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Identification of SBP Gene Family and Analysis of Expression Patterns Under Salt Stress in Quinoa

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Abstract: This study aimed to identify the Squamosa promoter Binding Protein (SBP) transcription factor from the whole genome of quinoa by analyzing its phylogenetic relationship, gene structure, chromosome location, gene replication, upstream cis-regulatory elements, tissue expression, and construction of the SBP protein interaction network, as well as the characteristics of its tissue expression pattern under salt stress. The researchers found that 23 genes of the CqSBP family were identified through bioinformatics analysis and showed diversity in their amino acid physical and chemical properties. These proteins were hydrophilic and all 23 CqSBPs were located in the nucleus. The SBP family genes were unevenly distributed across the 12 chromosomes of quinoa, mostly on the B chromosome group. The upstream cis-acting element analysis revealed the presence of 49 elements with plant hormones, stress, light response, and tissue-specific expression, and all CqSBPs contained one or more Tata box elements. Protein interaction network analysis showed that all CqSBP proteins appeared in the known interaction network of *Arabidopsis*. Different SBP genes were differently expressed in different organs and periods of quinoa, and SBP genes were expressed with certain tissue specificity. The expression of CqSBP showed many changes under salt stress.

Keywords: Quinoa, SBP Gene Family, Bioinformatics, Salt Stress, Expression Analysis

Introduction

Transcription factors are a class of proteins that regulate transcription. They can activate or inhibit the transcription of target genes by binding to specific sequences of DNA, thereby regulating gene expression (Riese *et al*., 2007). Squamosa promoter Binding Proteins (SBPs) are plant-specific transcription factors with multiple members. Klein *et al*. (1996) first isolated two proteins from the SBP-box family, namely AMPSBP1 and AMPSBP2, while studying the regulation of gene expression networks. With the completion of more and more plant genome sequencing, the SBP transcription factor family has been extensively identified genome-wide. SBP-box family genes have also been identified in *Arabidopsis*, rice, and other plants (Yang *et al*., 2008; Zhang *et al*., 2017a). Members of this family are widely involved in plant growth, development, and various physiological and biochemical processes (Guo *et al*., 2008).

The sequence analysis of these SBP proteins revealed that all known SBP transcription factor member proteins contained a highly conserved DNA binding domain consisting of 79 amino acid residues, including two zinc finger domains and 1 two-way Nuclear Localization Signal (NLS) (Birkenbihl *et al*., 2005). The DNA binding domain of the *Arabidopsis* SBP transcription factor comprises two independent zinc finger structures, composed of 8 amino acid residues and Zn^{2+} and the 8 amino acid residues include histidine and cysteine acid. The two zinc fingers are composed of (Cys3HisCys2HisCys) and (Cys6HisCys). Zn^{2+} binds to the front and rear 4 amino acid residues (Yamasaki *et al*., 2004). Zn^{2+} and nuclear localization signals are necessary for the protein DNA binding process. The C-terminal NLS partially overlaps with the C2HC type zinc finger structure sequence, which has the function of guiding the SBP-box gene into the nucleus to regulate the transcription and expression of their downstream genes. The revelation of these structural features will help to

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further analyze their regulatory role in the growth and development of higher plants. At the same time, it was pointed out that miR156 regulates many SBP transcription factor family members. Currently, 11 SPL genes containing miR156 recognition sites were found in both *Arabidopsis* and rice (Rhoades *et al*., 2002) The spatiotemporal expression of SPL3 during the vegetative development of *Arabidopsis* is regulated by miR156 (Schwab *et al*., 2005). Tissue-specific interactions between MIR156 and certain OsSPL genes also occur in rice (Xie *et al*., 2006).

Currently, the functions of many SBP-box genes have been identified in many species. For example, SPL2, SPL10, and SPL11 genes are involved in floral bud morphogenesis in *Arabidopsis* Thaliana (Shikata *et al*., 2009); Overexpression of ATSPL1 or ATSPL2 enhances heat tolerance in *Arabidopsis* Thaliana and tobacco (Chao *et al*., 2017); and ATSPL7 induces the flowering in grasses. ZmLG1 controls the ligule development in maize (Moreno *et al*., 1997); SPL13 regulates tomato inflorescence structure and side branch yield (Cui *et al*., 2020); OsSPL18 regulates grain weight and number in rice (Yuan *et al*., 2019); in wheat, yield-related traits are controlled by TASPL20 and TASPL21 genes (Zhang *et al*., 2020). The SBP box gene family is also involved in the stress response process of plants. Such as SBP transcription factor CRR1, which plays an important role in maintaining copper homeostasis in the body of *Chlamydomonas reinhardtii* (Kropat *et al*., 2005). Therefore, the SBP protein plays a vital role in flower formation and development, leaf morphogenesis, fruit development, environmental signal response (abiotic stress), and signal transduction. The SBP gene of cabbage and chrysanthemum is responsive to hormone treatment and abiotic stress (Song *et al*., 2016; Tan *et al*., 2015), suggesting that the SBP gene is an important gene related to drought resistance and stress resistance.

Quinoa (*Chenopodium willd*) is an annual dicotyledon of the family *Amaranthaceae*. Quinoa is cold-tolerant, drought-tolerant, salt, alkali, and barren-tolerant, with a high protein content in the grain, coordinated amino acid ratio, and rich in vitamins (A, B2, E) and minerals (Ga, Fe, Cu, Mg, Zn). It is known as the mother grain, golden grain, and sacred food, attracting the attention of agricultural and food experts and consumers at home and abroad. Quinoa genome sequencing was completed in 2017 (Jarvis *et al*., 2017). This has made it possible to reveal the functions of important gene families in quinoa at the genome-wide level. The SBP-box gene plays important roles in plant type, yield, stress resistance, etc. Therefore, the isolation and identification of important genes in the SBP-box family can provide candidate genes for crop genetic improvement. This study uses bioinformatics methods to identify the quinoa SBP-box gene family and analyzes the family members' sequence characteristics, chromosome location distribution, and gene structure. The RNA-seq data in public databases were used to study the expression patterns of the family members in different tissues and environments. At the same time, the expression patterns of the family genes under abiotic stress were analyzed by qRT-PCR. This provides important information for the in-depth study of the quinoa SBP box gene family and the cloning of important genes.

Materials and Methods

Search and Identification of SBP Members in Quinoa

The complete genome sequence, CDS sequence, protein sequence, and gene annotation files were downloaded from the Phytozome V12.1 database (Goodstein *et al*., 2012) (https: phytozome.jgi.doe.gov pzportal.HTML). We downloaded the file of the Hidden Markov Model sequence spectrum (PF03110) of the SBP protein family and constructed Hidden Markov Model (HMM) with Hmmer (V3.1B2, https: HMMER.org) and then searched for candidate sequences with SBP-box domain (E-value set to 1) in the quinoa protein database. The candidate sequences were passed through Pfam (https://pfam.xfam.org/family), NCBI-CDD (https://www.ncbi.nlm.nih.gov/cdd/), and SMART (https://smart.embl-heidelberg.de/). The SBP-box gene of quinoa was obtained by mutually removing the incomplete reading frame by hand and checking whether it was for the presence of the SBP domain.

Basic Physical and Chemical Properties of Protein and Phylogenetic Tree Analysis

The isoelectric point and relative molecular mass of all SBP amino acid sequences were analyzed by ExPASy (https://web.expasy.org/protparam/) and the subcellular localization was performed by Psort-Prediction (https://psort1.hgc.jp/form.html).

Known amino acid sequences of *Arabidopsis* and tomato SBP were downloaded from Plant TFDB v5.0 (https://planttfdb.gao-lab.org/tf.php?sp=Ppe&did=Prupe.I004500.1.p). The phylogenetic analysis of *Arabidopsis* Thaliana, tomato, and quinoa SBP protein was performed with Clusta lX (V2.1) (Thompson *et al*., 2003). The phylogenetic tree was constructed by the adjacency method and the results were compared using Mega (V6.0) for phylogenetic analysis (Tamura *et al*., 2013). The test parameter bootstrapping was repeated 1000 times, with other parameters set as default.

Gene Structure and Conservative Motif Analysis

According to the quinoa genome annotation file, the gene structure display system GSDS (http://gsds.cbi.pku.e-du.cn/)

was used to construct the gene structure of SR's gene exons/introns (Clouse, 1996). MEME (http://meme-suite.org/) was used to predict and analyze the amino acid conserved domains of the quinoa SBP transcription factor protein sequence. The upper limit of the number of conserved domains obtained by the search was 10 and other parameters were defaulted (Suyama *et al*., 2006).

Chromosome Location and Gene Duplication Analysis

The annotation information of the SRS gene was used in the quinoa database to determine the position of the family member on the chromosome and the map inspect tool (http://www.plantbreeding.wur.nl/uk/software_mapinspect.htl) was used to mark the position of each SBP gene on the chromosome to obtain the distribution of each SBP-box gene in the genome. MCScanX was used for gene family replication analysis (Wang *et al*., 2012a). The conditions for determining gene duplication events were based on the identification method of the Plant Genome duplication database (Lee *et al*., 2012); that is, gene duplication events must meet the following conditions at the same time (Zhou *et al*., 2004): (1) The length of the matching part of the two gene sequences is greater than the length of the longer sequence; (2) The similarity of the matching parts of the two gene sequences is greater than 80%; (3) The closely linked genes are involved in only one replication event. Also, the gene's position on the chromosome is used to determine whether a tandem copy or a fragmented copy has occurred.

Analysis of Cis-Acting Elements and Construction of Protein Interaction Network Diagram

Based on the quinoa annotation information file, 2000bp upstream of the SBP gene transcription initiation site was extracted using the sequence extraction function of TBtools (Chen *et al*., 2020), which was used as the promoter region, and the SBP promoter region was analyzed by the Plant Care database (http://bioinformatics.psb.ugent.be/webtools/plantcare/html/) (Lescot *et al*., 2002). String (http://STRING db.org/) was used to construct the protein-protein interaction network diagram (Szklarczyk *et al*., 2015) and the SBP network was constructed using the STRING software (confidence greater than 0.8) based on *Arabidopsis thaliana*.

Secondary Structure Analysis and Tertiary Modeling Prediction

The secondary structure of the family proteins was analyzed on NPS@: GOR4: (https://npsa-prabi.ibcp.fr/cgi-bin/npsa_automat.pl?page=/NPSA/npsa_gor4.html) (Combet *et al*., 2000). At the same time, we used the Swiss Model (https://swissmodel.expasy.org/) (Kelley *et al*., 2015) to predict the tertiary structure of proteins.

Plant Material and Treatments

Quinoa "Honghua Dajingyuan (HHDJY)" was used as the material which was grown in seed germination pouches (height: Width = 30: 25.5 cm). Uniform seeds of the same degree of fullness were subjected to surface sterilization and germinated in distilled water, with a germination box (10 × 8 × 6 cm) used as a bed for the seeds. After 2-3 days, seedlings were transferred to seed germination pouches and placed in the trough of a paper wick, inside a growth room (relative humidity 60-70%, light time 12 h, day and night temperature 28/18°C). Before transferring the seedlings to the pouch, 100 mL of MS culture medium was added to the pouch. When the seedlings were grown for one month, the seedlings were again transferred to another pouch with 100 mL of distilled water or 200 mmol/L NaCl solution, using the distilled water treatment as a control. The leaves were collected at 0, 2, 4, 8, and 12 h after treatment. Three biological replicates were performed at each time point. The collected leaves were temporarily stored in liquid nitrogen and then stored in a -80°C refrigerator for further analysis.

SBP Gene Expression Analysis, RNA Extraction, and Real-Time Quantitative PCR

The quinoa SBP gene expression data were obtained from the transcriptome data of different quinoa tissues (number: PRJNA394651) and data related to drought, high temperature, salt, and low phosphorus stress environments (number: PRJNA306026). The data was standardized by the Log2 method.

Total RNA was extracted with RNA plant plus reagent (Beijing, China) and cDNA was prepared with a superscript TM III reverse transcriptase kit (Invitrogen). RNA and cDNA were detected by ultra-micro ultraviolet spectrophotometer (UV-VIS spectrophotometer Q5000). qRT-PCR analysis was performed in the abi-viia 7 real-time PCR system of American applied biosystems using 2 × quantitect-sybr-green-pcr-mix (qiage) (Qiagen). The procedure was as follows: Denaturation at 95°C for 3 min, denatured for 10 s at 95°C for 40 cycles, then annealed/extended at 60°C for 1 cycle.

Results

Analysis of Physicochemical Properties of SBP Gene Family Proteins

A total of 23 members of the SBP gene family were obtained through sequence alignment and screening of proteins conserved sequence of quinoa. Analysis of basic properties showed that the size of the amino acids encoded by this family is between 189-1106, the average value was 574.3 and the molecular weight is between 21298.92-121757.34 Da, the average value is

63474.64Da. The theoretical isoelectric point varied relatively large, ranging from 5.74 to 10.24, the average value is 7.69, and weak alkaline. The instability index is between 43.72 with 81.14 and both are greater than 40, which are unstable proteins. The aliphatic index ranged between 56.30 with 87.87. GRAVY (grand average of hydropathicity) varied, but they were all less than zero. Therefore, all proteins in this family belong to hydrophilic proteins. Subcellular location showed that 23 CqSBPs proteins are located in the nucleus (Table 1).

Phylogenetic Tree Analysis

To understand the phylogenetic relationship and classification of CqSBP genes. We used 71 protein sequences from *Arabidopsis* (31), tomato (17), and quinoa (23) to construct a phylogenetic tree based on multiple sequence alignments (Fig. 1, Table S1). The SBP gene was divided into 10 subgroups (Group1-Group10). The SBP protein in 10 subgroups ranged from 2 to 16 and the largest number of CqSBP genes was found in Group10. Compared with other subfamilies, the Group8 protein contained a relatively long amino acid sequence, indicating that there may be some functional differences between this subfamily and other subfamilies. Among the CqSBP genes, we identified 8 pairs of paralogous genes (CqSBP01/CqSBP02, CqSBP06/CqSBP07, CqSBP08/CqSBP10, CqSBP14/CqSBP15, CqSBP16/CqSBP17, CqSBP18/CqSBP19, CqSBP20/CqSBP21, and CqSBP22/CqSBP23). Paralogous genes showed high sequence similarity between the two genes. This similarity indicates that they may have originated from a single gene in a distant common ancestor.

Gene Structure and Conserved Domain Analysis

Intron-exon structure, intron type, and number are typical evolutionary imprints of a gene family. Among the 23 sequences of the quinoa SBP gene family, the gene structure revealed relative similarity on the same branch of the phylogenetic tree, but differed in different branches (Fig. 2). The number of introns in the quinoa SBP genes family ranged between 2 with 14. Statistically, 8 CqSBP genes contain 2 introns (34.78%), 5 CqSBP genes contain 3 introns (21.74%), 2 CqSBP genes contain 4 introns (8.7%) and 8 CqSBP genes contain 9 or more introns (34.78%). The MEME analysis tool was used to predict all quinoa SBP protein sequences and the results showed that the 10 conservative functional motifs are statistically significant, each with an e-value less than $1e^{-300}$. The predictions of the conservative motifs of quinoa SBP genes mostly supported the classification of the SBP gene family phylogenetic analysis. The sequence characteristics and amino acid length of these conserved motifs are shown in Fig. 3. Motif 3 and Motif 4 are conserved SBP domains in all quinoa proteins. 15 SBP genes contain only three conserved motifs, Motif 1, Motif 3, and Motif 4, corresponding to the simple gene structure. CqSBP22 and CqSBP23 contain motif 2, Motif 3, Motif 4, Motif 6, and Motif 9. Some genes (CqSBP05, CqSBP06, CqSBP07, CqSBP013, CqSBP16 and CqSBP17) had 10 conservative motifs.

An unrooted phylogenetic tree was constructed based on the full-length sequences of CqSBP proteins using the N-J method in MEGA7. Bootstrap values based on 1,000 replications were calculated. (A) The distribution of motif in SRS proteins. (B) The exon-intron structure of the SRS gene.

Chromosome Location and Gene Duplication Analysis

23 CqSBP genes were located on 12 chromosomes of quinoa (Fig. 3) by chromosome mapping (of a total of 18 chromosomes of quinoa). The most distributed SBP genes (4) are on chromosome 11 and other genes are distributed on the remaining chromosomes between 1 and 3. A gene family is a group of genes derived from the same ancestor, through gene duplication; usually, they share obvious similarities in structure and function and code similar protein products. Genes from the same family can be packed closely together to form a gene cluster, but they are often scattered at different positions on the same chromosome or exist on different chromosomes (1). Gene duplication has a great effect on gene families. Gene duplication provides raw materials for new genes and facilitates the production of new functions (5). Gene duplication mainly includes genome fragment duplication, tandem duplication, and rearrangement at the gene and chromosome levels. Tandem and fragmental duplication often occur during the evolution and expansion of gene families (7). Tandem duplication usually causes gene clusters, while fragmented duplication may cause the dispersion of family members.

Meanwhile, we detected a replication event of the CqSBP box gene family. Using information from chromosome fragments and genomic repeats, 12 pairs of homologous (Table 2) genes with fragment repeats and tandem repeats were found and their sequence homology was high. Eleven pairs of repetitive genes belong to fragment duplication (91.67% of all replicated gene pairs). The pair (CqSBP06/CqSBP07) belongs to tandem repeats and the gene pairs with tandem repeats have high sequence similarity, often higher than 60%. The gene pairs with duplicated fragments were distributed in each subfamily of the phylogenetic tree and their distribution had a certain preference. Among them, ten pairs were distributed in the same phylogenetic subfamily, which may be due to the polyploidization process of the quinoa genome. Also, we found that there were 8 pairs of paralogous genes in the CqSBP gene. Further calculating the Ka/Ks between genes with homology, we found that all Ka/Ks is less than 1, indicating that these genes have undergone purification selection after duplication and the gene function is relatively conservative.

