate genes associated with flowering pathways of *Isatis indigotica*.

Gene name ^z	Unigenes (no.)	Flowering pathway
AP1	3	Photoperiod
AP2	1	Photoperiod
AGL6	1	Photoperiod
AGL8	1	Photoperiod
AGL14	1	Others
AGL15	1	Photoperiod
AGL16	1	Others
AGL17	1	Others
AGL18	1	Photoperiod
AGL19	1	Vernalization
CAL	2	Others
CCA1	1	Photoperiod/circadian clock
CO	2	Photoperiod/circadian clock
COL9	1	Photoperiod/circadian clock
CHS	2	Photoperiod
CRY1	3	Photoperiod/circadian clock
CRY2	1	Photoperiod/circadian clock
EBS	3	Photoperiod
ELF3	1	Photoperiod/circadian clock
ELF6	4	Photoperiod
ELF8	1	Photoperiod
ELF9	2	Photoperiod
EMF1	1	Vernalization
EMF2	1	Vernalization
ESD4	1	Vernalization
FD	1	Photoperiod
FKF1	1	Photoperiod
FLC	1	integrator
FLD	1	Autonomous
FLK	3	Autonomous
FPA	1	Autonomous
FPF	2	GA
FT	1	Integrator
GI	2	Photoperiod/circadian clock
HUA2	1	Vernalization
LD	3	Autonomous
LHY	1	Photoperiod/circadian clock
LKP2	1	Photoperiod/circadian clock
PHYA	3	Photoperiod/circadian clock
PHYB	1	Photoperiod/circadian clock
PHYD	7	Photoperiod/circadian clock
PHYE	1	Photoperiod/circadian clock
PIE1	1	Photoperiod
PIF3	2	Photoperiod
SEP1	3	Others
SOC1	1	Integrator
SPA	1	Photoperiod
TEM1	1	Photoperiod
TFL1	2	Photoperiod
TFL2	1	Photoperiod
TOC1	4	Photoperiod
VEL1	1	Photoperiod
VRN1	2	Vernalization
VRN2	1	Vernalization
WNK1	2	Photoperiod/circadian clock

^zAP1 = apetala1; AP2 = apetala2; AGL6 = agamous-like 6; AGL8 = agamous-like 8; AGL14 = agamous-like 14; AGL15 = agamous-like 15; AGL16 = agamous-like 16; AGL17 = agamous-like 17; AGL18 = agamous-like 18; AGL19 = agamous-like 19; CAL = cauliflower;

identified genes were involved in various flowering pathways (Table 6; Supplemental Tables 2 and 3), including photoperiod/circadian clock, GA, autonomous, vernalization, and aging pathways (Amasino and Michaels, 2010; Srikanth and Schmid, 2011). These include orthologs of the autonomous pathway genes such as flowering locus D (FLD), flowering locus with kh domains (FLK), and luminidependens (LD), orthologs of the GA pathway gene such as flowering-promoting factor (FPF) and orthologs of the vernalization pathway genes such as vernalization 1 (VRN1), embryonic flower1 (EMF1), and enhancer of AG-4 2 (HUA2), as well as a number of genes responding to the photoperiod pathway, such as agamous-like 15 (AGL15), CO, CCA1, CHS, CRY2, PHYA, PIF3, ELF3, LHY, TOC1, and terminal flower1 (TFL1). In addition, homologs of the key genes involved in flowering regulation, such as flowering locus C (FLC), flowering locus T (FT), CO, and suppressor of overexpression of col1 (SOC1), were also identified in this study. In addition, we identified several orthologs of the functional genes associated with floral meristem identity and flower development such as apetala1 (AP1) and sepallata1 (SEP1). There was a very high degree of similarity in the known genetic flowering pathways and a lot of critical flowering genes between *I. indigotica* and *A. thaliana*.

qRT-PCR ANALYSIS. To evaluate the reliability of RNA-Seq analysis, eight bolting and flowering-related genes, AGL15 (TRINITY_DN18713_c0_g1), AGL17 (TRINITY_DN59446_c0_g1), ELF6 (TRINITY_DN69071_c0_g2), ELF8 (TRINITY_DN69534_c0_g2), EMF2 (TRINITY_DN66245_c2_g3), FLC (TRINITY_DN69832_c1_g1), photoperiod independent early flowering1 (PIE1) (TRINITY_DN67850_c0_g2), and TFL1 (TRINITY_DN21486_c0_g1), were selected for verification in five tissues (roots, stems, leaves, flowers, and fruit) using qRT-PCR (Fig. 9). The primer sequences, RNA-Seq results, and qRT-PCR values are listed in Supplemental Table 4. The expression profiles of the eight genes revealed by qRT-PCR were generally consistent with the corresponding FPKM values derived from RNA-seq. The expression patterns of five genes (Fig. 9A, B, D, G, and H) fit well with the RNA-Seq results, whereas three genes (Fig. 9C, E, and F) had similar expression patterns, but

Table 6. Continued.

CCA1 = circadian clock associated 1; CO = constant; COL = constant-like; CHS = chalcone synthase; CRY1 = cryptochrome 1; CRY2 = cryptochrome 2; EBS = 24-epibrassinolide; ELF3 = early flowering 3; ELF6 = early flowering 6; ELF8 = early flowering 8; ELF9 = early flowering 9; EMF1 = embryonic flower1; EMF2 = embryonic flower2; ESD4 = early in short days 4; FD = flowering locus D; FKF1 = flavin-binding kelch domain F box 1; FLC = flowering locus C; FLD = flowering locus D; FLK = flowering locus with kh domains; FPA = flowering time control protein a; FPF = flowering-promoting factor; FT = flowering locus T; GA = gibberellin; GI = gigantea; HUA2 = enhancer of AG-4 2; LD = luminidependens; LHY = late elongated hypocotyl; LKP2 = lov kelch protein 2; PHYA = phytochrome A; PHYB = phytochrome B; PHYD = phytochrome D; PHYE = phytochrome E; PIE1 = photoperiod independent early flowering1; PIF3 = phytochrome interacting factor 3; SEP1 = sepallata1; SOC1 = suppressor of overexpression of col1; SPA = suppressor of phyA-105; TEM = tempranillo; TEL1 = terminal flower1; TEL2 = terminal flower2; TFL1 = terminal flower1; TFL2 = terminal flower2; TOC1 = timing of cab expression 1; VEL1 = vernalization 5; VRN1 = vernalization 1; VRN2 = vernalization 2; WNK1 = with no lysine kinase 1.

Fig. 9. Quantitative real time polymerase chain reaction (qRT-PCR) validation of eight putative genes involved in flowering pathways; RPKM = reads per kilobase of transcript per million mapped reads.

with very small inconsistencies compared with the RNA-Seq results. These results support the reliability of the RNA-Seq data.

Discussion

This study catalogs the occurrence of genes in *I. indigotica* that have sequence similarity to flowering gene *A. thaliana* and provides preliminary investigations of flowering-associated genes in *I. indigotica*. Furthermore, we compared transcriptomes of leaves, stems, flowers, and fruit with that of roots at the reproductive stages. Functional enrichment of the DEGs provided clues about the molecular basis of reproduction in *I. indigotica*.

I. indigotica is an important biennial herbaceous plant, and its dried leaves and roots have commonly been used as Chinese

medicines for hundreds of years. Because of the low number of available *I. indigotica* gene sequences in public databases, little functional investigation has been done for this plant. Tang et al. generated 28 million Illumina paired-end reads that were then assembled into 33,238 unigenes in a previous study (Tang et al., 2014). In this study, RNA-seq and differential gene expression profiling analyses were performed. About 150 million clean reads were generated and assembled into 124,508 unigenes. The numbers of high-quality reads and assembled unigenes exceeded the previous study. The unigenes assembled in this study were subjected to a BLASTx similarity search and annotation against the nr, SwissProt, COG, KEGG, GO, and Pfam databases. The most frequent GO term in the molecular function, biological process, and cellular component groups

were the cell part, metabolic process, and binding, respectively. These findings differ somewhat from the results in our previous study of the transcriptome of *I. indigotica*. The COG functional annotation of the unigenes revealed that the category “general function prediction only” was the most highly represented category. A large number of unigenes were also annotated to the category “replication, recombination, and repair,” which were similar to the previous study of the transcriptome of *I. indigotica* (Tang et al., 2014). These findings establish the basis for further genomic studies in *I. indigotica*.

Studies of *A. thaliana* flowering have revealed that multiple different flowering pathways converge at several flowering pathway integrators such as SOC1 and FT, which were regulated by two key upstream genes, CO and FLC that negatively control flowering (Lee and Lee, 2010; Moon et al., 2005; Srikanth and Schmid, 2011). In this study, two unique sequences, TRINITY_DN63019_c0_g1 and TRINITY_DN63019_c0_g2, were found to be the orthologs of AtCO. Moreover, some studies suggested that lots of genes associated with the vernalization pathway played important roles in flowering control (Jung et al., 2012; Srikanth and Schmid, 2011). As expected, the vernalization-response genes including EMF1, VRN1, and vernalization 2 (VRN2) were also identified in this study (Table 6) and the result was consistent with the previous studies of flowering gene discovery (Gao et al., 2014; Moon et al., 2003; Zhang et al., 2011, 2013). The unigene (TRINITY_DN38410_c0_g3) matched to AtSOC1 was found as well (Supplemental Table 3). The interaction of SOC1 and AGL24, which belong to the MADS-box gene family regulates the expression of LFY and determines the flowering time of *A. thaliana* (Liu et al., 2008; Seo et al., 2009). The family of MADS-box transcription factor is a major group of regulators controlling floral development and floral organ specification in *A. thaliana* (Becker and Theißen, 2003; Smaczniak et al., 2012; Theißen, 2001). Several members of the MADS-box family such as AP1, AP2, and AGLs were identified in this study and probably take part in the regulation of the development and flowering of *I. indigotica*.

Conclusion

Illumina sequencing and de novo assembly were performed for *I. indigotica* at the reproductive stages. As a result, more than 44.97 Gbp of data were obtained and assembled into 124,508 unigenes with an average length of 1027 bp, representing orthologs of known plant genes, as well as potential new genes. The assembly and annotation of the *I. indigotica* transcriptome achieved in this study revealed tissue-specific gene expression patterns and pathways. This study is the first to conduct systematic identification of flowering-associated genes based on transcriptome sequencing and assembly in *I. indigotica*. A total of 91 unigenes that showed high homology to the known bolting and flowering-related genes in *A. thaliana* were identified. The results presented herein could build a foundation for further investigation of bolting and flowering regulatory networks in *I. indigotica* and contribute to molecular and genetic research in the Brassicaceae plants.

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Supplemental Fig. 1. Gene ontology [GO (Boyle et al., 2004)] classification of differentially expressed genes (DEGs) in Fruit_vs._Root.

Supplemental Fig. 3. Gene ontology [GO (Boyle et al., 2004)] classification of differentially expressed genes (DEGs) in Root_vs._Stem.

Supplemental Table 1. Kyoto Encyclopedia of Genes and Genomes [KEGG (Wixon et al., 2000)] pathways of the assembled unigenes in *Isatis indigotica*.

Pathway	Pathway ID	Genes (no.)
Glycolysis/gluconeogenesis	ko00010	461
Citrate cycle (TCA cycle)	ko00020	296
Pentose phosphate pathway	ko00030	224
Pentose and glucuronate interconversions	ko00040	211
Fructose and mannose metabolism	ko00051	184
Galactose metabolism	ko00052	159
Ascorbate and aldarate metabolism	ko00053	170
Fatty acid biosynthesis	ko00061	98
Fatty acid elongation in mitochondria	ko00062	26
Fatty acid metabolism	ko00071	200
Synthesis and degradation of ketone bodies	ko00072	16
Steroid biosynthesis	ko00100	98
Ubiquinone and other terpenoid-quinone biosynthesis	ko00130	69
Oxidative phosphorylation	ko00190	713
Photosynthesis	ko00195	165
Photosynthesis - antenna proteins	ko00196	76
Purine metabolism	ko00230	541
Caffeine metabolism	ko00232	19
Pyrimidine metabolism	ko00240	434
Alanine, aspartate and glutamate metabolism	ko00250	207
Glycine, serine and threonine metabolism	ko00260	204
Cysteine and methionine metabolism	ko00270	288
Valine, leucine and isoleucine degradation	ko00280	202
Valine, leucine and isoleucine biosynthesis	ko00290	146
Lysine biosynthesis	ko00300	88
Lysine degradation	ko00310	88
Arginine and proline metabolism	ko00330	269
Histidine metabolism	ko00340	77
Tyrosine metabolism	ko00350	93
Phenylalanine metabolism	ko00360	219
Tryptophan metabolism	ko00380	168
Phenylalanine, tyrosine and tryptophan biosynthesis	ko00400	95
beta-Alanine metabolism	ko00410	125
Taurine and hypotaurine metabolism	ko00430	46
Selenocompound metabolism	ko00450	86
Cyanoamino acid metabolism	ko00460	123
D-Arginine and D-ornithine metabolism	ko00472	2
Glutathione metabolism	ko00480	269
Starch and sucrose metabolism	ko00500	375
N-Glycan biosynthesis	ko00510	154
Other glycan degradation	ko00511	65
Other types of O-glycan biosynthesis	ko00514	20
Amino sugar and nucleotide sugar metabolism	ko00520	323
Glycosaminoglycan degradation	ko00531	38
Glycerolipid metabolism	ko00561	151
Inositol phosphate metabolism	ko00562	222
Glycosylphosphatidylinositol (GPI)-anchor biosynthesis	ko00563	41
Glycerophospholipid metabolism	ko00564	215
Ether lipid metabolism	ko00565	81
Arachidonic acid metabolism	ko00590	63
Linoleic acid metabolism	ko00591	31
alpha-Linolenic acid metabolism	ko00592	87
Sphingolipid metabolism	ko00600	60
Glycosphingolipid biosynthesis - globo series	ko00603	24
Glycosphingolipid biosynthesis - ganglio series	ko00604	21
Pyruvate metabolism	ko00620	349
Glyoxylate and dicarboxylate metabolism	ko00630	168

Continued next page

Supplemental Table 1. Continued.

Pathway	Pathway ID	Genes (no.)
Propanoate metabolism	ko00640	166
Butanoate metabolism	ko00650	95
C5-Branched dibasic acid metabolism	ko00660	19
One carbon pool by folate	ko00670	67
Carbon fixation in photosynthetic organisms	ko00710	353
Thiamine metabolism	ko00730	26
Riboflavin metabolism	ko00740	28
Vitamin B6 metabolism	ko00750	30
Nicotinate and nicotinamide metabolism	ko00760	37
Pantothenate and CoA biosynthesis	ko00770	64
Biotin metabolism	ko00780	9
Lipoic acid metabolism	ko00785	13
Folate biosynthesis	ko00790	58
Porphyrin and chlorophyll metabolism	ko00860	149
Terpenoid backbone biosynthesis	ko00900	121
Indole alkaloid biosynthesis	ko00901	17
Monoterpenoid biosynthesis	ko00902	20
Limonene and pinene degradation	ko00903	167
Diterpenoid biosynthesis	ko00904	26
Brassinosteroid biosynthesis	ko00905	13
Carotenoid biosynthesis	ko00906	68
Zeatin biosynthesis	ko00908	40
Sesquiterpenoid biosynthesis	ko00909	17
Nitrogen metabolism	ko00910	168
Sulfur metabolism	ko00920	106
Phenylpropanoid biosynthesis	ko00940	273
Flavonoid biosynthesis	ko00941	62
Anthocyanin biosynthesis	ko00942	1
Flavone and flavonol biosynthesis	ko00944	18
Stilbenoid, diarylheptanoid and gingerol biosynthesis	ko00945	133
Isoquinoline alkaloid biosynthesis	ko00950	36
Tropane, piperidine and pyridine alkaloid biosynthesis	ko00960	55
Betalain biosynthesis	ko00965	1
Glucosinolate biosynthesis	ko00966	48
Aminoacyl-tRNA biosynthesis	ko00970	213
Biosynthesis of unsaturated fatty acids	ko01040	107
ABC transporters	ko02010	38
Ribosome biogenesis in eukaryotes	ko03008	369
Ribosome	ko03010	1333
RNA transport	ko03013	637
mRNA surveillance pathway	ko03015	413
RNA degradation	ko03018	312
RNA polymerase	ko03020	145
Basal transcription factors	ko03022	167
DNA replication	ko03030	140
Spliceosome	ko03040	709
Proteasome	ko03050	251
Protein export	ko03060	136
Base excision repair	ko03410	109
Nucleotide excision repair	ko03420	190
Mismatch repair	ko03430	83
Homologous recombination	ko03440	96
Non-homologous end-joining	ko03450	40
Phosphatidylinositol signaling system	ko04070	222
Plant hormone signal transduction	ko04075	520
Ubiquitin mediated proteolysis	ko04120	430
Sulfur relay system	ko04122	40

Continued next page

Supplemental Table 1. Continued.

Pathway	Pathway ID	Genes (no.)
SNARE interactions in vesicular transport	ko04130	108
Regulation of autophagy	ko04140	81
Protein processing in endoplasmic reticulum	ko04141	657
Endocytosis	ko04144	339
Phagosome	ko04145	372
Peroxisome	ko04146	306
Plant-pathogen interaction	ko04626	441
Natural killer cell mediated cytotoxicity	ko04650	76
Circadian rhythm - mammal	ko04710	43
Circadian rhythm - plant	ko04712	80

Supplemental Table 2. The coding sequence (CDS) of flowering-associated genes in *Isatis indigotica*.

Gene ID	Coding sequence
TRINITY_DN44529_c0_g2	ATGGGAAGGGGTAGGGTTGAAATGAAGAGGATAGAGAACAAGATCAATAGACAAGTGACAT TCTCTAAAAGAAGAGCTGGCCTTTTGAAGAAAGCCCATGAGATCTCGGTTCTTTGTGATGC CGAGGTATCCCTTATTGTCTTCTCCATAAGGGGAAACTG
TRINITY_DN59583_c0_g1	ATGAGACGTACGAAGTACTTTTCAAGTTCAAATATTTTCAATCCAAAAGACAACCTTAAAAC TAAACGGACAAAAGCTCATCTACGTACAGGCTGATGATCTGATTATATCAATCAATAGACT ATTTGAAAAACAGTGCTAATATTTTCTATCTATATTTAATTATAATGGTGCCGAAGCTA AGTGGAGATATGGAGATCTCG
TRINITY_DN60394_c3_g1	ATGTTTTTTATTATGGATGATTATAAAAAATATATATGGATCTTCATGCGGCAAAGCAGCCAAG GTTGCAGTTGTAGACGGGTTCAAGGGACAGATCAAGGTCGTTCTCTCATTGCCATTGGA TCTTCTTCTTGATACAGGCCACCCATGTTGAGAAAAGGAGATGGCTGATGAGAGAGCATG TATGGATGCTGCATTTGATGCTGCTGCGGGGGCGGAGGGGGAGGCATGTTTGGCCATGG TTCTGCTGGTCCCATTGCTCTTGTGTGCCCTAAGAACCTTTTCCCTCTCCTTGATCTGTTG GAAAGCATGCTGTTTGTCTGTATGGCTTTCTCCTTTCTTTGGAGCTCATTGATGGAGTC GTACATCAGTTGGTTTTCTAGAGCGGATATGCTTAAGAGCAGTGTCAAGCTGCTGCTCC AGATTCTGGAGCTCCTTAGGGCTCATTGCTTGCAAGTCTTCCCAAGATAGTGCCTCTGGT TTCTCTCCAAAAGCTCAATCTTAGCCTTAAGCCTGTTATACTCCATCGACCAGTTCGTATTG ACGTCGGACTCAGGTGCAATAAGCTGTCTCTCGGCGTAAGAGTACCTCTCATAGCGTTCAA GTATCTTCTCCATACAAGAATCAGTGGAGTATTCGAAGAGTTTCCCTTATGGGAGAAGAC AACAAGGGCAACTTCAGCATCACAGAGAACAGAAATCTCATGAGCTTTCTTCAAAAGACC AGCTCTTCTTTTCGAGAATGTACCTGTCTATTGATCTTGTCTCTATCCT
TRINITY_DN64890_c0_g1	ATGTGGGATCTAAACGACTCACCACACCAGACACTTAGAGAAGAAGAATCTGAAGAGTTCTG TTATTCATCACCGGGTAAACGGGTCCGATCTTTCTCGAATTCAAGTTCTTCCGCTGTAGTC ATCGAAGATGGATCCGATGAGGACGAACATAACCGGGTCAGACCCAACAACCCACTTGTC ACACATCAGTTCTTCCCGGAGATGGAATCTAGCGTCGGAGACGGCGGCGTAGGAGATGAT GGTGGTGGTCCCGGGTCGGGGTTTCTCGGGCTCACTGGTTTGGTGTGAAGTTTGTCAGT CCGATCTAGCCACCGGATCATCGGCGGGTAAACCCACCACTGTCGCCGCCGTGGTCGAGC CGGTGCAGCCTTTGAAAAGAGCCGGCGTGGACCACGGTCACGAAGTTCTCAGTATAGAG GCGTTACGTTTTACCGGCGAACCGBAAGATGGGAATCTCATATCTGGGACTGTGGGAAAC AGGTTTACTTAGGTGGATTTGACACTGCTCATGCAGCTGCTCGAGCATATGATAGAGCTGC TATTAATTCGGTGGAGTAGAAGCTGATATCAATTTTAACATCGAAGATTATGATGATGAC TTGAAGCAGATGACGAATTTAACCAAGGAAGAGTTCGTGCACGTACTTCGCCGACAAAGC ACAGGCTTCCCTCGAGGAAGTTTCAAGTATAGAGGTGTCACCTTTGCATAAGTGTGGTCGT TGGGAAGCTCGAATGGGTCAATTCTTAGGCAAAAAGTATGTTTATTTGGGGTTGTTTCGACA CCGAAGTTGAAGCTGCTAGAGCTTATGATAAAGCTGCAATCAAATGTAATGGCAAAGACG CTGTGACTAACTTTGATCCAAGCATATACGACGACGAAGTGAATGCCGAGTCATCAGGGA ATCCTATTCAACAAGATCATAATCTCGATTTGAGTTTGGGAAATTCGGTTAATTCGAAGCA AAAGGGTCAAGATATGCGGCTCAAGATGAACCAACAAGATTCTTCACTCTAATGAGAT TCTTGGATTAGGTCAAACCGGAATGGTTAACCATATCCCCAATTCAAATCACCAA
TRINITY_DN62832_c0_g1	ATGAGCGTGAAGGAAGTGAAGCGTTGGAGAGGCAGCTGGAAGCCGCTCTTACCGCAACTC GACAACGCAAGACTCAAGTTATGATGGAAGAAATGGAAGATCTTCGGAAAAAGGAGAGG CAACTCGGAGACATAAAACAACAACCTCAAGATTAAGTTTGAGACCGAAGGCTATGCGTTC AAAACGTTTCAAGACTTATGGTCAAATTCGGCAGCATCGGTGGCCGGTGATCCTAACAATT CTGAATTTCCGGTTCAGTCTTCTCATCTTCAATCAGTGGATTGCAACACTGAACCTTTTTC CAAATAGGGTTTCAACAAGATTACTACGTGCAAGGTGAAGGGTCTTCGGTATCAAAGAGT AACGTGGCATGTTGACCAATTTCTGTTCAAAATTGGGTTCTT
TRINITY_DN48318_c3_g1	ATGGGAAGGGGTAGGGTTCAGCTGAAGAGGATAGAGAACAAGATTAATAGACAAGTTAC TTTCTCAAAGAGAAGGTCTGGTTTGCTCAAGAAAGCTCATGAGATCTCTGTTCTCTGCGAT GCTGAGGTTGCTCTCATCGTCTTCTTCCAAAGGCAAACCTTCGAATATTTCCACCGACTC TTGCATGGAAGGATACCTTGAACGCTATGATCGCTATTTGTATTTCAGACAAACAACCTGTT GGCCGAGATATTTACAGAGTGAAAAATTGGGTTCTAGAACATGCTAAGCTCAAGGCGAGA GTTGAGGTACTTGAGAAGAAACAAAAGGAATTTTATGGGGGAAGACCTTGATTCTGTTGAGC TTAAAGGACCTTCAGAGCTTGGAGCATCAGCTCGATGCTGCTATCAAGAGCATTAGGTCA AGAAAGAACCAAGCTATGTTTGAATCCATATCAGCGCTCCAGAAGAAGGATAAGGCTTTG CAGGATCACAATAATACGCTTCTCAAAAAGATTAAGGAGAGGGGAGAAGAAAACGGGTCT GCAAGAAGGACAATTAGTCCAATGTCCAACAATTCATCAATCTTCAACCCCAATACTG CTTAACCTTCTCCAGAGATGGCTTTGTGGGGAGAGTTGGGGGCGAAGACGGCGGTGCATC GTCGTTGACGGAACCAAACTCTTCTTCTCCAGCTTGGATGTTACGTCCTACAACGAACGAG

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Supplemental Table 2. Continued.