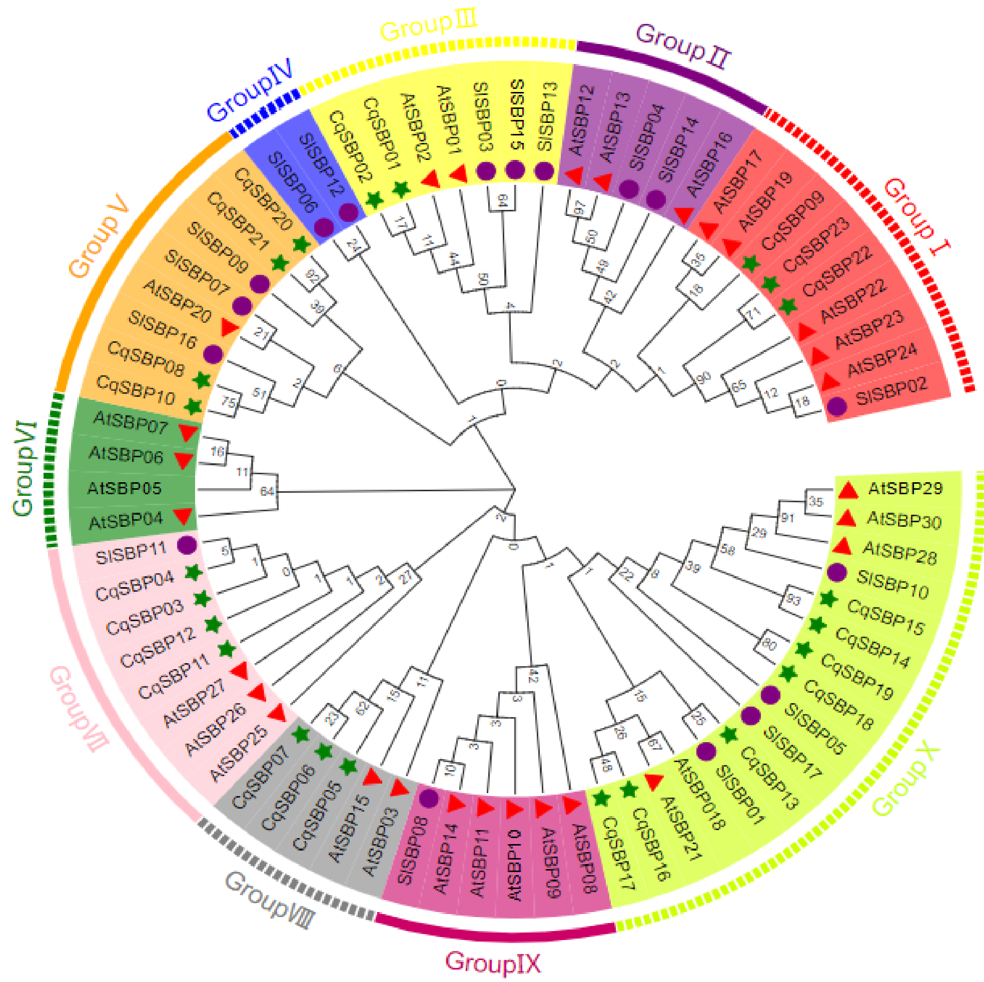

Fig. 1: Phylogenetic relationships of the SBP homologs in different species

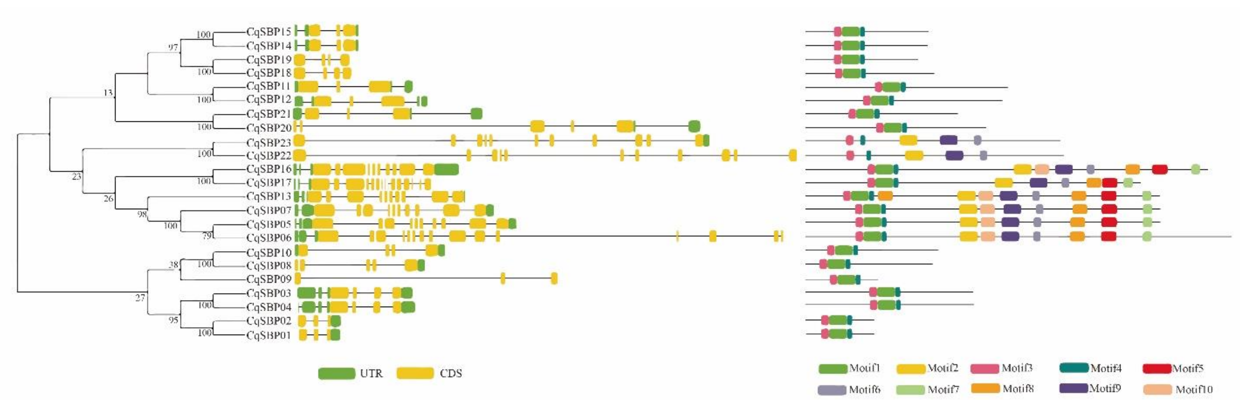

Fig. 2: Structural analysis of CqSBP genes in quinoa

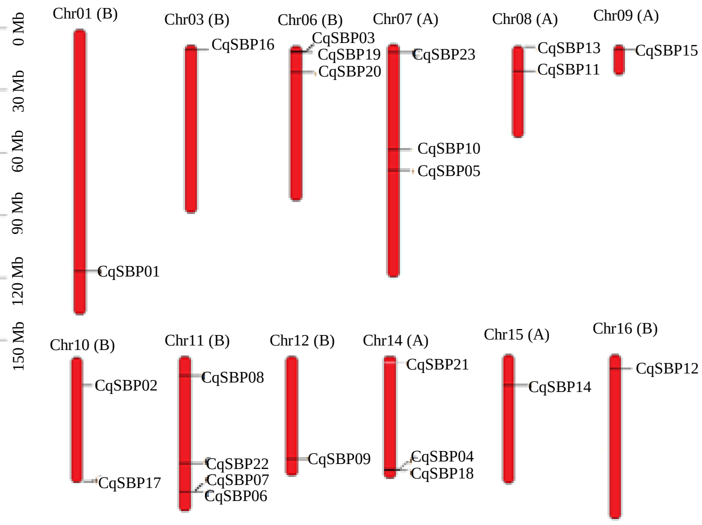

Fig. 3: Chromosome mapping of CqSRS genes in quinoa

Table 1: Information on the 23 SBP gene members in quinoa

Gene accession no	Gene	Size (aa)	Molecular weight (Da)	Isoelectric point	Instability index	Aliphatic index	Gravy	Subcellular localization
AUR62004146-RA	CqSBP01	189.00	21298.92	10.24	81.14	56.83	-0.803	nucleus
AUR62013707-RA	CqSBP02	189.00	21300.88	10.24	81.14	56.30	-0.796	nucleus
AUR62028919-RA	CqSBP03	462.00	50273.96	8.90	60.23	58.53	-0.643	nucleus
AUR62005629-RA	CqSBP04	462.00	50311.10	8.67	56.91	61.65	-0.580	nucleus
AUR62002563-RA	CqSBP05	978.00	108454.93	6.44	49.36	84.30	-0.358	nucleus
AUR62029983-RA	CqSBP06	1189.00	132135.72	7.01	48.63	87.87	-0.305	nucleus
AUR62029984-RA	CqSBP07	980.00	108865.55	6.30	46.74	84.13	-0.306	nucleus
AUR62024322-RA	CqSBP08	349.00	37731.32	7.64	61.14	53.04	-0.680	nucleus
AUR62019452-RA	CqSBP09	202.00	22122.73	9.81	68.39	58.86	-0.864	nucleus
AUR62012061-RA	CqSBP10	373.00	39563.29	8.45	59.28	51.98	-0.654	nucleus
AUR62032118-RA	CqSBP11	562.00	62082.24	6.87	50.08	71.25	-0.468	nucleus
AUR62039662-RA	CqSBP12	545.00	60397.78	6.26	55.10	64.88	-0.645	nucleus
AUR62011728-RA	CqSBP13	984.00	110161.02	5.76	50.96	78.58	-0.461	nucleus
AUR62029416-RA	CqSBP14	347.00	38017.36	8.76	62.86	58.70	-0.633	nucleus
AUR62003425-RA	CqSBP15	349.00	38422.77	8.74	65.21	58.11	-0.668	nucleus
AUR62035190-RA	CqSBP16	1106.00	121757.34	7.06	57.61	70.34	-0.510	nucleus
AUR62042534-RA	CqSBP17	922.00	101713.51	6.75	59.37	67.16	-0.541	nucleus
AUR62005645-RA	CqSBP18	359.00	38997.57	9.36	46.94	59.22	-0.574	nucleus
AUR62028905-RA	CqSBP19	317.00	34782.05	9.05	43.72	62.74	-0.653	nucleus
AUR62003075-RA	CqSBP20	499.00	55390.33	5.89	50.89	74.43	-0.448	nucleus
AUR62007890-RA	CqSBP21	423.00	46751.15	6.57	51.37	66.88	-0.671	nucleus
AUR62042853-RA	CqSBP22	716.00	80133.15	6.32	51.17	74.85	-0.378	nucleus
AUR62042654-RA	CqSBP23	707.00	79251.95	5.74	48.34	75.12	-0.404	nucleus
	Averrage	574.30	63474.64	7.69	56.81	66.77	-0.570	

Note: GRAVY represents the grand average of hydropathicity

Table 2: Gene duplication in the CqSBP family

Duplicated CAMTA gene1	Duplicated camta gene 2	Ka	Ks	Ka/Ks	Date(mya)T = Ks/2λ	Selective pressure	Duplicate type
CqSBP01	CqSBP02	0.006	0.123	0.048	7.240	Purifying selection	Segmental
CqSBP03	CqSBP04	0.017	0.077	0.225	4.536	Purifying selection	Segmental
CqSBP05	CqSBP06	0.040	0.103	0.392	6.066	Purifying selection	Segmental
CqSBP05	CqSBP07	0.040	0.098	0.410	5.776	Purifying selection	Segmental
CqSBP06	CqSBP07	0.032	0.081	0.400	4.767	Purifying selection	Segmental
CqSBP08	CqSBP10	0.013	0.077	0.164	4.551	Purifying selection	Segmental
CqSBP11	CqSBP12	0.028	0.062	0.445	3.664	Purifying selection	Segmental
CqSBP14	CqSBP15	0.014	0.061	0.230	3.577	Purifying selection	Segmental
CqSBP16	CqSBP17	0.022	0.094	0.228	5.563	Purifying selection	Segmental
CqSBP18	CqSBP19	0.072	0.135	0.533	7.945	Purifying selection	Segmental
CqSBP20	CqSBP21	0.018	0.072	0.257	4.237	Purifying selection	Segmental
CqSBP22	CqSBP23	0.033	0.114	0.286	6.738	Purifying selection	Segmental

Note: The non-synonymous (Ka) and synonymous substitution rate (Ks); millions of years ago (mya)

Analysis of Homeopathic Elements and Construction of Protein Interaction Network Diagram

The promoter sequence 2000 bp upstream of the start codon of the CqSBP gene was obtained through TBtools and analyzed by Plant care. A total of 49 functional elements were identified (Fig. 4, Table S2) related to tissue-specific expression, light response, hormones, and stress. Among them were 22 light response elements: ACE, AE-Box, Box-4, G-Box, I-Box, MRE, SP, and LAMP. Some elements only exist in specific genes (RY-element only exists in CqSBP13, AAAC-motif only in CqSBP05, and Gap-box only in CqSBP08), G-box and G-box GT1-motif were found in almost all CqSBP genes. There were 10 types of action elements that respond to hormones. Among them, 10 elements were involved in the methyl jasmonate reaction and 9 elements were involved in the gibberellin reaction (except SARE). 8 types of elements are involved in the abscisic acid reaction (except SARE and AuxRR-core). At the same time, a special element SARE (salicylic acid response element), was discovered, which only exists in CqSBP22. In addition, some elements involved in stress have been Discovered, including Low Temperature Response Elements (LTR, DRE), drought response elements MBS and WUN motif related to wound response. There are also the necessary action elements are which is involved in participating in anaerobic induction. Some functional elements rarely occur the element CAT box, which is related to meristem expression, the GCN4 motif involved in endosperm expression, and the HD-Zip1, which is associated with the differentiation of palisade mesophyll cells and ZEOL. O_2-site is an element related to the regulation of protein metabolism.

All promoter sequences (2000 bp) were analyzed. In order to get a closer understanding of the functions of this family of proteins, *Arabidopsis thaliana* was used as a template to construct a protein interaction network diagram (Fig. 5). We found that 22 CqSBP proteins (except CqSBP17) appeared in the known *Arabidopsis* interaction network diagram. Among them, the functions of *Arabidopsis* genes (AT1G69170 and AT1G76580) homologous to the 7 CqSBP genes of quinoa are unknown, while the functions of other *Arabidopsis* genes that are homologous to quinoa have been studied. As seen in the figure that ATSPL7 is at the center of the interaction network and it functions by interacting with multiple proteins.

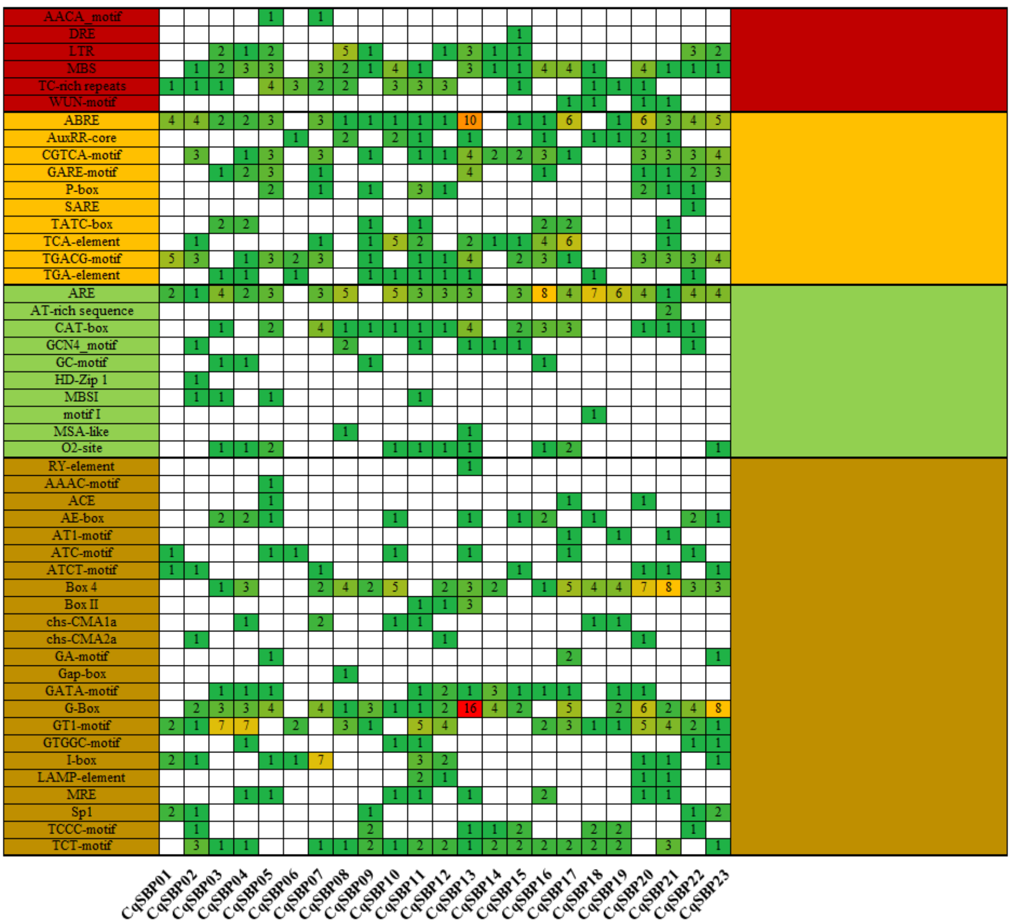

Fig. 4: Cis-acting components of Quinoa SBP genes

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Studies have shown that AtSPL7 directly upregulates SEPALLATA3 (SEP3) and MADS32 genes to induce phase transition and flowering of gramineous forages (Gou *et al*., 2019). In addition, this gene can regulate copper homeostasis-related genes in *Arabidopsis thaliana* (Araki *et al*., 2018). Therefore, the homologous CqSBP genes (CqSBP22 and CqSBP23) may have similar functions. AtSPL9 participates in the transition from nutrition to the reproductive stage and inhibits the germination of new leaves in the shoot apex meristem. Therefore, the CqSBP genes (CqSBP8 and CqSBP10) may also have similar functions. The overexpression of ATSPL1 (CqSBP05, CqSBP06, CqSBP07, and CqSBP13) enhanced the heat tolerance of *Arabidopsis Thaliana* and tobacco (Chao *et al*., 2017). ATSPL13B (CqSBP14, CqSBP15, CqSBP18, and CqSBP19) are involved in the vegetative growth and reproductive development of *Arabidopsis thaliana*. At the same time, ATSNZ can interact with SPL1/SPL3/SPL13B/SPL9/AGL8/AT1G69170 and so on, so CqSBP genes which are homologous with these genes may be regulated by CqSNZ genes.

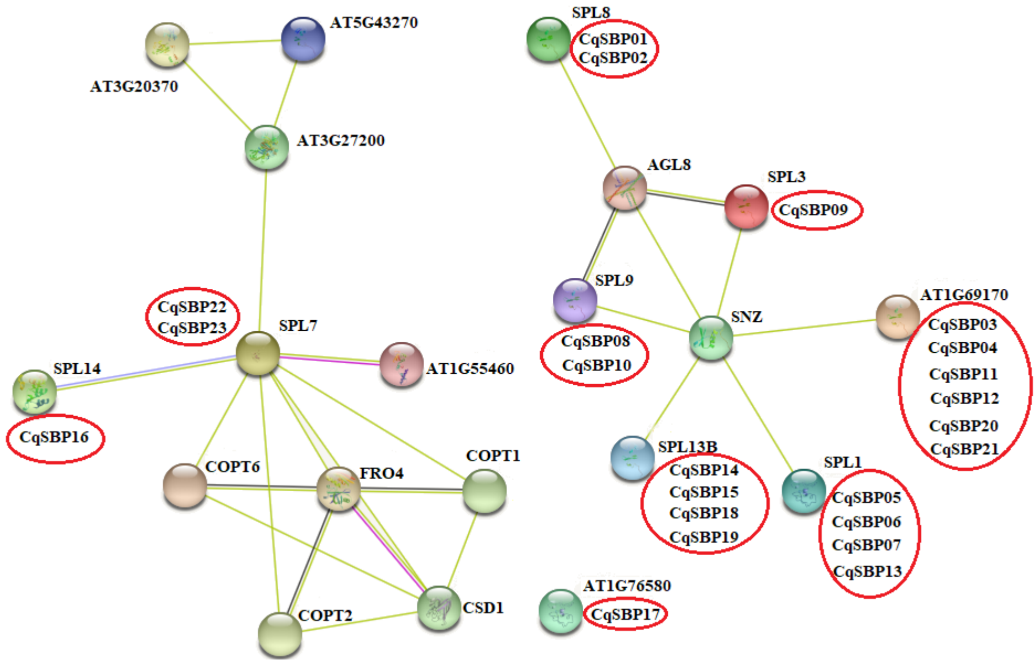

Fig. 5: The potential interaction network of CqSBP based on the *Arabidopsis* and quinoa

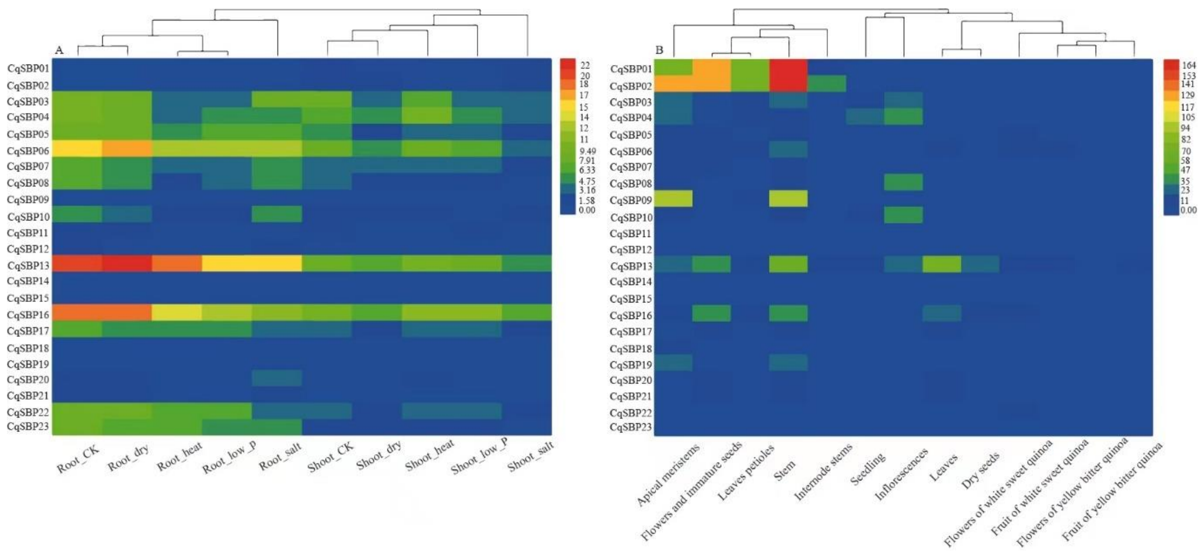

Fig. 6: The expression profiles of SBP genes in different treatments and developmental stages and tissues of quinoa