Gene ID	Coding sequence
TRINITY_DN68423_c2_g1	ATGATCAAAGCAACTTCAGCATCACAAAGGACAGATAAACTCGAAAAGCTTTCTTCAAAAAGTCC ATTTCTTCTCTTGGAGAAGGTCACCTTGCTGCTCGTTGCGTTTTCTATCCTCTTCATCTCGG TCTTTCCTCTCACCATCCCTCTTGATTTGTATTGTGTATGCGCTTTGGATGGATTGATGAGT TTATCTTTTTGTGTTTATATCTATCTGTGTGGGTGGAGA
TRINITY_DN18713_c0_g1	ATGGGTGCGAGGAAAAATCGAGATAAAGAGGATCGAGAATGCGAATAGCAGGCAAGTTACTT TCTCCAAGAGGCGTGCTGGGTTGCTCAAGAAGGCTCATGAGCTCTCTGTTCTCTGCGACGC CGAGGTTGCCGTCATCGTCTTCTCCAAGTCCGGCAAGCTCTTCGAGTTCGCTAGTACTGGC ATGAAGAAGACGCTTTTAAGATACGGAAACTACCAGAGTTCTTCAGATGCTCCTCTGACTA ATTCTAAAGCAGAGGACCAGAAGGATTGTAGAGAGGTGGACCTTTTAAAGGATGAGATTT CAAAGCTTCAAGAGAAACAACCTACAATTGCAAGGTAAGGGCTTGAATATTCTGAGCTTGA AAGAGCTGCAACACCTTGAGCAGCAACTAAATGTTTCATTGATATCAGTGAGAGAGCGAA AGGAACCTATTGTTGACTAAACAACCTGAAGAATCACGGCTCAAGGAACAGCGAGCAGAGC TGGAAAATGAGACCTTGCGTAGACAGGTTCAAGAACTCAGGAGTTTCTCCCGTCCATCAA CCAACACTCTGTTCCATCATACATCAAATGCTTCGCTATAGATCCCAAGAACCCACTCGTA AACAACCTCTAGCTTGACGACATAAACTGCAGCCTCCAGAAGACCAATTCAGACACAACCT TTGCAATTAGGGTTGCCGGGAGAAGCACATGATAGAAGGAAGAATGAAGGTAACGGAGA GAGCCCATCAAGTGATTTCGGTGACAACGAGTACGACTGGAGCAGCTGCACAAAGGATCG GGCTAGTT
TRINITY_DN69985_c0_g2	ATGGGAAGGGGAAGATCGCGATCAAGAGGATCGACAACCTCCACGAGCCGTCAGGTGACTT TCTCGAAGCGGAGGAACGGGTTGCTGAAGAAAGCCAAGGAGCTTGCGATTCTCTGCGATG CAGAGGTGCGGTGTCATCATCTTCTCCAGCACCAGGCGCCTCTACGATTTCTCCAGCTCTAG CATGAAATCGGTAATAGAGCGATACAGCGAGGCCAAAGGTGAAACCAACTCGGAAATTA ACCCAGCTTCAGAAATCAAGTTTTGGCAAAAGGAGGCCGCGATTCTAAAGCGACAGCTAC ATAACTTGCAAGAAAACACCGGTATGTTTTGCATCCTCTGAGTTCGTCAAACACTGTGCA TATTAACAAACTAGAACTGGGAACGATGTAC
TRINITY_DN59446_c0_g1	ATGGGGAGAGGGAAGATAGTGATCCAGAGGATCGATGATTTCGACGAGTAGGCAAGTCACTT TCTCGAAAAGAAGAAAGGGTCTCATCAAGAAAGCTAAAGAACTCGCTATTCTCTGCGACG CAGAGGTGGGTCTCATCATCTTCTCCAATACCGACAAGCTCTATGACTTTGCCAGCTCCAG TATGAAATCGGCTATTGAACGATTTAACAAGACCAAGATGGAGCAGCAACAACCTATTGAA TCCTGCGTCAGAAGTTAAGTTTTGGCAGAGAGAGGCCACAACCTCTAAGGCAAGAACTGCA CTCATTGCAGGAAAGTCATCGACAACCTAACAGGGGAGCAATTACATGGTCTGAGCGTTAA GGAGTTGCACAATATAGAGAGCCAACTTCAAATGAGTTTACATGGAATTCGTATGAAAAA GAGGGATCTTGTTTCATCAGGAGAACCTCGAATTGTGCGAAAAGGTACAAAGGATTCATCA AGAAAACGTCGAACTACACAAGAAGGCTTATGCAGCGTCAAGCAGAAATGGGTTGGGAC TTCGTGAGCTTGAAGATACAGCCGATGAGTCCCATGCACAGGTTTCGTCTGCAGCTAAGTC AGCCTGAACAGTCCCATTATCAGACCTCATCAAAGAGC
TRINITY_DN58069_c0_g1	ATGAAGAAGGCTAAAGAGCTCTCGATTCTCTGCGACGCCGATGTTGCTCTTATCATCTTCTCC AGCACC GGCAAGATTTACGATTTCTCCAGCGGCTGTATGGAGCAAATCCTTTCTAGATAT GGATACAGTGCTGCGCTGCTGATCATCATATAAACAGAGAGACAACAACCTTCTACTT TGTTCTTCACATGAAAATGGTGATGTGTTGCGAAAAGATGATTCCTTGAAGAGCGAACTC GAGAGATTACAGCTTGCAATTGAGAGACTGAAGGGTAAGGAGCTTGACGGTATGAGCTTC TCGGATCTTATTTCTCTTGAAAACAGTTGAATGATAGCTTGCATAGTGTCAAGGATCGTA AGACTCAAGTCCTGCTTAACCAGGTAGAAAGATCCCGGTTACAGGAGAAAAGAGCGTTGG AAGAAAATCAAATCTTGCGCAAACAGGTAGAGATGTTGGGGAGAGGTTTCATCAGCGCCAA AAGGGTTGAGTGAAATACCTCAGCTTTCTAGCCCAAGCGGAGCCTGAGAGTTCTTCATC AGACGATGACGAGAATGACAACGATGATCACCATTCCGACACTTCCTTGACAGCTGGGGTT GTCGTATCGGGGTAAGTGCAAAAGAGAAAGAAGCCGAAGATTGAATCGCCCTGCGATAA CTCTGGAAGTCAAGTAGCTTCTGAT
TRINITY_DN68423_c2_g2	ATGGTGAGGGTAAAGACGGAGATGAAGAGGATAGAGAACGCAACAAGTAGGCAAGTGACCT TCTCGAAGAGAAGAAATGGACTTTTGAAGAAAGCTTTCGAGTTATCGGTCTTTGTGATGC TGAAGTCGCTTGTATCATCTTCTTTTCAAGATCCAAGCTCTATGAGTTCTCTAGCTCTAGAG CATCCGTGAGGGCAATTATAGCTGGC
TRINITY_DN46328_c0_g1	ATGAAGAGGATAGAGAACAAAGATCAATAGACAAGTGACATTCTCTAAAAGAAGAGCTGGCC TTTTGAAGAAAGCCCATGAGATCTCGGTTCTTTGTGATGCCGAGGTATCCCTTATTGTCTTC TCCATAAGGGGAAACTGTTTCGAGTACTCCTCTGAATCTTGCATGGAGAAGGTACTAGAA CGCTACGAGAGGTACTCTTACGCCGATAGACAGCTGAAAGCACCTGACTCCCACGTTAAT GCACAGACGAACTGGTCAATGGAATATAGCAGGCTTAAGGCTAAGATTGAGCTTCTGGAG AGGAACCAGAGGCATTATCTGGGAGAAGATTTAGAATCAATTAGCATAAAGGAGCTCCAG

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Supplemental Table 2. Continued.

Gene ID	Coding sequence
TRINITY_DN60394_c3_g2	ATGTACGAGTCCCTCAACCACCTCCAAAGAAAGGAGAAGGAAATACAGGAGGAAAACAGCA TGCTTGCCAAACAGATAAAGGAGAGGGAAAGTATTCTAAAGACACATCAAAACCAATGGG AGCAGCAGAACCGCACCCACCATATACCAACCCAGTCGCAACCGCAATTACATCCTTACA TGATCTCTCATCAGACATCTCCTTTCCTAAATATGGGTGGACTGTACCAAGAAGAAGATCC AGCGGCGGTGAGGAGGAACAATCTC
TRINITY_DN68029_c0_g1	ATGTTGATCTTCCACTTCTGTCATTTAACTTCTTACTAGTGTTCATTGGAACCCAATAGATTTT TGTTTGTTTGCCTTTTTCTAGAGGGTAACAAGATTACTGTCATCTCTCAGGTAGAGAAAAGA GGCTGAAGCTAAAGGTGTACCAATGGGCCAAGCGCTAGACATAGCTATTCCTCCTCCACG GCCTAAACGAAAACCAAGCAATCCGTATCCTAGAAAGACGGGAAGTGGAGCTATCCCCAT GTTAAATCGGGTGTAATGATGGAAAAGAGTCCATTGGTTTCAGAAAAAGTTTCGCCTCC TGAGATGGCGAATGAAGATCTGCAGGAAGACAACCTGTTTCAGATTGTTTCACTCATCAACA CCTCTCTGCTGCGTCTTCCATGAATAAAAGTTCTGTAGAGACATCAAACGCAAGCACTTTT CGGGAGTTCTTACCTTCACGGGAAGAGGGGAGTCAGAATAACGGGATAAGAAAAGGAGCC AAACCCAGCGAATTACAGTGGTTTGAATGCAAAACATCTGGAAAACGATGTGGTAAATAA CGAGCAAGAACCTCAGACTTATCCAAGGCGTATCCCCGTTGTAGTGCCATTGGGAAGCTC GATAACAAGCTCTCTATCACATCCTCTTTCGATGCCAGACGAGAATGACGCCCCAAGAAA TAGTTATCCCCACACAGCTCAGTCGTTTCTGACCATATAATGTCAGCCCTTTCACAGACA CCGGCTCTATATACCGCAGCAACTTTCGCCTCATCGTTTTGGCCTCCAGATTCTGGTGGTG GACCACCTGGCCAAGGGAACCTTACCTCCGAATTTGGCTGCCATGGCTGCAGCCACTGTCTG CAGCTGCAAGTGCTTGGTGGGCTGCCAATGGATTGCTACCTTTATGTGCTCCCTTTAGTTC AGGTGGTTTGACCTGCCACCCTCCAACCTACTTTTGGACCATCCGGTGAAGTAGACCACACA AAAGCAGGCACTTTACTACATGTTTCTGCGCAGAGCCGAGAGCGGATGGACCAAGAACAC TCTGAGGCATCAAAGGCTCGATCTTCATTGGACTCGGAGGAGATTGAAAACGGGATTA CCAGATTGTCATGAGCAGCCTTCAGCAACAGCTGAGACTGATGTGAAAGGCTCAGATGGA GCAAGAGACAGAAAACAAGTTGACCGGTCTTCTGTGGTTCAAACACTCCCTCGAGTAGT GATGATGTCGAGGCGGATGCATCAGAGAGGCAAGAGAATGGCACCAATCCTGAAGTGAA AGAAGTGAATGCAGATACTACTAATCCACAACTGCAGAGTCCAATGCACGTCGCAGTAG AATCAGCTCCAACCTTAACCGATCCATGGAAGGCTGTTTCAGATGAGGGTTCGAATCGCTTTC CAAGCTCTCTTTGCCAGAGAAGTTTTGCCACAAAGTTTTTCATATCAGAAAGATTACAGAG AAGAGGATCAACAAGAACATAGATATCCAATGGAACCTTGATCTTAACTGCACAGCTCAAT TAGCTCCGGTTGATGATGATCAAGAGGAGAAGAGAAACATAGGGTTTTTGGGAATGGGAT TGGATGCCTCAAAGCAAAGTAGAGGAAGAACAGGTTTCAAACCTTACAAAAGATGTTCAA TGGAAGCCAAAGAAAGTAGAGTGATCAGCACCAATCCTATCATCCATGTGGAACAGAAAAG ATTCCAAACGGATTTCGGTTGGAACCCAGGCCTCCACA
TRINITY_DN63019_c0_g1	ATGGCCACTCACCACACAACAATGACCGATCCGGAGAACAGACTGGTGGTGGTTCAAGATG AGGAGGGTGAAAGAGGATGCCAAAGAGGCGGCTTCGTGGTTGTTCCCTAACTCAGACAAA AACAATGGGAATCACCAGAACAATGAATTGTTGTTTCAGTGATGAGTATCTAGACCTTGCG GATTACAACTCGAGCATGGACTACAAATTCACAGGCCAATACAATCAGTATCAGCGTCAA CAAGACTGCAGCGTACCACAGACAAGCAACGGAGGAGACAGGTTGTTCCGCTTCGACT TGAAGAATCAAGGGGAAACCTGCGCCACAAGCAACAGAATATCATATATGGCTCCTCAGC AAGTCACTACGTGTACAATGGTTCCAAAAAACAGAACGTAAGGCTTATGTATATTTGT
TRINITY_DN63019_c0_g2	ATGTTGAAACAAGAGAGTAACGACATTGGTAGTAGAGAGAACAACAACAGAGGGGCACGAG CCTGTGACACATGCCAGTCAACTGTCTGCACCGTGTACTGCCATGCTGACTCTGCCTACTT GTGCACGAGCTGTGATGCTCAAGTTCACCTCTGCCAATCGCGTTGCTTCCCGCCATAAACGG GTCCGTGTCTGCGAGTCATGTGAGCGTGCCCCGGCTGCTTTTCTGTGCGAGGCAGATGATG CGTCTCTATGCACAGCCTGCGATTACAGAGGTTTATTCCGCAAACCTCTTGCCAGACGCCA TCAGCGAGTTCCAATTCTGCCGGTTTCTGGAACTCTTACAGCTCCATGGCCACTCACCAC ACAACA
TRINITY_DN65596_c1_g1	ATGGGTTACATGTGTGACTTCTGTGGTGAACAAAGATCAATGGTGTATTGTGATCCGATGC AGCGTGTCTCTGCCTCTCCTGTGACCGGAGTGTTTCATTCCGCTAATGCATTGTCCAAACGA CACTCTAGGACACTTGTCTGCGAGAGATGCAATGCGCAGCCTGCAACAGTCAGGTGTGT TGAAGAAAGGGTTTCGCTCTGTCAAAACTGTGATTGGTCAGGCCACAACAATTCTTCTC GTCTTCTCGTCAAATAATCACAAGAGGCAAACGATTAGTTGCTATTCTGGTTGCCCTTCA AGCTCGGAGCTCGCCTCTATCTGGTCTTTCTGTTTGGACTTAGCCGGACAATCCGTTTGTGA ACAAGAAATGGGTATGATGAATATAGACGATGATGCTCAGACCAACCAAACTGTAAACGA TGATAAGAAAGATGCCATCGTAGGCTCCTCTTCAAGGCCTGAAACCAGTTCTGCAGCAC AACCGAATTCATCACTTGCTAAGGATGTTGGAGTGTGTGAAGATGACTTTTATGGAACCT

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Supplemental Table 2. Continued.

Gene ID	Coding sequence
	CGGTATGGATGAAGTTGACTTGGCCCTTGAGAACTATGAAGAGCTCTTTGGGACAGCCTT TAACCCCTCGGGAGAGCTCTTCGGACAAAGTGAATCGATAGTCTTTTCCAGAAGCATC AAGCAGCTCCTGAGGGCGGGAATTCGGTGCAGCCTGCTGGGAGCAATGATTCTTTCATGA GTTCAAAAACCGAGCCAATAATATGCTTCACATCGAAGCCAGCACATTTCGAACATATCT TTCTCTGGAGTCACAGGAGAAAGTAGTGCTGGAGATTTCGAAGAATGTGGTGCATCAT CTTCCATGCAGCTCTCGGGCGAGCCACCATGGTTTCCTCAAACATCACAGGATAATAATG CTTGCTCACACTCAGTGACCCGTAATAACGCGGTTATGCGTTACAAAGAAAAAAGAAGG CTCGCAAGTTTGATAAGAGAGTGAGGTATGCTTCTCGCAAAGCAAGAGCTGATGTGAGAC GCGGTGTAAAGGGGAGATTGTCAAAGCTGGTGAAGCTTATGACTACGACCCACTCACCC CAACCAGAAGCTAT
TRINITY_DN53874_c0_g1	ATGACTACGGTCATGGGTGCATTGTGCTTGGATGAGATCAGACATGCACAAAGAGCGGATGG ACCCGCAAGCATCTTGGCAATAGGCACGGCCAAACCCTGCGAACTATGTGATGCAGGCGG ATTATCCAGACTACTATTTCCGCATCACCAACAGTGAACACATGACCGATCTCAAGGCAA AGTTCAAGCGCATGTGCGACAGATCAATGATACGGAAGCGGTACTGCACT
TRINITY_DN61788_c0_g1	ATGCTTTTAACTACATTCCCCTGTGAGTTTGTGTTGCAGTGATGTCATCTCATGACTCAAT GGGGCTGGTTTTTAAAGTGCTTATCAAAGGAGCAGTTGACTTTCTCGTTAAGCCGATAA GAAAAACGAGCTTAAATCCTTTGGCAACATGTTTGGAGAAGATGTCAAAGTTCTAG CGGGAGTGGAAGTGAAAGTGAACACATCAAACCTCAAAGTCCGTGAAATCAAAGAGTA TAAAAAATCTGACAATGATTCCGGAAGCAGTGGTGAGAATGAAAACGGGAGCATTGGC CTGAATGCTAGTGATGGAAGTAGTGATGAGAGTGGTGCTCAGAGCTCTTGGACGAAAA AAGCTGTGGAGGTTGACAGTCCACGAGCGGTATCTCCATGGGATCGAGTTGATAGCACT TGCGCACAAGTGGTACATTCCAACCCCGAGGTTCCAGTAATCACTTGGTTGCAGCACC TGCTGAGAAGGAGACCCACGAACAGGATGAAAAATTTGAAGATGTCACAAGGGGTAG AGACTTGGAGATTAGTATTCATAGAAATTGTGATCTGACACTGGAGCCAAAAGATGAACC CCTAACCAAAACCACTGGCATTATGAGACAGGATAATTCATTTGAAAAGAGCTCTAGT AAATGGAAATTGAAAAGTTGGAAAAGGACCATTGGACCTCAGTAGTGAAAAGCCCTTCAA GTAAACAAATGCATGAAGATGGAGGGTTCGGGTTGCAAAGCTATCTCTTGCCACCTTC AAGATAACAAAGAACTCGAGGCGCCTAACACACACTGCAAAACTTCAGATACCTGTGAA GCTGCCGTCAAAAACGCTGAAGAGCTAATGGACGTTGAACATAGTTCAAAGAGGCATA GAGGAATAAAGATGATGGGGTAATAGTTAGAGATGACCGCAATGTGCTGAGGCGTT CAGAGGGTTCAGCTTTCTCAAGGTATAATCCAGCCTCAAATAACAACAAGCTTTCTGGCG GGAACCTGGGAAGCAACTCTCTTCAAGATAATAATTGTCACTCAAACATGAACGAGAGC CTCCCAATAATCATCACTCACGCGTCGGTAGCAATAACTTAGAAATGAGCTCCACA ACTGAGAACAACGCATTCAAAAAGCCTGGAGCTCCAAAAGTAAGCTCGGCAGGATCTTCA TCAGTAAAGCATTATCGTTTCAGCCTCTACCTTGTGATCATCATCAGTCCTTCTAT AATCTTGTTCACGCCCCGTGAGCGGAAGTTACCGCCACAATGTGGATCCTCAAATGTGTAC AATGAGGCGATTGAAGCTAACAACAACACAGTGAATTACAGTGTGAATGGAAGTGTA TCAGGTAGTGGTCATGGAAGCAATGGGCCATATGGAAGCAGCAACGGCATGAATG CTGGAGGGATGAATATGGGAAGTGATAATGGTGCTGGCAAAAGCGGAAGTGGCGATGG TAGCGGAAGTGGAAGTGGAAGCGGAAGCGGGAATGTGGCAGATGAAAAATAA GATCTCTCAAAGAGAAGCTGCTTTGACGAAGTTCCGCCAGAAGAGAAAAGAGAGG TGCTTCAGAAAGAAGGTACGATACCAAAGCCGGAAGAACTAGCGGAACAACG GCCTCGTGTCCTGGCCAATTCGTCCGTAAGACAGCTGCTGGAACAGATGATAACGACA TAAAAACGCCGAGGATAGC
TRINITY_DN29253_c0_g1	ATGCATACACCAAAACAAAACATAACCCACAAGACTAAAGATTATTCCAAACACAAAGAT GATATCTTTTAAAGCAAACCTTAATAAAAAAATCAAGAGAGGGAAGGGAGATGAA CACAGACCATACAAGTGTTGAAGAAGATC
TRINITY_DN45325_c0_g1	ATGTTTAAACCGGAGTTACAGCCCTTATGAAGTTCCTCTCCTTTTGCATCTTCAGTTTTCCCTT TTTACCTATAAAACAGACAGACCACAGCAAATTTTCAAACATGAAAATCGATACTA CTGGGTAAACACCAAGTGTAC
TRINITY_DN66742_c0_g1	ATGTCTTATTCTGGCTCTGGTTCTGGTGGTGGTGGTGGTGTAGTATTGTATGGTTTAGA AGAGATCTCAGGGTTGAAGATAATCCAGCTTTAGCTGCAGCTGTAAGAGCTGGCCCTG TAATTGCAGTGTGTATGGGCACCAGAGGAAGAGGGACACTATCATCTGGTAGGGTT TCAAGGTGGTGGCTCAAGAATAGTTTGGCTCAGCTTGATTCTTCTCTTAGAAGCCTTGG TACATGTCTCATACCAAGAGATCTACTGATAGTGTGCTTCACTTCTTGAAGTTGTAA ATCCACTGGTGGTCTCAGATCTTCTCAACCACTTGTATGATCCCTTATCATTGGTCCGT GATCATCGTGCTAAGGACGTTCTGACAGCGGAAGGCATAGCGGTTAAATCATTCAACGC

Continued next page

Supplemental Table 2. Continued.

Gene ID	Coding sequence
	AGATTTGCTTTACGAGCCATGGGAAGTGACCGATGAATTAGGCCGTCCTTTCTCAGTG TTTGCTGCCTTTTGGGAAAGATGCCTTAGCATGCCTTATGACCCTGAGTCTCC TCTTCTCCACCTAAGAAGATCATTTCAGGGGATGTGTCCAAGTGTGTT GCGGATACATTGGTCTTTGAAGATGAATCAGAGAAAGGAAGTAATGCACTTCTCG CTCGTGCTTGGTCTCCGGGTGGAGTAATGGTGATAAAGCTCTCACAACGTTTCAT CAACGGACCATTGATTGAATACTCTAAGAACCGCAGAAAAGCCGATAGTGCCACGACC TCGTTTCTTTCTCCACACTTGCATTTTCGGGGAAGTGAGTGTGAGAAAAGTTTCCATCTTG TCAGGATCAAACAGGTGGCATGGGCAAACGAAGGGAACAGGCTGGTGAAGAAAAG CGTGAATCTTTTCTCAAATCTATTGGTCTCAGGGAATACTCAAGATACATAAGCTTTA ACCATCCATACTCTCATGAAAGACCGCTTCTTGGCCATCTAAAGTTTTCCCTTGGG CTGTGGACGAGAACTATTTCAAGGCGTGGAGGCAAGGCCGACTGGATACCCTTTGG TCGATGCCGGGATGAGAGAGTTATGGGCTACTGGTTGGTTACACGATCGCATAAGAG TAGTTGTTACAAGCTTCTTGTAAAGTGCTTCAATTGGCATGGGGGATGAAG TATTTCTGGGACACACTTCTTGATGCAGATTTAGAAAGCGATGCTCTTGGTTGGCAATACA TTACTGGTACTCTCCCTGATAGCCGAGAGTTTGATCGTATTGATAACCCACAGTTTGAAGG ATACAAGTTTGATCCAAATGGGGAATACGTACGGAGATGGCTTCCTGAACCTTTCAAGACTC CCTACAGAGTGGATACATCACCCATGGAACGCACCTGAATCTGTGCTTCAAGCTGCTGG TATCGAGCTTGGTTCAAACATATCCTCGACCAATTGTAGGATTAGATGAAGCAAAAAGCA AGGCTTCATGAAGCACTTTCACAGATGTGGCAACTAGAAGCTGCTTCAAGAGCTGC AATAGAGAACGGATCCGAAGAAGGACTTGGAGATTCTACTGAGTTTGAGGAAGC TCCTATCGAGTTCCCTAGGGATATCACAATGGAAGAGACTGAACCAACCAGACTCAACCC TATTAGGAGATATGAAGATCAGATGGTTCCAAGCATTACTACTTCTTTGATCAG ACCTGAAGAAGACGAAGAATCGTCTCTGAATGTGAGAACTCAGTAGGAGATAGCA GAGCAGAGGTTCTATGAACATGGTCAACGCCAACCAAGCTCAGCAGCAGCCGAGAGCA GAACCGGTTTCAAACCAAATCACAGCTATGATTCCAGAATTCAATATCAGGATTGTTG CAGAGAACACTGAAGACTCGACAGCTGAATCTTCAAGCAGCGGAAGGAGAGAGAGGGA CGGAGGCATAGTCCCCGAGTGGTCAGGGTACTCAGAACAGTTTGCTAGTGAAGAAA ATGGGATTGGAGGAGGAAGTACAACATCTAGCTACTTGCAGAATCACCATGAAATACTC AACTGGAGACGGCTTTCACAAACTGGG
TRINITY_DN67410_c0_g1	ATGATAAACATATGTTCTGAACCCCTAGTAGAGGCTACAGTTCGGACCATGTCTAAGTGGTT CATAAGCTCAGGAAAGCTTGAAAATGATCAGAGGTCTTTGCTGTGGAGGCTTGTAACCT GGCTCTAATCACTCGTTGGGAAGGAAAACACCATAATTATTTCTGGAAGTACCGGATCT CAGAAGCACTTTTGTCTGTTGTGGAGAATTTTCGTAGTCAATCCTTGGAGAATTATGT GTCGCTGGAAAAAGAAATTTCAAGTTGCTGAGAAGGTACTGAATGCGAATTTTCTTCTAGT CTGAGGTCATATGTTTGGGATATAATTGGATTCTTGGCAGCTCACTGTGAGGAAGAGTTC GATTCCATTTTGGTGGAGATGAATCCGCCTCAACTTTCTTGTACATGCGCATGCTTG ACCTTTTCAAGGTCGGTTCAGAAAGGCTATCAAATATGCCAAAACGATATTATCAGCGCCT CCCAAAGTGAGTCGGCGTCAAGAGCAGTCTAATGATGATATATTCTCCCTCCAAATATA TATCATCAAGGGCCAGAGTTACCCTCTCGTTTATCCTAGGAGGATGGTGACAGAAAT TTGAATTCCCTTGTAATTTCTTAAGTTATATTCCATCTTCTGGAGGTTATGTACTGCCAAA TATACTGCAAACTACCGTCTGCTTAGTGGGCTTGGCATGCTATTATCGATCCCTCAGT ATGCGAGTTTCATTTAAGAAACCAGGGTTTGGAGATACTGATATCCTTCTGTAGTTGGT ATCAAAGGAATCGTGACAATATAGGACCATCGAGTTTGTCTCTTATCCCCAGAGCATTGC TGAGAAGAGGATATGTTGCTGGGAATGTACGGAAGACTGGGACAACAAAGATGCTATT CTTCTCTATGCTCTCTTGGCTTTGGCCGAGTTGGTTACTCATTCTTCTCTGAACAGAAATCA CGCCGAAGAATTTCAATGAAGAGAGATAGCGTGAAAGATCTGTTATGCACCACACTTCA GGAGATCCGAGATGGAAGTTATGGCTCTGGTCCAAAGTGGTATGCTGCACACATCCTAA CCTATCTTGGATATTATGGCTTCCAACATAAGTTGGGGAAAAGGCTCATGGGAGCTTACG AAAATGAGGAATGTAGCGATCTGCGATTCTTTTGTAGTGGGAATAGTGCGAGCCTA CACAAAGTTATTCTCGCTGTCAGGTGCCAACGTTACTGCCTCCCAAGGAGGGAGCTC ACAGTGGCTCAATTGAATCAAATGAGAGATCGCAGAGAACCAATTCAAGAAATCCGATG TCTGCGAATGTGGATACTTGGGCGCTTGTGAAGTTGTTGGAATTTGCTTACTCTGGGTAT GTGGAAGTAGAAAACACGGCACGGAAGAAAGTTGAAAACCTTTGGCGAGACATTGTAAGT CAAAGGTTCTGCTGCAGATGCTGTGCAGAAAAAGACCCAGATGGGGATCTTCAATACC CAGAATTGATCTACCACTTGCCCTCACTCCTAAACTCATTCTTCTCGGATGTTATATTA GTACCTAAAGAAACAGACATAGCTGGCTTCAACTGCTGTTCTGTTTCTTTACATCTCC TCATGCTCACTCTACCGAGTTATACTGTCGTCAGGCTGTGAATACCTACGTGCCTTGT

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Supplemental Table 2. Continued.