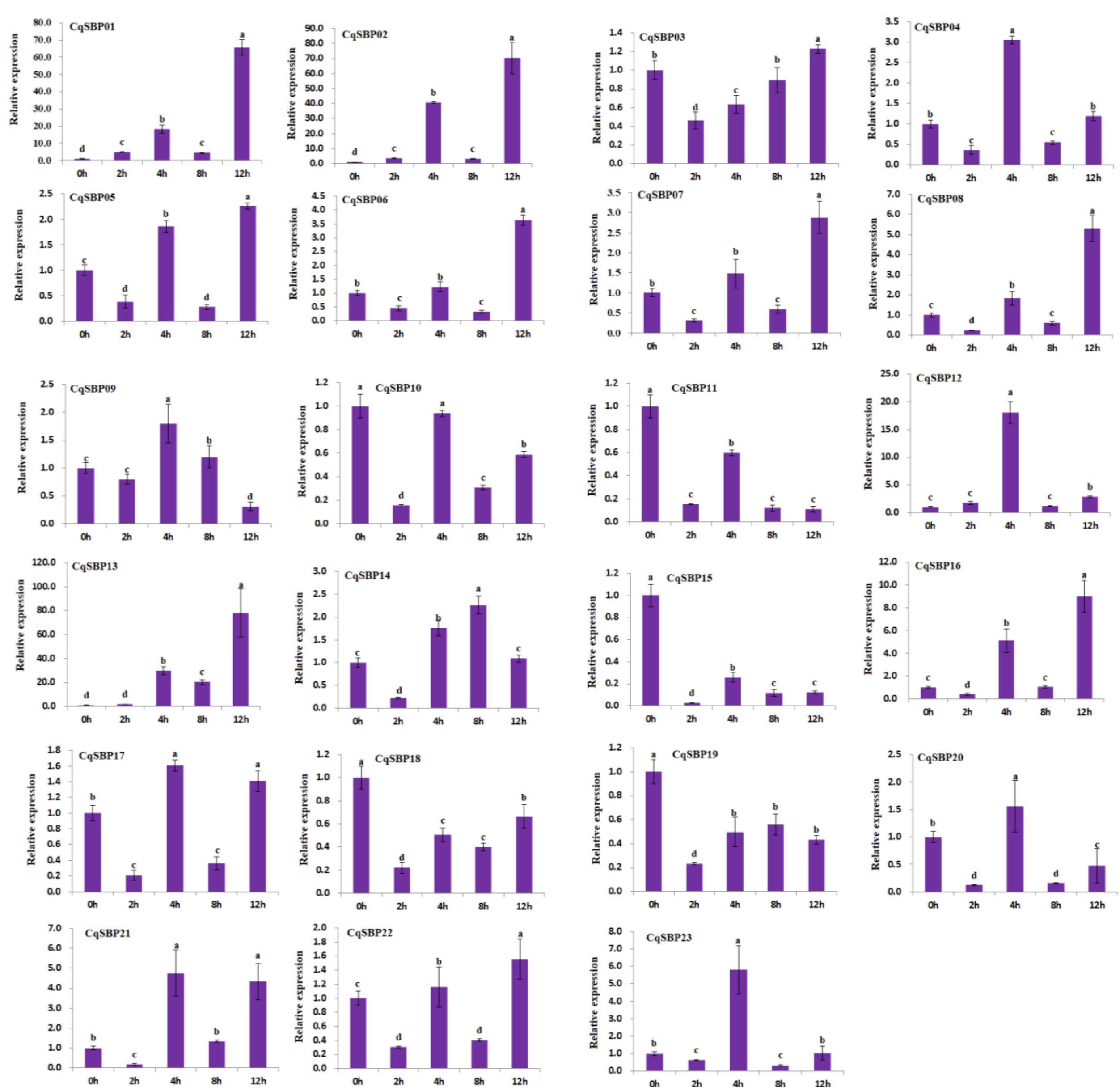

Fig. 7: Expression profiles of 23 SBP genes using qRT-PCR analysis in quinoa

Analysis of Expression Patterns

The analysis of quinoa gene transcriptome data obtained gene expression profiles of 23 quinoa CqSBP genes in 13 quinoa tissues and 10 different treatments. TBtools software was used to draw a gene expression map (Fig. 6, Table S3). In the figure, red and blue indicate the intensity of gene expression where red indicates strong signal strength and blue indicates weak signal strength. The results showed that most of the genes in the SBP family were strong expresses under different treatments (CqSBP03/CqSBP04, CqSBP05/CqSBP06, CqSBP07 CqSBP08/CqSBP10, CqSBP13, CqSBP16/CqSBP17, CqSBP22/CqSBP23). The expression of some SBP genes was expressed at very low under different treatments (CqSBP01/CqSBP02, CqSBP14/CqSBP15, CqSBP18/CqSBP19, and CqSBP09).

There are differences in expressing different SBP genes in different organs and periods of quinoa. Further analysis revealed that the expression of SBP genes has certain tissue specificity. Gene expression in the same branch of the evolutionary tree was similar. For example, CqSBP11/CqSBP12, CqSBP14/CqSBP15, and CqSBP20/CqSBP21 genes are expressed very low in different tissues of quinoa. CqSBP13 is expressed at very high levels in various tissues. CqSBP01/CqSBP02 genes were highly expressed in Apical meristems, stems, Flowers, immaturity seeds, and Leaf petioles of quinoa. Also highly expressed in apical meristems were CqSBP09, CqSBP13, CqSBP08/CqSBP10, and CqSBP16/SBP18. (A) CqSBP expression patterns at different treatments. (B) CqSBP expression patterns at different developmental stages and tissues. FPKM was used to calculate gene expression and the data was standardized using the Log2 method.

Q-RTPCR Analysis

To investigate whether the CqSBP gene family has a certain expression pattern under salt stress. We used qRT-PCR to detect the expression changes of each gene in leaves under salt stress (Fig. 7, Table S4-S5). The results showed that most of the repeated gene pairs have similar expression patterns, such as CqSBP01/CqSBP02, CqSBP05/CqSBP06, CqSBP16/CqSBP17, CqSBP18/CqSBP19 and the expression patterns of individual repeated genes also differed significantly (CqSBP08/CqSBP10, CqSBP11/CqSBP12, CqSBP14/CqSBP15). Most of the genes respond significantly to salt stress. The expression levels of CqSBP01, CqSBP02, CqSBP12, CqSBP13, and CqSBP16 genes under salt stress increased by 10 times or even 100 times. Among them, the expression level of CqSBP13 under salt stress was 78 times that of the control. This gene plays an extremely important role in salt stress, but its function still needs further research. Most of the genes (CqSBP03, CqSBP04, CqSBP05, CqSBP06, CqSBP07, CqSBP08, CqSBP09, CqSBP10, CqSBP14, CqSBP17, CqSBP20, CqSBP21, CqSBP22, and CqSBP23) expressed more frequently after stress treatment, at the same time, we found that some genes also showed down-regulated under salt stress (CqSBP11, CqSBP15, CqSBP18, and CqSBP19), suggesting that these genes might play a negative role in salt stress. These results suggest that the CqSBP gene in quinoa may be involved in salt-stress adaptation through complex mechanisms. Values represented the mean ± Standard Error of the Mean (SEM) of three biological replicates with three technical replicates at different treatments. Error bars indicated the SEM among the three experiments.

Discussion

The SBP box protein family is a type of plant specific transcription factor which regulates the expression of downstream genes by binding to cis-acting elements in the promoter region of downstream genes. The number of members of this family varies greatly among different species, 17, 19, and 49 SBP gene family members were identified in *Arabidopsis*, rice, and soybean respectively (Schmutz *et al*., 2010; Yang *et al*.,2008). This study identified 23 SBP genes of quinoa. The changes in SBP genes in different species illustrate biodiversity and the evolutionary relationships among different species. The 23 CqSBP genes are distributed on 12 chromosomes. The number of amino acids, isoelectric points, and molecular weights of CqSBP proteins varied considerably. This may be due to the different functions of the SBP family during growth and development.

Interestingly, we found that all CqSBP genes are located in the nucleus, indicating that CqSBP can be the transcription factor in the nucleus. Gene duplication is of great significance for the evolution of gene families, mainly because gene duplication can provide the most primitive material for generating new genes, which in turn promotes the generation of new functions (Rensing, 2014). There are three main ways of plant gene replication: fragment replication, tandem replication, transposition events such as retro trans position, and repeated transcription. Fragment duplication is the most important way because most plants undergo a chromosome doubling process and retain many repeated chromosome fragments in the genome (Wang *et al*., 2012b). This study identified that 11 pairs of homologous genes were generated by fragment duplication and 1 pair of homologous genes was amplified by tandem duplication, indicating that the amplification of the quinoa gene family was mainly amplified by fragment duplication. SPL10/SPL11 in *Arabidopsis* has the same gene structure. The sequences are highly similar (82.1%) and they are chromosomally contiguous. They may be produced by the repeat mechanism. The corresponding SBP-box in quinoa has tandem replication. The family members CqSBP06/CqSBP07 also have high homology. Quinoa is a hetero tetraploid plant whose genome has undergone a process of doubling during evolution so that many genes exist in multiple copies in the quinoa genome. Recent studies have shown that a genome-wide duplication event occurred in Quinoa between 3.3-6.3 Million Years Ago (MYA), supporting the idea that genes exist in multiple copies (Jarvis *et al*., 2017). This study found that multiple copies of SBP genes are scattered on different chromosomes. Micro collinearity analysis showed that there are 8 pairs of SBP paralogous genes in the quinoa genome, which provides favorable evidence for the doubling of the quinoa genome.

From a phylogenetic point of view, SBP genes are composed of multiple members in most plants. For example, 3, 4, and 8 SBP homologous gene pairs were identified in *Arabidopsis*, rice, and soybean genomes. They are horizontally homologous genes, in the same evolutionary branch and are formed after speciation. Compared with *Arabidopsis* and rice, quinoa has more

SBP homologous gene pairs, which strongly indicates that more repetitive events of SBP genes occur after quinoa speciation. Generally speaking, SBP genes with complete SBP functional domains can often be found in EST sequences, which means that these SBP genes are transcriptionally active. The 23 CqSBP genes in this study all included typical SBP functional domains.

The C-terminus of the conserved domain of the SBP transcription factor is the nuclear localization signal region. In analyzing the conserved domains of SBP, this study found that the domain of quinoa SBP protein contains about 79 amino acid residues with two zinc finger structures, C3H (C-C-C-H) and C2HC (C-C-H-C) types. Most transcription factors have an NLS site at the C-terminus of the SBP-conserved domain. In addition, CqSBP genes located in the same branch share similar intron/exon structures and most CqSBPs of the same branch have similar motifs. Therefore, genes from the same phylogenetic group may have similar roles in quinoa. This indicates that the evolution of the SBP-box gene family may be closely related to the diversity of gene structure. In addition to the conserved CqSBP motif, several unique group-specific motifs have also been observed, such as CqSBP05, CqSBP06, CqSBP07, and CqSBP13 subfamily the motifs in 2, 5, 6, 7, 8, 9 and 10. These specific motifs may be important for the specific roles of the CqSBP genes and their functional differentiation may have occurred during the evolution of different lineages.

Gene expression profile analysis showed that the expression patterns of genes in this family are different in different tissues. These results may be an important research resource to further reveal the function of CqSBP genes in quinoa development. Most SBP genes are widely expressed in the meristems, flowers, inflorescences, petioles, internodes, stems, and leaves of quinoa, suggesting that they play a key role in these biological processes. At the same time, most CqSBP genes are highly expressed in the apical meristem, which indicates that they are widely involved in cell differentiation. Studies have shown that AtSPL8 mediates other development, flowering, cell differentiation, floral organ development, and stamen filament elongation (Unte *et al*., 2003; Zhang *et al*., 2007). BrcSPL8 plays an important role in developing Chinese cabbage flowers (Zhang *et al*., 2017b). In this study, CqSBP01 and CqSBP02, homologous to AtSPL8, are highly expressed in inflorescence and apical meristems. It is hypothesized that they may be involved in differentiating meristems and flower formation. CqSBP08 and CqSBP10 are highly expressed in stems and they may participate in stem development and regulation of organ formation, which has been verified in the study of the homologous gene ATSPL9 (Zhang *et al*., 2020).

ATSPL14 plays a role in developing normal plant structures and is sensitive to fumonisin B1 (Stone *et al*., 2005). It is highly expressed in all organizations. OsSPL6 and OsSPL15 are also highly expressed in all tissues. In our study, CqSBP16 (the homologous gene of ATSPL14) is highly expressed in all tissues and it may affect the plant structure of quinoa. The qualitative analysis of the role of the quinoa SBP transcription factor in the growth and development of quinoa is of great significance to the study of the function of the quinoa SBP gene. It provides a certain theoretical basis to study the regulation mechanism of cotton fiber (with economic value). Therefore, increasing the research on these SBP genes may help better understand specific physiological processes. Q-TR-PCR showed that CqSBP01, CqSBP02, and CqSBP13 expressed extremely significantly under salt stress, indicating that these three genes may play a key role in salt stress. By analyzing the regulatory network related to SPL genes, 112 genes were found to be closely related to SPL genes and the promoters of these genes all contain a core motif of GATC, speculating that SBP transcription factors may be involved in plant tissues development, biotic and abiotic stress response and activation of other transcription factors and membrane proteins (Wang *et al*., 2009). At the same time, the SPL gene may also be involved in the metabolism of glucose, inorganic salts, and ATP as well as in carbohydrate transport. The SBP gene was discovered in the gene regulation network that studies the path of flower formation and therefore was considered to be closely related to flower development. In recent years, it has been discovered that the SBP gene has a wide range of biological functions. The SBP genes have been found in many plants, but their functions are still poorly understood. One reason for this is that almost all functional studies are carried out through mutants, for example, by constructing over-expression or silencing vectors of related genes, then using transgenic technology to transfer them into corresponding plants and observing the phenotype of the transgenic plants. The functions of the genes are interpreted.

Conclusion

The SBP gene family of quinoa has 23 members encoding weakly alkaline hydrophilic proteins. The SBP family genes are unevenly distributed on 12 chromosomes of quinoa, mainly on the B chromosome group. Upstream cis-acting element analysis revealed 49 elements related to plant hormones, stress, light response, and tissue-specific expression and all CqSBPs contain one or more Tata box elements. Protein interaction network analysis showed that all CqSBP proteins appear in the known interaction network of *Arabidopsis*. The expression of different SBP genes varied at different organs and periods and the expression of SBP genes has certain tissue specificity. The expression of CqSBP showed many changes under salt stress.

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Author's Contributions

Weihai Hou: Conceived and designed the research, conducted experiments, as well as wrote the manuscript.

Jianlin Wang: Prepared seed materials.

Zongyu Zhang: Data analysis for the research.

Inzamam Ul Haq: Help with experiments.

Xibo Feng: Designed the research, funds acquisition, and project administration.

Ethics

This study was performed in line with the principles of the declaration of Helsinki. Approval was granted by the bioethics committee of Tibet agricultural and animal husbandry university. The authors declare that there is no conflict of interests.

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Supplemental files

Table S1-S5

Table S1: The70 Sbp gene-coding protein sequence information in this study

GENE ID	GENE NAME	PROTEIN SEQUENCE
AT1G02065.1	ATSBP01	MLDYEWDNPSSIVLSGDERNPDSDPTRSSFSFFDPISHYNNDHRHITISPPLLSSFSNQQ QQHHLTLYGQTNSNNQFLHHHHHHHSLYGSTTTTTPYGASDPIYHPHSSAPPASLFSYDQ TGPGSGSGSSYNFLIPKTEVDFTSNRIGLNLGGRTYFSAADDDFVSRLYRRSRPGESGMA NSLSTPRCQAEGCNADLSHAKHYHRRHKVCEFHSKASTVVAAGLSQRFCQQCSRFHLLSE FDNGKRSCRKRLADHNRRRRKCHQSASATQDTGTGKTTPKSPNDSGVKASSSPSSNAPPT ISLECFRQRQFQTTASSSTSASSSSNSMFFSSG
AT1G02065.2	ATSBP02	MLDYEWDNPSSIVLSGDERNPDSDPTRSSFSFFDPISHYNNDHRHITISPPLLSSFSNQQ QQHHLTLYGQTNSNNQFLHHHHHHHSLYGSTTTTTPYGASDPIYHPHSSAPPASLFSYDQ TGPGSGSGSSYNFLIPKTEVDFTSNRIGLNLGGRTYFSAADDDFVSRLYRRSRPGESGMA NSLSTPRCQAEGCNADLSHAKHYHRRHKVCEFHSKASTVVAAGLSQRFCQQCSRFVPPKV ATFDLF
AT1G20980.1	ATSBP03	MDEVGAQVAAPMFIHQSLGRKRDLYYPMSNRLVQSQPQRRDEWNSKMWDWDSRRFEAKPV DVEVQEFDLTLRNRSGEERGLDLNLGSGLTAVEETTTTTQNVRPNKKVRSGSPGGNYPMC QVDNCTEDLSHAKDYHRRHKVCEVHSKATKALVGKQMQRFCQQCSRFHLLSEFDEGKRSC RRRLAGHNRRRRKTTQPEEVASGVVVPGNHDTTNNTANANMDLMALLTALACAQGKNAVK PPVGSPAVPDREQLLQILNKINALPLPMDLVSKLNNIGSLARKNMDHPTVNPQNDMNGAS PSTMDLLAVLSTTLGSSSPDALAILSQGGFGNKDSEKTKLSSYENGVTTNLEKRTFGFSS VGGERSSSSNQSPSQDSDSRGQDTRSSLSLQLFTSSPEDESRPTVASSRKYYSSASSNPV EDRSPSSSPVMQELFPLQASPETMRSKNHKNSSPRTGCLPLELFGASNRGAADPNFKGFG QQSGYASSGSDYSPPSLNSDAQDRTGKIVFKLLDKDPSQLPGTLRSEIYNWLSNIPSEME SYIRPGCVVLSVYVAMSPAAWEQLEQKLLQRLGVLLQNSPSDFWRNARFIVNTGRQLASH KNGKVRCSKSWRTWNSPELISVSPVAVVAGEETSLVVRGRSLTNDGISIRCTHMGSYMAM EVTRAVCRQTIFDELNVNSFKVQNVHPGFLGRCFIEVENGFRGDSFPLIIANASICKELN RLGEEFHPKSQDMTEEQAQSSNRGPTSREEVLCFLNELGWLFQKNQTSELREQSDFSLAR FKFLLVCSVERDYCALIRTLLDMLVERNLVNDELNREALDMLAEIQLLNRAVKRKSTKMV ELLIHYLVNPLTLSSSRKFVFLPNITGPGGITPLHLAACTSGSDDMIDLLTNDPQEIGLS SWNTLRDATGQTPYSYAAIRNNHNYNSLVARKLADKRNKQVSLNIEHEVVDQTGLSKRLS LEMNKSSSSCASCATVALKYQRRVSGSQRLFPTPIIHSMLAVATVCVCVCVFMHAFPIVR QGSHFSWGGLDYGSI
AT1G27360.1	ATSBP04	MDCNMVSSSQWDWEHLIMSNPSRTEDDSKQLPTEWEIEKGEGIESIVPHFSGLERVSSGS ATSFWHTAVSKSSQSTSINSSSPEAKRCKLASESSPGDSCSNIDFVQVKAPTALEVSVAS AESDLCLKLGKRTYSEEYWGRNNNEISAVSMKLLTPSVVAGKSKLCGQSMPVPRCQIDGC ELDLSSAKGYHRKHKVCEKHSKCPKVSVSGLERRFCQQCSRFHAVSEFDEKKRSCRKRLS HHNARRRKPQGVFSMNPERVYDRRQHTNMLWNGVSLNARSEEMYEWGNNTYDTKPRQTEK

Table S1: Continue

		SFTLSFQRGNGSEDQLVASSSRMFSTSQTSGGFPAGKSKFQLHGEDVGEYSGVLHESQDI HRALSLLSTSSDPLAQPHVQPFSLLCSYDVVPK
AT1G27360.2	ATSBP05	MDCNMVSSSQWDWEHLIMSNPSRTEDDSKQLPTEWEIEKGEGIESIVPHFSGLERVSSGS ATSFWHTAVSKSSQSTSINSSSPEAKRCKLASESSPGDSCSNIDFVQVKAPTALEVSVAS AESDLCLKLGKRTYSEEYWGRNNNEISAVSMKLLTPSVVAGKSKLCGQSMPVPRCQIDGC ELDLSSAKGYHRKHKVCEKHSKCPKVSVSGLERRFCQQCSRFHAVSEFDEKKRSCRKRLS HHNARRRKPQGVFSMNPERVYDRRQHTNMLWNGVSLNARSEEMYEWGNNTYDTKPRQTEK SFTLSFQRGNGSEDQLVASSSRMFSTSQTSGGFPAGKSKFQLHGEDVGEYSGVLHESQDI HRALSLLSTSSDPLAQPHVQPFSLLCSYDVVPK
AT1G27360.3	ATSBP06	MDCNMVSSSQWDWEHLIMSNPSRTEDDSKQLPTEWEIEKGEGIESIVPHFSGLERVSSGS ATSFWHTAVSKSSQSTSINSSSPEAKRCKLASESSPGDSCSNIDFVQVKAPTALEVSVAS AESDLCLKLGKRTYSEEYWGRNNNEISAVSMKLLTPSVVAGKSKLCGQSMPVPRCQIDGC ELDLSSAKGYHRKHKVCEKHSKCPKVSVSGLERRFCQQCSRFHAVSEFDEKKRSCRKRLS HHNARRRKPQGVFSMNPERVYDRRQHTNMLWNGVSLNARSEEMYEWGNNTYDTKPRQTEK SFTLSFQRGNGSEDQLVASSSRMFSTSQTSGGFPAGKSKFQLHGEDVGEYSGVLHESQDI HRALSLLSTSSDPLAQPHVQPFSLLCSYDVVPK
AT1G27360.4	ATSBP07	MDCNMVSSSQWDWEHLIMSNPSRTEDDSKQLPTEWEIEKGEGIESIVPHFSGLERVSSGS ATSFWHTAVSKSSQSTSINSSSPEAKRCKLASESSPGDSCSNIDFVQVKAPTALEVSVAS AESDLCLKLGKRTYSEEYWGRNNNEISAVSMKLLTPSVVAGKSKLCGQSMPVPRCQIDGC ELDLSSAKGYHRKHKVCEKHSKCPKVSVSGLERRFCQQCSRFHAVSEFDEKKRSCRKRLS HHNARRRKPQGVFSMNPERVYDRRQHTNMLWNGVSLNARSEEMYEWGNNTYDTKPRQTEK SFTLSFQRGNGSEDQLVASSSRMFSTSQTSGGFPAGKSKFQLHGEDVGEYSGVLHESQDI HRALSLLSTSSDPLAQPHVQPFSLLCSYDVVPK
AT1G27370.1	ATSBP08	MDCNMVSSFPWDWENLIMSNQSKTENEKKQQSTEWEFEKGEGIESIVPDFLGFEKVSSGS ATSFWHTAVSKSSQSTSINSSSPEDKRCNLASQSSPGDSSSNIDFLQVKPSTALEVPIAS AESDLCLKLGKRTYSEEFWGRNNNDLSAVSMNLLTPSVVARKKTKSCGQSMQVPRCQIDG CELDLSSSKDYHRKHRVCETHSKCPKVVVSGLERRFCQQCSRFHAVSEFDEKKRSCRKRL SHHNARRRKPQGVFPLNSERVFDRRQHTSMLWNGLSLNTRSEEKYTWGTTYETKPTQMES GFTLSFQRGNGSEDQLFTGSTLSFSAFQTSGGFSAGKSNIQLPDKGVGECSGGLHESHDF YSALSLLSTTSDSQGIKHTPVAEPPPIFGTFPSHFI
AT1G27370.2	ATSBP09	MDCNMVSSFPWDWENLIMSNQSKTENEKKQQSTEWEFEKGEGIESIVPDFLGFEKVSSGS ATSFWHTAVSKSSQSTSINSSSPEDKRCNLASQSSPGDSSSNIDFLQVKPSTALEVPIAS AESDLCLKLGKRTYSEEFWGRNNNDLSAVSMNLLTPSVVARKKTKSCGQSMQVPRCQIDG CELDLSSSKDYHRKHRVCETHSKCPKVVVSGLERRFCQQCSRFHAVSEFDEKKRSCRKRL SHHNARRRKPQGVFPLNSERVFDRRQHTSMLWNGLSLNTRSEEKYTWGTTYETKPTQMES GFTLSFQRGNGSEDQLFTGSTLSFSAFQTSGGFSAGKSNIQLPDKGVGECSGGLHESHDF YSALSLLSTTSDSQGIKHTPVAEPPPIFGTFPSHFI
AT1G27370.3	ATSBP10	MDCNMVSSFPWDWENLIMSNQSKTENEKKQQSTEWEFEKGEGIESIVPDFLGFEKVSSGS ATSFWHTAVSKSSQSTSINSSSPEDKRCNLASQSSPGDSSSNIDFLQVKPSTALEVPIAS AESDLCLKLGKRTYSEEFWGRNNNDLSAVSMNLLTPSVVARKKTKSCGQSMQVPRCQIDG CELDLSSSKDYHRKHRVCETHSKCPKVVVSGLERRFCQQCSRFHAVSEFDEKKRSCRKRL SHHNARRRKPQGVFPLNSERVFDRRQHTSMLWNGLSLNTRSEEKYTWGTTYETKPTQMES GFTLSFQRGNGSEDQLFTGSTLSFSAFQTSGGFSAGKSNIQLPDKGVGECSGGLHESHDF YSALSLLSTTSDSQGIKHTPVAEPPPIFGTFPSHFI
AT1G27370.4	ATSBP11	MDCNMVSSFPWDWENLIMSNQSKTENEKKQQSTEWEFEKGEGIESIVPDFLGFEKVSSGS ATSFWHTAVSKSSQSTSINSSSPEDKRCNLASQSSPGDSSSNIDFLQVKPSTALEVPIAS AESDLCLKLGKRTYSEEFWGRNNNDLSAVSMNLLTPSVVARKKTKSCGQSMQVPRCQIDG CELDLSSSKDYHRKHRVCETHSKCPKVVVSGLERRFCQQCSRFHAVSEFDEKKRSCRKRL SHHNARRRKPQGVFPLNSERVFDRRQHTSMLWNGLSLNTRSEEKYTWGTTYETKPTQMES GFTLSFQRGNGSEDQLFTGSTLSFSAFQTSGGFSAGKSNIQLPDKGVGECSGGLHESHDF YSALSLLSTTSDSQGIKHTPVAEPPPIFGTFPSHFI
AT1G53160.1	ATSBP12	MEGKRSQGQGYMKKKSYLVEEDMETDTDEEEEVGRDRVRGSRGSINRGGSLRLCQVDRCT ADMKEAKLYHRRHKVCEVHAKASSVFLSGLNQRFCQQCSRFHDLQEFDEAKRSCRRRLAG HNERRRKSSGESTYGEGSGRRGINGQVVMQNQERSRVEMTLPMPNSSFKRPQIR
AT1G53160.2	ATSBP13	MEGKRSQGQGYMKKKSYLVEEDMETDTDEEEEVGRDRVRGSRGSINRGGSLRLCQVDRCT ADMKEAKLYHRRHKVCEVHAKASSVFLSGLNQRFCQQCSRFHDLQEFDEAKRSCRRRLAG HNERRRKSSGESTYGEGSGRRGINGQVVMQNQERSRVEMTLPMPNSSFKRPQIR
AT1G69170.1	ATSBP14	MDSWSYGRSVFMSNETLLPCDTFAKNRRFEQRLSNNDDVLISDMAGNSNGFSAVSITKVV PEEEDEENISSSSKFSSQELNRIDFKLRSFLDLGNDDDDTSSRGFALPSKKSRASNLCSQ NPLCQVYGCSKDLSSSKDYHKRHRVCEAHSKTSVVIVNGLEQRFCQQCSRFHFLSEFDDG KRSCRRRLAGHNERRRKPAFYFLPGKRHKLLRTSQDVVGNKFLENSSLVLPESFPGSLLY RVIDEDDHRTSRLVSFKDEPTCSMFPTNEQNSSRTYESKPAIYSTEVSSIWDLHETAASR STRALSLLSAQSQQHLSKFPNTTFSITQPNQNLNHSSSTDYHQMEQPLWIDPGKTNSAGS SSCKGKGTSTVDLLQLSSHLQRIEQQRNYTGDVKQEYNELYFPGS
AT1G76580.1	ATSBP15	MGELPKDDWQMNRWKWDGQRFEAIELQGESLQLSNKKGLDLNLPCGFNDVEGTPVDLTRP SKKVRSGSPGSGGGGGGNYPKCQVDNCKEDLSIAKDYHRRHKVCEVHSKATKALVGKQMQ RFCQQCSRFHLLSEFDEGKRSCRRRLDGHNRRRRKTQPDAITSQVVALENRDNTSNNTNM DVMALLTALVCAQGRNEATTNGSPGVPQREQLLQILNKIKALPLPMNLTSKLNNIGILAR KNPEQPSPMNPQNSMNGASSPSTMDLLAALSASLGSSAPEAIAFLSQGGFGNKESNDRTK LTSSDHSATTSLEKKTLEFPSFGGGERTSSTNHSPSQYSDSRGQDTRSSLSLQLFTSSPE EESRPKVASSTKYYSSASSNPVEDRSPSSSPVMQELFPLHTSPETRRYNNYKDTSTSPRT SCLPLELFGASNRGATANPNYNVLRHQSGYASSGSDYSPPSLNSNAQERTGKISFKLFEK DPSQLPNTLRTEIFRWLSSFPSDMESFIRPGCVILSVYVAMSASAWEQLEENLLQRVRSL VQDSEFWSNSRFLVNAGRQLASHKHGRIRLSKSWRTLNLPELITVSPLAVVAGEETALIV RGRNLTNDGMRLRCAHMGNYASMEVTGREHRLTKVDELNVSSFQVQSASSVSLGRCFIEL ENGLRGDNFPLIIANATICKELNRLEEEFHPKDVIEEQIQNLDRPRSREEVLCFLNELGW LFQRKWTSDIHGEPDFSLPRFKFLLVCSVERDYCSLIRTVLDMMVERNLGKDGLLNKESL DMLADIQLLNRAIKRRNTKMAETLIHYSVNPSTRNFIFLPSIAGPGDITPLHLAASTSSS DDMIDALTNDPQEIGLSCWNTLVDATGQTPFSYAAMRDNHSYNTLVARKLADKRNGQISL NIENGIDQIGLSKRLSSELKRSCNTCASVALKYQRKVSGSRRLFPTPIIHSMLAVATVCV CVCVFMHAFPMVRQGSHFSWGGLDYGSI
AT2G33810.1	ATSBP16	MSMRRSKAEGKRSLRELSEEEEEEEETEDEDTFEEEEALEKKQKGKATSSSGVCQVESCT ADMSKAKQYHKRHKVCQFHAKAPHVRISGLHQRFCQQCSRFHALSEFDEAKRSCRRRLAG HNERRRKSTTD
AT2G42200.1	ATSBP17	MEMGSNSGPGHGPGQAESGGSSTESSSFSGGLMFGQKIYFEDGGGGSGSSSSGGRSNRRV RGGGSGQSGQIPRCQVEGCGMDLTNAKGYYSRHRVCGVHSKTPKVTVAGIEQRFCQQCSR FHQLPEFDLEKRSCRRRLAGHNERRRKPQPASLSVLASRYGRIAPSLYENGDAGMNGSFL GNQEIGWPSSRTLDTRVMRRPVSSPSWQINPMNVFSQGSVGGGGTSFSSPEIMDTKLESY KGIGDSNCALSLLSNPHQPHDNNNNNNNNNNNNNNNTWRASSGFGPMTVTMAQPPPAPSQH QYLNPPWVFKDNDNDMSPVLNLGRYTEPDNCQISSGTAMGEFELSDHHHQSRRQYMEDEN TRAYDSSSHHTNWSL