Gene ID	Coding sequence
	TCCGCTCCGGGATGCAAGAGAGCCATTTGGATAGACTAAACGTTCTGTGAGTTGGCT GGGGTTAACCAAGCTTGTGAAGTGGTTCTACGGTGATGAATTGCCAACCCCTCCATCGG GTTGCAAATGGAATAACATGGACACCGATGCAAACTACATGAGCTTCAAGCTTACGT GGAGATATACTCGCTCACCAGTGGTGGATAATGGAAGATCTTCAGAACGACTGTGCT AAAGTGATTCTCTCTTGCTTGAATCCGCTAGAGAGTTATCGATCAAAACAATCGAATTA GCTGCAAGTTTCTCGATGTGGAACTGGTGAAGCAGCTGCTGAGCATGCAGCTCCTAT ATACCATCAGCTTCGTGACTCAGGGGAGCTCGATGAGCTAGATGATGAGCTGGTTAACT TGATCCGAACCGCTGCTGTTCACTTTTCTCAACAGGGTGGT
TRINITY_DN69128_c1_g2	ATGGCGAAAACACGACCTGGTGTGCTTCTCCGAAGAGCAAGCTGGGCAAGAGAGATATCG ATTCGTTTACTATCAGAGGCACCAACAAAGTTGTTGAGCGGGAGATTGTGTGTTAAT GCGTCCAGTGGATGCTGGTAAGCCTTCTTATGTGGCACGTGTTGAGAAAATTGAAGCGG ATGCAAGGAACAATGTGAAGGTGCATTGTGATGGTATTACCGTCTGAGGAATCAGAT GGAGGAAGGAGACAGTTCCATGGAGCCAAAGAGCTTTTCATCTCTGATCACTTCGATGT CAGAGCGCACACTGCATTGAAGGAAAATGCATCGTTCACACCTTAAAACTACACGAG GCTTGAAAACGTTGGAGCCGAAGACTATTATTGTAGGTTGAGTATAAAGCTGCTAC GGGCGCATTTACCCCTGATCGAGTTGCTGTG
TRINITY_DN62817_c0_g1	ATGGCGAAAACCTGACCTGGTGTGCTCTCGAAAATCAAGCCTGGGAGGAAGGAGCTGG ACTCTTATACCATCAAAGGCACAAACAAAGTTGTGAGAGCTGGAGATTGCGTGTGTGAT GCGCCCATCGGATGCTGGTAAGCCACCATACGTGGCCCGTGTGAGAAGATCGAAGCG GATGCAAGGAACAATGTGAAGGTGCACTGTGATGGTATTACCGCCCTGAGGAGTCTCT TGGTGGTAGGAGACAGTTCCATGGAGCTAAAGAACTTTCTTGTCTGACCATTTCGATG TTCAAAGCGCACACACCATTGAGGGAAAATGCATTGTTACACCTTAAAACTACACAA GGCTTGAAAACGTTGGTGGGAGGATTATTATTGTAGATTGAGTACAAGGCTGCTACTG GCGCGTTTACCCCTGATCGTGTGCTGTGTAAGTGCATGCAAAATGTGAAATGCCTTACAATCCAG ACGATCTCATGGTGCATGCGAAGGCTGCAAGAGCTGGTACCATCCTGCGTGTGTTGGC ATGACGATTGAAGAAGCAAAGAAGCTTGATCACTTTGTATGTGCTGAATGCAGCTCTGA TGACGATGTCAAGAAATCGCAGAACGGGTTTACTGCATCTCCGGCTGATGATGTCAAGGT GGAAACGAAGCGCAGGAAAAGA
TRINITY_DN50493_c0_g1	ATGCACTGGGTTGATGGTGCTTTGCTGAATGGGGAAAGGCCAGACAGATACAGTTTGTGGTT CTTGGTCCTGTCTGGATCTGATCTACGCTTAAAGTTGCTCCAGTTCTTGTCTGCAGAACATT CTGTCTGTAAAGGTGGAACGAAGCGCAGGAAAAGA
TRINITY_DN58990_c1_g1	ATGAAGAGAGGGAAAGATGAGGAGAAGATACTGGAACCGATGTTTCCTAGACTTCATGTG AATGATGCAGACAAAAGGAGGGCCAAGAGCTCCTCCAAGAAAACAAGATGGCTCTCTATG AGCAACTTAGCATCCCTTCTCAGAGGTTTAGTGATCATGGTACCTTGCCCTCGTAACACA ACCACTTTGGTTCCCTTCCGGACCATCTAACCAGCCTTGTGGCGTGGAAGAACTTACCTG CGCAACATCTTGATTCTTCAGCTGCGGGCCAAGCAACTGATAAGTTTCGTCTCCCAAATG TCCTTCATGGAAAATGTGAGAACCTTGGCACAGAATGATCAGAGGAAAATAGTAAGA GAGGAAGATGATTTGCGAGTTCCCGTATTTATTAAGTCAAGAAAGTTTCAGTGTCTAGGCA GAAGCAAGAGTGCGATTGTGAAGGAGAAACACTCCACAATCGTAAGACCAAGTCAAG GGGAGTGCAAAAGCGAGGTGGCTTTGTGAAGTCTTCAGAAATATCAGCTACAGAGGAGATG GATCTTGAAGTATCAGCATCGAGTTGTGACAGAGTAAATGATTGCAGTGCTTCCGTGAG ACAAGAGTCTAGAAATTGGTTAGACCGAGATGGTGGTGAACACAAGTGATGGACAG TAATAACGGAGTCGAATCTCACTTGGCATCGGAAAGTCATACAGAAGAAGGTCGTGGCA ATCCTAATGACGTTGAGAATGGTCGTGAACACTGCAGAAGTGAGGATACGCCTCTATG CAGCAGATAAACGAAGAGGCAAGTGATGATGTTTCTGATAATTGATGGTGGATTCTA TATCCAGTGTAGATGTCTCCCCGATGACGTTGTGGGAGTATTAGGTCAAAAACGTTTCTG GAGAGCAAGGAAAGCTATTGCCAATCAACAAAGAGTATTTGCTGTTCAACTATTTGAGTT GCACAGACTAGTCAAGGTTCAAAGACTTATTGCTGCATCACCAGGATGCTTGTCTGATGA CATCAGTTATCTTGGAAAAGTTACTGCTAAAAGCTATCCAGTAAAGAACTCATTCATCA GAATTCATTGTAAAGCCTCCTCTACCACAGGTTACCAACACAGAAGCGTCGACTCAGA CAAGACTGACCAACATAAACTGGAATGTTTCAGCTGAGAAGCTGGTGGGAAAGTTGTCAA ACCAAGCTCATCACCATCATCAACAACCTTCCAACACTACATGCCTTTTCCGACCAACC AACCACCGCTTACCAGGTGTAACCGGATGTTGCTATCCTCCTCATCCTCCTACCTCCG GAGGAAACAGCAATGGTTGATCCCTGTAATGTCTCCTTCCGAAGGGCTGATATACAAGC CGCACCTGGTCCGGGACACACAGGGCCGGTCTGTGGAGGGTATTATGGTCATTTTCATG CCTGCACCGATGGTTATGGGTAACCTTCATGGGTGGTGGTGGTCCGCTCCTCCGTTT CATCCTGGTAATGGCTACTTCCCTCCATATGGTATAATGCCTCCTACCATGATGAACCCTT

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Supplemental Table 2. Continued.

Gene ID	Coding sequence
	ACTATCCTGGCCAACAACAGCAACAACAACATCAACCAAATGAGCAAATGAATCAG TTTCAGAACGCATCTGCTTTGAACACTCAACAACAGAGCTCTGTGAATGAAGCGGCTGC GCAACAGCAGCCGACGAAGTCTTATCCTCGGGCTAGAAAGAGCAGGCGAGGGTCTACA GCAAGCAGTCCAAGTGGTCCAGAGGGAATCTCTGGTAAGAACTCGTTTCGGCCATTCTT AGCGGTTGATGATGACGACAACAACAACATCAACAACGCACCTGAGCAAATGATGAC GACAACCACAACGACGACAAGAACTACTGTTACTCAGACAACAAGAGATGGAGCAGGA GTGACGAGAGTGATCAAGGTGGTTCCACACAACCCCAAGCTGGCGAGTGAGAACGCTG CGAGGATTTTCCGGTCAATACAAGAAGAGCGTAAACAGTACGACTCCTTCTCTAACTA CCCT
TRINITY_DN69071_c0_g2	ATGGTGCTGCTATCTCTGCTTCTTCATCTTCAGAGGCCAAAAAATGAACTTGAGGAGGGTC ATTCTGGAGTGCAGAATAAAGAGAGCACTAATCTTTTAGAGGAGTTGAGTTTGTTCATGG AGAAGCTGAAAGATGTATATTACGACGATGATGATGGTCTGCTTAATGACTTCCAAGT TGATTCTGGAACCTTGGCATGTGTGGCGTGTGGCGTTCTTGGCTTCCCTTTATGTCTGTG GTACAGCCTTCTGAAAATGCATTAATAAGATCTCTCAGAGAGACAAGGCGAGATAGAT GCTCAGGATATTACGGCACTGTCAATTAGAAAAGTGTGGCGGTGAATGGAACACGTCATC CAGATATATAAGACCTCGCATTTTCTGCCTCGAACACACTATTGAACTTCAGAGACTG CTGCAGTCAAGGGGTGGACTGAAGTTCCTTGTAATCTGCCATAAAGATTTTCAAAAATTTA AGGCACATGCGGCTATAGTGGCAGAGGAAGTCAAAGTCCCTTTCAGCTATGATGATGT CCTGTTAGAGAGTGCATCTAAGAAGAGTTGAGTCTAATTGATCTTGCAATCGAAGAT GAAGAAAACAACGAACACGGCGTAGACTGGACCTCAAACTTGGTATCAATTTACGGTA CTGTGTTAAAGTGAGGAAAAATCCCCCTACTAATAAAAATTCAGCATGCACTGTCACTAGGT GGCTTGTTCTCCGACACAAGCCACATGCTAGATATGTCAACTATCAAATGGCTGCAGAGA AAATCACGCTCAAAGGCTAACCCAGCTCTACCTCAAGTTTCACACCTCGTGAACATCT TGAAGTAAAAGTAGACAGAAATTTAGGGGAGGAAGGAAGAAAAGATCATCCAGTA CTCGAGAAAAGAAAATGTTGAATCCCAAGCCGGAAGAAAGGAAGAAAAGATCATCCAG
TRINITY_DN51551_c0_g1	ATGGGTAATGTTGAGATTCCCAATTGGCTAAAAGCCTTGCCATTGGCGCCTGTCTTTAGACC TACAGACACCGAGTTCGAGATCCTATTGCGTATATATCGAAAATCGAGAAAGAAGCCA GTGCCTTTGGGATCTGCAAGATCATTCTCTTTACCAAAGCCGTCGAAGAAGTATGTTT TCTACAACCTGAACAAGTCTCTTTTGGGTGTCCTGAATTGGCTTCGGATGTAGACAT TTCGAAAGTGTGTCAGGAGGATAGAGCTGTATTCACCACTAGGCAGCAAGAGTTAGGCCA GGCTAGACAAAAAACCAAAGGACGAGAGAGCAGTAATTCTCAAAGGAGTGGTGTAA GCAGGTGTGGCAAAGTGGTGGCGTATATACATTGGAGCAGTTTGAAGTCAAAGTTCGA AAACCTTTCTACAAAAGCCAGTTAGGAACGATTAAAGAAGTGTACCAGTTGTGGTTG AGGCATTGTTCTGGAAGCAGCTTCAGAGAGGCCTATATACATAGAGTATGCAAATG ATGTGCCTGGCTCCGCTTTTGGTGAGCCAGAGGGTCATTTGAGGCATTTCCGGCAGA GAAAGAGGAGGGGGAGAGGATCTTATCAGAGGAAGGCAGAGATCAATGAGGACAG CAGCGTCGAAAAAAGGACGGAAGGAGACAATTATCAAGAACCATCCTGTAAGAATGG TGAGAAAACATTGCCTGAGGTACCAAGGCATCTCTTGCTTCTCCAAGTTTCATTA TCTCAAGATCCGTCCAAGAGGAAGAACATG
TRINITY_DN69458_c0_g3	ATGTCTCCAACCTAAGTAGTCATGTTGTGGACCTTGTTGTAAGTCCGACCATACATGCT TCTACAGTCGATAATCATGATGGCCCAATAAAGTTGACCGGTGAGTACATCTGCAGCTA TGTGTCTGTACGTAATGTTGATGAAGCGGTTGAAAGGAGCGACCAAGAGTTTCAAGA ACCTAGGTCTACTGTCGCTAACATTGAGGAGGAACAGCAATCGCAGGTGGTGAACCAAC CGAAAGAGAAGCTGTATTTGGTGATAACACGCGAGGTGGAGGGAGAGGAAGCTATGTGT ACCATAGAAAACCTGTGCTCTGAAGATATTATGCATACTGAGCAACAGGAAGAGCAAACA CATTCTTCAGCTCAATTGGATTAAAAAGTTTCTGAACTAACATTGCCAGTGAGAACAT AGTTGTGGACATAATTCATGATGATGAACCTCTGGCAAGCAACTGTGATCAAGCGTCTTCA AATGGACTGCAAGCTGCAGATAATGAGATTAGCATGGATAGCGAAGTTGCAAGCTCAGG AAACACCGAAGTTATCGAGGCGCCCAATTCTAATATGGGGAGAGCAAAGAAGAAGCG GAAAATGGAATTAGAGTCTGAGACAAATGATAATCCAGAGAGTAGCATTGGTTTCA TAAGGAGTCCTTGTGAAGGGTTGAGGTCAAGGGGTAGGAGGAAAGTGACATGTGAAACA TCATTCAATCTCACTGAAGCGAGCGACGAAGAGAAGAAACCCACTGCGAAAAGGCTCA AGAAAACCTCAAATACTCGC
TRINITY_DN95956_c0_g1	ATGCCCTGTCTTCCGTCTGTGGCGGCTATAATCCGACACAAACCTAAACGACAGTCCACA CTCGTCGACCTTGCAATTTGTATGGTCGTTCTCCAGTGTGCAGACGCAAATGCTCGG TCCTCGCCCACTGCCATTTGAAGTTCATGGAACATCCTTTCCAAGGGCACGCGAA AGGTCTATCATCGTTATGAACACGTTGATGAAGCACCAGATATTTGTGAGCCCTGAAT TTCTTTCCACACCTTCTGTGTGCAGCGGTTTCTTGTGAGCTTGCAAGTCCGCTCTA CTCTTGAAAGTCATCTTGCATCCCTC

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Supplemental Table 2. Continued.

Gene ID	Coding sequence
TRINITY_DN69534_c0_g2	ATGCGTAATGAGAAAAGAAATCCAAAATTAGAAGCGACACATCTGGAGAAGGCCA AGGAACTTTATACTAAAGTCTGACTCAGCATAATTCCAACATGTATGCTGCCAACG GTTCTGGCATTATATTAGCAGAGAAAGGACAATTTGATATTGCCAAGGATCTTTTCA CTCAGGTTCAAGAAGCTGCAAGTGGAAGTGTGTTTCTTCAGATGCCTGATGTAT GGGTGAATCTGGCTCATGTGTACTTTGCTCAAGGGAATTTTGCCTTAGCCGTGAAA ATGTATCAAACTGCTTGCGGAAGTTCTTTTACAACACAGACTCTCAAATCTCTCT TTACTTGGCCCGTACCCATTATGAGGCTGAGCATTGGCAAGAGTGCAAAAAGA CGCTGCTAAGGGCCATTCACTTGACTCCTTCAATTACACATTTGATTTGATTGG GTGCTGTAATGCAGAAATCATCATCTTCCACACTACAAAAGAAAAAGAGAACA GCTGATGAGGTGCGCTCAACAGTCACGGAAGCAGAGAATGCTGTTCCGCTATTCA CTCAGTTGTCTGCTGCGTCAGACCTCCATGTTTCATGGGTTTGATAGTAAAGAAATAC AAACCCATGTTTCAGTATTGCACGCACTTACTGGAAGGAGCGAAAAGTTCACCGTGAA GTAGCTGAGCGTGAGGAGCTGCAGAATCGGCAGAGACTAGAAGTTGCTCGTCAGGCTG CTTTGGCAGAAGAAGCACGCCGTAAAGCTGAAGAACATAGGAAATATCAGTTGGAAAA AAGAAAAAGGAAGACGAGCTGAGACGCCTCAAGCAAGAAGAAGAAAAAATTCAACG TATAAAGGAACAATGGAAGAGCAACCCACATGGATCTCATAAGCGTAAGGATAGAG TTGAAGATGATGATGGGGAAGGTAGGCCAGTGAGCGGAAAAGAAAAGGCGGGA AGAGAAGAAAGAAGGACAAAGGCTCAAGGGCTCGACACTATGAGGACGATGATGAAG AAGCCGCTACTATGGATGATCATAATGAAGTGGAAGACGAAGACGCCAACACTA ATTATAATAGGGAAGAGGAGAATCAAGAAGCTGAGGAGCCTGTGGATGATGATGCTCAT GACCTTCTTGCCGCTGCAGGGCTCGAAGATCCTGATGCTGATGATGAGGTACCTGCTTC AGTTGCGAGGCGAAGAACGGCGCTTTCGTCATCAGATGAAGAAGGTGAATTGATGGAG AGTCAGCCAAATTCAAGCCCCCAAAAAGAGAATTCTCCGGGGAGGCAAGAAGAGAGC AATGTGGAAGAAGAAGAGACTAACCTGGACAACGAGGAGGCCAAT
TRINITY_DN67027_c0_g1	ATGACCTTTGCTGAAGAAGACGAAGTAATTCGACAATAAACATTCTTGATACTTCTGTTG ATAAGGAGGATGCCTCGAAGGATGATGTGGCTGCTAAAAAAGAAGAAGATGGCTCTG ATCAGACCGCGGAAATAAACAAACGGAAGAGGAAGCTGCCAGAAAAAGAAAC TGAAAAGAAGGAAGCAAACAAGCCTCCGGAATCGTGGTTTGAGTTAAAAGTAAACCCAC ATATATATGTGACTGGGTTACCCAAGGATGTCACCATCGAGGAAGTAGTTGAAGTTT TTTCTAAATGCGGCATAATTAAGGAGGATGACACTGGTAAGCCTCGCATAAAGCTTTACA GTGACAAGGCAACAGGAGAGTTAAAAGGCGATGCTCTTATCACGTATATGAAGGAGCC GTCAGTTGATCTTGCAATTCAAATCTTAGACGGGGCTCCTTTACGTCCCCTGACAAGCT CCTCATGTGAGTTTCTCGAGCTAAATTCGAGCAAAAAGGGGAGAGATTTATAACGAAGCA AACCAGACAACAAGAAGAAAAAAGCTTAAAAAGGTCGAGCAAAAGTTGCTTGGAT GGGGTAAGTTTTTTTTTTTTCTTTGAAT
TRINITY_DN67027_c0_g2	ATGTCCAGCTCCGAGAATCTACAGGTTCCACAATCATCTTCAGACTCTACTGATGTTGGTT GGTACATTCTTGGTGAACCAACAAAACCTCGGTCCATATACCTTCTTGGAGCTCTGTG ACCATTTCAGGAATGGTTACCTACAGGAACTACCTAGTCTGGGCTGAAGGAAGA AGCGAATGGCAGCCACTTTCTACCATCACTGAGTTGATGTCAGGATTCTGGAGCTGA GGTTGACTATTGAGCTGGAGGTGCTATAAATGGATATAATGCTGGAACCAACCAAGAGAA GCAAGATAATACTGCCTCT
TRINITY_DN57304_c0_g1	ATGGGATCCTCAATAAAGATCAACGCAATATCCATAGATCTCGCAGGCGCTGCCAACGA GATTGATATGGTAACATGTGATCATTTCTCCATACGTGGATTCTGATGCTGAAACGCG CGAGAGAGATCCTAAGAAATGTTGGCCGTTTTTCGGAGGAGAGTGTAGTTTGGGAGA CCAACAAAGCCATTCCCTTCTTCTTGTCTGTTCCAAAGTTTATAGTGGTGGCGTTGCA TGAGCTGCATCAGAGATATCGATGCTGATGGTACAAACGATTGTGGACTGCCTTCAAAC TCGAGAAGTATAATTAGCGGGAAAAAGCTCGATGGAAGCTCTTCGGTCATACCTAGCC AAAGCAAACCGAATACTCTAACTGTCGTTGATCAGGAGAAAGAAAGGAATATTAATAT CGCAGGTAGTGCTATTGTGGAGAAGGAGGATGTAACTGCGAAAGTTCTCGGAAGAAT GATCAGAGAGCTACTACGTCTCTCAAGAAAGTTCATCCTCCATCTATGAATGTTTCT ACTGTTAGGAGCAAGGGCAGAAAGCTGGCGAGTCCAGAGCAAGTAGGAAACAAGAGA CCTAAAGTCAACAAATCCTCCACGGATATTAGCAGCGTGAAAGAGACACAAAACGTGGA TCAGCTGGCTGTGACAACCTGTTGCCTCATCTGAGATCGCTCGTGTGGTTGAGGATAGGCC GCCTAATGAGTCATCAGAGAGTAGGAAGCTTGCCACAAGTGGGTTGCAGCGTAGGA AAACCTCGTCGAATGAGCGAGCTGGTTTACAATGATACCCAGAAAAAGCCGAAAGGAAGC CGACTACCAGCAAAAAAGAGTCTTGTTCGAAAAAGGAACCGGTTAAAGGTACAAA AAGAAAGGTATCACCTGAAAAAATTTATGCCAGCAGGAAAGCCGGCGCAACTTCTG

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Supplemental Table 2. Continued.

Gene ID	Coding sequence
	AAAATGCCTCCAAAAGCCGTGGCTCTGATCAAGGTGATAGTGAATCAACTGATAGTGGGT TTGACAGAGATCCTATTAACGGTAAGCAAAAAGAACAGAAGATTCCAGATTGTTGAC GAGTTTGTAGTACCATCATGTCCTTCCCAAGAGGGCGTCCGTGAGAATGATGCAGAT CCCGGTAAGAGTGCTTTATCAACTCCTGTGCACTCTTTAGTCAAGGAAAAAGATTCTGT TCCTTCTCCTCTGAGAGCTCAGAGAACAGATCAGAAGCTCAGTTTAGCTAGGAA GAAGAAAAATAAGTCAGAAATAGATAGCGTGAAGAGTAGCCTAATCAGTTTGTAGT TCCGGAGTGGATGAAGGAAGTCAGGTCAAACCGCGAACCGGTCTTCCATAAACGC AAGTTCCCAACCTACTCGGGAATTCTTGAATGAGAAAAAGGTGGGTCAGTGTACTTG ACGATCGTCTTGCTTCACAAGGATATGTCAGAAAACCTATCCCTCAGGTTAATGACAG GCCAGTCCTTTCTTTGCATATGCCAGACAATGAGCATATGAGGTCAACAGATGCAGAA GCAAACGTGTGTTGAGAGTTCGGTTCCTCTTCTAATTCCAACACAGGTGGATGGCTGA GTGCTCTAGTGGATGCTGTTGACTTCAGCAGCAACAGCAACTAATCTAAGAATC ACCTCGTCTTCTACACAAGTTGCAGACCCATCTTCTGTGACGCAAAAGGATGCTTCTGGT GCAGACAGAAAAGGGGAAGAGAGTAATGGTCCAAAATCATCATGGAGCACTCGGAA GCCAAAGCCATGACAGAAAAGGAGAATAGGCCAGAAGAGCAAAACGGTGATATTCTCAAG GCTATAGCCGAACCTCTGGCCAAAAAACTAGACGAAAAATGTCTAACCAACAAAGA AGAGGACGTTGGCAACAAGCAGCCACCACAAGAACCAGCACACAAATCCAAGAATGCTC TACTGAT
TRINITY_DN66245_c2_g3	ATGCCAGGCATTCTCTCGTGACTCGTGAAACTTCTTCTTGTTCAGAAGCACAGATCAGA TGTGCCATGAAGACTCCCGTGTGCATATGTCTGAAGAGGAGGAGATTGCTGCTGAAGAGA GCTTGGCTGCGTATTGCAAGCCTGTAGAATCTACAACATTCTTCAGCGGCGTGCTATTA GGAATCCCTTGTTTCTTCAAAGATCTTTCATTATCAGATTGAGGCAAAACATAAAAGG AGAATACAAATGACTGTGTTCTTTCGGGGACTATAGATGCTGGGGTACAACTCAAAA GCTGTTCCCTCTCTATATCCTGTTGGCAAGACTCGTTTCTCTTAAGCCTGTTGCCGAGT ATTCTGCAGTATATAGGTTTCAGTCGAGCATGTATTCTTACTGGTGCTCGGGGTTGATG GAGTTAGTCAAGCACAAAGCCAACCTTCTTCTCCTGATATGAATAAACTCGCGTT GGAGGCAAAATCAGGATCACTCGCTATCTTATTATTAGCTTTGCTGGTGCGCAAAATT CACAATTTGGCATTGATTTCAGGCAAGATCCATGCAGGAAATATAGGAGGACATTGCC TATGGAGCAAAATACCTCTTCAATCACTCTATTCTTCGTGGCAGAAATCTCCAAACATGG ACTTGGGACAGAGAATAGACTCAGTCTCTCTTGTGAAATGCAGCCTTGCTTCATAAAGT TAAAGTCTATGAGTGAGGAAAAGTGTGTCTCGATTTCAGGTTCCAGCAATCCCCTCACCTC GAGCTCACCGCAGCAAGTGCAAGTCACCATATCTGCAGAAGAGGTTGGGGCAACGGA AAAATCTCCTTATAGTTCATTTTCATATGATGACATCTCTTCTCTTCACTGTTGCAAA TTATCAGGTTGAGAACACGGAATGTAGTTTTCAATTACAGATACCATAACAACAAAC TGCAGAGGACTGAAGTAACTGAAGACTTTTCTTGTCCATTTTGCTTAGTAAAATGTGCCA GTTTGAAGGGCCTCAAATATCATTGGCCATCAACCCATGATCTCTTCAATTCGAGTT TTGGGTAAGTGAAGAATATCAGGCTGTAAATGTGTCTCTCAAGAGTGAGACAATGATC GCCGAGATTAATGAGGACGGCGTTGACCCGAAGCAGCAAAACATTCTTTTCTCTTCA AAGAAAGTCAGACGTAGGAGGAAAAAGAGTCAAGTACGGAGTCAACCGCAGGCA ATCATCTTGGACTAGGCTGCGAGGTGCTGGATAAAGACTGATGATGCTCATTCTGCGAGAA GTGAGAAGAGCCGAATACCAGCTGGAAAGCAGTGCGAAAGAATTGGGGGTGCTGA GTCGTCTGGTCAAAGAGTTCCTCCTGGCACGAGTCTGTCAGACGTGCAATCAGGTGC TGATCCAGATAATGTGCAGTCGATAGCTGGAAGTACGATGTTGCAATTCGCAAAAAC GAGGAAGCTATCTATAGAACGGTCGGACTTGAGGAACCGTAGCCTCCTTCAGAAGAGACA GTTCTTCCACTCTCATCGAGCTCAGCCCATGGCTCTAGAGCAAGTACTTTCTGACC GAGATAGTGAAGATGAAGTTGATGATGATGTGGCAGATTTTGAAGATAGACGGATGCTCG ACGATTTCTGTTGATGTGACCAAGGATGAGAAGCAGATGATGCACATGTGGAACCTCG TTTGTGAGGAAGCAGCGAGTATTAGCAGATGGTCACATTCCATGGGCATGTGAGGCGTT CTCAAGATTACATGGACCCGTCATGGTTTCAACACCCCATTTGATCTGGTGCTGGAG AATGTTTATGGTGAACTGTGGAACCATGGCCTTCTTGACGCCCCGACCATGAACAGC TGTAATACCTTTCTCGAACAGCTCCAAAGT
TRINITY_DN70231_c1_g3	ATGCTTGATTCTTGTCTTAGGTAGAGAAGAGACGAGCCTCGAAGCCTATAGGAAGCTTTT GCAAAGTGACAGAGGCGGAACCCGAAGTTGGAAGCTTTGGGTTTTGAGATTTTGT TTAATGAGAAGCGCTTGTACAGCTTCGCCAGTCTCGCCAAAGCCTGTGGAGAAGCC TCTCAAGAAGGTGCCTCTTGAACCTTTTATACCTCTCACAAAGGAGGAGGAGGCTGAAGTC TATCGAGCCTTTTCTGGCAAAAACAGAAGGAAAAGTCTTGGCTACTCATGCAAAATTCG AACATTGATATTACTGGAGAAGTTTTACAATGCCTTACACCATCTTCATGGCTCAACGACG AGGTTATCAATGTCTACCTGAACTACTCAAAGAGAGAGAACTAGAGAGCCCCAAAAGT ATTTGAAGTGTCATTTCTCAATACCTTT

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Supplemental Table 2. Continued.

Gene ID	Coding sequence
TRINITY_DN64502_c0_g2	ATGTTGTCATCAGCAAAGCATCAGAGAAACCATAGAGTCTCTGCAACAAACAAGAACAAGA TTCTCAACAAAGTTTCTTCCATTTTCATCCTCATCATCACCACCATCATCATCACCATCATCA TCCTCATCATCCTCATCCTCATCCTCATCCTCATCATCTCCTTTACACTCACAGGACTCCCA AGGCCAGAAGAGATCTCTAATCACCATGGAAGAAGTATGGAAAGACATCAACCTTGCTTC CATCCACCACCTTAACCGCCACAGCCAACATCCACAACACAACCATGAGCCAAGGTTTCAG GAGCCACAACCACCAGAACCAAAACCCCTAACTCCATCTTCCAAGATTTTCTTAACAGACCT TTGAACCAGGAACCAACAATACCCACAAGCCTCACCATGGGTCTTCCTCTAATGGCGATA CCACCACTGTCAGTCTCTCTTCAGCAGCTCTCCTTTGGCACCTCCTGCAACTGTTCTGA GCTTGAATTCGGTGCTGGCTTCGAGTTTCTCGATAACCAAGATCCTCTTGTCAACCCCTAA CTCTAATCTGCATAGCCACAATCACCTCCCAAACGTTTCTTCATTCAACACCCCTTTT GAGGCTCTCGTTACATCCACTTGTCTTGGTAAGAAAAGAGGCCAAGATTCCAATGAAGG TTCAGGGAATAGAAGACATAAGCGTATGATCAAGAACAGAGAATCTGCGGCTCGTTC CAGAGCTAGGAAACAGGAATGTGCCTCTCCTCTCCTGACCTTCTACTCGAAAAA GAAATGTGGTTTTGCCATCAAAATGCTTTTGATC
TRINITY_DN69998_c3_g1	ATGGCGAGAGAACATCCGAATGAAACGATCGGAAAACGGAAGAAGCGTGGCAGAGTTG AAGAAGAAGAAGAAGAAGAATACATGGGCGATGGAATCGGAAAGGAAGTAGAAGAAGA TGTAGGAGACGAGAAGCTTCCATTACAAGTTGGGATGTTCTATTACCCAATGACACCA CCTTCGTTTATCGTATCCGATGCTCTGGAGCCAGATTTTCTTTGATCTACGTAAACA GAGTCTTCGAGGTCTTCACTGGTTATCGAGCCGACCAAGTTCTTGGTCGGAAGTGTGCG ATTCTTACAGTACAGAGATCCTCGTGCTCAAAGGCGACACCCATTGGTAGATCCTGTG GTTGTGTCTGAGATTAGAAAATGTCTTGAGGAAGGTATCGAGTTTCAAGGAGAGCTTC TCAATTCAGAAAAGATGGTACTCCTTTGGTTAACAGACTACGGCTTGCTCCAATACG CGACGATGATGGAACCATACACACGTGATTGGGATACAGGTCTTCTCTGAGACGACT ATAGACCTTGACCGTGTCTCATATCCTGTCTTCAGGCAACAGTTTGACCAGACATCTC AAGACTTGGCTCCAAGCGGGAGCCCCGAGGTCCAGAGAGGATCATCAACATGTCTGTGG GATACTCCAGCTGTCTGATGAAGTCTTGGCCCATAAACATCTTATCCGGTTAACTTCA AGGGACGTTGCTTCCATTGGTTCTGCCTGCAGGAGGATGAGACAGCTCACGAAAAACG AAAGCGTGAGGAAGATGGTTTGTGAGAATGCGTGGGGAAAAGAGATAACCGGAACGTT GGAGATCATGACTAAGAAGCTAGGATGGGGTCGGTTAGCTAGAGAGCTCACTACCCTT GAAGCTGTGTGTTGGCGCAAATTCCTGTTGGAGGGATTGTACAACCTTCGCGATGCA ACTTCAGTGCGTGTGCTGTTGGGAACAGGCTTGTGCTATTTGGTGGGGAAGGGGTAA TATGCAGCCAATGGATGATACTTTTGTCTCAATCTTGATGCAGAGTTTCCCAAGTGG CAACGTGTGAAAGTGAAGTCATCTCCTCCAGGACGTTGGGGACACACTCTCTCGTGCC TCAACGGGTCTGTGGTTAGTAATATTTGGAGGGTGTGGAAGACAAGGATTGCTTAATGA CGTATTTGTACTTGATCTAGACGCTAAGCATCCGACGTGGAAGGAAGTAGCTGGAGGG ACTCCTCCATTGCCCTAGATCTTGGCACAGCTCTTGCACCATTTGAAGGCTCGAAGCTGG TCGTCTCAGGTGGCTGTACAGACGCTGGGGTGTCTCTCAGCGACACCTTTTTGTGGA TCTAACGACAGATAAAACCGACATGGAGAGAGATCCCGACATCATGGGCTCCTCCTTCT AGACTTGGCCACTCTCTATCCGTCTTGGTTCGGAATAAATCTTAAATGTTGGTGAC TTGCAATAGCGGCCATTTAAACTAAGGTCTGGAGAGGCATACACTATAGACTTGGA AGACGAGAAACCGAGATGGAGAGAGCTCGAGTGTAGCGGTTACAGGCGAGGTTGCA CCGCTGCAAGACTAGACCACGTGGCTGTGAGCATGCCCTGTGGTCGAGTAATCATCT TTGGTGGGTCTATCGCAGGGCTTCACTCACCTTCGAGCTGTTCTTATAGATCCTGC GGAAGAGAAACCATCATGGAGGATCCTGAATGTCCCGGGGAAACCGCCAAAGTTTGCT TGGGGACATAGCACTTGTGTTGTGCGAGGGACTCGAGTATTAGTTCTGGGTGGTCACA CCGGTGAGGAATGGATACTCAATGAGTTACATGAACTCTGCTTGGCTAGCCGCCAGGA CTCGGATATG
TRINITY_DN69832_c1_g1	ATGGGAAGGAGAAAGGTGGAGATCAAACGAATTGAGAACAAAAGCAATCGACAAGTCA CTTTTGTAAACGACGCAATGGTCTCATGGAGAAAGCTCGCCAACCTCTCTATTCTCTG CGACTCCTCCATCGCTATTCTCATAGTTTCATCCACCGGAAAACCTATACCTCCTCC TCCGGCGATAGCATGGCCAAGATCCTCAAGCGTTATGATATACACATGCTGATAAAC TTAAGAAAATGGGTCTTGCAGAAAAAATCGGATTATCTTTACACAAGGAGTTGCT AGAAATAGTCCAGTGCAAGCTTGAAGAAAGCGAAAAGTGATAACATAAGTGTGGAGTCC CTAACTGCCCTGGAAGAGCAGTTCAAGACTGCTGTGTCTGTGACTAGAGCTAGGAAGA ACGAATAATGATGGAGATAGTGAAGACCCTTCAAGAAAAGGAGAAGCTGTTGAGAGA AGAGAACCAGGTTTTGGGTAGCCAGCTTACAAAGATGGAGAAGAAAAGGTTTCTG

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Supplemental Table 2. Continued.

Gene ID	Coding sequence
TRINITY_DN67304_c0_g1	<p> ATGATGAATCCACCGGAGAAGAACGAAGATAATGTCCCTTCTGTATCTCACTTCAAT TTTCCACTCTTACTCCACAATCGAACTCGAATCCTAATCCAGACCCAAGTTGAATCA ATTCCCGAGCTCGATCTCCAGCTCAAGCCCTAGTTTTGAGCAGATGGTATCATTCTCC GCGCCAAAGAAACGAAGGAGAGGACGGTCTCAGCGCTCAGCGTCCTCGTTTCACATCC TTCCCGTCCCTAACGTCGGCGTCTTCCCGGTAACAGCAATTCGTGTCACCTTCAGC TTCTTCTCCGGTAGACCGAACGTAGAGGGCAATGGATCGAACCAGACTGTAAAAATT TATCCTGGGATAGGTGACGAGATCATCACGATCAACAAGGAAGCTACCACCGAAGCTT TGCTTGCGCTCACAGCTGGGTTCCCTGCTGATTCACTTACAGAGGAAGAGATTGAGTT CGGTGTGGTTCCTGTGGTTGGAGGAATCGAACAAGTGAATTACATATTGATTAGGAAC CACATCATATCGAAATGGAGAGAAAATGTATCTAGTTGGGTACAAAAGGACATGTTTC TCGATTTCGATTCTAAACACTGCACTAGTCTCTTGGATTTCGGCTTATCATTACTTGGT CATGCATGGATATATCAATTCGGTGTAGCACAGGCAATCAAAGACAAGATTCTGCT CAATCAAGCAAGCCTAGTGTGGTTATAGTTGGTGGTGGTTATCTGGTTTGGCTGCAG CGAGGCAGCTTCTGAGGTTTGGGTTTAAAGTCACGGTTTTGGAGGGTAGGAAACGACC CGGTGGACGGGTTTATACAAAAAAGATGGAAGGTAATAGAGTAGTCGCTGCAGCGGAT TTAGGAGGAAGTGTCTGACTGGAACGTTAGGAAACCCTCTGGGGATTATAGCCAAGC AGCTAGGTTGTTCTCTTTTAAAGTACGAGATAAGTGTCTCTTTATAGAGTGGATGG TAAACCGGTTGATCCCGATCTGGATATGAAGGTCGAGGCAGCTTTTAAACCGGCTTCTT GACAAGGCAAGTAACTTAGGCAGTCGATGGGTGATGTTTCCATGGATGTCTCCCTTG GGGCAGCGCTCGAGACATTCAGGCAGGTTTATGGGGACGCGGACGATGTGGCCACCGA GGAGATGAGTTTGTTAATTGGCATCTTGCTAACTTGAATATGCAAATGCGGGTTTA GTATCAAAGCTCTCTCTTGCATTCTGGGATCAGGATGACCCATACGATATGGGTGGAG ACCACTGCTTTCTGCCTGGAGGAAATGGAAGGCTGGTTCAGGCTTTGGCTGAAAAATGT ACCAATCTTATATGAGAAGACCGTTCAAACAATCAGATATGGTGCAGATGGTGTGAAG GTTACTGCTGGAAATCAAGTGTATGAGGGTGATATGGTGTGTGTACGGTTCCTTGTG GTGTTCTTAAGAACGGGTCCATCAAATTTTGGCCGGAGTTGCCTCAGAGAAAGCTTGA TTGTATAAAGAGACTAGGTTTTGGGTTATTGAACAAAGTTGCAATGCTCTTTCCGTAT GGATTTTGGGGCACAGATCTCGATACCTTTGGACATCTTACTGAGGATCCGAACATC GAGGTGAATTCTTTCTGTTCTATAGCTATGCACAAGTTGCAGGTGGTCTCTACTGAT CGCGTTGGTTGCGGGAGAAGCTGCTCATAAGTTTGAGACAATGCCACCCACTGACGCA GTGACTCGTGTTCTTCAGATTCTTAGGGGTATGTATGAACCACAAGGAATAAATGTCC CTGATCCAATTCAAACGGTCTGCACCAGATGGGGCGGGGATCCATTACGTTTCGGATC TACTCTAATGTTGCAGTGGGAGCTTCAGGTGATGATTACGACATATTAGCAGAAAAGT GTGGGAGATGGAAGGCTTTTCTTTGCCGGAGAAGCCACGACAAGGCGGTACCCTGCAA CCATGCATGGAGCTTTCGTAACCTGGTCTGCGAGAAGCTGCTAATATGGCTCATTCTGC AAAGGCCCCGAGGCATAAGGAAGAGAATCGATAGGAACCCCTTCAAAGAATCCCTATTCT TGTGCTACCCCTTCTTGCAGATTGTTCAGGGACCCTGATCTGGAGTTTGGGAGTTTTT CCATAATCTTTAGTCGAAGGAATCCGGACCCAAAGTCTCCTGCAATTATGAGGGTAAC GCTAAGCGAGCCTCTTAAGAGGAACGAAGACCCAATAGCAGATCAGCATCAAACAAG ATACTGTTTCAGCAGCTTCAGTCTCATTCAACCAGCAGCAACAGATTTCAGGTGTATA CGTTATTGACTAGACAACAGGCTCTTGACCTGAGAGAAGTCAGAGGTGGTGTGAGAA GAGACTTCACTACCTATGTGAGACACTGGAGTGAAGCTGGTGGGAAGAAAAGGTCTA GGAATTGGAGCTGATTCCGTATCGCTTCTATTAAAGCTGAGCGAACCGGTGCAAGC CAGCGTCATCATCTTCCGGCACAAAATCTGGTTGGGCTGTA </p>
TRINITY_DN40841_c0_g3	<p> ATGGCCGAAGCTGAGGAACAACAAAATTTTGTGCGACACAATGGAGATGAGGTGCATA ATGGTTTACAGTACCAGGTCCATGACGAGACCCCTTGCTACCAACCATACGAGGTTC AGACCCGATTCTTGAACCTCAGCAGTACGAGGTTCAAGATCCGACCCCTGAACCCAG CAGTACGGTGGTCAATTAGAGTACCAAGACTTCCAGGTGCAGGACCAGGCTAATGAAG AAGTCCACGATCAGCCGCAAGATGAACTACAATATCAACCTCAAGAGCAGGAGCAGTA TCAGTTGCACGACCAGGCTCATGGTCAGGCGCAGTATCAGGTTGAAGGCGAGGCACAG GATCAGGATGGTGATGAAGTGCAAGATCAAGTTGACGGTGAGGAAGAAATTCCTGAGC ATGTTGAGTCTCTACAGAAATCAGAGCTTGAAAGTGATATAAGTATAACAGGCGGAGG TGAGGAGAAGCGATGGCCGGGGTGGCCCGGAGAAACAGTGTTCCGTATGCTGGTTCTT GCACAGAAAAGTGGGTAGCATCATTGGTCGCAAAGGTGATGTATTAAAGAAAATAGTTG AGGAGACAAGGGCTCGGATAAAGATTCTTGATGGTCTCCAGGCACAACCGAAAGAGC TGTTATGGTTTCTGAAAAGAAGAGCCCAATCATCTCTGCCTCCTTCTATGGATGGC CTTCTGAGAGTCCACATGCGGATAGTTGATGGTCTAGATGGTGAAGCTTCTCAGGCCC </p>

Continued next page

Supplemental Table 2. Continued.

Gene ID	Coding sequence
TRINITY_DN40841_c0_g2	<p>CTCCGCCTACAAAGGTTTCAACAAGATTACTAGTCCCAGCATCTCAGGCTGGAAGTTT GATTGGAAAACAAGGAGCAACAGTTAAAGCCATTCAAGAAGCATCTGGCTGTATAGTT AGAGTCCTCGGATCAGAGGATTTGCCTGTTTTTGCTCTTCAAGACGATAGGGTTGTTG AAGTTGTGGGGGAGCCAACAAGTGTTCATAAAGCCTTGGAGCTAATTGCATCACATCT CAGAAAGTTCTTGGTTGACCGTAGCATCATCCCATACTTTGAAAATCAGATGCAAAAAG CCAACTCGCCAGATGGATCATATGCCGCCACCACACCAGGCCTGGGGTCCACCTCAAG GCCATGCCCCAACTGGTGGCTATGGTAGTGTCAACCCACCTCCATATATGCAACCACC ACCAAGACATGATAATTACTATCCTCCTCCTGAAATGCGTCCACCTACAATGGAGAAA CAGCCTCATCAAGGTATATCTGCATACGGAAGGGAGCCTCCTATGAATGTGCATGTAT CATCGGCCCCACCTATGTCCGCTCAGCAAGTTACGCAGCAAATGCAGATTCCACTGTC TTACGCAGATGCTGTGATTGGGACATCAGGTTCAAACATAAGCTACACTCGACGTCTT AGTGGAGCAACAGTAACCATTTCAGGAAACCAGAGGAGTACCTGGTGAAATGACTGTTG AGGTTAGCGGAAGTGGTTCACAAGTCCAGACCGCTATGCAGCTTATCCAGAAGTTAT GGCTGAAGCTGGAGCGCCGGCACCAGCACAGCCGCAAGCTGTAGCACCAGAGCAGCAA GGCTATAACCCCTATGCAACCCACGGGTACGTCTATGCAACGGCTCCGACGAACCCGC CTGGAGGATACGCTACGGATTACAGCTCAGGCTATGGTTAC</p> <p>ATGGCCGAAGCTGAGGAACAACAAAATTTTGTGCGACACAATGGAGATGAGGTGCATA ATGGTTTACAGTACCAGGTCCATGACGAGACCCTTGCTCACCAACCATACGAGGTTCA AGACCCGATTCTTGAACCTCAGCAGTACGAGGTTCAAGATCCGACCCTTGAACCCAG CAGTACGGTGGTCAATTAGAGTACCAAGACTTCCAGGTGCAGGACCAGGCTAATGAAG AAGTCCACGATCAGCCGCAAGATGAACTACAATATCAACCTCAAGAGCAGGAGCAGTA TCAGTTGCACGACCAGGCTCATGGTCAGGCGCAGTATCAGGTTGAAGGCGAGGCACAG GATCAGGATGGTGATGAAGTGCAAGATCAAGTTGACGGTGAGGAAGAAATTCCTGAGC ATGTTGAGTCTCTACAGAAATCAGAGCTTGAAAAGTGATATAAGTATAACAGGCGGAGG TGAGGAGAAGCGATGGCCGGGGTGGCCCGGAGAAACAGTGTTCCGTATGCTGGTTCCT GCACAGAAAGTGGGTAGCATCATTGGTCGCAAAGGTGATGTTCATTAAGAAAATAGTTG AGGAGACAAGGGCTCGGATAAAGATTCTTGATGGTCTCCAGGCACAACCGAAAGAGC TGTTATGGTTTCTGGAAAAGAAGAGCCGAATCATCTCTGCCTCCTTCTATGGATGGC CTTCTGAGAGTCCACATGCGGATAGTTGATGGTCTAGATGGTGAAGCTTCTCAGGCCC CTCCGCCTACAAAGGTTTCAACAAGATTACTAGTCCCAGCATCTCAGGCTGGAAGTTT GATTGGAAAACAAGGAGCAACAGTTAAAGCCATTCAAGAAGCATCTGGCTGTATAGTT AGAGTCCTCGGATCAGAGGATTTGCCTGTTTTTGCTCTTCAAGACGATAGGGTTGTTG AAGTTGTGGGGGAGCCAACAAGTGTTCATAAAGCCTTGGAGCTAATTGCATCACATCT CAGAAAGTTCTTGGTTGACCGTAGCATCATCCCATACTTTGAAAATCAGATGCAAAAAG CCAACTCGCCAGATGGATCATATGCCGCCACCACACCAGGCCTGGGGTCCACCTCAAG GCCATGCCCCAACTGGTGGCTATGGTAGTGTCAACCCACCTCCATATATGCAACCACC ACCAAGACATGATAATTACTATCCTCCTCCTGAAATGCGTCCACCTACAATGGAGAAA CAGCCTCATCAAGGTATATCTGCATACGGAAGGGAGCCTCCTATGAATGTGCATGTAT CATCGGCCCCACCTATGTCCGCTCAGCAAGTTACGCAGCAAATGCAGATTCCACTGTC TTACGCAGATGCTGTGATTGGGACATCAGGTTCAAACATAAGCTACACTCGACGTCTT AGTGGAGCAACAGTAACCATTTCAGGAAACCAGAGGAGTACCTGGTGAAATGACTGTTG AGGTTAGCGGAAGTGGTTCACAAGTCCAGACCGCTATGCAGCTTATCCAGAAGTTTAT GGCTGAAGCTGGAGCGCCGGCACCAGCACAGCCGCAAGCTGTAGCACCAGAGCAGCAA GGCTATAACCCCTATGCAACCCACGGGTACGTCTATGCAACGGCTCCGACGAACCCGC CTGGAGGATACGCTACGGATTACAGCTCAGGCTATGGTTAC</p>
TRINITY_DN40841_c0_g1	<p>ATGGCCGAAGCTGAGGAACAACAAAATTTTGTGCGACACAATGGAGATGAGGTGCATA ATGGTTTACAGTACCAGGTCCATGACGAGACCCTTGCTCACCAACCATACGAGGTTCA AGACCCGATTCTTGAACCTCAGCAGTACGAGGTTCAAGATCCGACCCTTGAACCCAG CAGTACGGTGGTCAATTAGAGTACCAAGACTTCCAGGTGCAGGACCAGGCTAATGAAG AAGTCCACGATCAGCCGCAAGATGAACTACAATATCAACCTCAAGAGCAGGAGCAGTA TCAGTTGCACGACCAGGCTCATGGTCAGGCGCAGTATCAGGTTGAAGGCGAGGCACAG GATCAGGATGGTGATGAAGTGCAAGATCAAGTTGACGGTGAGGAAGAAATTCCTGAGC ATGTTGAGTCTCTACAGAAATCAGAGCTTGAAAAGTGATATAAGTATAACAGGCGGAGG TGAGGAGAAGCGATGGCCGGGGTGGCCCGGAGAAACAGTGTTCCGTATGCTGGTTCCT GCACAGAAAGTGGGTAGCATCATTGGTCGCAAAGGTGATGTTCATTAAGAAAATAGTTG AGGAGACAAGGGCTCGGATAAAGATTCTTGATGGTCTCCAGGCACAACCGAAAGAGC TGTTATGGTTTCTGGAAAAGAAGAGCCGAATCATCTCTGCCTCCTTCTATGGATGGC</p>

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Supplemental Table 2. Continued.