Table S1: Continue

AT2G47070.1	ATSBP18	MEARIDEGGEAQQFYGSVGKRSVEWDLNDWKWDGDLFLATQTTRGRQFFPLGNSSNSSSS CSDEGNDKKRRAVAIQGDTNGALTLNLNGESDGLFPAKKTKSGAVCQVENCEADLSKVKD YHRRHKVCEMHSKATSATVGGILQRFCQQCSRFHLLQEFDEGKRSCRRRLAGHNKRRRKT NPEPGANGNPSDDHSSNYLLITLLKILSNMHNHTGDQDLMSHLLKSLVSHAGEQLGKNLV ELLLQGGGSQGSLNIGNSALLGIEQAPQEELKQFSARQDGTATENRSEKQVKMNDFDLND IYIDSDDTDVERSPPPTNPATSSLDYPSWIHQSSPPQTSRNSDSASDQSPSSSSEDAQMR TGRIVFKLFGKEPNEFPIVLRGQILDWLSHSPTDMESYIRPGCIVLTIYLRQAETAWEEL SDDLGFSLGKLLDLSDDPLWTTGWIYYVRVQNQLAFVYNGQVVVDTSLSLKSRDYSHIISV KPLAIAATEKAQFTVKGMNLRQRGTRLLCSVEGKYLIQETTHDSTTREDDDFKDNSEIVE CVNFSCDMPILSGRGFMEIEDQGLSSSFFPFLVVEDDDVCSEIRILETTLEFTGTDSAKQ AMDFIHEIGWLLHRSKLGESDPNPGVFPLIRFQWLIEFSMDREWCAVIRKLLNMFFDGAV GEFSSSSNATLSELCLLHRAVRKNSKPMVEMLLRYIPKQQRNSLFRPDAAGPAGLTPLHI AAGKDGSEDVLDALTEDPAMVGIEAWKTCRDSTGFTPEDYARLRGHFSYIHLIQRKINKK STTEDHVVVNIPVSFSDREQKEPKSGPMASALEITQIPCKLCDHKLVYGTTRRSVAYRPA MLSMVAIAAVCVCVALLFKSCPEVLYVFQPFRWELLDYGTS
AT3G15270.1	ATSBP19	MEGQRTQRRGYLKDKATVSNLVEEEMENGMDGEEEDGGDEDKRKKVMERVRGPSTDRVPS RLCQVDRCTVNLTEAKQYYRRHRVCEVHAKASAATVAGVRQRFCQQCSRFHELPEFDEAK RSCRRRLAGHNERRRKISGDSFGEGSGRRGFSGQLIQTQERNRVDRKLPMTNSSFKRPQI R
AT3G57920.1	ATSBP20	MELLMCSGQAESGGSSSTESSSLSGGLRFGQKIYFEDGSGSRSKNRVNTVRKSSTTARCQ VEGCRMDLSNVKAYYSRHKVCCIHSKSSKVIVSGLHQRFCQQCSRFHQLSEFDLEKRSCR RRLACHNERRRKPQPTTALFTSHYSRIAPSLYGNPNAAMIKSVLGDPTAWSTARSVMQRP GPWQINPVRETHPHMNVLSHGSSSFTTCPEMINNNSTDSSCALSLLSNSYPIHQQQLQTP TNTWRPSSGFDSMISFSDKVTMAQPPPISTHQPPISTHQQYLSQTWEVIAGEKSNSHYMS PVSQISEPADFQISNGTTMGGFELYLHQQVLKQYMEPENTRAYDSSPQHFNWSL
AT3G60030.1	ATSBP21	MEARIEGEVEGHSLEYGFSGKRSVEWDLNDWKWNGDLFVATQLNHGSSNSSSTCSDEGNV EIMERRRIEMEKKKKRRAVTVVAMEEDNLKDDDAHRLTLNLGGNNIEGNGVKKTKLGGGI PSRAICCQVDNCGADLSKVKDYHRRHKVCEIHSKATTALVGGIMQRFCQQCSRFHVLEEF DEGKRSCRRRLAGHNKRRRKANPDTIGNGTSMSDDQTSNYMLITLLKILSNIHSNQSDQT GDQDLLSHLLKSLVSQAGEHIGRNLVGLLQGGGGLQASQNIGNLSALLSLEQAPREDIKH HSVSETPWQEVYANSAQERVAPDRSEKQVKVNDFDLNDIYIDSDDTTDIERSSPPPTNPA TSSLDYHQDSRQSSPPQTSRRNSDSASDQSPSSSSGDAQSRTDRIVFKLFGKEPNDFPVA LRGQILNWLAHTPTDMESYIRPGCIVLTIYLRQDEASWEELCCDLSFSLRRLLDLSDDPL WTDGWLYLRVQNQLAFAFNGQVVLDTSLPLRSHDYSQIITVRPLAVTKKAQFTVKGINLR RPGTRLLCTVEGTHLVQEATQGGMEERDDLKENNEIDFVNFSCEMPIASGRGFMEIEDQG GLSSSFFPFIVSEDEDICSEIRRLESTLEFTGTDSAMQAMDFIHEIGWLLHRSELKSRLA ASDHNPEDLFSLIRFKFLIEFSMDREWCCVMKKLLNILFEEGTVDPSPDAALSELCLLHR AVRKNSKPMVEMLLRFSPKKKNQTLAGLFRPDAAGPGGLTPLHIAAGKDGSEDVLDALTE DPGMTGIQAWKNSRDNTGFTPEDYARLRGHFSYIHLVQRKLSRKPIAKEHVVVNIPESFN IEHKQEKRSPMDSSSLEITQINQCKLCDHKRVFVTTHHKSVAYRPAMLSMVAIAAVCVCV ALLFKSCPEVLYVFQPFRWELLEYGTS
AT5G18830.1	ATSBP22	MSSLSQSPPPPEMDIQPPALVNDDPSTYSSALWDWGDLLDFAADERLLVDQIHFPPVLSP PLPPLIPTQTPAESELDPSPEESGSGSDRVRKRDPRLICSNFIEGMLPCSCPELDQKLED AELPKKKRVRGGSGVARCQVPDCEADISELKGYHKRHRVCLRCATASFVVLDGENKRYCQ QCGKFHLLPDFDEGKRSCRRKLERHNNRRKRKPVDKGGVAAEQQQVLSQNDNSVIDVEDG KDITCSSDQRAEEEPSLIFEDRHITTQGSVPFTRSINADNFVSVTGSGEAQPDEGMNDTK FERSPSNGDNKSAYSTVCPTGRISFKLYDWNPAEFPRRLRHQIFQWLANMPVELEGYIRP GCTILTVFIAMPEIMWAKLSKDPVAYLDEFILKPGKMLFGRGSMTVYLNNMIFRLIKGGT TLKRVDVKLESPKLQFVYPTCFEAGKPIELVVCGQNLLQPKCRFLVSFSGKYLPHNYSVV PAPDQDGKRSCNNKFYKINIVNSDPSLFGPAFVEVENESGLSNFIPLIIGDAAVCSEMKL IEQKFNATLFPEGQEVTACSSLTCCCRDFGERQSTFSGLLLDIAWSVKVPSAERTEQPVN RCQIKRYNRVLNYLIQNNSASILGNVLHNLETLVKKMEPDSLVHCTCDCDVRLLHENMDL ASDIHRKHQSPIESKVNPPSSGCCCVSSQKDIPSRILNFNKDPEAGLDCKERIQADCSPD SGGKETDPLLNKEVVMNVNDIGDWPRKSCIKTHSALAFRSRQTMFLIATFAVCFAVCAVL YHPNKVTQLAVAIRMRLVHKI
AT5G18830.2	ATSBP23	MSSLSQSPPPPEMDIQPPALVNDDPSTYSSALWDWGDLLDFAADERLLVDQIHFPPVLSP PLPPLIPTQTPAESELDPSPEESGSGSDRVRKRDPRLICSNFIEGMLPCSCPELDQKLED AELPKKKRVRGGSGVARCQVPDCEADISELKGYHKRHRVCLRCATASFVVLDGENKRYCQ QCGKFHLLPDFDEGKRSCRRKLERHNNRRKRKPVDKGGVAAEQQQVLSQNDNSVIDVEDG KDITCSSDQRAEEEPSLIFEDRHITTQGSVPFTRSINADNFVSVTGSGEAQPDEGMNDTK FERSPSNGDNKSAYSTVCPTGRISFKLYDWNPAEFPRRLRHQIFQWLANMPVELEGYIRP GCTILTVFIAMPEIMWAKLSKDPVAYLDEFILKPGKMLFGRGSMTVYLNNMIFRLIKGGT TLKRVDVKLESPKLQFVYPTCFEAGKPIELVVCGQNLLQPKCRFLVSFSGKYLPHNYSVV PAPDQDGKRSCNNKFYKINIVNSDPSLFGPAFVEVENESGLSNFIPLIIGDAAVCSEMKL IEQKFNATLFPEGQEVTACSSLTCCCRDFGERQSTFSGLLLDIAWSVKVPSAERTEQPVN RCQIKRYNRVLNYLIQNNSASILGNVLHNLETLVKKMEPDSLVHCTCDCDVRLLHENMDL ASDIHRKHQSPIESKDPEAGLDCKERIQADCSPDSGGKETDPLLNKEVVMNVNDIGDWPR KSCIKTHSALAFRSRQTMFLIATFAVCFAVCAVLYHPNKVTQLAVAIRMRLVHKI
AT5G18830.3	ATSBP24	MSSLSQSPPPPEMDIQPPALVNDDPSTYSSALWDWGDLLDFAADERLLVDQIHFPPVLSP PLPPLIPTQTPAESELDPSPEESGSGSDRVRKRDPRLICSNFIEGMLPCSCPELDQKLED AELPKKKRVRGGSGVARCQVPDCEADISELKGYHKRHRVCLRCATASFVVLDGENKRYCQ QCGKFHLLPDFDEGKRSCRRKLERHNNRRKRKPVDKGGVAAEQQQVLSQNDNSVIDVEDG KDITCSSDQRAEEEPSLIFEDRHITTQGSVPFTRSINADNFVSVTGSGEAQPDEGMNDTK FERSPSNGDNKSAYSTVCPTGRISFKLYDWNPAEFPRRLRHQIFQWLANMPVELEGYIRP GCTILTVFIAMPEIMWAKLSKDPVAYLDEFILKPGKMLFGRGSMTVYLNNMIFRLIKGGT TLKRVDVKLESPKLQFVYPTCFEAGKPIELVVCGQNLLQPKCRFLVSFSGKYLPHNYSVV PAPDQDGKRSCNNKFYKINIVNSDPSLFGPAFVEVENESGLSNFIPLIIGDAAVCSEMKL IEQKFNATLFPEGQEVTACSSLTCCCRDFGERQSTFSGLLLDIAWSVKVPSAERTEQPVN RCQIKRYNRVLNYLIQNNSASILGNVLHNLETLVKKMEPDSLVHCTCDCDVRLLHENMDL ASDIHRKHQSPIESKVNPPSSGCCCVSSQKDIPSRILNFNKDPEAGLDCKERIQADCSPD SGGKETDPLLNKEVVMNVNDIGDWPRKSCIKTHSALAFRSRQTMFLIATFAVCFAVCAVL YHPNKVTQLAVAIRMRLCSTELSHNSFSESFPSERDRI
AT5G43270.1	ATSBP25	MECNAKPPFQWELENLISFGTSTAEVPRKLKPMEWEIDGFDCTSLYSSSFAYAGSSGSDI AHAFSKSSKSTSISSSSAEVRTHNFTSETGESLPGEFAKGIDTSPSLELSFGSGDPVLGL KLGKRTYFEDFWEVENAKGLGLPVTLASSSVSPVKKSKSIPQRLQTPHCQVEGCNLDLSS AKDYHRKHRICENHSKFPKVVVSGVERRFCQQCSRFHCLSEFDEKKRSCRRRLSDHNARR RKPNPGRTYDGKPQVDFVWNRFALIHPRSEEKFIWPSSKHVPSRVLMPQPAKTEISDTEH NRFGLLDPKTKTARAELFSKEKVTISSHMGASQDLDGALSLLSNSTTWVSSSDQPRRFTL DHHPSSNLQPVAHRSAAQLNSVSGYWQPDPPAVEGPTALHRNGVGQFNENYFSLNQFYN
AT5G43270.2	ATSBP26	MECNAKPPFQWELENLISFGTSTAEVPRKLKPMEWEIDGFDCTSLYSSSFAYAGSSGSDI AHAFSKSSKSTSISSSSAEVRTHNFTSETGESLPGEFAKGIDTSPSLELSFGSGDPVLGL

DOI: 10.3844/ajbbsp.2023.91.120

Table S1: Continue

		KLGKRTYFEDFWEVENAKGLGLPVTLASSSVSPVKKSKSIPQRLQTPHCQVEGCNLDLSS AKDYHRKHRICENHSKFPKVVVSGVERRFCQQCSRFHCLSEFDEKKRSCRRRLSDHNARR RKPNPGRTYDGKPQVDFVWNRFALIHPRSEEKFIWPSSKHVPSRVLMPQPAKTEISDTEH NRFGLLDPKTKTARAELFSKEKVTISSHMGASQDLDGALSLLSNSTTWVSSSDQPRRFTL DHHPSSNLQPVAHRSAAQLNSVSGYWQPDPPAVEGPTALHRNGVGQFNENYFSLNQFYN
AT5G43270.3	ATSBP27	MECNAKPPFQWELENLISFGTSTAEVPRKLKPMEWEIDGFDCTSLYSSSFAYAGSSGSDI AHAFSKSSKSTSISSSSAEVRTHNFTSETGESLPGEFAKGIDTSPSLELSFGSGDPVLGL KLGKRTYFEDFWEVENAKGLGLPVTLASSSVSPVKKSKSIPQRLQTPHCQVEGCNLDLSS AKDYHRKHRICENHSKFPKVVVSGVERRFCQQCSRFHCLSEFDEKKRSCRRRLSDHNARR RKPNPGRTYDGKPQVDFVWNRFALIHPRSEEKFIWPSSKHVPSRVLMPQPAKTEISDTEH NRFGLLDPKTKTARAELFSKEKVTISSHMGASQDLDGALSLLSNSTTWVSSSDQPRRFTL DHHPSSNLQPVAHRSAAQLNSVSGYWQPDPPAVEGPTALHRNGVGQFNENYFSLNQFYN
AT5G50570.1	ATSBP28	MDWNFKLSSGYLSGFDQEPDLSPMDGSISFGGSSQSKADFSFDLKLGRNIGNSSSVFGDT EQVISLSKWKDSALAKPEGSRSSSSKRTRGNGVGTNQMPICLVDGCDSDFSNCREYHKRH KVCDVHSKTPVVTINGHKQRFCQQCSRFHALEEFDEGKRSCRKRLDGHNRRRRKPQPEHI GRPANFFTGFQGSKLLEFSGGSHVFPTTSVLNPSWGNSLVSVAVAANGSSYGQSQSYVVG SSPAKTGIMFPISSSPNSTRSIAKQFPFLQEEESSRTASLCERMTSCIHDSDCALSLLSS SSSSVPHLLQPPLSLSQEAVETVFYGSGLFENASAVSDGSVISGNEAVRLPQTFPFHWE
AT5G50570.2	ATSBP29	MDWNFKLSSGYLSGFDQEPDLSPMDGSISFGGSSQSKADFSFDLKLGRNIGNSSSVFGDT EQVISLSKWKDSALAKPEGSRSSSSKRTRGNGVGTNQMPICLVDGCDSDFSNCREYHKRH KVCDVHSKTPVVTINGHKQRFCQQCSRFHALEEFDEGKRSCRKRLDGHNRRRRKPQPEHI GRPANFFTGFQGSKLLEFSGGSHVFPTTSVLNPSWGNSLVSVAVAANGSSYGQSQSYVVG SSPAKTGIMFPISSSPNSTRSIAKQFPFLQEEESSRTASLCERMTSCIHDSDCALSLLSS SSSSVPHLLQPPLSLSQEAVETVFYGSGLFENASAVSDGSVISGNEAVRLPQTFPFHWE
AT5G50670.1	ATSBP30	MDWNFKLSSGYLSGFDQEPDLSPMDGSISFGGSSQSKADFSFDLKLGRNIGNSSSVFGDT EQVISLSKWKDSALAKPEGSRSSSSKRTRGNGVGTNQMPICLVDGCDSDFSNCREYHKRH KVCDVHSKTPVVTINGHKQRFCQQCSRFHALEEFDEGKRSCRKRLDGHNRRRRKPQPEHI GRPANFFTGFQGSKLLEFSGGSHVFPTTSVLNPSWGNSLVSVAVAANGSSYGQSQSYVVG SSPAKTGIMFPISSSPNSTRSIAKQFPFLQEEESSRTASLCERMTSCIHDSDCALSLLSS SSSSVPHLLQPPLSLSQEAVETVFYGSGLFENASAVSDGSVISGNEAVRLPQTFPFHWE
SOLYC01G068100.2.1	SLSBP01	MEASVGERFYHMGGTDLRGLGKRSLEWDLTDWKWDGDLFIATPLQQNPSNYQSRQFFPVE TGNLASSNSSSSCSDEVNHGMEQQRRELEKRRRVIVVDEDDSGPLSLKLGGQGEPAADAG REMSNWDGAAGKRTKLAAPAAARAVCQVDDCGTDLSKAKDYHRRHKVCEMHSKASRALVG NVMQRFCQQCSRFHALQEFDEGKRSCRRRLAGHNKRRRKTQSETVANNNSLNDGQTSGYS LMSLLKILSNMHSNGANHTEDQDLLSHLLRSLASQGPTNGDKSLSGLLQESSNLLNNRSI LRNPEIASLISNGSQAPPRPKERQFTNSAAEMPQKRLEDARTASSQSPGILFPIQSNSQA YTPGRESTTGRSKLIDFDLNDAYVDSDDCGDDIDRSPVPECPSWLQQDSHQSSPPQTSGN SDSASAQSPSSSSGDNQNRTDRIVFKLFGKGPSDFPFVVRAQILDWLSHSPTEIESYIRP GCVVLTIYLRLPESAWEELSYDLSSSLSRLLDVHGGDSFWTKGWIYIRVQNQIAFVCDGQ VLLDMSLPCVSNDGSTLLSVRPIAVPVSDRVQFLVKGYNLTKPSTRLLCSLEGNYLDPEA DNEVEEQVAGGDKDDKLQSLNFTCSIPAVGGRGFIEVEDHGVSNSFFPFIIAEEDVCSEI RMLESDLELTSLDYVKGQTNNIEARNQAMDFIHELGWLLHRNNLRARLEHFGPNAVLHPL KRFKWLVEFSVDHEWCAVVKKLLNILLDGTVGGDDSSLKYALTEMGLLHKAVRRNSRPLV ELLLTYTPTNVADDLCSEYQSLVGVGGQFLFRPDCVGPGGLTPLHIAAGIDGYEDVLDAL TDDPGKVAIEAWKNTRDSTGFTPEDYARLRGHYSYIHLVQRKISKKANSGHIVVDIPRVP SVVENSNQKDEVCATTSLEISMTERKAIPRPCRLCDRKLAYGSRSRSLLYRPAMFSMVAM AAVCVCVALLFRGSPEVLYIFRPFRWEMVDFGTS*
SOLYC01G080670.2.1	SLSBP02	MISSLLSGDDPAASSNFDWSDLLDFDLHEQLNISFDDPLHQEQQPETEFVAPVIPSSEDS PHSQDTDAGRIRKRDPRMACSNFLAGRIPCACPELDEKMEEEEMAGIGPGKKRARTVRAS AGAGARCQVPDCEADISELKGYHKRHRVCLRCANATSVVLDGHSKRYCQQCGKFHILSDF DEGKRSCRRKLERHNNRRRRKATDTSKTSAEKESQQLTTADDVSGDDDIVKDNTCMGSQL GEKEILLESEGHVPICSTQGIQNNHSDSFTASGETQVDAEKENYKNSHSPSYYDNKSALS SVCPTGRISFKLYDWNPAEFPRRLRHQIFQWLASMPVELEGYIRPGCTILTVFVAMPTFK WGKLLEDPAAHLYELIASPGNMLRGRGSFLIYLNNMVFRVTKGENSVVKVKLKGPAPKLM SIYPTCFEAGKPMEFFACGSNLMQPRFRFLVSFGGRYLGNDINVVPSDCKYEGDSSSTEH QLLKIHVPRTEADLFGPAFVEVENESGLSNFIPILIAEKDICAEMKEIQRKFCSGGSECT AVCSPCEASTSRKSEFSEFMLDVAWLLREPSSENVQILASVQMQRFNYLLNILMESQSTI ILERVLSYFENIVKRNMLAGITDADMTLFQKNILEKNILLKERLHLKEYFAGDSGQIMQE LPNLQDTAVPHKHNIEFGPTYWELTSRVPLLDAELPLRVKEQQSGKSCGFLVRKTLLTSR TLVFVISGFALCLGLCATFLHPRKVGDIAMTIRRCLFDKT*
SOLYC01G090730.2.1	SLSBP03	MLDYEWENQSSFMFTSDQNTQEENDQNNNQFLDPQAHFPHITSYQHPQQQQQQLQNPHF PQFQATPNNTHLISSMYDPRAYGVPYTQTHDTSMLSLQPTGGFMVVPKSEPQFGGGIHDF SSSSSRIGLNLGGRTYFASSSEDDFVNRLYRRTRAVDAGSVNSPKCQAEGCNADLTHAKH YHRRHKVCEFHSKASTVIAAGLTQRFCQQCSRFHVLSEFDNGKRSCRKRLADHNRRRRKN IQQENNKKQPQPSSKSPAESGAQSSTVTVAISPPRIPVDGFRQRTYQQVTTSSSFPMGD*
SOLYC02G077920.2.1	SLSBP04	METNKWEGKRSITEAEKEEDEHGSVEEDSKRKRVLTLSGRKLVGEGSAHPSCQVDQCTAD MADAKPYHRRHKVCEFHSKSPIVLISGLQKRFCQQCSRFHLLAEFDDAKRSCRRRLAGHN ERRRKITYDSHGENLG*
SOLYC03G114850.2.1	SLSBP05	MESWSYFSGGKGFVSEESVSVNDGMRRVKNGVMGWELKTQSSYGMCTTDNQGFHELGSPN LMRKPMFTDQMRDGFASSKHWGGGGGSIVGAFSGEDKSSSKLSSSAVDSISRDSSLIDLK LGRFPDHHVDGNIFKSAKTLSSSTSAESILPAKRMRAGGLNSHKPFCQVQGCGKDLSPCK DYHKRHKVCEVHSKTAKVIVNGIEQRFCQQCSRFHLLAEFDDGKRSCRKRLAGHNERRRK PPHTGMYQISWNFFCNVTLCMPRHT*
SOLYC04G045560.2.1	SLSBP06	MFGSGFDSPPVGVYEKNSNCTVEEGCTSSAAPMMYGLGKRNNSSVELPLPSLSKKTKSST HNPLKPHCQVDSCNLDLSSAKQYHRKHRVCHIHSKCPKVIILGRHRRFCQQCSRFHSLSD FDENKRSCRTRLSDHNARRRKPQFNSTSTRFSSLFYDNKQSMNLVFNNAPLVHSKPTADS TWETSEVSKFTLTRGLTLKPYKADSFNGQSLVGGFKLSGTTEMQTNASNLYSVSNDTKAE VFSQGVKETTFSLNMGVAPELPRALSLLSNENEFISIGHSKHVNQIIIPEQVTHAIPQSL PFESSERWQAEQHLFNPHIHTLVANGHSGGSFQEIQLSKDPFDDSYMSMD*
SOLYC04G064470.1.1	SLSBP07	MKSKDSSDCTEQALFDELKALEEHLKAHMSLAPKMYHLEVALGHFKKWSVTESLSHVRNY MKLDPFLLPVVQGSILVHVLEEFDEGKRSCRRRLTGHKKRRRKTHPENVANGASVNDEGN YLLISLLRILANVQCNSLYGFHGFPAIYSFCMTKDVGKINKVIAFTQ*
SOLYC05G012040.2.1	SLSBP08	MEPLSYALEGRGLIFPDNVELSVDTVSRNRSIVKEWNLNPFCDVDKSICGFSQEVTENTE FLGSGIADILKKSAASNPCPGVLSGEMSDGCGKMLSSTSMFNSFEPIPGEVGLGAMFNNS ATKSNNPMSSLIDLKLEELTDHGELRTNQSSKESSILSSPESSLAAGKAQTKSSHSRFSI SQVHDQKEEESTTVYREVKSNQSLKRNSALTSVNSSLQGKRLRTTNFHSEIPVCQVHGCN KDLSSSKDYHKRHKVCNEHSKTAIVIVNGIEQRFCQQCSRFHLLAEFDEGKRSCRKRLAG HNERRRKPQFDTHWGSRFLDMTSQRRVPFLFPEIFPGSFFYQENYEDNNNSKHPKLEHKP FGISQLAISVKNEQFPAKSIQHQYGMRKQDPSKVHTGGTTLSIQEFSKGQNSSCALSLLS AHSQNLLHNSTDVSPTLRWTVEPNHHVYVKGRDHNLEKSPRVSVVKSLTPTELYSSDVAE QDVVVQVPDCEAVSFGIQRDHGHDQRSNSINSKNCLSLEGGPTMDLVQLSSHLQRVEQQK