Gene ID	Coding sequence
TRINITY_DN70605_c0_g2	<p> CTTCTGAGAGTCCACATGCGGATAGTTGATGGTCTAGATGGTGAAGCTTCTCAGGCCC CTCCGCCTACAAAGGTTTCAACAAGATTACTAGTCCCAGCATCTCAGGCTGGAAGTTT GATTGGAAAACAAGGAGCAACAGTTAAAGCCATTCAAGAAGCATCTGGCTGTATAGTT AGAGTCTCTGGATCAGAGGATTTGCCTGTTTTTGTCTTCAAGACGATAGGGTTGTTG AAGTTGTGGGGGAGCCAACAAGTGTTCATAAAGCCTTGGAGCTAATTGCATCACATCT CAGAAAGTTCTTGGTTGACCGTAGCATCATCCCATACTTTGAAAATCAGATGCAAAAG CCAACTCGCCAGATGGATCATATGCCGCCACCACACCAGGCCTGGGGTCCACCTCAAG GCCATGCCCCAACTGGTGGCTATGGTAGTGTCAACCCACCTCCATATATGCAACCACC ACCAAGACATGATAATTACTATCCTCCTCCTGAAATGCGTCCACCTACAATGGAGAAA CAGCCTCATCAAGGTATATCTGCATACGGAAGGGAGCCTCCTATGAATGTGCATGTAT CATCGGCCCCACCTATGTCCGCTCAGCAAGTTACGCAGCAAATGCAGATTCCACTGTC TTACGCAGATGCTGTGATTGGGACATCAGGTTCAAACATAAGCTTACACTCGACGTCTT AGTGGAGCAACAGTAACCATTACAGGAAACCAGAGGAGTACCTGGTGAAATGACTGTTG AGGTTAGCGGAACTGGTTCACAAGTCCAGACCGCTATGCAGCTTATCCAGAACTTTAT GGCTGAAGCTGGAGCGCCGGCACCAGCACAGCCGCAAGCTGTAGCACCAGAGCAGCAA GGCTATAACCCCTATGCAACCCACGGGTCACTGTATGCAACGGCTCCGACGAACCCGC CTGGAGGATACGCTACGGATTACAGCTCAGGCTATGGTTAC </p> <p> ATGGCGTCAGTTACGAAGCCGTTTCAGAGCACGTGAATCCGAAGATGCCGGTTTCACAT CGAACAATCTATGGGTGGGTAGCCTGACGATGGATACGACGGAGTCAGATCTGACGGA GTTGTTTGAAGGTTTCGGCGATATCGACAGAATCACGGCGTACTCGTCCCGTGGCTTC GCCTTCATCTACTACAGACACGTCGAGGAAGCTGTGCGGGCGATGGAGGCCCTCCAAG GGGCGAATTTGAACGGAAGTCAGATTAAGATCGAATACGCGCGACCGGCAAAACCTTG TAAGAGTCTCTGGGTGGGCGGAATCAGCCCGAGTGTTTCAAAGGATGACCTGGAGGCA GAATTCAGTAAATTTGGAAGAATCGTGGATTTTAGGTTTCTTAGGGAACGCAAGACAG CTTTCATTGATTATTACGAAATGGAAGATGCCGTACAGGCAAGAAGCATGAGTGGCAA GCGAATGGGTGGTAGCTATTTGCGCGTTGATTTTCTCCGGTCAACAAGCGCCAGAAAA GAACAATGGGGTGGCTCTTACGATAACAGGAATGGCAATGTGAATCATAAACCGCAGT ATCCTCACTCGCATGAAGATGCCAAAGGAGATGACCAGCCAAGTAAGGTTCTGTGGAT TGGGTACCCTCCTTCTGTTCAGATAGATGAGCAGATGCTACACAATGCAATGATACTC TTTGGTGAGATCGAGAGGAAAAAAGTTACCCGTCAAGGCATTTTCACTTGTGGAGT TTAGGAGCGTGGAAGAAGCTCGCCAAGCCAAGGAAGGGCTACAGGGGAGGTTATTCAA AGATCCTAGAAATCACAATTATGTACTCAAACGATGAGATACCTCCTGAGCAAGATGAT ACTAGTTTTTATTCTGGCGTGAAACGGTCAAGGCCAGATATGTTTCATCAATGATCCTA CTGGGTCTGTGAGGCCCTTCAGAGGTAGCAATGAGCGTCCTTATAATGGTTCAGAATA CAGTGACGTTGCTGGTAAGGAGCCAAACTGGAGGAGGCCGTCTCAAATGGAAGTGGGA ATACTCCCATCTCCAACGGGACATGGAATTCTCCCATCTCCTGCACAAGGTATGAGGA ACCTATGAGGTCAAACCCCGGTTTCATGGGAAGGATATGATCCTGCTCAGTTGGGATAG AGAAAGCAAACGAACCAGAAGAGATGGATCGGTTGACGGTTTTACTCCAATGGGTGTG GATGAGAGGTCAATTTGGGCGTGTTTCAGTTGCTGCTAGGCCATACCTGGTTACCCTG ATTCTGACTACATGTGGAGAGGAATGATTGCCAAGGGTGGAACCTCCCGTCTGTTGTGC TCGTTGTGTACCTATTGGAAGGGGATCGAAACTAAGCTCCCCGAGGTCGTCAATTGT TCAGCAAGAAGTGGTCTGGATATGCTCGCCAAACATTACACCGAAGCCATTGGATTTG AGATAGTTTTCTTCTTACCAGACAGTGAAGAGGATTTTGCCTTACACTGAATTTCT CCGCTACCTTGGCTCGAAAAATCGAGCTGGTGTTGCTAAATTAGATGATGGAACAACT TTATTCTTGGTACCTCCTTCAGATTTTTTAACTGACATACTCAAAGTGTCGGTCCAG AACGGCTATATGGTGTTGTTCTCAAGTTGCCTCCGCCAGCCGTTCTGTGCGAGCAAC ATACAGACAAGAATCTCAATCCAATCCTCTGCCTTATATGGATCAAGCGCGGGATTCA CTGCCAATGCCGGTCACAGTTTATATCCTCCTCGGGAATAATTACAATAGGGGTGCAC TAGAACAGTTGACAGCTCCTTCAAGACCATCGGTTAGCGAGCCACTCAGAATACCTAA CAATGCAGCGGCGTCTCAAGCTGGGGTTAGTTTAACTCCGGAGCTTTTAGCCACCCTG GCATCTATTCTCCCTGCAACTTCTCAATCTGCTGCTCCCGAGAGTACCAACCTGTGT CAGGTACTTCAACAGTCGTTTCCACAGTACCTCAGTACAATGGAGAAGCAGCAGCCTCA AGCTTGGAATAGAGATCCGCAACAGTGCATGATGCCTCAAATCAGTCTTTCCAACAA TATGGAATCAGTACAATCCAGCCGGGCAACTACCTCCTCCTGCGCGTTATCCTC CAGCTTCAAACAGCCCTAACCCCACTACTCTAGTGGAATCGTCCGTGGCAACATGCA GTATCAAGGCCAAGGACAATCTGTTAACATGCCTCAGATGTCTCCGTTACCGAATATG CCTCAAATAATTATGCCATGTACACTCAGGGTTCGTTAAATCATCCTGTTTCTCAGC </p>

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Supplemental Table 2. Continued.

Gene ID	Coding sequence
TRINITY_DN60601_c0_g2	CCATGACGCAGCAATACCAACCAGAAGCTTCCGTACCAAACCAAATTATGGTGCCGT TCCAAGTTACCAGCAAGGTAAGTATTATGGTTTAAACAACAAATCAGGCGCATAATATA AATCCTTCCCAATTTCAAGCTGCCATGCAACCACCAGCTGACAAGGCAAACCTTAGAGC CACAAAGCCAAGCAGCACAGCCTATGCTCTCTGGGGCTGGTCAGGGTACAACAAATGG GGAGGTCGAGAAGGACGAGAGATATCAGAAAACACTACAGTTTGAGCAAGCCTTCTT CTCCAGATAAAGCAGAATCAGCAGCAGCCGCTTCAGGTACTCCGGCTGGACAGGGGCTT ATGTCAGGAGTTTGGGTGTTCAACAACGGAGTGATACGTCTAGTAGAAAACCCAAACC AGTCCGGTGGAGCGACCACTCAGACGCACGGCCGGAGGAATGTCTTGGTTTACTTGCC TACGGGTGAAGTAGTCTCTTCTTACTCGTCACTGGAACAGATCCTAAGGAGTCTTGGG TGGGAAAGATACTTCAATGGAGACTCCGATCTCATCAATACCACAAACGTTCCCTCTA TCGACCTCATCTCCTTACCAAGAGACTTCTCCAAGTTCAACTCTGTTTACATGTACGA CATCGTCGTCAAGAACCCTAATTCCTTCCACGTCCGTGATTTCAT
TRINITY_DN47820_c0_g1	ATGTCAGGCGTGTGGGTGTTCAAGAACGGAGTGATAAGGCTTGTGGAGAAATCCTAACC AGTCAGGAGGCGACACACACAGCCGAAGGAAAGTGATGGTCTATTTACCGACAGGAGA AGTGATCTCATCTTACTCGACGCTCGAGCAGATCCTTCGCAGTCTTGGGTGGGAGAGG TACTTCGGTGGCGGCGACACAGATCTCCTCAATTCCACAAACGCTCATCCATTGATC TCATCTCTCTCCCTAAAGATTTACCAAATTCAGTCCGTTTACATGTACGATATCGT CGTCAAGAACCCTAATTACTTCCACGTCCGGGACTCCAAT
TRINITY_DN67831_c2_g1	ATGTCGTCCGAGTTGAAACAGCTAATCGTCGTTGCTGAAGGCACTGCAGCGTTGGGTC CTTATTGGCAAACCATCGTCTCCGACTATCTCGAGAAAATCATCAGGTCTTTCTGTGG CAGTGAGGTAAACGGAGAGAGGAACCTGTTTCTAATGTTGAGCTATCACTGGTCATC TTCAATTCTCATGGTTCATATTGTGCTTGCTTGGTACAAAGGAGTGGCTGGACAAAAG ATGTCGATATTTTCTTGCAATTGGCTTTCGTCCATACAATTTGCCGGTGGTGGTTTTAA TGAGGCTGCCACAGCTGAAGGGCTTGCCGAAGCATTGATGATGTTTCTCCTCCTTCA GGCCAAGCACAGCCAAGCAATGATCTGAAAAGGCACTGTATCCTAATCACAGCCAGCA ATCCTCACTCGTTGCCAACACCTGTATATCGTCCAAAAGTGCAAAATGCGGAACGGAA TGAAAATGGTGATGCGCATTCTGAAAGTCGTTTATCAGATGCCGAAAACGTGGCATCA TATTTTCTAGGTGCTCTGTTTCATTGTCTGTTGTGTGTCGAAAGCAGCTTCCGAAGA TAAGAGCACTATACAATGCGGGAAAGCTCAATCCACAAAGTGCGGACTTGTGATTGA CACGGTTAAGAACGCATTCTATCTTGCTCAATCTCGGAGAATTTGTGGAGGCACGT GCTGCCTTGAGTCATTCTGCTACAAATTTGCCACAGACCACCCAAAGCCCTGTGAAAG TGGACAGGGCCACTGTTGCTCCATCTCTTCCAGTCACTGGGCAACCTCCAGTCTCTGT GCCATCAGCTAATGGACCTATTCTTAATCGGCAACCAGTTTCTGTTGGACCAGTTCCA ACTGCTACTGTGAAAGTTGAGCCTAGCACTGTACCATCTATGGCAGCAGTTCCAACTT TTCCCCATATCCCCTCCGTAGCTCGGCTGCTACACAAGCAAATCCTTCTATTCAAAC ATCTACAGCATCTCCAATTTCTCAAGAAATGGTCACCAATGCCGAGAATGCACCAGAT ATTAAGCCTGTGGTTCGGTGAATGACGCCACCATTGCGTACTGGTCTCTGCTGGTGGAG CTAACGTGAATCTGCTGAACAATCTTCTCAAGTTTCGACAAGTCATGAGTCTGCAGC TCTGGCGGGTGCAGCCTCGTCGGTGGGCAAAAGTGCGGTTGCAATGCATGTCAAAT ATGATATCAACAGGAATGGCTACATCTCTGCCTCCTTCACAAACTGTGTTTTCATCTG GACAGCAGGGAATTACTTCAATGGTTGGTTTCGGGTGCATTAATGGGAATGCACAAGC GGGACAAAGCCCAGGTCTTAATAATTCCTTTAGTCCTCAACAACGTCAAATGTTGCT TCAAACCTTGGTGTCTTCAACCAATGCAAGGGGTGAACCAAGGAAGTCATTCTGGAG CACAGATGATGCAATCCATGAACCAAAACATGATGAGTGGTCTCGGCCAAGGAAATGT CTCCTCTGGAACAGGTGGAATGATGCCTACTCCAGGAGTTGGCCAACAAGCGCAGCCA GGAATACAACAACTCGGTGGCAGTAACAGTTCAGTCTCTAATATGCAGTTGTACAGC CATCATCGGGGGCTATGCAGACTCCTCAATCCAAATATGTTAAAGTCTGGGAGGGAAA CTTATCTGGGCAAAGACAAGGGCAGCCTGTTCTTATCACCAGACTTGAGGGTTACCGA AGCGCTTCTGCCTCTGATTTCGTTGGCAGCCAATTGGCCACCGACTATGCAGATCGTTC GTCTCATATCCCAGGATCATATGAATAACAAGCAATATGTTGGCAAAGCTGACTTCCT TGTTTTTCGGGCCATGAGCCAACATGGGTTTTTGGGACAACCTCAGGATAAAGAAGCTT TGTGCAGTCATCCAGCTGCCATCAGACGCTGCTTCTCTCCGTCTCTGACAAGGCTT GCCGCTTGATTGGAATGCTTTTCCAGGGGATATGGTTGTGTTAAGCCGCAAATTCC GAATCAGCAACAACAACAGCAACAACAGCTGCAGCAGCACCAACAACAGCAGCAGCAG CAGCAACAGCAACAGATCCAGCAGCAGCAGCAGCAACAACAACACCACCACCAACAGC AACAGCTGCCACAACCTCCAGCAGCAGCAGCAGCATCAAATGTCACAGCTCCAACATCA TCAGCAGCAACAGCAACAGCAGCATCAGTTGTACAGCTCCAACATCATCACCAGCAG

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Supplemental Table 2. Continued.

Gene ID	Coding sequence
TRINITY_DN67682_c0_g1	<p> CAGCAGCAGACGTACCCGCTGAATCAGATGCAGCAACAGACTTCGCCACTGAATCAGA TGCAGCAGCAGCAGCAGCAGCCTCAACAGCTAGTTGGGTGAGGAGTGATGGGTGGTCA AACTTTTGCACAAGCTCCTGGAAGATCTCAACCAGGCGGCGGTGGGCAGCCTACCATG CCGGGAGCTGGCTTCATGGGA ATGGCTACTACTTCATCTGAGAGGTGGACCGATGGTCTTCAGTTCTCCTCCTTGTTAT GGCCTCCGCCACGAGACCCTCAACAACATAAAGGATCAAGTCGTTGCTTACGTCGAGTA CTTTGGTCAATTCACATCAGAGCAATTCCTTGATGACATTGCTGAGTTGGTCCGCCAT CAGTATCCATCAACCGAGAAGCGCCTTTTGGATGATGTTCTGGCAATGTTTGTCTTC ATCATCCGGAGCATGGTCATGCGGTTATCCTTCCAATTATTCATGTCTCATTGATGG CTCTCTGGTGTACAGCAAGGACGCTCATCCCTTTGCCTCTTTCATATCGTTAGTTTGC CCAAGTAGTGAGAATGACTATTCGGAGCAATGGGCTTTGGCGTGCGGAGAAATCCTCC GCATTTTGAATCATTACAATCGTCCCATATAAAGACCGAGCACCACCAATGGAGAAAC AGAGAGAAATTGCCTGAGCAAAGCTTCGACTAGTGGGTCTACGCTTTCAGAGCCTAAG GTTGTATCACCGGTACAGCATGAAAGAAAACCGTTAAGGCCTTTGTCTCCATGGATCA GTGATATACTACTTGCTGCGCCCTTGGGTATAAGAAGTGACTACTTTCGTTGGTGTAG TGGGGTTATGGGTAAATATGCTGCTGGAGAGCTCAAGCCGCCAACCATGCTTCTCGA GGATCTGGTAAACATCCTCAATTGATGCCTTCAACACCAAGATGGGCGGTTGCTAATG GAGCTGGTGTCTACTGAGTGTTCGATGATGAAGTTGCTCGATATGAGACTGCTAC GCTAACAGCGGTTGCTGTCCCTGCACTTCTTCTCTCTCCCCCACGACATCCTTAGAT GAGCATTTAGTTGCTGGCCTTCCAGCTCTTGAGCCATACGCACGTTTGTTTCATAGAT ATTATGCCATTGCAACTCCAAGTGCTACTCAGAGACTTCTTCTTGGACTTTTAGAAGC CCCGCCGTCGTGGGCTCCAGATGCACTTGATGCTGCTGTACAGCTTGTTGGAACCTCTT CGAGCTGCTGAAGATTATGCATCTGGTGTAAGGCTACCCAGGAAGTGGATGCATTGCT ACTTCTTGGTGCAATAGGAATTGCTATGTCTATGAGGGCAGGTGTTGCTGCTGATGC TGCAGCCGCTTTGCTTTTCCGCATACTCTCACAGCCGCACTGCTTTTCTCTCCGCTA AGCCAAGTTGAGGGAGTAGAAATTCACACGCGCCTATTGGTGGCTACAGTTCAAATT ACAGAAAGCAGATAGAAGTTCCTGCAGCAGAAGCAACCATTGAAGCCACTGCTCAAGG AATTGCCTCAATGCTTTGTGCGCATGGTCTGAAGTCGAGTGAGAAATTTGCACTATA TGGGAAGCTGCCTATGGATTGATTCTTTAAATTCCTCAGCGGTTGATCTCCCCGAAA TCATTGTCGCTACCCCACTGCAACTTCCTATCTTGTCTATGGAATCTATACATTCCACT CCTGAAAGTACTTGAATATCTTCCACGGGGGAGTCTTCCGGAAGCATGCTTGATGAAA ATATTTGTCGCCACCGTGGAACAATCCTCAGTAGAAGCTTTCCGCCAGAAATTTCCG GGGAACATATCAGGAAAGCCAGATCGAGTTTACC GCGAGATCAGCGACCAAAAAACCT TGCTATGGCTGAGCTTCGTGCTATGGTCCATGCTCTCTTTTAGAATCATGCGCTGGT GTTGAGATAGCGTCACGCCTACTTTTGTGTTTGTGACTGTATGTGTTAGCCATGAAG CACAGTCTAGTGGGAGCAAGAGACCGAGAAGCGAATATGCTAGTACTGCAGAGGAGAA TCAATCTGTATCTGACAATCAAAGTAGTAACCGTAAAAGTAGGAATGTCAAGGGACAG GGACCTGTGGCAGCATTTGATTACATCGTTCTCGCTGCTGTTGCTGCTCTTGTG AGGTTTCAGCTGTATCCTATGATCTCTGGAGGGGAAACTTTTCCAATACGAGTTGC TGCGACGATTCCGAAGTCTGTAAAAATAAATGGGTCTACTAACGAGTATGGAGCTGGG ATTGATTCGGCAATTAATCATACACGCCGAATCTTGGCAATTCTAGAGGCACTCTTTT CACTGAAACCGTCTTCTGTGGGGACTCCATGGAGCTACAGTTCTAACGAGATAGTTGC TGCGGCCATGGTTGCAGCTCATATCTCCGAATTGTTTAGACGTTCAAAGGCTTTGACG CATGCGTTGTCTGGGTTGATGAGATGTAAGTGGGACAAGGAAATTCACAAAAGAGCAT CGTCTTGTATAACCTCATAGATGTTTCATAGCAAAGTCGTAGCATCAATTGTCGACAA AGCTGAACCTTGGAAGCATATCTTAAGAATGCACCGGTCCAGAAGGATTCTCTGACA TGTCTTAACTGGAAACAGAACACGTGTGCAAGCAGCGCAGGCTTTGGTACAGCAGTGA CGTCCACGTACGTAGTGAAATGACTCCAAGAGGCAACCATAAGTATGCTAGACATTC AGATGAAGGCTCAGGGACTAGACCTCAGAGAAGGGTATCAAAGATTTCTCTTGGAT GCTTCTGATCTAGCGAATTTCTCAGAGCTGATAGGCTCGCGGGGTTTATTGTGGTA CACAAGTTCTTTGAGGTCAGTACTGCAAAGAAACCGGAGCTTTCTTTCTCCGTTGT TTCAGTTATGGCACAACCTGATCTGCTCCGGAATCCAGCCACAGCGGAAAGC ACCTCTGCTCAACAAGGATGGAGACAGGTAGTTGATGCACTATGCAACGTCGTATCTG CAACGCCAGCAAAAGCAGCTGCAGCAGTTGTTCTTCAAGGCTGAGAGAGAGTTGCAGCC TTGGATCGCCAAAGATGATGAAGAAGTGCAGAAAATGTGGAATAAACAACGGATA GTGAAAGTGATGGTGGAGCTGATGCGAGATCATGAGAGGCCAGAGTCACTGGTGATTT TGGCAAGTGATCGGATCTTCTTCTGAGGGCAACTGATGGAATGCTTGTTGATGGAGA </p>

Continued next page

Supplemental Table 2. Continued.