Table S1: Continue

		NSVQVKQENDIFCSFTST*
SOLYC05G015510.2.1	SLSBP09	MEWNVKWDWGNLVMFGSKASESPKELQLTDWGVEEEGELDGGSFNLSSGGSGTGGYGSDL KCGSSIKSSISASTDSSPKDGFKVSNFAFETFNASPEDPSKKLESSKAEVSRNSPPMEAS VGSVEPVIGLKIGKRTCETFGGGSSAKVSSFPPNPASSAAATKKAKSSTQNAPIPHCQVE GCNLDLSSAKEYYRKHRVCDSHSKSPKVIVAGVARRFCQQCSRFHSVSEFDDKKRSCRRR LSDHNARRRKPHQETIQFNSARLSSLFYDSRQPMNLVLNEAQLIHSRAAANATWESTQDS KFSITREFTPKPERTGSTNGKSLLERNQFSRAVGAHSNASSLLLPSKGTTAEVFNRGAKE SMFNMVTGPEFPRALSLLSTNSWGSSEPESVSLNHANQTSMPEQMMQAIPPHMSSQYWQA GQHSSDPRYHTLAAANSNSGGSFQEMGVFKAPFDTDFYLNALN*
SOLYC05G015840.2.1	SLSBP10	MESSSSSSKRAKAPGNIAHCLVDGCNADLSECREYHRRHKVCEVHSKTAKVTIAGRDQRF CQQCSRFHSLVEFDDGKRSCRKRLDGHNRRRRKPQPDSMAKNSGILFGQQGTKLLSFSSQ QIFPSAVVSSAWAGVVKTDSDMVLYNNQSHMNGMDSQNSFPDSSGHSYKGGSQFQFMQGS DRSLTEAPLFEHPTSAAGISSSGQKIFSSGLNDIVDSDRALSLLSSAPAVTREIGLSHMV QQPASIPRSQSHGLQYDGLSHFPFAQDFNSKPQDSHVSNSSSPLHFHDMLQNAQDESSTI PASQQTLAFMWD*
SOLYC05G053240.2.1	SLSBP11	MEARNFHGPVVSNMEVSGKKSREWDSNDWVWDGDRFTAEPLNSLPSDCRSKQLFPIGSEI PETATGIFNGFSSGAGELTLGNDKGRKELEKRRRTIVIDDDDEQNGEAGSLNLKLGEQLY PVMEEEVEKWEGKNGKKTKISGVSSNRAVCQVQDCRADLSSAKDYHRRHKVCEVHSKAAK ALVGNVMQRFCQQCSRFHVLEEFDEGKRSCRRRLAGHNKRRRKTHPENVANGASVNDEGG SNYLLISLLRILANVQFNSSDQTKDQDLLSHLLRNLASLAGAANERNASGLLPAPSDLQN PGTSMEAPKEDSLRPNANCLTIPASEVKEKRMDRGTSDAERGISQNLCALRPETLCCRKE SLPINANASVTTSAPLKLNIDLNNIYDDSQGGIQKLQNSDVFVNPGAASSGCPLWISHDP HKSSSTRTSLNSGSTSSLSPSSSSGEAQSRTDRIVFKLFGKDPGEIPTGLRKQVLDWLSH SPTDIESYIRPGCIILTIYLRMDKPIWEELYSDLNSSLRKLLNASAGSFWRTGWVYSRVK DRVAFLFNGQVVLDTPLPSHRSCGISIIKPIAVCASERVQFLVKGFNLSRPTTRFLCAME GKYLVQGNCTDVMVGADSCMDYNEIQSLSFPCTVPNATGRGFIEIEDHGLSSNFFPFIVA EKDVCSEIRTLESIIEAAKMDDGFLRGTEEFQARDQALDFLHELGWLLHRCHLKFRVGSG ASLNLFPFQRFHRLIDFSIDHDWCAVVKKLLDVFFNGVVDVGQQSSLDIPLQEVGILHRA VRRKCRSMIDVLLKYRHHGAFDKSGLQTQQDDRGYLFRPDTVGPGGLTPLHVVASLAGYE NILDALIDDPGEVGIEAWKSARDSTGLTPNDYACLRGHYSYVHMVQKKINQKPGDGHVVL DIPGSLLDSNLKQKLSDGHRSVKVTSFQTEKSLGKPIHRQCKQCKQKLSYGNSGTSLVYK PAMLSMVAIAAICVCVALLFKSSPEVLYSFRPFRWELLNTTWIGLATGIVVVDASDLCPI MLCKISKLLCILTICTANCLHLWF*
SOLYC07G053810.2.1	SLSBP12	MEKNDDLLVISTSENTNKKIITTNNNKKLLSNSSSSSSLIRSCQAEKCNVDLSDAKQYHK RHKVCEYHAKSQVVVVAGLRQRFCQQCSRFHELTEFDESKRSCRRRLAGHNERRRKSTSS SSSSSSSADRIHISIQENPTHKNFHLR*
SOLYC07G062980.2.1	SLSBP13	MANNDAGEGVVMQVMKHYCQVETCEANLDGAKKYHKRHKVCQVHAKAPIVLLAGLKQRFC QQCSKFHELSEFDGTKKSCRLRLDGHNKRRRKTPLPIELEDNQCRLINGEARPHMDMTLS SRNTIYTADISG*
SOLYC10G009080.2.1	SLSBP14	MENNKWEGKRSMEEDDDEEDEDVVEDTKRKRVLTRSGRKVSTAEGSRQPSCQVEECTADM VNAKTYHRRHKVCEFHAKAPEVLIDGLRQRFCQQCSRFHQLAEFDDAKKSCRRRLAGHNE RRRKSAQDYPGEGSS*
SOLYC10G018780.1.1	SLSBP15	MLDYNWGEQSSVMLSNDEQNQENEQNREFFDPYGPNTQTYTENPYPHQHFPNIQHQNHQF FHTQNNPTTLYDPRSYETCYTPHPHPQSSMLQQNSGFMVVPKSEPNQFVGNGSGIDFGSS SSSRIGLNLGGRTYFSSSEDHDFVNRLYRRSRAVETAGSIMNTPRCQAEGCNADLTHAKH YHRRHKVCEFHSKASTVIAAGITQRFCQQCSRFHLLSEFDNGKRSCRKRLADHNRRRRKN QQANLENSNKDTTTNSPSDTLARSPADSGAHCSSVTVAISPPRISLDVFRQRP*
SOLYC10G078700.1.1	SLSBP16	MELGSVSSSGNSSSSDSLNGLKFGKKIYFGNAGVGVQVKNGCGSSPVNGDGNLPPAPATT KRGRGGLVQGGHPPRCQVEGCQADLSDAKAYYSRHKVCGMHSKSPTVVVAGLEQRFCQQC SRFHQLTEFDQGKRSCRRRLACHNERRRKPPSGSLFSTHYGNLSSSIFENNSSRSGSFLV DFSSHQNVNESSWPNTRASEQGWDHQSSGKFLQRPWLNNSENAASELVLQGSATRTSYHG VPSGDYFPGVSDSSGALSLLSNRSWGSRNRPPSLGVNSQVHIDGVHTIQPSGSHGAPTNH FSSPSLSFKGNEASSSSHEMPPDLGLGQMLQASDNPYCGELGMAQHGDGRQYMELDQSKG YHPSVQNVHWTL*
SOLYC12G038520.1.1	SLSBP17	MESWSYVSGGKGFVSEESVSVDDGITPCSWSQQGVKVGSQIRDAFGGEDESSSKHSSSSF IDLKLGRGRFLDVKNFSLSSTKRNRAGGLNSFCQVQGCGKDLTSCKDYHKRHKVCEIHSK TAKVIVNGIQQRFCQQCSRFHLLAEFDDGKRSCRKRLAGHNERRRKPHTGLHSGRAGKHF QPYSGTRFQGSSFVTSSFICQDILGGSLLHQPKHDMHDWYKNVKVEHCSDYSPELTMPFT NKHSQPRPLFTSYHTDKHCPALHDEGITTITRSKNNESSNSYLNDIGGSDFVSRSLFHST SIGSDVLNVMDSDSPFQGISNSGCALSLLSSQSQDSSNYSSVVPPSAHHLITPRSYNHYN MTQTSECFPEASPKGSTSTVSTIYNLSEVISAKGQLEHILRNNCGSLQGSDYVNTKNLLS CEDGTTIDLLQLSSQLHQVEHQRRSMK*
AUR62004146-RA	CQSBP01	STVIAAGLTQRFCQQCSRFHLLSEFDNGKRSCRKRLADHNRRRRKSNNQRITSTAPSMSSGEN AQSSPSQTILRSPSDSG MNSSSSVTIAVSPPRVSFDSSLMQMRSFE*
AUR62013707-RA	CQSBP02	MQIPKTEPDLFTNRPIGLNLGRRTYFSADDDLVSRLYRRSRAVEPALHSPKCQAEGCNADLSHAKHYHR RHKVCEFHSKASTVIAAGLTQRFCQQCSRFHLLSEFDNGKRSCRKRLADHNRRRRKSNNQRITST APSMSSGENAQSSPSQTILRSPSDSG MNSSSSVTIAVSPPRVSFDSSFMQVRSFE*
AUR62028919-RA	CQSBP03	MSAISMMELNAKSPFLWDWENLVMFNTKAAETPKKLQSDSEIEGIEGFEAGSFYSSGGRSDGGTGSDLG YASSSKSSKSASVDSSADRELKGNQFSLEATDCFQQDLRGKRDLVNSSGTTRASPTIESSVASGESLIALE LGKRTYFEDVS GASNVKNTARSSIPPDSAAKKTKSSSPSIENPRCQVEGCNLDLSSAKDYHRKHRVCENH SKSPKVVINGLERRFCQQCSRFHGLSEFDQKKRSCRRRLSDHNARRRKPKPEVIQFNSMRLTSSLYEGR NQLNFAFDQVPMHQTRHGTWDSARESKVTLAKPGFFTTMKSGGTDQLHSTHSGLPSPTTKVSPVS TQLLPSKGVPSDVFQRGLPVSVAPSNLAAAQDFRALSLLSTSSWSSCDPEPPALNH SMHTNHASLAPSLPPMHPLPLGGPPISSEFWQADQPASGGPGSHTSTFQLFKAPNESSFYLY*
AUR62005629-RA	CQSBP04	MSAISMMELNAKSPFLWDWENLVMFNTKAAETPKKLQSDSEIEGIEGFEVGSFYSSGGRSD GGTGSDLGYVSSSKSSKSASVDSSADREFKGNQISLEATDCFQQDLRGQRDLVNTSGTTRAS PTIESSVASGESLIALELGKRTYFEDVSGASNVKNTARSSIPPDSVAKKTKSSSPSIENPRCQVE GCNLDLSSAKDYHRKHRVCENHSKSPKVVINGLERRFCQQCSRFHSLSEFDQKKRSCRRRLSD HNARRRKPKPEVIQFNSMRLTSSLYEGRNQLNFAFDQVPMHQTGHGTWDSARESKVTLV GGTDQLLSTHSGLPSPTTKVSPVSTQLLPSKGVPSDVFQRGLPVSVAPSNLTAAQDFRALSLLSTSSWG SCDPEPPALNHSMHTNHASLAPSLATMHPVPLGGPPISSEFWQADQPALGGPGSHTSTFQLF KAPNESSFYLY*
AUR62002563-RA	CQSBP05	MEAEMGGKTDVYCSAVMPVSDPKAVGKKTLEWDLNDWKWDGDLFLAAPLNTTHTPLDCRSKQLF PLGPELASNNNVGSEESNKTNEKEKREMEKRRRVVVVPHEELNDEGRPLNLKLGEQVYPIAEDEADKL EGKSVKKSKSAGTGTSQPACQVEGCTADLSNAKDYHRRHKVCEVHSKVSEAFVGNVIQRFCQQCSRFH ALPEFDEGKRSCRRRLAGHNKRRRKTLPETSPNVGSLTDEKSSGYLLVSLLRILSNLHSNGSDETKDQ DLISHLLRNLASQV SGSNLPELQQGSQSLHNAGISIGVPEKNPSSAQELCQAVPSAEARIGLLTR ENQHQKEKTQCASQPGIFHPTDGSIATKGSVPGAYLGIDLNNVYDDSQECVDIPGNG HGSIACAFRS EHLQKSSLPQTSGNSDSNSGHSSSSGSDSQGRTDRIVFKLFGKDPNDLPNQLRTQILDWLSHKPSDIEGYIRPGCIVLTV YLRLNKSLWEELCYDMSSSLSRLLSLSDDPFWKTGWIYTRVQQSAAFICDGRVVLDTPLPFKSRGSRISSISPIAVPTAE TVQLVVKGSNLSGPTSRLLCAIEGKYLVQDSCYSLVESTAAEHNEIQSLSFHCSIPNVVGRGFIEVEDYGLSGCFFPFIV

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Table S1: Continue

		AEPEICSEICMLERVMEIAGTDEGIERRNDALEFIHEMGWLLHTNRLSSMSGQTNIHLDLFPFVRLKWLIDYSINHDWCA VLRKLLDLLFSGIVDTGNHASVENALSEISLLHTAVQRNSRSMVEFLLRYIPKKVKNTIGLEQKQSHYVLPSSFLFRPDV TGSNGLTPLHLAASCAGFENMLDALLEDPGMVGIGAWENARDSTGLTPKDYAYLRGHNHYIDLFQSKVNKNSSGKHVVVD ILGLSNLEYKQKPSDELKLAKFNSLYTEKRQISQNCKLCEQRPNYGFRGTSLTCRPVVMSLVTIAVVCVCTALLFKSMPR VCYVFVPFRWDSLKYGAM*
AUR62029983-RA	CQSBP06	MEAGMGGITDVYSSAVLPVSDPKAVGKKTLEWDLNDWKWDGDLFLATPLNTTHTPLDCRSKQLFPLGPELAMNNNVGSEE ISITNEKGKREMEKRRRVVVVPHEELNEEGRPLNLKLGEQVYPIAEDEADKLEGKSVKKSRSAGTGTSQPACQVEGCMAN LSNAKDYHRRHKVCEVHSKVSEAFVRNVMQRFCQQCSRFHALPEFDEGKRSCRRRLAGHNKRRRKTLPETSPNVGSLTDE KSAGYLLVSLLRILSNLHSNGSDETKDQDLISHLLRNLASQVSGSNLPELQQGSQRLLNAGISVGIPEKNPSSAQELCQA VPSAEAHIGLLTRENQHQKEKTQYASQPGIFHPADGSIATKGSVPRAYLGIDLNNVYDDSQECVDIPGNGHGSIACAYWP EHLQKSSPPQTSGISDSNSGHSSSSGSDSQGRTDRIVFKLFGKDPDDLPHQLRTQILDWLSHKPSDIEGYIRPGCIVLTI YLRLNKSLWEELCYDMSSSLSRLLSLSDDPFWKTGWIYTRVQQSAAFICDGRVVLDTPLPFKSRGSQISSISPIAVPAAQ TVQLVVKGSNLSGPTSRLLCAIEGRYLVQDSCYSLVESTAEQDEVQSLSFHCSIPNVVGRGFIEVEDYGLSGCFFPFIVA EPEICSEICMLERVMETVGTDEGINRRNDALEFIHEMGWLLHADRLSSMSGQPNIQLDLFPFVRLKWLIDFSMDHDWSAV LRKLLDLLFSGIVDTGNHASVKNALSEMPLLHTAVQRNSRSMVEFLLRYIPKKVKNTKGSEQKQSHYEPPISFLFRPDVT GSNGLTPLHLAASCAGFENILDALLEDPGMVGIGAWENARDSTGLTPKDYAYLRGHNHYIVLFQSKVNKISSGKHVVVDI LGLSNLNSKQKQSDELKSAKFNSLYTEKRQISQNCKLCVQRPNYGFRGTSLTCRPVVMSLVTIAVVCVCTALLFKKKRSD EAEKLAVIVDVLVQNRFELIEEINTSFVLGVGWDLIMEMQKLEKTSNEPRIVESYHFVSVLAESEYGLQIHDLSSEIMYR LDLYAFLYEMKCKAVDSLNKPSPPKKNKWPVPPVRPQGDKYICIDYINVMRVVVATKARVSLIEVAELAAAKWVVSTCKS AKQDATKRAIQFLRVCYNVDIIDLNYGKGVYAGIKCALSRENNIFPTPALPPAAPRKPKASSSFGEHAV*
AUR62029984-RA	CQSBP07	MEAEMGGKADVYSSAVMPVSDLKAVGKKTLEWDLNDWKWDGDLFLATPLNTTHTPLDCRSIQLFPLGPELATNINVGSEE ISKTNEKGKREMEKRRRFVVVPHEEVNEEGRPSNMKLGEQVYPIAEDEADKLEGKSVKKSKSLGTGTSQPACQVEGCTAD LSNAKDYHRRHKVCEVHSKVSEAFVGNFMQRFCQQCSRFHNLPEFDEGKRSCRRRLAGHNKRRRKTLSETSPNGGSLTDE KSAGYLLVSLLRILSNLHSNGYDETKDQDLLSHLLRNLASQVSGSNLPELQQGFQRVLNAGISVGIPEKNPSSAQELCQA VPSAEAHIGLLTRENQHQKEKTQYASQPGIFHPADGSIATKGSLPGAYLGIDLNNVYDDSQEFVDIPGNGHGSIACAYWP EHLQKSSPPQTSGISDSNSGHSSSSGSDSQGRTDRIVFKLFGKDPDDLPHQLRTQILDWLSHKPSDIEGYIRPGCIVLTI YLRLNKSLWEELCYDMSSSLSRLLSLSDDPFWKTGWIYTRVQQSAAFICDALFSCAEGRVVLDTPLPFKSRDSRISSISP IAVPAAQTVQLVVKGSNLSGPTSRLLCAIEGKYLVQDSCCYSLVDSTAAEQDEVQSLSFHCSIPDVVGRGFIEVEDYGLS GCFFPFIVAEPEICSEICMLERVMEIVGTDEGIDRRNVALEFIHEMGWLLHTNRVSSMSGQTNIQLDLFSFVRLKWLIDF SVDHDWCAVLRKLLDLLFSGIVDTGHHASVENALSEMPLLHTAVQRNSRSMVEFLLRYIPRKAKNTKVSDESPSSFLFRP DVTGSNGLTPLHLAASCAGFENMLDALLEDPGMVGIRAWENARDSTGLTPKDYAYLRGHNHYIVLFQSKVNKISSGKHVV VDILGLSNLNSKQKQSDELKSAKFNSLYTEKRQISQNCKLCVQRPNYGFRGTSLTCRPVVMSLVTIAVVCVCTALFFKSM PRVCYVFLPFRWDTLKYGAV*
AUR62024322-RA	CQSBP08	MGSNYMTVEGSSTVSSGLSDSINGLKFGQKIYFEDGGKAVLQSGQPPRCQVEGCNTDLSDAKTYYSRHKVCGMHSKSPIV IVAGIEQRFCQQCSRFHRLPEFDQGKRSCRRRLAGHNERRRKPPPGSLLSSRLGRLSSSFFGDNTSKNGGFLLDFSSYSR QSEKDLWPGSETSEQVSGSQSRSIMWPGHSEDHPSKMYLHGSASESSYSFPSGECITGVSSDSSCALSLLSNQSWGSRNS SSGTALGNSMNVDGTPVSQCNAAHGVTVAHFPNSSSSWGYKGNNDASCGSDGVPSGHLGLGQISQPHYNGQFHGVLLMDH VQDGGRQYMDVDHSRAYNSNNTNHVDWSL*
AUR62019452-RA G	CQSBP09	MMVVVQSNPLFKIAVGREERGKVVGEIWGCRVAGGGNEEPSLVLGRSDKRWQLRGGGKGGDGGDGGGSGGLLLGLARCQA EKCTVDLTEAKRYHRRHKVCEHHAKAPSVLVSGLRQRFCQQCSRFHELSEFDETKRSCRRRLAGHNERRRKSASESQGEG STSSQSKGSNLQLRTGDQAQLSYSGNNNNNCTSSYKQFQIR*
AUR62012061-RA	CQSBP10	MGSNYMNVEGSSTSSSGLSDSINGLKFGQKIYFEDVGSGGGGSGKSSGAGGGGCGPVKKGGKAVLQSGQPPRCQVEGCNT DLSDAKTYYSRHKVCGMHSKSPIVIVAGIEQRFCQQCSRFHRLPEFDQGKRSCRRRLAGHNERRRKPPPGSLLSSRLGRL SSSFFGDNTSKNGGFLLDFSSYSRQSEKDLWPGSETSEQVSGSQSRSIVWPGHSEDHPSKMYLHGSASESSYSFPSGECI TGVSSDSSCALSLLSNQSWGSRNSSSGTALGNSMNVDGTPVSQCNAAHGVTVAHFPNSSSSWGFKGNNDASCGLHGVPSG HLGLGQISQPHYNGQFHGDLLMDHVQAGGQQYMDVDHSRAYNSNNTNHVDWSL*
AUR62032118-RA	CQSBP11	MILIVFSGAKHQIKNLIANFCLGISYVVFGILILLYIMESWWFDSLDKGFESNEAISQSDAIVRGKNVLIGWEHKITNED SVLTPSQQSVENRSYSELGIAEMVRIQCPTDSTRNELEDNGSVGDFYSSYVTTNAFSGDDESSSKFSSSVMDSSSRESSL IDLKLGGFGDNPNSSSTRTATAHVLSSADSPTPPKRARVSSQAVHCQVYGCHKDLSSAKDYHKRHKVCDVHSKTPKVIVN GIEQRFCQQCSRFHLLGEFDDGKRSCRKRLAGHNERRRKPQVGFSNRNGRSFQSYTGSNFQGFTPTSTSFICQDILPRGI SHTVKYGTNDWVKHIKVEDGTGCTQMPTYSCINRQLQPKSILPPQDFEKQFPFIDNTNNTGTQFPFGKNVNQHTPVIVSH SLFQTNSPRNEDLALLDATSTVQELAGISESGCALSLLSFQSQNSSGHSSAMPGCHPVIIPSSSPQYSVNEVSEKIFGNG AQALKSEVQNRYSSVIVSSTGRNQPSFMSVLNYGNNAHSEFGNEIHHRSKFMNIKDHLLCEDGTTIDLLQLSSQLHGKPE AV*
AUR62039662-RA	CQSBP12	MESWWFDSLDKGFESNEAISQSDSIIKGKNVLIGWEHKSPLSNEDSVLTPSQRSVENRSFSELGIAEVVRRQCPTDSTRN ELEDNGSDGDIYSSYVTTNAISGDDESSSKFSSSVMDSSSRESPLIDLKLGGFGDNPNSSSTRTATAHVLSSADSSTPPK RVRVISQAVHCQVYGCHKDLSSAKDYHKRHKVCDVHSKTPKVIVNGIEQRFCQQCSRFHLLGEFDDGKRSCRKRLAGHNE RRRKPQVGFSNRNGRSFQSYTGSNFQGFTPTSTSFICQDILPRGISHTVKYGTNDWVKHIKVEDGTGCTQTPTYSCINRQ LQPKSILPPYDFEKQFPFIDNTNNTGTQFPFGKNVNQHTPEIVSHSLFQTNSPRNEDLALLDAASTVQELAGISESGCAL SLLSFQSQNSSGHSSAMPGCHPVVIPSSSPQYSVNEVSEKIFGNGAQALTSEVQNRYSSVIVSSTERNQPSFMSMLNYGN NAHSEFGNEIHHRSKFMNIKDHLLCEDGTTIDLLQLSSQLQRVENQKLSEPLKQDTENSFCLGMI*
AUR62011728-RA	CQSBP13	MMEQAHRLSELRKRGIEWDLNDWKWDGDLFIATPSNSQGQQFIPLVPVPGNSSNTSSSCSDDVDDGTGRRDLERKRRVFV VDQDSLEEAAPLTLKLGVPHRERDHWETSTAKKTKLPSTSSTRAVCQVEDCEADLTKAKDYHRRHKVCELHSKATKALVA NVMQRFCQQCSRFHALQEFDEGKRSCRRRLAGHNKRRRKTQPETAVQGNSMDDQTNSVLLMSLLRILSNMHGNNRANQTT DQDLVAQLLKSLANPSGLHSGKGLSGLLHESQKLLNGGMATGNGHSEKMSAYLSNDQQNTPRVIDQHVQLPDSEIPRKGL YPANSRGSEIQAVSLEEPKSLFPIKDSPPAYSETTEGRMKLNNFDLNDAYVDSDDGMEDLERSPVNENFATGSVDFPSWA RQDSHQSSPPQTSGNSDSASAQSPSSSSGEAQSRTDRIVFKLFGKEPNDFPIMLRGQILDWLAHSPTEIESYIRPGCIIL TIYLRLAESSWEELCSDLSSRLTQLFDISDDTFWRMGWVYYVRVQNQIAIVHNGEVVLDTSLSLKDNNCCRILSVMPIAVS MNEQVQFKVRGFNLSQSTTRLLCALEGKYLDQEVSQESEVGDFLEDDDETDHANLSCIIPKATGRGFIEVEDHGLSSSFF PFIVAEKDVCSEIRTLENVLELKKTDEEAYEINKTLESWCQAMDFINEMGWLLHRSHLKSRLADLDPNTVIFSFRRFKWL MDFSMDHDWCAVVKKLLDILFAGTVGLGEHSSLKVALSEMGILHRAVRRNSRPMVEFLLRYAPLNVSEEFISSNDGGQVR FLFRPDAQGPAGLTPLHVAAGRDGSEDILDALTDDPGKNGIDAWKNARDSTGATPEDYARLRGHYAYIHIVQRKIYRSST SGHVVVDIPGEQSVAPRQDGALSFEVGRSASLAMNQSCKLCDQKKMSVYYGSRSRASLVYRPAMLSMVGIAAVCVCVALL FKSMPNVVCLFQPFRWEMLNYGSS*
AUR62029416-RA	CQSBP14	MEWDSKSCAWNGVSKVEFQDNGYHHHLATLAGSSGTGINNMFSVDLKLGRLGDMGDVSMDTLKNSMPLNMASSSSPSPVL ALSKRGRPGNSGAQSTVICSVDGCASDLNQCREYHRRHKVCERHSKTPVVLVGGKEQRFCQQCSRFHSLEKFDEVKRSCR KRLDGHNRRRRKRQPETFNMPDSAGGVLSSQTADGMLQYSCPQMHTVNWPTMSQPDLYFQNNQETIYQPLLNDVAPTGSR RGGLRVSPDNSGCALSLLSRYSSQSSDIRVGPVMQPTVMSSATAQGSSTSLHLNNSYQLPCSQGLDDIESSASLSSSSNT NAPNIGGFHTGHAGFRENTRIFPFGWE*
AUR62003425-RA	CQSBP15	MEWDSKSCAWNGVSKVEFQDNGYHHHLATLAGSSGTGISNMFSVDLKLGRLGDMRDLSMDTLKNSMPLNMASSSSPSPVL ALSKRGRPRNSGAQSTVICSVDGCASDLNQCREYHRRHKVCERHSKTPVVLVGGKEQRFCQQCSRFHSLEEFDEVKRSCR KRLDGHNRRRRKRQPETFYMPDSAGGVLSSHTADGMLQYSCPQMHTVNWPTMSQQPDLYFQNNQETIYQPLLNDVAPTGS RRGGLKVSPDNSGCALSLLSRYSSQSSDIRVGPAMQPTVMSSATAQGSSTSLHLNNSYQLPCSQGLDDIESSASLSSSSN TNAPNIGGFHTGHAGYRENSSRIFPFGWE*
AUR62035190-RA	CQSBP16	MEEVGTQVASPLYIHQNIGGRFCEGALIGSKRSLCYNSGSNHHQQQQQHSQIHRSGHGWNPKDWEWDSSHFLARSRPLES DRLRLGSLHEVSTPNNKEVVNPVLSSSFTSKSSSPPHDDQQSGNSLRLQLGGVVDNNGTGTSFNKTSVGNVQSSNSTEDP VSSSRPNKKVRSGSPGGGNYPMCQVDSCSEDLSKSKDYHRRHKVCELHSKATKALVGKQMQRFCQQCSRFHPLAEFDEGK RSCRRRLAGHNKRRRKTQAEDTTSPAIQPTDSHKTGYGNLDIVNLLTVLARGQGNAEQNVPPCPSLPDKNQLMQILSKIN SLPLPTDIAANPHIPPCSTKNGFEQGALGQSNMDVDAASRSTTDLLAVLSATLAASSPDSLAFFSQKSNPASCVDKNKST DMDKDTGSDACKKPSIELQSLGGERSSSSYQSPTEDSDSQVQDTRTNLPLQLFSSSPGDDSSPNLVTSRRYFSSDSSNPT EERSHSSAAPVTRKLFPLETASESARPVRMSFSEEANVNVEASRTETSASRMTLELFTMGNKAASNSLQNLPHQAGYTSS

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Table S1: Continue

		SGSDHSPPSFNSDPQKDRTGRIIFKLFDKDPSQLPGALRTQIYNWLSNSPSDMESYIRPGCVVLSIYVSMSSAAWEQLEE SFLQRVDALVQDSDFEFWRSGRFSVNIGRQLAVHKDGRIRICKPWSTVSSPELFVVSPLAVVSGQDTSLVLRGRNLTSPG TKIHCAYMGGYSSKEVLKSSDQGLPCEEIRLSEFNVHAAADSVLGRCFIEVENGVRGNCFPIIIADAKICQELRLLEREF CEAKDSDVITDDQAQYVASPHSHEALHFLNELGWLFQRQKSSDIAVNDFMLHRFQYLLTFSTERDYSALVKTLLDIFVEA ESTMDGLSTECVEALSNMHLLHRAVKRSSRKMVDMLVHYSAPCGSDSSKKYIFPPNLRGPGGITPLHLAACTSGSYDIVD ALTNDPMQIGLHSWKSLLDDGGQSPYSYALMRNNHTLNSMVAQKLSDRKNKQVSVTIGNEIVESMVPAEVRQRPSLPLDT KQKSCSKCAMRSYSRMPGSHGFLHRPFIHSMLTIAAVCVCVCLFFKSLHVNSVTPFMWDNVDFGAM*
AUR62042534-RA	CQSBP17	MEEVGTQVASPLYIHQNIGGRFCEGALIGAKRSLCYNSGSNHHQQQQHSQIHRSGHGWNPKDWEWDSSHFLARSRPLES DRLRLGSLHEVSTPNNKEVVNPVLSSSFTSKSSSPPHDDQQGGNSLRLQLGGVGDNNGTGTSFNKTSVGNVQSSNSTEEP VSSLRPNKKVRSGSPGGGNYPMCQVDSCSEDLSKSKDYHRRHKVCELHSKATKALVGKQMQRFCQQCSRFHPLAEFDEGK RSCRRRLAGHNKRRRKTQAEDTTSPAIQPTDSHKTGYGNLDIVNLLTVLARGQGALGQSNMDVDAASRSTTNLLAVLSAT LAASSPGSLAFFSQKSNPGSCVDKNKSTTMDKDTGSDACKKPSIELQSLGGERSSSSYQSPTEDSDSQVQDTRTNLPLQL FSSSPGDDSSPNLVTSRRYFSSDSSNPTEERSHSSAAPVTRKLFPLETASESARPVRMSFSEEANVNVEASRTETSASRM TLELFTMGNKAASNSLQNLPHQAGYTSSSGSDHSPPSFNSDPQKDRTGRIIFKLFDKDPSQLPGALRTQIYNWLSNSPSD MESYIRPGCVVLSIYVSMSSAAWEQLEESFLQRVEALVQDSDFEFWRSGRFSVNIGTQLAVHKDDPFRFVTLWTEGFAFA NLGAQNLTSPGTKIHCAYMGGYSSKEVLKSSDQGLPCEEIRLNEFNVHAAASSVLGRCFIEVENGVRGNCFPIIIADAKI CQELRLLEREFYEAKDSDVITDDQANMLQYLLTFSTERDYSALVKTLLDIFVEAESRMDGLSTECVEALSNMHLLHRAVK RSSRKMVDMLVHYSAPCSYDIVDALTNDPMQIGPHSWRSLLDDGEVRQRPSLPLDTKQKSCSKCAMRSYSRMPGSHGFLH RPFIHSMLTIAAVCVCVCLFFKSLHVNSVTPFMWDNVDFGAM*
AUR62005645-RA	CQSBP18	MGYKLTKNYCDLAELKKGGIATISAIFGSSSFDTEKAIGERLVDLKLGRLGDFGKGLVNNFKGHSNSIMDPFSPTAGSSK RPRTPGTTSQVVSCLVDGCKADLSKCRDYHRRHKVCEMHSKTPRVTIGGNEQRFCQQCSRFHPLGEFDEGKRSCRKRLEG HNRRRRKPQPEPLPVNQGNFFSASQGSRFLAFSNQPIIPATSVVTTAWSGAVKSESNPTLYNSAAPSSYSQAYRGRQFPF LQVPESPLTGVSSAVIDSDRALSLLSSNAETPEMGLGHTFHHPSLVNPTRAMLSSLHYNSVPSQYPGSSQGHGMEGHPTG SGLFSDLRSSNSLCQDVFQNNTGASSTSGGHQTLSFSWE*
AUR62028905-RA	CQSBP19	MGYKLTKNYCDLAELKKGGIATISAIFGSSSFDTEKAIGERLVDLKLGRLGDIGKGLVNNFKGHSHSIMDPFSPTAGSSK RPRTPGTSTQVVSCLVDGCKADLSKCRDYHRRHKVCEMHSKTPRVTIGGNEQRFCQQCSRFHSLGEFDEGKRSCRKRLEG HNRRRRKPQPEPLPVNHGNFFSASQEKQAQAELSLPDPQLPLIVELKPFLNQVIDSDRALSLLSSNAETPEMGLGRTFHH PSPINPTRPMLSSLHFNSVPSQYSGSSQGHGMEGHPTGSGLFSDLRSSNSLCQDVFQNDTGASSTSGGHQTLSFSWE*
AUR62003075-RA	CQSBP20	MFASSVERRWHFLGVEEMGVLLRLVEISMLALPSWCVEGEEMVFLGVEDMCCTHEHCVWESKGCFVRVGAWSIVMDSWKH MGCEIKTMFNVESYPLISNTQALERMDFMDLGFPDDIRKSYSISSEPSGEVFSDEIGTDYPQFGEESNHQQDFSLVDLKL GRLEDGGIDKDSELSKINAAESSVMLSSPAKKARSSMSINRSSNCQVLGCNKDLSSFKSYYKRHKVCDVHTKTPKVIVDG IEQRFCQQCSRFHLLAEFDDIKRSCRRRLSAHNKRRRKPQLASEPGSGIIDFSSSLAFPEVMPSVYLGPSKYEEGIDNSI KSSNFLLQMGCVGEKINKFPANVKDDIAGFAKPTNETLSSIQQTSRALSLLSAQSHSISSQLLETASATLTNRGNHADSN PGHSLNHSAGIFNKVSASGPHEPGIYSMDADEDGPTMINHNNSNTVGLHLPSDGISRPGLRNTDCHHPKERGIILNLLQL SSNLQRVEQQKHSTENEAG*
AUR62007890-RA	CQSBP21	MDSWKHMGCEFKPMFNGETYPLISNTQALERMDLMDLGFADDIRKSYSISSEPSGEVFSDEIGTDYPQFGEESNHQQDFP LVDLKLGRLEDGGIDKDSEFSKFNAAESSVRLSSPAKKARSSMSSNRSSNCQVLGCNKDLSSFKSYYKRHKVCDVHTKTP KVIVDGIEKRFCQQCSRFHLLAEFDDTKRSCRRRLSAHNKRRRKPQLASEPGSGIIDFSSSLAFPEVMPSVYLGPSKYEE GIDNSIKSSNFLLQMGCVGEKINKFPANVKDDIAGFAKPTNETLSNIQQTSRALSLLSAQSHSISSQLLETASATLTNRG NHADSNPGHSLNHSAGIFNKVSASGPHEPGIYSMEEDGPTMINPNNSSTVGLHLPNDGISRPGLRNTDCHHPKERGIILN LLQLSSNLQRVEQQKHSTENEAG*
AUR62042853-RA	CQSBP22	MDLPPLTGGGEESGAPFEWSDLFDFTIDDQLLLNLDVSDHPKEQPPVLLPPVTNAEDNGKTVAVNGGESGSSDRVRKRDP RMICKNFLAGRVPCACPELDALMAEEEEEEAGPGKKRPRMGRTPGVAKCQVPGCEVDIRELKGYHRRHRVCLVCANATSV VIEDFDEGKRSCRRKLERHNNRRRRKSADYRGTVEKEPQGDVQTEDVFSDGEAGKENAWSGGQIEKEDSKDKTLSNLCSA LESQNIESDSNLTFTPVDKVVDNLEREYSPPSDTKSAYTSACPTGRISFKLYDWNPAEFPRRLRHQIFQWLASMPVELEG YIRPGCTILTVFVSMPQYMWVKLFEDPVSYVQNSVGHGGILSGRGAALVYLNDLRFRVMREGASVMKVKVAVRAPRLHYI YPPCFEAGKPMDFVACGSNLLQPKFRSLVSFAGKYLAHDYYVAFPRGKEDKPAIDYDYQLCRIYVPHTEPSYFGPAFVEV ENECGLSNFIPILIGDAHVCSEIKLIHQKYDCSNCRKKSQCMPSGSSYGTCEVSCSRQAALSEFMLDVAWLLKQPCSEKL HCILTSSQIQRYNCLINAHNKELILKQGGECVSNVYTCLGSFSRDDMLSVDHTACQVTKLRAEMNCTFLEHSDSQGEGES ISLINREVAMNVNDSRDWPKNSCHSVISKKFTSTRPFIYAIAVVAVCFGVCAVVLHPYKVTKFAVTIRRCVFDNSS*
AUR62042654-RA	CQSBP23	MDLPPLTGGGEESGAPFEWSDLFDFTIDDQLLLNLDVSDQPKEQPPVLLPPVTNAEDNGKTVAVNGGESGSSDRVRKRDP RMICENFLAGRVPCACPELDALMAEEEEEETGPGKKRPRMGRTPGVAKCQVPGCEVDIRELKGFHVLSDFDEGKRSCRRK LERHNNRRRRKSADYRGTVEKEPQGDVQTEDVFSDGEAGKENAWSSGQIAEKEDSKDKTLSNLCSALESQNIESDSNLTF TPVDKVIDNLEREYSPPSDTKSAYSSACPTGRISFKLYDWNPAEFPRRLRHQIFQWLASMPVELEGYIRPGCTILTIFVS MPQYMWVKLFEDPVSYVQNSVGHGGILSGRGAALVYLNDLSFRVMREGTSVMKVKVAVRAPKLHYVYPPCFEAGKPMDFV ACGSNLLQPKFRSLVSFAGKYLAHDYYVAFPRGKEDKPAIDYDYQFCRIYVPHTEPSYFGPAFVEVENECGLSNFIPILI GDEHVCSEIKMIHQKYDCSNCRKKLQCIPSGSSYGTCEVSCSRQAALSEFMLDVAWLLKQPCSEKLNCILTRLLKEYIAQ ANDFLRQSAYNKELILKQGGECVSNVDTCLGSFPHDDLLSVDHTACQVTKLRAETNHTFLEHSDSRGEGESVSLINREVA MNVNDNRDWPKKSCHNIISKKFTSTRPFIYAIALVAVCFGVCAVVLHPYKVTKFAVTIRRCVFDDSS*