Gene ID	Coding sequence
	AGCTTGACATTACCTCAACTTGAGCTACTTGAAGCCACGGCAAGGGCAATACAGCCG GTGCTAGCTTGGGGGACATCTGGACTAGCAGTGTTGACGGTTTATCCAATCTATTGA AGTGTCTGTCTACCGGCAACAATACGGTGCCTTTCACACCCAAGTGACACGTACGTGC CTTGAGCACTTCAGTACTACGCGACATCATGAACCAAAGCTCCATAACCATCAAGGTA ACTCCAAAACCGCCGCCAACACAGAGAAGAACGGGATGCACAGCCCGTCTATCGGT TCTTCAACGCGGCCACCATAGACTGGAAAGCAGACATCCAGAAATGTTTGAAGTGGGA AGCTCACAGCTTGCTCTCAACGACCATGCCTACTCAGTTTCTTGACACCGCGGCTCGA GAACTAGGCTGTACCATATCGTTGTCGTCCCAA
TRINITY_DN84722_c0_g1	ATGTCACGAACAGAAAATTCGTGTAAAATGTTTATGGCTTGTCTTGTCTCAAAGGTTA TACTTTTATGCTCTAGTATATTGAATGGTCGGTCTTGTGTTATTAACAGGCTGAGAGA GAGTTGCAGCCTTGGATCGCCAAAGATGATGAAGAAGGTCAGAAAATGTGGAAAATCA ACCAAC
TRINITY_DN69595_c0_g1	ATGGCTCTGGGCGTAAAGAGGAGCGAGCAAGGCCAAGGACAAGGGGCAGTTGATTC TCGGTGATCTCGTTCTTGCCAAAGTCAAAGGCTTCCCTGCTTGGCCTGCTAAGATAAG CCGGCCTGAAGAGTGGGATCGTGCTCCAGACCCGAAGAAGTACTTTGTTTCAGTTCTTT GGAACACAGGAAATAGCTTTTGTGACCCGCTGATATCCAAGCCTTCACTAGTGAGG CAAAGAGCAAATATTAGCAAGATGTCAAGGTAAAACAGTAAAGTATTTTGCACAAGC TGTAACGGAAATATGCACCGCATTTGAAGAGTTGCAAAACCACAAGTCTAATGTTTTG GGCAATGGGGATCCTCCCGATGCTACGGAGCCTGGGTTGACAAAGGCTAAGATAGTAG ATGGAATAGATCATATAGTCACTGATTCTGATGGAAGTGAACGGTGATTCTAGGGC GGATCCTTGCGTCCCCAAATTAGAAAAGAATAGTGGTGAAGAGACAGAGGCTGAGACA GGGAAGCAGGAATCATCTCCGTTTCGGGAGTCAAAGATCACAACCACATCCTCGGGTA GCGAGTCATTGGAGCATGGTTCATATGACTCTAAAATAAAGGAAGAAGATATTGATAA AGGAACCGACGCGATGATTGCATTGATGGTCAAAGAATCTGGCCAACGGTAAGGGA ATAAAGAAGGTAGCAGGTGGCTCGGACAAAAAAGGTGATACAGTTTCATATAGAAAAAA GCAGTAACTCACATGTGCATGATGGTCGAGCTGCTAGTGGAATCTGATTCCAAGAA GTCAAAAGGTTTGTGACAGAGAAATCTAGTTCCAAAAGTGTCTGGAGGTAAGCGTGAA AGTTTCGCTGGCGTTAAGGGTGGTCTTTCCGGCAAGAAAAAGGAGGCTTGAAAGTGAAC TAGGGAAGCATGCACCAAGAGTAGAAAAAGCTCACCTGCTTCTAAAAAGCGGCGATG TGATGGTAAAACAGACAAAGGAAAGTGTGAGATTGATGATGAATCTGATTGTACTGAG GCTGTGTCAGATATTAAGCGTGAAATTGTTTTAGGAGTAAGTGCTCGTGAGGAAATT TACAATATGATAAAGAAGTAGTTGCATATACAAAGCGCCGACAGCAAGCAGTTGAGCA TGATACCTCTCCTCTTTTCTGGGTCTCGGGATAAATCCGGGAAAGGTCAACTAGAA CAGAAAAACCGTTCATCTTCTATTAGTGATAAATCCGGG
TRINITY_DN69302_c0_g3	ATGTGTTTCCTGGTAGATTCATCCGCAGAAGTTAGCAACAGTTTTGGGCCCTGCGACGATTT TAGCCTCCTGCCGTTCTCTGACCTTCCATTTGAGAGACTAAGAATATCTTCTCTGTT TCAGAAGCAATTGACTCTGCGAATCAACTGCGAAATGTTACGATTTTGTTCCTTCA
TRINITY_DN69302_c0_g1	ATGAAGAAACAAAATCGTAACATTCGCAAGTTGATTTCGACAGTCAATTGCTTCTGA AACAGAGTATTGCTGAAATCATGGGTGATAGTAGCAATCCTGAAGATATTCTTAGTCT CTCAAATGGAAGGTGAGAGAACGGCAGGAGGCTTAAATCGTCGAGGGCCCCAAAACCTG TTGCTAACTTCTGCGGATGATTCCACCAGGAAACACATGCTTGGTTCAACTCCATCAT ATAATAAAGAACGCAGGAAAGTTCAGATGGTGGAGCAACCAGGCCAAAAAGCTGCTGG AAGAAGCCCTCAGACAGTTAGAATAGGAAGTTCAGTTCGAAGCCGCCCTATGTCTGCT GATGATATTCAGAAAGCGAAGATGCGTGCTCTGTATATGCATAGCAAGAATAGTAGAA AGGATCCCTTATCAAGTGCGATTAGTGATTGAGAACCATATTCTGAGAAGCCCTT GGCTCTTCTGTGACCAAGGATTCTCCACCTAGTGAGAACAATGAAGCTAAGACTGAA GATACACCTGAACCTTCTGCTGTACAGCCTGTCAATTCACCGCCTGTAAATCTCCCGG TTCAGCCTGTCAATTCACCGGTTGTAGATGTCCCGGTTACAGCCTGTGCTTCTCCGGC TGTAATGTGCCGGTACAAGCTGATGAATTTAGAAAACCTTCAACACCTCCTAAAAGC ATTTCTAGTAAGGTGGGAATCTTGTTGAAAATGAGCCACAACTATTCTAAAGAATT GCAAGAAAAAACAGACTGATTGGCATGTACCACCAGAAATGAGACTTGACGACCTCTG GAGAGTAGCTGCTGGTGGTAATAGCAAGGAGGCAGATGTTTCAGAAAAACCGAAACCGG AGAGAAAAAGAAACAACATATCAATCTCTTCAAACCTATACCGTTGAATCCTAAGGAAC CATGGGACAGGGAAGTGGACTTTGATGACAGTTTGACACCTGAAATCCCGTCTCAGCA GCCACCAGAAGAAAGTATAGCAGAACCAGAGGAATCACTTGATGATCGGCGAACTGCT GCTGGTGCTGCCACAACCTCTTCATCTCAAAGTAGTACCATGGAACCTGATTTTGAGT TATTAGCCGCCTTACTTAAGAACCCGGATCTTCTATATGCGCTGACTTCTGGTAATCC

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Supplemental Table 2. Continued.

Gene ID	Coding sequence
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TRINITY_DN69302_c0_g2	ATGTGTTTCTGTTAGATTTCATCCGCAGAAGTTAGCAACAGTTTTGGGCCCTGCGACG ATTTTAGCCTCTGCGGTTCTCTGACCTTCCATTTGAGAGACTAAGAATATCTTCTCTG TTACAACACGAAAAAAGGTTTAATAGAACTGATGTGGAGCACC
TRINITY_DN68323_c1_g1	ATGGATACAAATACATCTGGAGGAGAAGAACTATTAATAAGGCAAGAAAGCCATATA CGATTACAAAGCAGCGGGAACGATGGACAGAGGATGAGCATGATAGGTTTCTAGAAGC CCTGAGGCTTTATGGAAGAGCTTGGCAACGTATTGAAGAACATATTGGGACAAAGACT GCTGTTTCAGATCAGAAGTCATGCTCAAAAGTTCTTCACAAAGTTGGAGAAAAGAAGCTG AAGCTAAAGGCATTCTGTTTGTCAAGCTCTGGACATCGAAATTCCACCTCCTCGTCC CAAAAGAAAACCAATACTCCTTATCCTCGGAAGCCTGGCAATAACGGTCAATCGTCC TCACAAGTATCATCAGCAAAAGATGCAAACTTGTATCGTCGGCCTCTTCTTACAAT GTAACCAGGCGTTCTTGAATCTGGAGGAAGTGCCGATTTCTGAGAAAACATCAACTGG GAAAGAGAATCAAGATGATAACTGCTCAGGGGTTTCCACTGTGAACAAGTATCCCTTA CCAAAAAAGTAACCTCCAGGGAACCGAAAGACGTTTCATGGAATCTGACCCGTCTCTAA GAAAGGCAAGTGCTGATAATGAAACAAGTAAGGACTCAAATGTAGACAACATGGTTCA AGATGTTCCCGAGAAGAGCAAAAGACAGAGATGGTGACGGCATGCACAGCGCAAGGAAC TACCCTTGGCATTTCCCGGCGGATTTTGTAAACGGAAATATGGCAAAATGCTCTCAAT TCCATCCCCCAGGTATGGTATCTCAAGACTTCATGTTTTGTCTATGGGAGATCGAGT TCACGGGCACTCTAGTTCGCACGTGAATCTTCCAGCTACAACAACATCATCTGCGACT ACTACTACAGCTTCTCAGCAAGCGTTTCCAGCGTGCCATTCCCAGGATGATTTCCGTT CGTATCTCCAGATCTCTTCTACTTTCTCCAATCTTATTATGTCAACTCTCCTACAGAA TCCTGCAGCTCATGCTGCAGCCACATTCGCTGCTTCTGTCTGGCCTTATACGAATGTC GGTAATTCGGGAGATTTCATCAACGCAAAATGAACTCTTCTCCTCCAAGTATAGCTGCCA TCGCTGCTGCTACAGTAGCTGCTGCAACTGCTTGGTGGGCTTCTCATGGACTTCTTCC TGTATGTGCTCCTACTCCAGTCGCATGCCTTCCATTACCAACCGTTGCAGTTCCAAT CCAGCGATGGATAAGATGGATACCGTTGAAAATGATCAACTACCGCTTGAGAAACAAA ACACAGCTCTGCAAGATCAAAACCTGGCCTCAAAATCTCCAGTCTCATCATCCGACGA TTCAGAAGAGACTGGAATAACCAAGCTAAACGCTGACTCAAAGACAAATGCTGACAAG GAGGAAGTTGTTGTTGGTGCTGCTGCTTTGCATGATTCAAACGTTTCCCAGAACAAAA AGTTGGTGGACCGCTCATCGTGTGGGTCAAACACACCTTCAGGGAGCGACGCGGAAC AGACGCTTTAGATAAAATGGAGAAAGATAAAGAGGATGTCAAGGATGTCAAGGAGGCA GATGCAAAATCAGCCAGGTGTTATTGAGTTAAGTAACCGTCGGAGTAAAATCAGAGACA CCAACAACCAAACTACTGATTCATGGAAGGAAGTCTCCAAGGGGGTCTATAGCGTT TCAGGCTCTCTTTCAGAGAGAGAGACTGCCTCAGAGCTTTTCACCTCCTCAAGTGGA GAGAATGTGAATGGAACAAAGTGACACTTCAATGCCAATGGCTCCTGATTTCAACA AAATTCAAGAATCTTGTGATGCAGACCAAGAAAGTGTAGTAATGATCGGTGCTGGACC GGGAAGAGCCTCAAAACGAGACAAACAGGGTTTAAGCCATACAAGAGATGTTCAATG GAAGTGAAAGAGAGCCAAGTTGGGAACACAAACAATCAAAGCGATGAAAAAGTCTGCA AGAGGCTTCGATTGGAAGGAGAAGCGTCAACA
TRINITY_DN63261_c1_g1	ATGCAAAATCAAATGGAGTGGGATAGTATCCGATCTCAGCGGCGGAGATGAGGTAG CTGAAGATGGTGAATGGTTCGGCGGAGATGACGGACCGATTCCGTTCCCGGTGACTAG TCTTCTGGAACCTGGGCGGTGTGGGTTCGTGGTCAGCGACGCTCTTGAGCCTGACCAA CCTATCATTTATGTTAACACCGTCTTCGAGATTGTCACTGGGTTTCGAGCTGAGGAAG TTATTGGTAGAAATTGTCGGTCTTGCAGTGTAGAGGTCCGTATGCTAAAAGAAGGCA

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Supplemental Table 2. Continued.

Gene ID	Coding sequence
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TRINITY_DN31883_c0_g1	<p>ATGATCCTAGCACTGTGTCTTGACCGCCTCGAGCCCTCAGAGGCCCTGGCTCGGCCTAG ACCCTGACATGTTTTTCTAGCTAAACCCAGAAACACGACGCAACTGCTGCAGGAATC ATCCTCCCGTGTCCACTATTCAATGATTATCATTCACAAAGCAACAAGCAACTGAA CCACTT</p>
TRINITY_DN76871_c0_g1	<p>ATGTCAGGGTCTAGGCCGAGCCAGGCCTCTGAGGGCTCGAGGCGGTCAAGACACAGTG CTAGGATCATTGCCAGACCACTGTTGATGCAAAACTCCATGCTGATTTTGAGGAGTC AGGCAGTTCCTTGATTACTCAACGTCAGTGCGTGTACTGGCCCGGTTGCGGAGAAC CAGCCACCGAGGTCTGACAAGGTGACCACGACTTATCTTCATCACATACAGAAGGGAA AGCTGATTACAGCCCTTCGGTTGTTTGCTCGCCTTGATGAGAAGACCTTCAAAGTCAT TGCATACAGCGAGAATGCTCCTGAGCTGTTGACAATGACCAAGTCATGCTTCTCTAGT GTTGGCGAGCACCTGTTCTAGGCATTGGGACGGATATAAGGACGCTTCTTACTGCTC CTAGTGCCTCTGCATTGCAGAAAGCCCTTGATTTGGAGATGTCTCCCTGTTGAATCC CATTCTTGTGCACTGCAAGACTTCTGCAAAGCCCTTTATGCGATCGTACACAGGGTT ACAGGGAGCATCATTGTCGACTTTGAACCGGTGAAGCCTTATGAAGTTCCCATGACAG CTGCTGGTGTCTTGAATCATAAACTCGCTGCGAAAGCAATCACTAGGCTGCAATC TTTGCCAGCGGGAGCATGGAAAGGCTTTGCGATACGATGGTTCAGGAGGTTTTTGAA CTGACGGGGTATGACAGGGTGATGGCTTATAAATTTTCATGACGATGATCATGGTGAGG TTGTCTCTGAGGTTACAAAACCTGGACTGGAGCCTTATCTTGGGCTGCATTATCCAGC CACCGACATTCTCAAGCAGCCCGTTTTCTGTTTATGAAGAACAAGGTTAGGATGATC GTCGATTGCAATGCAAAACATGTTAGGGTGCTTCAAGATGAAAAGCTTTCCTTTGATC TTACCTTGTGTGGCTCCACCCTTAGGGCACCACACAGCTGCCATTTGCAGTACATGGC CAACATGGATTCAATAGCATCTCTGGTGATGGCGGTTGTAGTAAACGAGGAAGATGGA GAAGGGGATGTCCCTGATGCTACTACACCTCAAAAGAGAAAGGCTATGGGGTTTTGG TGGTTTGTCAACACGAGTCCGAGGTTTGTTCGGTTTCCCTCAGGATAGCCTGTGA GTTTCTAGCTCAAGTGTTTGCATACACGTCAATAAGGAGGTAGAATTGGAGAATCAG ATTGTGGAGAAGAACATTTTGCACACAGACGCTCTTGTGCGATATGCTGATGCGTG ATGCTCCGCTGGGTATTGTGACACAGAGCCCCAACATAATGGACCTTGTGAAATGTGA TGGAGCAGCTCTTGTATAAAGACAAGGTATGGAAGCTGGGAGTAAGTCCAAGTGAG TTCCATCTGCAAGAAATAGCTTCATGGTTGTGTGAATACCACACGGACTCAACGGGTC</p>

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Supplemental Table 2. Continued.

Gene ID	Coding sequence
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Supplemental Table 2. Continued.

Gene ID	Coding sequence
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Supplemental Table 2. Continued.

Gene ID	Coding sequence
	GCAGACACTGTTATGCGATATGCTTCTGCGTGACTCGCCTGCCGAATTGTTACACAG AGTCCTAGTATCATGGACTTGGTGAAATGTGACGGTGACGCTTTCTTTACCACGGGA AGTATTACCCGTTGGGTGTTGCTCCGACTGAAGCTCAGATAAAAGACGTTGTGGAGTG GTTGCTTGCGAATCACGCGGATTCAACTGGGTAAAGCACAGATAGTTTAGGCGATGCT GGATATCCCGGTGCAGCTGCGTTAGGGGATGCTGTGTGCGGTATGGCGGTTGCGTATA TCACGAAAAGAGATTTCTTTCTGGTTCCGATCTCACACCGCTAAAGAAATCAAATG GGGAGGTGCTAAGCATCATCCCGAGGACAAAGATGATGGGCAACGGATGCATCCTCGT TCCTCTTTCAAGGCTTTTCTTGAAGTTGTTAAGAGCCGGAGTCAACCATGGGAACTG CGGAAATGGATGCGATTCAATCGCTCCAGCTAATTCTAAGAGACTCTTTTAAAGAATC GGAGGCAGCTATGAACTCTAAAAATGCAGATGGTGCGGTTCCAGCCTTATAGGGATATG ACAGGAGAGCAGGGAATCGATGAGTTAGGTGCAGTTGCAAGAGAGATGGTTAGGCTCA TCGAGACAGCAACTGTGCCGATATTGCTGTGGACGCTGGAGGATGCATCAATGGATG GAACGCTAAGATTGCGGAATTGACTGGTCTCTCAGTTGAAGAAGCTATGGGGAAGTCT CTGGTTTCTGATCTAATATACAAAGAGAATGAAGAAACTGTGCGATCAGCTCATTTCTC GTGCGCTGAGAGGAAACGAGGACAAGAATGTGGAGATAAAGCTGAAAACCTTTCAGTCC CGAACTACAAGGGAAGCGGTATTTTGGTTCGTGAATGCGTGTTCGAGCAAGGACTAC TCAAGCAACATTGTGCGCGTGTGTTTTGTGGGACAGGATGTTACTGGTCAGAAAATCG TAATGGACAAGTTCATCAACATACAAGGAGACTACAAAGCCATTGTTTCATAGCCCAA CCCGCTGATTCCACCAATCTTTCGCGCGGACGAGAACACTTGCTGCTTGGAGTGGAAC ACTGCGATGGAAGGCTCACGAATTGGTCTCGCAGTGAAGTGATTGGGAAAATGCTTG TTGGGGAGGTTTTTGGTAGCTGTTGCAGGCTAAAGGGTCTGATGCTTTAACCAAGTT CATGATTGTATTGCATAATGCGATCGGTGGCCAAGATACGGATAAGTTCCCTTTCCCG TTTTTGTACCGCAACGGGAAGTTTGTTCAGGCTCTATTGACTGCAAACAAGCGGGTAA GCCTCGACGGAAGGTTATTGGGGCTTTCTGTTTCTTGACAGATCCCGAGTCTGAGCT GCAGCAAGCTTTAGCAGTCCAACGAAGGCAGGACACAGAGTGTTCACGAAGGCGAAA GAGTAGCTTACATTTGCCAGGTGATAAAGAATCCTTTGAGCGGTTTGCGTTTCACAA ACTCATTGTTGGAAGCTACGGAAGTTGAACGAGGATCAGAAACAGTTTCTTGAAACGAG TGTTTCTTGCGAGAAACAGATCTCGAGGATTGTCAGTGACATGGATCTTGAAAAGATT GAAGACGGTACGTTTGAGCTAGATAGAGCGGAGTTTTTACTCGGAAGTGCATAAACG CGATTGTAAGCCAGGCGATGTTCTTATTGAGGGAGAGAGGTGTTTCAGCTGATCCGTGA CATTCCCGAAGAGATCAAATCGATAGCTGTTTATGGAGACCAGACAAGGATTCAACAG CTCCTAGCTGAGTTTCTGCTGAGTATAATCCGGTATGCACCGTCCCAAGAGTGGGTGG AGATCCATCTAAGCCAAGTTTCGAAGCAAATGGCTAATGGATTCTCCGCTATCCGCAC AGAATTTAGGTACATTTTCATTGCACCCGCTTTTGTCTCCTCATCTCTGTAACCATCAT TACGCAATCTGTTTTACAGTTCCATATTTTTGGTTTATGAAGAAGTTTTGATCGATT CCTTTTTAAAAAGTTTTGATTGTGCTTGGTTGTTGCTTGTGTTGGATATAGAATGGTT TGGTTTTTGGATCGTTATC
TRINITY_DN27276_c0_g1	ATGGTCTGCGGAGGCGGTGGCGAAACCAGCGGTAGAGGTGCGAACGGAGAGGCATCTT CGTTGAGCCACCGTGTGGATCAGAACAATCACCGCGGAAAACAGGCTCAGTCGTCGGC AAGCAAACCCCTAAGGTACAGAAATCAGCCGCGAAGCCACGCCGGCACGGAGTCCGTG AGCAAAGCTATCCAACAGTACACTGTGACGCGAGGCTCCACGCCGTCTTCGAGCAGT CTGGAGAGTCCGGCAAGTCGTTGACTACTCCCACTCCCTTAAACGACGACGTGCGC TTCTTCCGTACCGGAGCAGCAGATCACGGCTTATCTCTCGCGGATCCAGCGCGGCGGC TACATCCAGCCTTTCGGTTGCTTGATCGCCGTCGACGAATCCACCTTCACCGTCATCG GACACAGCCAAAATGCGCGGGAAATGCTAGGGCTCATGTCCCAA
TRINITY_DN27276_c0_g2	ATGGTCTGCGGAGGCGGTGGCGAAACCAGCGGTAGAGGTGCGAACGGAGAGGCATCTT CGTTGAGCCACCGTGTGGATCAGAACAATCACCGCGGAAAACAGGCTCAGTCGTCGGC AAGCAAACCCCTAAGGTACAGAAATCAGCCGCGAAGCCACGCCGGCACGGAGTCCGTG AGCAAAGCTATCCAACAGTACACTGTGACGCGAGGCTCCACGCCGTCTTCGAGCAGT CTGGAGAGTCCGGCAAGTCGTTGACTACTCCCACTCCCTTAAACGACGACGTGCGC TTCTTCCGTACCGGAGCAGCAGATCACGGCTTATCTCTCGCGGATCCAGCGCGGCGGC TACATCCAGCCTTTCGGTTGCTTGATCGCCGTCGACGAATCCACCTTCACCGTCATCG GACACAGCCAAAATGCGCGGGAAATGCTAGGGCTCATGTCCCAA
TRINITY_DN68291_c0_g1	ATGGATGCGATTCACTCGCTGCAGCTTATTCTAAGAGATTCTTTCAAAGAGTCCGAAG CGATGGACTGTAAACCAATGCAGTTGGGGAGGTTTCAGCCACATGGAGAGTATATGAC AGAGCAAGGGATGGAGGAGATAGGTGCAGTTGCGAGAGAGATGGTTAGGCTCATTGAG ACTGCGACGGTCCCTATATTTGCTGTGGACATTGACGGCTGCATCAATGGGTGGAACG

Continued next page

Supplemental Table 2. Continued.

Gene ID	Coding sequence
TRINITY_DN68291_c0_g2	<p>CCAAGATTGCAGAGCTGACTGGTTTTTCCGTTGACGAAGCTATGGGAAAGTCTCTTGT CAGGGATTTAATCTACAAAGAATACGAAGAAACCGTTGATAGGCTTCTTTATGGTGCT CTCAGAGGGGACGAAGGAAAGAATGTGGAGGTCAAGCTGAAAACTTTCGGTCCCGAGC TGCAAGGAAAGGCGGTGTTTGTGGTTGTCAACGCATGCTCAAGCAAGGACTACTTAAA CAACATTGTTGGGGTCTGCTTTGTGGGACAAGACGTAACCTGTCAAAAAATTGTTATG GACAAGTTCATCAACATACAA</p> <p>ATGGATGCGATTCACTCGCTGCAGCTTATTCTAAGAGATTCTTTCAAAGAGTCCGAAG CGATGGACTGTAAAACCAATGCAGTTGGGGAGGTTTCAGCCACATGGAGAGTATATGAC AGAGCAAGGGATGGAGGAGATAGGTGCAGTTGCGAGAGAGATGGTTAGGCTCATTGAG ACTGCGACGGTCCCTATATTTGCTGTGGACATTGACGGCTGCATCAATGGGTGGAACG CCAAGATTGCAGAGCTGACTGGTTTTTCCGTTGACGAAGCTATGGGAAAGTCTCTTGT CAGGGATTTAATCTACAAAGAATACGAAGAAACCGTTGATAGGCTTCTTTATGGTGCT CTCAGAGGGGACGAAGGAAAGAATGTGGAGGTCAAGCTGAAAACTTTCGGTCCCGAGC TGCAAGGAAAGGCGGTGTTTGTGGTTGTCAACGCATGCTCAAGCAAGGACTACTTAAA CAACATTGTTGGGGTCTGCTTTGTGGGACAAGACGTAACCTGTCAAAAAATTGTTAT GGACAAGTTCATCAACATACA</p>
TRINITY_DN68291_c1_g4	<p>ATGGAaaaaATCACAGGCTGGCCTCGCAATGAAGTGATTGGTAAATTGCTTGTTAAGG AAGTGTGTTGGGAGCTGCTGCAGGCTAAAGGGTCTGATACGTTGACTAAGTTCATGAT CGTATTGCATAATGTGATTGGTGGCCAAGACACGGATAAATTCCTTTCCCGTTCTTT GACCGCAGAGGAAACTCATTACGGCTCTCTGACTTTGAACAAACGGGTGAGCCCCG ATGGTCAGGTCAATTGGGGCTTTTTGTTTCTTGCAAGTCCGAGTCCCGAGCTGCAACA AGCTCTGGAGATCCAGCGGAGGCAGGAAAGTGAGTGCCTCTCGAGGGGGAAAGAGTTG GCTTACATATTTCAAGCTATAAAGAATCCATTGAGCGGTTTGCGTTTCACAAATTCAT TGCTGGAGGCCACGAATTTAAGCGAGGATCAGAAGCAGTATCTTGAAACAAGTGTTC ATGCGAGAAGCAGATCTCTAAAATTGTAGAAAACATGGACGCCAAAAGCATTGAAGAC GGTCACTTGAGTTAGAGAGAAACAGAGTTCTTCATTGGCAGCGTCATAAACCGCAGTGG TAAGCCAAGCAATGTTGGTTGTAAGAGAGAGAAATCTACAGCTGATATGTAACATCCC CATGGAGATCAAATCCATGGCTGTCTACGGTGACCGGATAAGGATCCAACAAGTCTTG GCGGAATTTCTGCAGAGTATCGTCCGTTATGCACCCATTGAAGGCTCCGTGGAGCTGC ACTTGCACCCGTTCTGAAACAAATGGCTGATGGATTCTCCGCTATACGCATGGAGTT CAGGATGGCATGTGCAGGGGAAGGCGTACCTCCGAGAAAGTGCAAGACATGTTCCAC AGTAGCCAATGGACGAGTCCAGAAGGATTGGGGCTAAGCGTTTGAGGAAGATTCTTA AGCTAATGAACGGAGAGGTTACGTACATAAGGGAATTGCAACGCTCTTATTTCCTAAT CGTTATCGAACTCCCAGTTCGCGCGC</p>
TRINITY_DN68291_c2_g1	<p>ATGATCGCCGTCGACGAATCCACCTTACCGTCATCGGACACAGCCAAAATGCGCGGG AAATGCTAGGGCTCATGTCCCAATCTGTCCCAAGCATAGATGAGAACGCAGAAGCTCT AGCGGTTGGCACGGACTTGCCTCCCTCTTCAGGCCATCGAGCTTCTTCTCCTCGAA CGCGCCTTCGTGGCTCGAGAAATCACGCTCCTTAATCCGCTTTGGATTCACTCCAAGA ACACTGCTAAACCTTTTTACGCGATTCTCCATAGGGTCGATGTAGGATCCTGTATCGA TTTAGAACCGGCGAGAACCGAAGACCCCGCGCTTTCGATCGCCGGTGCGGTCCAGTCC CAGAACTCGCAGTCCGCGCGATTCTCGTTTACAATCGCTTCTGGGGGAGACATCA AGCTCCTCTGTGACACTGTTGTGGAAAGCGTCAGGGATCTCACTGGGTACGACCGAGT TATGGTGTACAAGTTTCATGAAGACGAGCACGGCGAGGTTATCGCGGAGAGTAAGCGG CATGATTTAGAGCCTTACATCGGCCTGCATTATCCCGCCACTGATATTCCTCAGGCAT CTCGGTTCTTGTCAAGCAGAACCGTGTTAGGATGATCGTGGATTGCCATGCGTCGCC GGTTCGTGTGGTCCAGGACGATAGGCTCACGCAGTCTATATGCTTGGTGGGTTCGACT CTACGAGCTCCTCACGGTTGTCACGCTCAATACATGGCTAACATGGGCTCTATTGCGT CCTTGGCCTTGGCCGTGATTATAAATGGAACGAAGAAGACGGGAACGGTGGAGGAAG AACTCGATGAGGCTTTGGGGTTTAGTCGTTTGCCACCACACCTCTTCTCGCTGCATA CCGTTCCCTCTTAGGTATGCTTGTGAGTTTCTAATGCAGGCGTTT</p>
TRINITY_DN68291_c3_g1	<p>ATGCAAGCTTTTCGGTTTACAGCTAAACATGGAGTTGCAATTAGCAGGTGTCTG AGAAACGAGTTCTGAGAATGCAGACTTGTGTGCGATATGCTTCTGCGTGATTCCCC TGCCGGGATTGTTACGCAAAGTCTAGTATCATGGATTTAGTGAAATGCAACGGTGCT GCGTTTCTTTACCAAGGGAAGTATTATTCGTTGGGTGTGGCTCCGTCTGAGGTTTACA TAAATGACATTGTGGAGTGTTGCTTGCTAACCATTCGATTGACTGGCTTAAGCAC</p>

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Supplemental Table 2. Continued.

Gene ID	Coding sequence
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Supplemental Table 2. Continued.

Gene ID	Coding sequence
TRINITY_DN67850_c0_g2	<p> TGACGATGATGGCTATGTCCATCTACAGTTCAGGATGATACATCCTGGAAAAGGACTT CCTTCAGAGATGTTAAGTGATATGTTTGAGACTCGAGATGGATGGGTACGCCTGATG GGTTAGGACTTAAGCTTTCAAGGAACTGCTGGAGCAGATGAATGGTCGTGTGAGTTA TGTCCGAGAAGACGAACGTTGTTTCTTTCAAGTGGATCTTCAAGTCAAAACAAGGTTA GGTGTGAGACCAGAGAAAACAGAAGATGGTTCAAGCATAAAG ATGCCTATTGAAGAATTGCTTGCAAGGTATAAGGAGGATTCGGTGACAAGGATTTGT CTGAAAATGACTCTGGTTATACATGTGCTCTATCTGAAGACTTTGTAGTAGAATCTCA CAAAACCAGGCAGCAAGCTGATTCAGATGACGAAAACGTTGATTTAGCAGAATGTAAG CCAGATTTGCAGCCTTGACAGAGAAAAGATGAAGGCACATCCAATGAACTGAAAGAAG ATAACGAGAAAAGATAGTAGCGATAAAATTGCCGATGCCGCAGCAGCAGCAAGATCTGC GCAGCCAACTGGATTTACATACTCTACAACAAAAGTTCGAACGAAATTGCCGTTTCTT CTTAAGCATTCTTTGCGTGAGTACCAACACATTGGTTTGGACTGGCTTGTACAGATGT ATGAGAAAAGATTGAACGGGATTCTAGCTGATGAAATGGGTCTTGGAAAGACCATCAT GACCATCGCTCTTCTCGCACATCTTGCTTGTGATAAAGGGATATGGGGGCCCCATCTG ATTGTGGTTCCAACAAGTGTGATGCTTAATTGGGAACTGAATTTCTTAAATGGTGTC CTGCTTTTAAAATTCTCACCTACTTTGGGAGTGCAAAGGAGCGGAACTCAAGAGACA AGGATGGATGAAGCTGAACTCCTTTCATGTATGCATAACAACCTATAGGCTAGTTATC CAGGACAGTAAAATGTTCAAGCGCAAGAAGTGGAAAGTACTTGATTCTTGACGAAGCCC ATTTAATTAAGAATTGGAAGTCACAGAGATGGCAAACCTCTGTTGAACTTCAATTCTAA ACGCAGGATTTTGTGACTGGTACACCGCTGCAGAACGATCTTATGGAATTGTGGTCA TTAATGCATTTTCTGATGCCACATGTCTTCCAGTCTCACCAGGAATTCAAAGATTGGT TCTGTAACCCGATAGCAGGGATGGTGGAGGGACAAGATAAGATCAACAGAGAAGTTAT TGATCGCTTGATAATGTCCTCCGTCCTTCTCTACGGCGCTAAAAAGGGATGTG GAGAAACAACCTTCCTTCGAAACATGAGCATGTTATTTATGTAGATTATCTAAGAGGC AGCGCAACTTGTATGAGGACTTCATAGCAAGCACAGAAACACAGGCTACACTTAACAG TGGAAGCTTTTTTGGGATGATAAGTATCATAATGCAACTGCGGAAAGTTTGTAAATCAT CCTGATCTCTTTGAGGGTCGGCCTATTGTTAGTCTTTTGATATGGCTGGCATTGATG TGCAGTTGAGTTCGAGAATCTGCTCTCTGCTTATGAAAAGTCCATTTTCCAGGGTCGA TCTTGAGGCTCTGGGATTCTTATTCACCCATCATGATTTTCTATGACTGGTTGGGAA GGGGATGAGATCAAAGCTATTTCAACGCCCTCAGATTTGATCAAGCAGCGCTGGACT TGAAGGATAATTTAGAAGAAATCCCTCTGAGTTTAGTAAACCGTAAAAACCTGCAAGG GACAAATATTTTGAAGAAATTCGAAAGGCCGTCTTTGAGGAAAGGGTTAAAGAATCT AAGGATCGGGCGGCAGCCATTGCATGGTGGAACCTCTTGAGATGCCAGAGAAAACCTA CTTACTCTACATCTCTAAGAAGTCTTTTAACCATTAAGGGTCCCTCTTGATGACATACA CCATCTTAAGGCAAATCGTCCATCTTACATGTATTCCTCAATGCTGGCTGACATAGTT CTTTCACCAATCGAGCGTTTTCAAGGTAATTGAGCTAGTCGAAGCTTTTACGTTTG CGATTCCAGCTGCACGAGTGCCTTACCTGCTTGTGCTGGTGCAGCAAAAGTGACTCTCC TGTTTTCTTAGTCCATCGTACAAGGAGAAAGTTACAGATCTATTGTACCTCTTCTG TCTCCGATTAGACCTGCTATTGTTAGGAGACAAGTATATTTCCAGATAGGCGCTGA TACAGTTTGAAGTGTGGAAGCTGCAGGAGCTTGCCATGTTACTGAGAAAATTAATAAT TGGGGGTACAGAGCGTTGATATTCACGCAAATGACCAAGATGCTTGACATCTTGGAG GCTTTCATTAGTTTATACGGTTATACTTACATGCGTCTTGACGGCTCTACTCCACCAG AAGAGAGGCAGACATTAATGCAGCGGTTTAACACAAATCCCAAGATTTTCTTTTCAT TTTGTCAACTCGAAGTGGGGGTGTTGGCATAAACCTCGTTGGTGCAGACACGGTTATT TTCTATGACAGTGACTGGAATCCCGCAATGGATCAACAAGCACAAGATCGCTGCCACA GGATTGGTCAGACACGGGAAGTGCAATTTACCGGTTGATAAGTGAGAGCACCATTGA AGAGAATATCTTGAAGAAAAGCAAACCAGAAGCGTGCGCTTGATAACCTAGTGATTGAG AATGGTGAATATAACACCGAGTTTTTCAAGAAGCTCGACCCCATGGAATTGTTCTCTG GGCATAAGGCTCTGACCACGAAGGATGAAGAGGTCAAAGCAAGAATTGTGGGGCGGA GCTCCCTCTGTCAAATGCAGATGTTGAGGCTGCTTTAAACATGCAGAAGATGAAGCG GATTATATGGCTCTCAAAGAGTAGAAGAAGAAGAAGCTGTGGATAATCAAGAGTTTA CAGAAGAACCTGTAGAGAGACCAGAAGACGATGAGCTAGTAAATGAGGATGACATAAA GTCAGATGAGCCTGCTGATCAAGGTGTAGCTGCAGCAGGGTGCAGCAAGAAGAAAT CCATTGTTACCTACTGATAACAGGGATGAGAGAGCTGACATCACTATTTTAAGCCAAG AAGAAGATAATGATGTACCAGACGATGTCAAGCAAATGGCTGCAGCAGCCGCCGCTGC TGGACAAGCTATCTCATCTTTTGAGAATCAGCTGCGTCCTATTGATAGATATGCGATT AGATTTTTAGAGGTTTGGGACCCCATCATTGTTGAGGCTGCGTTGGAAAATGAAGCGG </p>

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Supplemental Table 2. Continued.

Gene ID	Coding sequence
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TRINITY_DN46533_c0_g1	ATGCTTCGAGGATCTCGCTTCTCTCTTCCCCGACTTCGATCTCTTCACTTTCCACCA CCCTCTTCTCTCAGGATCAACTCTCTGTGAAAGATTCTGTCTGTAAGCGCAACACCAT GCCTCTGTTTGAGCTATTGAGGCTCGCCAACGCTAAGCTTGAATCTGCTCAAGACAAT AACACTCCTCCACCTGTGGATGAAGTTGTGAGCTGGTTTGGGAAAACGGTCAGATTT CTACTCAAAGTCAGTCGAGCAGATCGAGGAACATTCTCCACCACAATCTGTTTCATCA AGCAAGCTCTTCGAGACCTAGAGAGATTGGAATGGCTCGAAGACGACGATGGTGGAC GAGATCCCTATGTGAGTCCGTCTCTAATGACGGGTTTGAGTCAAGACGATGACTTGG TTCCATGGCTGAATCATCATCAATCCCTAGATGGATACTGCTCTGATTTCTTGACGGA CGTGTCTCCTGTTACTGTCAACGAGCAAGAGAGCGACATGGCGGTAAATCAAAGTGT TTCCCGTTGTTCCAGAGAAGAAACAATGGCAATGAATCAGCTCCTGCTGCTTCTTCAT CGCAGTATAACGGTTTCCAATCACATTCTCTGTATGGAAGTGATAGAGCTAGAGATCC TGTGAGCCAACAGCCAAACCTGATCGATTTACTCAGCCACAGGAACAGTAGTCACT ACTAGTAACAAGCCTGGTTTGATCAACTTTTCGCATTTCTTACGCCCTGCAACTTTGG CTAAGACTAATAACCCTCATTGCACTAAAGAGAAGAGTCCCTCAAAGCCCGCCGAATGT GTTTAAGACCAAAGTTCTTGGAGCTAAAGACTCTGAAGTTAAGGTTCTTGACGAGTCT GCTCCTTCTGCAATGCCGAAGGATAACCAAAAGGCTTGCTTAATAACAGAAGACTCAG GTAGAAAAGAACAAGAGAGTGAAAAGGCCGTTGTATGTTCTTCTGTTGGCTCGGGTAA TAGTCTCGATGGCCATCGGAAAGTCTTCTGCTTTCTTTAAAAAGAAACATTCCGAT GTTTCAGGACATGGACTGTGATAGCGAAGATGTTGAAGGAGAATCGGGAGATGGAAGAA AAGAAGTAGCTCCATCTCGAACGGGCATGGGTTGGAAGAGAAGCCGCTCGGCCGAAGT ACATAATCTGTCTGAAAGGAGACGACGTGATAGGATTAACGAGAAGATGCGTGCGCTT CAAGAATAATAACAACTGCAACAAGGTCGGCCTTTTCTCCTTTGTGTATACTTGG TCACTCCTTTTCCGCCTTTCAAGGTATTGCTGCAACCAGTTTTTTCGTATGTGATCAG CTTCACTAACTGAATGCTTTTTTTTATTGTTGTAAGGTGGACAAAGCTTCTATGC

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Supplemental Table 2. Continued.

Gene ID	Coding sequence
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TRINITY_DN44852_c0_g2	ATGTTGGCTATGGACATCATCAGGCTCAGTCTCATGGATTATTCCAGTCTCTTGAATG TGATCCCACCTTTGCAAATGGGTAAACCAACAACCTTCTTTGCATTTTACACATCAA CTGG
TRINITY_DN51213_c0_g1	ATGTTTCCTACGCGCATCATCAAGCTCAGTCTCAAGGACTATATCAGCCTCTTGAATG CAATCCAACCTCTGCAGATCGGGTAAATCCTTTGTGATCTTTGCCTTGAAAAATCATCT GCAAACCAGCTTGTGTACTTCACTACCAAGATTGTATTGTTTGAGGCTCTT
TRINITY_DN51213_c0_g2	ATGTTTCCTACGCGCATCATCAAGCTCAGTCTCAAGGACTATATCAGCCTCTTGAATG CAATCCAACCTCTGCAGATCGGGTAAATCCTTTGTGATCTTTGCCTTGAAAAATCATCT GCAAACCAGCTTGTGTACTTCACTACTAAGATTG
TRINITY_DN38410_c0_g3	ATGCAAGATACCATAGATCGTTATCTGAGGCATACCAAGGATCGAATCAGCAGCAAAC CGGTTTCTGAAGAAAATATGCAGGTTAATTATGATATTGCGTACCAATTTCTTATAAC AACTTTAGTACAGAAT
TRINITY_DN69209_c0_g2	ATGAATGTTATGGAAAGAGTCGGTGAAGAAACAGTGGCGAGTAACAAGATACAATTGA AAGCACGAGTGGATGATGTTCTTGTAAAGCTTGATGCTCATCATATGGTGACCGAATC AGAAGCTGGGAACGATTGTCTGAGGAGCGACTGTCCTGGAAGCTCAGCTCACAGGAAT GTAGATATAAACAAGCCTCCCGAGGAATCCAAGATTTCTGTGCAAGAGCTGACATTGG GGAAGTATAGGGCAGTTCAAGGGAGTCATAATATGGATAGTGTCTTAGGGCTGGCAA GTTTGAGCATCTCTATCGTCTTGCTAGAGGCTCTTCTGCGTTTAGGGCAGGTGATGGG GATCTTGATTCTCAACCTCGTGACATGGATCAAATGCTTTCCAGAATTAGACAACAGC TTGCTGGAGCTCCTTCCGAGAGGCAAACTTGAAACCTATTATGAATCGGAGGAGCGA TCAGAATCTTGAAGCCTTCTCTGAACGTCTTAGAGCTGCTGGCGAGAACAGCATTATG AACGCTCCTGCGTGGATCAACGATGGTGTCCACTTGAAGAGTACGCTTTGAGTTCTT CCAGTTTTTCTCAGCTGATTCTTAAAGAGCTATGAAGGGGAAAGGGGTAGTAGGAAG AAACCAAGAACTCCTCCTGAACCTTGGCTGTGATCAAGATATAGGATGCAAGGACAAA AAGTTGGATAACAGCAAGTCGCCTATTCCCCACGATGTTTTGACTCTAAATCAAGTC CGAAAGGAAATGGGATTGTATCACATGGTGAAGGGATTCTACTAAATCTTCTGTGG AATCAGTTTGAGGGAGTTTCTTAGATCAAGTTCTGGTAAACGAGAGAAACGACACGGA CTTTCTCTATTTCCGAGCTGGTGGAGCTGGTTGACTCAGCGCACTCACAAGGATTAT TCTTGCTGGACTTGAGACCATCCCTTTTCGCTTTGGTCCCATCGAAGAACTTAGATA TACTGGTACTTTCCGAAAGAACAATTTAGACTCAGATGATGTTGATGAAGATTGAAT AGGAAGAGGTCCGGGATTCAGGAATCGTCTATTGTGGGCAGGGATCTGAAGAAAAGAA AAATGGACGTAAATGTGCCTTCTCCAGGAATCAACTTCAGGCCACTTCAAGTGGAG ACCTTTCAAAAGGAAAAGCCCTGTTATTGATTAAATGTGGTTGATGCACGAAATCCG GACAGCTGTGAACCTCAACAGCAACACTATATAAAAAATGTAGGCGTGTCTTCAATGA CGAGAAAACAGTCTATGTCCACATGGCTAGAAGAGCAATGGTATACTTGTCCAGAGGA GATAAATGGAGAAGATATCGGAGAAAATCAAATATATATGCCCTTGGTGTCTTCTG TTTGAGTTGCTATGCCATTGTGAGTCCAGCGAGATGCATGCTGCGATGATGGCAGATT TACGTCATCGGATTCTCCACCTGCATTCTTTCAAGATACCCAAAGGAAGCTGGATT TTGTCTTTGGCTTCTACATCCTGTACCCTCCTCCCGACCAACATCTAGAGAAATACTG AAGTCTGAGTTGATATGCGAGGATGATTCAAGTTATATCGACTGCTGCTGATGAGGAGA TATCTGAGCTGTTACTTCATTTTTTGTCTTCACTAGAAAGAGCAGAAGAAGAAAAATGC ATCTAAGCTTATGCAAGACATCCAGACCTTGGAGGATGATATCAAGGAGGCCGAGCGA AGATATTCTTCAAATGCATCTTTGGTGAGATCTCATGAAGCTATTGAAAGAAGAGGGC AATCATCTCCCATAGACGAGCGCTGTACAACACTTCTGGCGCTTGTGTGTTACCAAC CGTAATACAGACAGGCTGATGAGTAATATACGTCAACTTGAAGATGCATATTTCTTC ATGAGATCACAAATGAAGTTATCGGATTCTGCGCTAGTGCCCGTTCTGACAAAGGCC TTCTAAAGGACAGGGACAGGTGGTCTGAAAACCAAAATGAGAATCAGAATACGAGAAC CAAAGGAACTCTTCAGATCAACTGGAAGTGTTTTTTCGAGGGGTTGTGCAAAATTTGCT CGGTATAGCAAGTTTGAAACCTGTGGGACAATCAGAAGTGGAGACCTTTTAAACTCTG CTAGTGTGGTCTGCTCATTGAGTTTTGACCCTGATGAGGAACACATAGCAGCAGCTGG

Continued next page

Supplemental Table 2. Continued.

Gene ID	Coding sequence
	GATATCAAAGAAAATCAAGATTTTGGACTTCAATGCGTTTATGAATGAATCTGTCCGT GTTCAATTATCCACTAGTGGAGATGGTCAACAAATCGAAATTAAGCTGTGTTTGCTGGA ATAGTTACATCAAAACTACTTGGCCTCGACTGACTACGATGGTGTAGTTTCAGATATG GGATGCCGGGACTGGACAAGGATTTTCGCAGTACACAGAACACCAGAAGAGAGCCTGG TCAGTTGATTTTCTCCATCTGACCCGACAAAATTTGTCAGTGGAAGCGATGACTGTT CGGTAAAGCTTTGGAGCGTCAATGAGAAACGGTCACTAGGCACAATCTGGAGCCCAGC AAATGTGTGTTGCGTGCAATTCTCTTCATATTCCAATCACTTATTGGCATTGTTGGTCA GCTGATTACAAGGTCTATTGTTATGATCTTCGGTATGTCAAAACTCCTTGGTGTACCT TGGCGGGCCATGAGAAAGCTGTAGCTATGTGAAATTTATGGATTCAGAGACCATTGT TTCTGCTTCCACGGATAATTCTCTCAAGCTTTGGAATCTTAACAAGACGAATTCCTCT GGTTTGTCTCCTGGTGCTTGTTCATTGACGTATAAAGGACATACAAATCAGAAGAATT TTGTCGGATTATCGGTCTTGGATGGATACATAGCCTGTGGTTCAGAGACCAATGAGGT ATATAGTTACTATAGATCCTTACCGATGCCAATGACTTCGTACAAGTTTGGATCAGTG GATCCCATTTCTGGAAACGAATACTTTGATGACAATGGACAGTTTGTGTGAGCGTCT GTTGGAGAAAAAGTCTAATATGCTTGTAGCTGCGAATTCGACTGGAAACATGAAGCT ACTTAAACTGGTT
TRINITY_DN52784_c0_g2	ATGGAAGCTGTGAGTAGTATTGACGAGAGCTCGACAAGTACTGATTCCATTCCACTC CGGCGAAGATTCCGCCGCCGACGACGAGAAAGTCGTCATCTCCGGCGAGTTTATACAG AATGGGAAGCGGATCAAGCGTGGTTTGGATCCCGAGAACGGCGTCAAGCCGAATCA AGAAAGCTCCCGTCGTCGAGATTCAAAGGCGTCGTCCCTCAGCCAAACGGAAGATGGG GAGCTCAGATTTACGAGAAGCACCAGCGCGTGTGGCTCGGCACCTTCAACGAGGAA
TRINITY_DN33790_c0_g1	ATGCATGGAACAACCGATATTGTCCGGGAGCGGAGAAATCTAGTTACGACGGCCCGCG GAAGTCAGTCAACGGCGTCTAGCGGCGGTTTCACGCTGGCAGTTGAAGAAAACAGCTG CAACGGGGAGGCCGAGATCGTTCTCATGTGCAAAACATTCTGGTGTGAACTGGTCTCT GTAAGACGGGCACAGAAACCACACTTCTCTTCGTTCTGCTTGAAAAGCAAATACACA AATCGGTGGATCCCTATGTTTGGCCGAGGCATCTCGTACCCTACAATCTCCTTTCCAA ATGTCACGTCGGTTGTCCCTGGGATATCGGTAACAATCCAGTGCAAGTGCTCTCTCAG ATAAGGATCACTAGGTCCAGGAACATCAGGATCAGTCATGACCTTAGGTTTGTGTTGA ACTGCAGAAGGGAAAAGTTCATGGCCGTTGTAGAC
TRINITY_DN21486_c0_g1	ATGGAGAATATGGGAAGTAGAGTGATAGAGCCATTGATAGTGGGAAGAGTGGTCCGGAG ATGTTCTCGATTTCTTCACTCCAACAATTAATAATGAATGTGAGTTACAACAAGAAACA AGTCTCCAATGGCCATGAGCTTTTCCCTTCGTCTGTCTCCTCCAAGCCTAGAGTTGAG ATTCATGGTGGTGATCTCAGATCCTTCTTACCCTGGTGATGATAGACCCTGATGTT CAGGTCCTAGTGACCCCTTTCTAAAAGAACACCTGCATTGGGTCGTACAAAACATCCC CGGTACAACAGATGCTACATTTGGAAAAGAGGTGGTAAGCTATGAGTTGCCAAGGCCA AGCATAGGGATACACAGGTTTCGTGTTTGTCTGTTCAAGCAGAAGCAAAGACGTGTTA TCTTCCCAAATATTCCTTCCAGAGATCACTTCGACACTCGCAAATTTGCGATCGAGTA TGATCTTGGTCTCCCTGTGCGGGCTGTTTCTTTAACGCTCAGAGAGAAACCGCAGCT CGCAGACGT
TRINITY_DN61367_c0_g1	ATGGTCCGACAAGTTAGTTTGGTTGAAGAGGAGAAAGAATACGATCCGACACTCAGCG AGCTAAGGGGACCAGTCATCAACAGTAACGGTGCAGGGGTGTTCCCAAGGAGGAGGCAT TGGTTCAGAAGGTGATAATGTAAGACCGAATGGCCTTCTCAAGGTATATTCTAAGGAG CTTGATAAGAACAGTCGTTTCATGGGTGCTAAGCGGAGAAAGTCTGGTTCTGTGAAAA GATTCAAACAAGACGCATCCACGAGTAACAACCACACAACAACCTGCAGATCAGAATGC AACACCAGAGTTGGCCACATTAGACTCTTTTGGTGAATCGCGAGGATAGGGAATGAG TATCCTGGTGTGCTGGAAAATAATAATTTATCTCAGAAAAGCAAAATGGAAGAAGTGG ACATCGCGAGGATCCTTAAACCAGTGAAATTTTCTTATCTGTAACAAACAATGTACA AGACGTGTTGGTGACCTTTTGGCGCTAAGGTCTGATGGGAAAGAAGTGATGGTAGAC AACAGATTTCTCAAGGCTCACAATCCTCTTCTGCTGATTGAATTCTACGAGCAACATC TCAAGTACAATCCCGAAAGG
TRINITY_DN70446_c2_g2	ATGGATTTGAACGGCGAGTGTAAGGGAGGAGATGGGTTTATTGACAGAAGCAGAGTCA GGATTTTGCTTTGTGACAATGATTCAAGAGCTTGGGAGAGGTTTTCACCCTCCTTTC ACAGTGTTCTTATCAGGTGACATCAGTGAAATCAGCAAGGCAAGTGATTGATGCACTA AATGCAGAGGGACCTGATATCGATATAATTCTGGCGGAAATTGATCTCCCAATGGCCA AGGGTATGAAGATGCTGAGGTACATCACAAGAGACAAAGATCTTCGGAGAATCCCTGT GATAATGATGTCGAGGCAAGACGAGGTACCTGTTGTCGTAAAGTGCTTGAAGCTTGGT GCAGCTGACTACCTTGTGAAGCCTCTTCGGACCAACGAGCTTCTGAACCTGTGGACAC

Continued next page

Supplemental Table 2. Continued.

Gene ID	Coding sequence
	ACATGTGGAGAAGAAGACGCATGCTAGGACTTGCTGAGAAGAATATGTTTAGCTATGA TTTTGATCTCGTGGGATCTGATCCAAGTGATCCAAACACAAACAGTACCACCCTGTTT TCTGATGATACAGATGACAGAAGTATTAGGTCCACCAACCCGCAGAGAGGAACCTTTAA GCCATCAGGAAAAGGAGTGGCCTGTTGCTACGGGTTCGTTTGTGCTGGCGATGGTGC TGATGGCACAGCCACTTCAAGTCCTGCTGTTGCTATTATAGAGCCTCCATTGAATCAT CTTCCTGGGTCTCACCATGAGCCTACGAAAAGAAATACCAATCCAGCGCAATTTCTT CAGTGCCAAAGAAAAGTAGATTGAAGATTGGAGAGTCCTCCGCGTTCTTCACATATGT CAAGTCTACTGTCCTTGGTACCAACTGTCAGGATCCTCCCCGTGTCAATGGAATGGC TCACTTCATCTTCATCCAGGTATGGCGGAGAAGTTTCAAGCGGTGGCCAGTGAGGTGA TCAACAACACTAAACAAACACGCCGAGGTAGAGAGGCCGAGAAAACCTGTTCTCAAGG AGAGAACTTACAGAATGGCGCCAGCTATCCAAATTCCTTGAGCGGTCTCGCACGCTT CCAACACCAATGGAACCTTCATGGTAGGAGTTACCAAGAAGGAAATATGAATACTCCCC GGGATGCTATAAGCAGAAAGTAAGGATTTCATCTCAAGTTGATGCTTCGAGTTTCGCTGC ACAGAATGCCTATCCTTACTATATGCATGGTGTCTATGAACCAAGTTATGATGCAATCA GCAGCCATGATGCCTCAGTATGGTCATCAACATCCTCATTGCCACCTAATCATCTGA ATGGAATCACAGGATTTCTTATTACCACCACCCCATGAACACATCGTTACAGCACAG CCAGATGCCACAGAATGGTCAGGTGCCTTTACAGAGTGGTCAGATGTCTTTACAAAAT GGTCAGATGTCTATGGTTCATCATATTTCGTGGCCACCGGTGGGAAATCCGTCTTCTA ACGAGGTGAGAGTGACTAACTTGACAGAAGAGAGGAAGCTTTGCTCAAATTTAGACG TAAAAGAAACCAAAGGTGTTTGATAAGAAGATTAGGTATGTGAATAGGAAGCGCCTT GCTGAGAGGAGACCGCGTGTTAAGGGTCAGTTTGTTAGGAAAATGAACGGCGTAAATG TTGACTTAAACGGGCAGCCTGACTCTGCTGACTATGATGACGAGGAAGAGGAGGAAGA AGAAGAAGAAGAGGAGAATCGGGACTCATCTCCTCAGGATGATGCTCTGGGAAT
TRINITY_DN34145_c0_g1	ATGCGATTGATCGTGATTTTGTGTTGGCAGCTAGGACTTGCTGAGAAGAATATGTTTA GCTATGATTTTGATCTCGTGGGATCTGATCCAAGTGATCCAAACACAAACAGTACCAC CCTGTCCTCTGTA
TRINITY_DN55625_c0_g1	ATGCATCTAAAACTATGAATATGGTAGGAAAATCAACAAAAGAGGTTACTTCAAAAT GTCTATTTTTTTTTATCACATCTGATCAAGGAACCAGGGCAAGGAACAACAACCTCATT TAAAAGCTTGCGTAGCACAAGAATGGCGAAGGCCACAAGAACCC
TRINITY_DN55625_c0_g2	ATGTTCTCGTGCTACGCAAGCTTTTTAATGAGTTGTTGTTCTTGATCAGATGTGATA AAAAAAAAAGACATTTTGAAGTAACTCTTTGTTGATTTTCTACCATATTCATAGT TTTAGATGCATTTATAATGTCTGTTGCCTTCTTTTGAACCTTTTGACAATGAATATT GTGGATGTGTGCTTTTTATTGGAATGCAGTGACATCAGTGAAATCAGCAAGGCAAGTGAT
TRINITY_DN64509_c0_g1	ATGGATTTCGTCTCTCGATGGAGCTGCAGGTGACTCATCGAAGTGACGTGAAATGAGTG TTGATGAGAAGAGACAGCTTGTTTATGAACTGTGCAAGCAATCACATCTAGCTTCTGA AGTGTGTCAGGCATGGAGCCGCCAAGAGATTCTACAGATCTTATGCGCAGAAATGGGA AAAGAAAGGAAATATACTGGCTTGACCAAAGTCAAGATCATAGAGACTCTATTGAAAA TTGTATCTGAGAAAAAATCTGGAGAGTATGATGGGAAGAAGAGAGATTCTGACTGTGT GCCTGTTTCAGAGAAACTCAAAGAGACAAAGGAAGGTGATAATCCTACTCGTTATGTG ATTCCAACGAGCAACAATGCCTCAGGAAGCTGCAACTCGGTTAATACTAAAGGTGAGG AGAATACTATCTACTGCAACAATTTGGCTTGCCGGGCCATATTGAGACAGGAAGACTC GTTTTGCCGAAGGTGTTCTTGTGTCATTTGTCGTAAGTATGATGATAACAAAGATCCT AGTCTCTGGTTGACATGTAGCTCAGATCCTCCATTTGAAGGTGATTCTTGCGGATTCT CGTGTCTCTTGAAGTGTGCTTTCAAGAGTGAAAAATCTGGTCTTGCAAAAGACAAGCA AAGTGAGGGTTGCTGCTTCTACTGTGTCTCTTGCGGTAAACCAATAGCTTGCTTGAA TGTTGGAAGAAGCAACTGACGATTGCTAAAGAAACCAGAAGGGTAGACATACTATGCT ACCGTCTTCTATTGGTCCAGAACTAATAAAAGGCTCTACTAGATACCCAAATCTGTG TGAATTTGTGGATGAAGCTGTGAAGAGTCTTGAAGCTGATGTGGGTCCTCTCACTGGT CTTCCTATGAAAATGGGTAGAGGAATTGTAAACAGACTACAATCAGGACCCGATGTGC AGAACTTTGTTCTTCTGCTCTTGAAACACTAGAACTACACCTCCCGAAGTCGCTGC ATTGCCCTCACCTCGCAGCTACAAGATGCAGCACGATTGTTCTTACGGATTGAGCAAT GAGATATCTGCAGATACAGCAACCACAGTATCAACCAAGATTCAGATTGAGGATGTTA ACGCGACTTCGCTCACAGTGATTCTCGCCTCTAACGAAGTCGCTCACCTGCAACAT CGTTCACTACAGTATCTGGCATCGTAAGGTACCGAGAAAAGATTACCAGGAGAAGTCG ACTTGACATTTGTTTACTCCAAACGCAAGATTTGTTGTCTCTGGATTAGCTCCAGCGT CTGAGTATTGCTTCAAAGTTGTGTCCTTACGCGGTACACGAGAACTAGGCGTCGATGA

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Supplemental Table 2. Continued.

Gene ID	Coding sequence
TRINITY_DN53167_c0_g1	AATCAATGTTTTTACGCGTAGCCCTGAAGAAGGAGCGAATTGCTCTTCGGTAGTCGAA AGAAGCGAAAGCCCTCTCACAATTGCAGCACGTTGTCTTCGAATCCTTCTTCTGTTG AAGCTGAATCCAACAACGGTTACATTGCTCCTCAGAATCCCTCGCAGAACGACAAAAA AGATTCTCCTTCGACTGAGGAAAATGCTGCGAAAAGGACAACCGATTACAGACATTGTG CAGACTGAGAAAAACGTTGAAGTGTGTTGGATGAAGAAGCTGTTCCCGACAAGAACG GAGGAACCTAGTCCCGGTTAGTACGACAAATCTTGTTAGTAATCGAAACAGTTCAGA TGCGAGTTTGCCAATTACTCCCTTCAGGTCAGACCAAACCAAGAACCGTCAAGCTAGA AACGGAAAAATCGGTTAAAGAAAACGGTAATAACGGTGATCATCACTCAGCGAACGGAG GATCAGAGAGCGGATTAGAGCATTGTGTGAAGATCATAAGACAGCTTGAATGTTCAGG ACATATCGAGAAGGATTTACAGACAGAAGTTTCTGACTTGGTATAGCTTAAGAGCGACG CCACAAGAGATTAGAGTTGTGAAGATATTCATCGATACGTTTACTGATGATCCCATGG CTTTAGCTGAGCAGCTCGTTCATACCTTCAACGACCGCGTTTCGATTAAGCGTTCTGC GATTGGCAATGGTGCGTCTGCGTTGTCCATTCTGGATTCTGCATGAAGTTGTGGCAT ATGCCACGCCCTTTCTTCCACAAGTTGATTTTCTCATCCACTATCCAAGAAAAACGTC TGAGAGTTCCAGATAAGTTTGTGAGTAAATTCAAGGATGAGCTTTCGGTTGCGGTTGC ACTCACAGTACCTGATGGTCATGTTTGGCGTGTAGGACTAAGGAAAGCTGACAACAA ATCTGGTTTCAAGATGGTTGGCAAGAGTTTGTGACCGTTACTCCATTTCGATTGGTT ATCTTTTGATTTTATAGATACGAAGGGAACCTCTGCCTTCAGCGTCTACATTTTCAATCT ATCACACTCGGAGATCAACTACCATTCCACCGGTCTCATGGATTCCGCACACAACCAC TTCAAACGCGCCCGTTTGTGTTGAAGACCTGAAGACGAAGACGCCGAGGTCTGTTATC CTTCTTCCGTGTATCCTTCACCGCATCTGAAACTAATGTACCCGCCAATAAAGGGTA TACGAGTTCAGCCATCCAAAGCTTGTTCACTGGACCTGTTAAAGCTGAAGAGACAACA CCAACCCCAAAAGTTCCGAAAAAAGAGGGAGGAAGAAGAAAAACGCTGATCCTGAGG AAATAAACTCATCTGCTCCGCGCGATGATGACCCAGAGAGCCGTTCAAAGTTCTACGA GAGCGTTCTGCGAGAAAGAGAACCCTGACCGCAGAAGAGAGAGAGAGGGCCATCAAT GCAGCCAAAACGTTTCGAGCCAACAACCCTTCTTCAGAGTTGTTCTGCGACCATCCT ATCTATACAGAGGTTGCATCATGTATCTGCCTTCTGGGTTTGTGAGAAGTATTTAAG TGGGATCTCCGATTATCAAGGTCCAGCTCGCGGAGAAACAATGGCCCGTGAGATGC CTCTACAACGCAGGGAGGGCCAAATTCAGCCAAGGTGGGACGAGTTCACGCGGGAGA ATAACCGAGAGAGAGGGCCATCAATGCAG
TRINITY_DN52604_c0_g1	ATGTATCTGCCTTCTGGGTTTGTGAGAAGTATTTAAGTGGGATCTCCGGATTTCATCA AGGTCCAGCTCGCGGAGAAACAATGGCCCGTGAGATGCCTCTACAAAGCAGGGAGAGC CAAATTCAGCCAAGGATGGTACGAGTTCACTCTGGAGAATAACCTAGGAGAAGGTGAC GTCTGCGTGTTCGAGCTGCTCAGAACCAGAGATTTCTGTTCTGAAGGTGACGGCCTTTC GAGTCAACGAGTACGTC
TRINITY_DN21929_c0_g1	ATGTGTAGGCATAATAGTCGAGCGAAAGCCTCGCAGGAGGAGGTGGCTTACCTGATG AGGATCTCTTGGTATTTTCTAAACCTGTTTCGACTATACAACATTCTTCTCCGTCGCTC TCGATACAACCCATCGTTCCTTCGAAGATGCTTGAAGTACAAAAATCCAAGCAAAGGGC AAAACAAAGTCCGAATCTGGTGGGAAGGTAGTTTCACTACAAGGATTGTAATAACA CATTGCAGAAAACCTGAAGTTAGGGAGAATTGTTCTTGTCATTTTGTATATGCTATG TGGTAACTTCGAGGGGCTGCAACTTCATTTGAACCTCATTTTCATGGCTTATTTGAATTC GAGTGCATGCGTTCAGGAGAAGAGCAGAGAGTTAATGTCTCTGTAAGACTTGATAGAT TCGAATCTGAGGACGAAGAAACTCAATATGAAAAATTTGAGGAGCACTCTTCTGCTC GAAACCTCGTAAGCGTAAACAAAGAGGTGGTGGTGGTGGAAATATGGCCAAGCGACTT AAAATAAGCATTTTACCATTGGATTACCCAGTTTAGCCAATGCCACAGAAAAATGGAA TCGCCCTGCTGAATAGTGATCTTGCTAGACAAGTTGGGATGAATTCACCAGCCGTAGC TCAATCTTCTCTGGACTCTGATGCTAATGCTATGTTACTAAGCGAAGCTGTGGTTGCT GCTGCCAAGACGAGAAAGTTATCTGCTGAGCGATCAGAAGCTAGAAGCAACCAACTTC TCCTGAAACGCCAGTTCTATCTTCTCACAAGTTTCAGCCAATGTCAATTGAGCAAGT AATGTCTGATCGAGATAGCGAAGATGAAGTTGATGATGACGTTGCAGAATTTCGAAGAT CGCCAGCTGCAGATGCTTGATGATTTGTAGACGTAGACAAAGAGGAAAAAGAGATTCA TGCATCTTTGGAACACATTTGTAAAGAAAGCAAGGGTTGTGGCGGATGGTCATGTTCC TTGGGCGTGTGAAGCATTTTCAAAGTTTCAACAAGAAAGACTTGAACCATTCCTACGA CTCTCCTGGTGTGGAGATACCATCTGATTAACCTCTGGGACCTTGGGCTTATCGACG CGGTCACCATGAACAACCTGCTCTCTCATTACCTGGAGAAATGCGATGACAACCTCAGA CAACGCGAGTGTGGATCATCAGTCAGACAACAACAATGTCGATCATGGCATTGAC TAAACACTAACGATAGGATGGATGTTGAGGAGGATGTCAATGACAGAAAAGACAAG

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Supplemental Table 2. Continued.

Gene ID	Coding sequence
TRINITY_DN33663_c0_g1	ATGATGGTGGCTTATTCTTGCGTCTTAGGATCACCGACAAAGAAGGTAACAGCTATCA CTTTTACTATTGCTCTTATCCGTAATTTAATTCATAACCTA
TRINITY_DN54268_c0_g1	ATGAACAATCTGAGTTATCTTGAACCAGATTACTCTGAGTTTGTGGAAGTTGATCCTA CCGGAAGATATGGAAGATATAATGAAGTTCTGGGTAAAGGAGCTTCAAAGACTGTTTA CAGAGCATTTGATGAATATGAAGGGATCGAAGTAGCATGGAACCAAGTGAAGCTCTAC GATTTCTTACAGAGCCCTGAGGATCTCGAGAGGCTTTACTGTGAGATTTCATCTCCTTA AGACCCTAAACACAAGAATCATGAAATCTACACCTCTTGGGTGATACCGCCAA TCGAAACATCAATTTTGTCACTGAAATGTTCACTTCTGGCACCTTAAGACAGTATAGA CTCAGGCATAAGAGAGTGAACATAAGAGCGGTGAAACATTGGTGTAGACAAATCTTGA GAGGCTTGCATTATCTTCACAGCCATGACCCTCCTGTAATCCACAGGGATCTCAAATG TGACAACATTTTCGTTAATGGGAATCAAGGAGAGGTCAAGATTGGAGATCTTGGCCTC GCTGCCATTTTAAGAAAGTCCCACGCTGCTCACTGCGTCGGGACGCCTGAGTTCATGG CTCCTGAAGTTTACGAAGAAGCGTACAACGAACCTGGTTGATATATACTCGTTCGGTAT GTGCATTTTGGAAATGGTTACGTTTGATTACCCGTACAGCGAATGTACTCACCTGCT CAGATCTACAAGAAAGTCATGTCGGGCAAGAAACCGGATGCGTTGTACAAGGTGAAAG ACCCCGAGGTTAAATATTTTCATCGAGAAATGCTTGGCCACCGTATCGCTGAGAGTCTC AGCTCGTGAGTTACTAGATGACCCTTTTCTTCGAATAGACGATGGTGAATTTGATTTG AGATCAGTTGATTTGGATGATTCCGTGGGGCCACTAGTTAGGCAGCCGCATCATCTTG CTGACTACTACAACCTACCCGTGCAACAGTAGCTCTTTGAATCGTCAGTACTCAAATGG TTATAACAGCCACCACGAGTATCAAAACAGATGGGCGTATAATCCAGCTGAGACAGAG GAGACTCACGGAATCGAGCTCTTTGAGTGTGCAAAACGATAATGATCGTGAAGAAGACA AGAGCTCTGGTAATGTTGATATAAGCATCAAAGGCAAGAGAAGAGATGATGGTGGCTT ATCTTGCGTCTTAGGATCACCGACAAAGAAGGGCGTGTCCGAAACATTTACTTCCCA TTTGACATCGAGACAGACACGGCATTGAGCGTCGCGACAGAGATGGTAGCGGAACCTTG ATATGGACGATCACGGAGTCACAAAAATCGCCAACATGATTGACGGTGAGATATCTAC TCTTGTGCCTAGTTGGAGACCGGGACCTGAATTCGAAGAATCTCTTGCGGCCGCGGCG GCAGCAAATGCGAACATTTGCAGCAACTGCGTATCGAACCGCACCTCAATGGGATCGG TGATGGATTTCTGAGGACCAACCCTGGTGCAAATGTTGCACAGTGTTGCAGAAACGG GTGCGGCGAGACTCATGGCCGGTTTGAAGAGATCACGATAAGAGAAACCGAGGTTCTG CTTAGAGAGATATGGAAGCTGCAGCAACAGCAGGAAAGTCGTGAGCTTAGCTCGATAG ACTCGGGGCAAAACCACTCCGAAGAAGAAGAGGAAGAAGAAGTATACGAGAACCCGA AATCACGTTTTCTTGTGAGGCAAGTAACGCGCTAAACCATCTATCCGGTTCTGGATCG TTCTCGTTTTTGCCGTCTTTATACTGTGACGAGCTAGCCGAGAAAACCGAAAGTCAGG TCCAACAAGAGTTGAGATGGCTTAAAGCTAAATGCCAAATGGAGGTCAGAGAGATGCA GGATGAACAATAAAATCCCGGTGGCCGGAATCAGGAGAAGAAGAAGCGGAAATATGT CTGCAAGACGGGTTCTCGGGTTCCGGTTTCGGGCTTGGGAAGTGGAGATGAAGATAAGG TGAAAGAGAAGATGTTTGGAGGAAGATTAGTACCAAAATGTCTTAAAGGACAACCTC ACTTCCTGTTGATGCCATTGAATCT

Supplemental Table 3. Detailed information of the identified candidate genes associated with flowering pathways of *Isatis indigotica*.

Gene name	Unigenes (no.)	Gene ID
AP1	3	TRINITY_DN44529_c0_g2 TRINITY_DN59583_c0_g1 TRINITY_DN60394_c3_g1
AP2	1	TRINITY_DN64890_c0_g1
AGL6	1	TRINITY_DN62832_c0_g1
AGL8	1	TRINITY_DN48318_c3_g1
AGL14	1	TRINITY_DN68423_c2_g1
AGL15	1	TRINITY_DN18713_c0_g1
AGL16	1	TRINITY_DN69985_c0_g2
AGL17	1	TRINITY_DN59446_c0_g1
AGL18	1	TRINITY_DN58069_c0_g1
AGL19	1	TRINITY_DN68423_c2_g2
CAL	2	TRINITY_DN46328_c0_g1 TRINITY_DN60394_c3_g2
CCA1	1	TRINITY_DN68029_c0_g1
CO	2	TRINITY_DN63019_c0_g1 TRINITY_DN63019_c0_g2
COL9	1	TRINITY_DN65596_c1_g1
CHS	2	TRINITY_DN53874_c0_g1 TRINITY_DN61788_c0_g1
CRY1	3	TRINITY_DN29253_c0_g1 TRINITY_DN45325_c0_g1 TRINITY_DN66742_c0_g1
CRY2	1	TRINITY_DN67410_c0_g1
EBS	3	TRINITY_DN69128_c1_g2 TRINITY_DN62817_c0_g1 TRINITY_DN50493_c0_g1
ELF3	1	TRINITY_DN58990_c1_g1
ELF6	4	TRINITY_DN69071_c0_g2 TRINITY_DN51551_c0_g1 TRINITY_DN69458_c0_g3 TRINITY_DN95956_c0_g1
ELF8	1	TRINITY_DN69534_c0_g2
ELF9	2	TRINITY_DN67027_c0_g1 TRINITY_DN67027_c0_g2
EMF1	1	TRINITY_DN57304_c0_g1
EMF2	1	TRINITY_DN66245_c2_g3
ESD4	1	TRINITY_DN70231_c1_g3
FD	1	TRINITY_DN64502_c0_g2
FKF1	1	TRINITY_DN69998_c3_g1
FLC	1	TRINITY_DN69832_c1_g1
FLD	1	TRINITY_DN67304_c0_g1
FLK	3	TRINITY_DN40841_c0_g3 TRINITY_DN40841_c0_g2 TRINITY_DN40841_c0_g1
FPA	1	TRINITY_DN70605_c0_g2
FPP	2	TRINITY_DN60601_c0_g2 TRINITY_DN47820_c0_g1
FT	1	TRINITY_DN67831_c2_g1
GI	2	TRINITY_DN67682_c0_g1 TRINITY_DN84722_c0_g1
HUA2	1	TRINITY_DN69595_c0_g1
LD	3	TRINITY_DN69302_c0_g3 TRINITY_DN69302_c0_g1 TRINITY_DN69302_c0_g2
LHY	1	TRINITY_DN68323_c1_g1
LKP2	1	TRINITY_DN63261_c1_g1

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Supplemental Table 3. Continued.

Gene name	Unigenes (no.)	Gene ID
PHYA	3	TRINITY_DN31883_c0_g1 TRINITY_DN76871_c0_g1 TRINITY_DN76871_c0_g2
PHYB	1	TRINITY_DN68291_c2_g2
PHYD	7	TRINITY_DN27276_c0_g1 TRINITY_DN27276_c0_g2 TRINITY_DN68291_c0_g1 TRINITY_DN68291_c0_g2 TRINITY_DN68291_c1_g4 TRINITY_DN68291_c2_g1 TRINITY_DN68291_c3_g1
PHYE	1	TRINITY_DN69481_c0_g1
PIE1	1	TRINITY_DN67850_c0_g2
PIF3	2	TRINITY_DN46533_c0_g1 TRINITY_DN46533_c0_g2
SEP1	3	TRINITY_DN44852_c0_g2 TRINITY_DN51213_c0_g1 TRINITY_DN51213_c0_g2
SOC1	1	TRINITY_DN38410_c0_g3
SPA	1	TRINITY_DN69209_c0_g2
TEM1	1	TRINITY_DN52784_c0_g2
TFL1	2	TRINITY_DN33790_c0_g1 TRINITY_DN21486_c0_g1
TFL2	1	TRINITY_DN61367_c0_g1
TOC1	4	TRINITY_DN70446_c2_g2 TRINITY_DN34145_c0_g1 TRINITY_DN55625_c0_g1 TRINITY_DN55625_c0_g2
VEL1	1	TRINITY_DN64509_c0_g1
VRN1	2	TRINITY_DN53167_c0_g1 TRINITY_DN52604_c0_g1
VRN2	1	TRINITY_DN21929_c0_g1
WNK1	2	TRINITY_DN33663_c0_g1 TRINITY_DN54268_c0_g1

Supplemental Table 4. List of gene-specific primers used in quantitative real time polymerase chain reaction (qRT-PCR).

Gene	Sense primer (5'–3')	Anti-sense primer (5'–3')
ELF6	TTAAGGCACATGCGGCTAT	TTTGAGGTCCAGTCTACGC
ELF8	TGGATCTCATAAGCGTAAGG	TTAGTGTTGGCGTCTTCGT
EMF2	CGGCGTGCTATTAGGAATC	AGTCTTGCCAACAGGATAT
PIE1	AAAGCCGTCTGACAGTATGG	TCCTGAGGCAACCAAGAAT
AGL15	CCTTGCGTAGACAGGTTCA	ACGAGTGGGTTCTTGGGAT
AGL17	CCAATACCGACAAGCTCTA	ATAGTTGTTGCTGCTCCAT
TFL1	GGGAAGAGTGGTCGGAGAT	GAGGAGACAGACGAAGGGA
FLC	CTTGATCGTCAGTCGAAATG	GGGCGTTCTCAAGGTGGTC