Table S2: Cis-acting elements in the promoter region of CqSBP genes

Gene ID	Gene Name	Element	Function	Function category
AUR62004146-RA.v1.0	CqSBP01	ABRE	cis-acting element involved in the abscisic acid responsiveness	Phytohormone responsiveness
AUR62004146-RA.v1.0	CqSBP01	ABRE	cis-acting element involved in the abscisic acid responsiveness	Phytohormone responsiveness
AUR62004146-RA.v1.0	CqSBP01	ABRE	cis-acting element involved in the abscisic acid responsiveness	Phytohormone responsiveness
AUR62004146-RA.v1.0	CqSBP01	ABRE	cis-acting regulatory element involved in the MeJA-responsiveness	Phytohormone responsiveness
AUR62013707-RA.v1.0	CqSBP02	ABRE	gibberellin-responsive element	Phytohormone responsiveness
AUR62013707-RA.v1.0	CqSBP02	ABRE	gibberellin-responsive element	Phytohormone responsiveness
AUR62013707-RA.v1.0	CqSBP02	ABRE	gibberellin-responsive element	Phytohormone responsiveness
AUR62013707-RA.v1.0	CqSBP02	ABRE	gibberellin-responsive element	Phytohormone responsiveness
AUR62028919-RA.v1.0	CqSBP03	ABRE	cis-acting regulatory element involved in the MeJA-responsiveness	Phytohormone responsiveness
AUR62028919-RA.v1.0	CqSBP03	ABRE	cis-acting regulatory element involved in the MeJA-responsiveness	Phytohormone responsiveness
AUR62005629-RA.v1.0	CqSBP04	ABRE	gibberellin-responsive element	Phytohormone responsiveness
AUR62005629-RA.v1.0	CqSBP04	ABRE	gibberellin-responsive element	Phytohormone responsiveness
AUR62002563-RA.v1.0	CqSBP05	ABRE	cis-acting regulatory element involved in the MeJA-responsiveness	Phytohormone responsiveness
AUR62002563-RA.v1.0	CqSBP05	ABRE	cis-acting regulatory element involved in the MeJA-responsiveness	Phytohormone responsiveness
AUR62002563-RA.v1.0	CqSBP05	ABRE	cis-acting regulatory element involved in the MeJA-responsiveness	Phytohormone responsiveness
AUR62029984-RA.v1.0	CqSBP07	ABRE	cis-acting element involved in the abscisic acid responsiveness	Phytohormone responsiveness
AUR62029984-RA.v1.0	CqSBP07	ABRE	cis-acting element involved in the abscisic acid responsiveness	Phytohormone responsiveness
AUR62029984-RA.v1.0	CqSBP07	ABRE	cis-acting element involved in the abscisic acid responsiveness	Phytohormone responsiveness
AUR62024322-RA.v1.0	CqSBP08	ABRE	gibberellin-responsive element	Phytohormone responsiveness
AUR62019452-RA.v1.0	CqSBP09	ABRE	cis-acting element involved in the abscisic acid responsiveness	Phytohormone responsiveness
AUR62012061-RA.v1.0	CqSBP10	ABRE	cis-acting regulatory element involved in the MeJA-responsiveness	Phytohormone responsiveness
AUR62032118-RA.v1.0	CqSBP11	ABRE	cis-acting regulatory element involved in the MeJA-responsiveness	Phytohormone responsiveness
AUR62039662-RA.v1.0	CqSBP12	ABRE	cis-acting element involved in salicylic acid responsiveness	Phytohormone responsiveness
AUR62011728-RA.v1.0	CqSBP13	ABRE	cis-acting element involved in the abscisic acid responsiveness	Phytohormone responsiveness
AUR62011728-RA.v1.0	CqSBP13	ABRE	cis-acting element involved in the abscisic acid responsiveness	Phytohormone responsiveness
AUR62011728-RA.v1.0	CqSBP13	ABRE	cis-acting element involved in the abscisic acid responsiveness	Phytohormone responsiveness
AUR62011728-RA.v1.0	CqSBP13	ABRE	cis-acting element involved in the abscisic acid responsiveness	Phytohormone responsiveness
AUR62011728-RA.v1.0	CqSBP13	ABRE	cis-acting regulatory element involved in the MeJA-responsiveness	Phytohormone responsiveness

Table S2: Continue

AUR62011728-RA.v1.0	CqSBP13	ABRE	cis-acting regulatory element involved in the MeJA-responsiveness	Phytohormone responsiveness
AUR62011728-RA.v1.0	CqSBP13	ABRE	cis-acting regulatory element involved in the MeJA-responsiveness	Phytohormone responsiveness
AUR62011728-RA.v1.0	CqSBP13	ABRE	cis-acting regulatory element involved in the MeJA-responsiveness	Phytohormone responsiveness
AUR62011728-RA.v1.0	CqSBP13	ABRE	cis-acting regulatory element involved in the MeJA-responsiveness	Phytohormone responsiveness
AUR62011728-RA.v1.0	CqSBP13	ABRE	cis-acting regulatory element involved in the MeJA-responsiveness	Phytohormone responsiveness
AUR62011728-RA.v1.0	CqSBP13	ABRE	auxin-responsive element	Phytohormone responsiveness
AUR62003425-RA.v1.0	CqSBP15	ABRE	cis-acting element involved in the abscisic acid responsiveness	Phytohormone responsiveness
AUR62035190-RA.v1.0	CqSBP16	ABRE	cis-acting regulatory element involved in the MeJA-responsiveness	Phytohormone responsiveness
AUR62042534-RA.v1.0	CqSBP17	ABRE	cis-acting element involved in salicylic acid responsiveness	Phytohormone responsiveness
AUR62042534-RA.v1.0	CqSBP17	ABRE	cis-acting element involved in the abscisic acid responsiveness	Phytohormone responsiveness
AUR62042534-RA.v1.0	CqSBP17	ABRE	cis-acting regulatory element involved in auxin responsiveness	Phytohormone responsiveness
AUR62042534-RA.v1.0	CqSBP17	ABRE	cis-acting regulatory element involved in the MeJA-responsiveness	Phytohormone responsiveness
AUR62042534-RA.v1.0	CqSBP17	ABRE	cis-acting regulatory element involved in the MeJA-responsiveness	Phytohormone responsiveness
AUR62042534-RA.v1.0	CqSBP17	ABRE	gibberellin-responsive element	Phytohormone responsiveness
AUR62028905-RA.v1.0	CqSBP19	ABRE	cis-acting element involved in salicylic acid responsiveness	Phytohormone responsiveness
AUR62003075-RA.v1.0	CqSBP20	ABRE	cis-acting element involved in salicylic acid responsiveness	Phytohormone responsiveness
AUR62003075-RA.v1.0	CqSBP20	ABRE	cis-acting element involved in salicylic acid responsiveness	Phytohormone responsiveness
AUR62003075-RA.v1.0	CqSBP20	ABRE	cis-acting element involved in the abscisic acid responsiveness	Phytohormone responsiveness
AUR62003075-RA.v1.0	CqSBP20	ABRE	cis-acting regulatory element involved in auxin responsiveness	Phytohormone responsiveness
AUR62003075-RA.v1.0	CqSBP20	ABRE	cis-acting regulatory element involved in the MeJA-responsiveness	Phytohormone responsiveness
AUR62003075-RA.v1.0	CqSBP20	ABRE	cis-acting regulatory element involved in the MeJA-responsiveness	Phytohormone responsiveness
AUR62007890-RA.v1.0	CqSBP21	ABRE	cis-acting element involved in salicylic acid responsiveness	Phytohormone responsiveness
AUR62007890-RA.v1.0	CqSBP21	ABRE	cis-acting element involved in salicylic acid responsiveness	Phytohormone responsiveness
AUR62007890-RA.v1.0	CqSBP21	ABRE	cis-acting element involved in salicylic acid responsiveness	Phytohormone responsiveness
AUR62042853-RA.v1.0	CqSBP22	ABRE	cis-acting element involved in the abscisic acid responsiveness	Phytohormone responsiveness
AUR62042853-RA.v1.0	CqSBP22	ABRE	cis-acting element involved in the abscisic acid responsiveness	Phytohormone responsiveness
AUR62042853-RA.v1.0	CqSBP22	ABRE	cis-acting element involved in the abscisic acid responsiveness	Phytohormone responsiveness
AUR62042853-RA.v1.0	CqSBP22	ABRE	cis-acting element involved in the abscisic acid responsiveness	Phytohormone responsiveness
AUR62042654-RA.v1.0	CqSBP23	ABRE	gibberellin-responsive element	Phytohormone responsiveness
AUR62042654-RA.v1.0	CqSBP23	ABRE	gibberellin-responsive element	Phytohormone responsiveness
AUR62042654-RA.v1.0	CqSBP23	ABRE	auxin-responsive element	Phytohormone responsiveness
AUR62042654-RA.v1.0	CqSBP23	ABRE	cis-acting element involved in the abscisic acid responsiveness	Phytohormone responsiveness
AUR62042654-RA.v1.0	CqSBP23	ABRE	cis-acting element involved in the abscisic acid responsiveness	Phytohormone responsiveness
AUR62029983-RA.v1.0	CqSBP06	AuxRR-core	cis-acting regulatory element involved in auxin responsiveness	Phytohormone responsiveness
AUR62024322-RA.v1.0	CqSBP08	AuxRR-core	auxin-responsive element	Phytohormone responsiveness
AUR62024322-RA.v1.0	CqSBP08	AuxRR-core	cis-acting element involved in salicylic acid responsiveness	Phytohormone responsiveness
AUR62012061-RA.v1.0	CqSBP10	AuxRR-core	cis-acting regulatory element involved in the MeJA-responsiveness	Phytohormone responsiveness
AUR62012061-RA.v1.0	CqSBP10	AuxRR-core	cis-acting regulatory element involved in the MeJA-responsiveness	Phytohormone responsiveness
AUR62032118-RA.v1.0	CqSBP11	AuxRR-core	gibberellin-responsive element	Phytohormone responsiveness
AUR62011728-RA.v1.0	CqSBP13	AuxRR-core	cis-acting element involved in gibberellin-responsiveness	Phytohormone responsiveness
AUR62035190-RA.v1.0	CqSBP16	AuxRR-core	cis-acting regulatory element involved in the MeJA-responsiveness	Phytohormone responsiveness
AUR62005645-RA.v1.0	CqSBP18	AuxRR-core	cis-acting element involved in gibberellin-responsiveness	Phytohormone responsiveness
AUR62028905-RA.v1.0	CqSBP19	AuxRR-core	cis-acting element involved in salicylic acid responsiveness	Phytohormone responsiveness
AUR62003075-RA.v1.0	CqSBP20	AuxRR-core	cis-acting regulatory element involved in the MeJA-responsiveness	Phytohormone responsiveness
AUR62003075-RA.v1.0	CqSBP20	AuxRR-core	cis-acting regulatory element involved in the MeJA-responsiveness	Phytohormone responsiveness
AUR62007890-RA.v1.0	CqSBP21	AuxRR-core	cis-acting element involved in salicylic acid responsiveness	Phytohormone responsiveness
AUR62013707-RA.v1.0	CqSBP02	CGTCA-motif	cis-acting element involved in the abscisic acid responsiveness	Phytohormone responsiveness
AUR62013707-RA.v1.0	CqSBP02	CGTCA-motif	cis-acting element involved in the abscisic acid responsiveness	Phytohormone responsiveness
AUR62013707-RA.v1.0	CqSBP02	CGTCA-motif	cis-acting element involved in the abscisic acid responsiveness	Phytohormone responsiveness
AUR62005629-RA.v1.0	CqSBP04	CGTCA-motif	cis-acting element involved in the abscisic acid responsiveness	Phytohormone responsiveness
AUR62002563-RA.v1.0	CqSBP05	CGTCA-motif	cis-acting regulatory element involved in the MeJA-responsiveness	Phytohormone responsiveness
AUR62002563-RA.v1.0	CqSBP05	CGTCA-motif	cis-acting regulatory element involved in the MeJA-responsiveness	Phytohormone responsiveness
AUR62002563-RA.v1.0	CqSBP05	CGTCA-motif	auxin-responsive element	Phytohormone responsiveness
AUR62029984-RA.v1.0	CqSBP07	CGTCA-motif	cis-acting regulatory element involved in auxin responsiveness	Phytohormone responsiveness
AUR62029984-RA.v1.0	CqSBP07	CGTCA-motif	cis-acting regulatory element involved in the MeJA-responsiveness	Phytohormone responsiveness
AUR62029984-RA.v1.0	CqSBP07	CGTCA-motif	cis-acting regulatory element involved in the MeJA-responsiveness	Phytohormone responsiveness
AUR62019452-RA.v1.0	CqSBP09	CGTCA-motif	cis-acting element involved in the abscisic acid responsiveness	Phytohormone responsiveness
AUR62032118-RA.v1.0	CqSBP11	CGTCA-motif	gibberellin-responsive element	Phytohormone responsiveness
AUR62039662-RA.v1.0	CqSBP12	CGTCA-motif	cis-acting element involved in salicylic acid responsiveness	Phytohormone responsiveness
AUR62011728-RA.v1.0	CqSBP13	CGTCA-motif	gibberellin-responsive element	Phytohormone responsiveness
AUR62011728-RA.v1.0	CqSBP13	CGTCA-motif	cis-acting element involved in the abscisic acid responsiveness	Phytohormone responsiveness
AUR62011728-RA.v1.0	CqSBP13	CGTCA-motif	cis-acting regulatory element involved in auxin responsiveness	Phytohormone responsiveness
AUR62011728-RA.v1.0	CqSBP13	CGTCA-motif	cis-acting regulatory element involved in auxin responsiveness	Phytohormone responsiveness
AUR62029416-RA.v1.0	CqSBP14	CGTCA-motif	cis-acting element involved in the abscisic acid responsiveness	Phytohormone responsiveness
AUR62029416-RA.v1.0	CqSBP14	CGTCA-motif	cis-acting element involved in the abscisic acid responsiveness	Phytohormone responsiveness
AUR62003425-RA.v1.0	CqSBP15	CGTCA-motif	cis-acting regulatory element involved in the MeJA-responsiveness	Phytohormone responsiveness
AUR62003425-RA.v1.0	CqSBP15	CGTCA-motif	cis-acting regulatory element involved in the MeJA-responsiveness	Phytohormone responsiveness
AUR62035190-RA.v1.0	CqSBP16	CGTCA-motif	cis-acting element involved in salicylic acid responsiveness	Phytohormone responsiveness
AUR62035190-RA.v1.0	CqSBP16	CGTCA-motif	cis-acting element involved in the abscisic acid responsiveness	Phytohormone responsiveness
AUR62035190-RA.v1.0	CqSBP16	CGTCA-motif	cis-acting element involved in the abscisic acid responsiveness	Phytohormone responsiveness
AUR62042534-RA.v1.0	CqSBP17	CGTCA-motif	gibberellin-responsive element	Phytohormone responsiveness
AUR62003075-RA.v1.0	CqSBP20	CGTCA-motif	cis-acting regulatory element involved in the MeJA-responsiveness	Phytohormone responsiveness
AUR62003075-RA.v1.0	CqSBP20	CGTCA-motif	cis-acting regulatory element involved in the MeJA-responsiveness	Phytohormone responsiveness
AUR62003075-RA.v1.0	CqSBP20	CGTCA-motif	gibberellin-responsive element	Phytohormone responsiveness
AUR62007890-RA.v1.0	CqSBP21	CGTCA-motif	cis-acting element involved in the abscisic acid responsiveness	Phytohormone responsiveness
AUR62007890-RA.v1.0	CqSBP21	CGTCA-motif	cis-acting element involved in the abscisic acid responsiveness	Phytohormone responsiveness
AUR62007890-RA.v1.0	CqSBP21	CGTCA-motif	cis-acting element involved in the abscisic acid responsiveness	Phytohormone responsiveness
AUR62042853-RA.v1.0	CqSBP22	CGTCA-motif	cis-acting regulatory element involved in the MeJA-responsiveness	Phytohormone responsiveness
AUR62042853-RA.v1.0	CqSBP22	CGTCA-motif	cis-acting regulatory element involved in the MeJA-responsiveness	Phytohormone responsiveness
AUR62042853-RA.v1.0	CqSBP22	CGTCA-motif	cis-acting regulatory element involved in the MeJA-responsiveness	Phytohormone responsiveness
AUR62042654-RA.v1.0	CqSBP23	CGTCA-motif	cis-acting regulatory element involved in the MeJA-responsiveness	Phytohormone responsiveness
AUR62042654-RA.v1.0	CqSBP23	CGTCA-motif	cis-acting regulatory element involved in the MeJA-responsiveness	Phytohormone responsiveness
AUR62042654-RA.v1.0	CqSBP23	CGTCA-motif	cis-acting regulatory element involved in the MeJA-responsiveness	Phytohormone responsiveness
AUR62042654-RA.v1.0	CqSBP23	CGTCA-motif	cis-acting regulatory element involved in the MeJA-responsiveness	Phytohormone responsiveness
AUR62028919-RA.v1.0	CqSBP03	GARE-motif	cis-acting regulatory element involved in the MeJA-responsiveness	Phytohormone responsiveness
AUR62005629-RA.v1.0	CqSBP04	GARE-motif	cis-acting element involved in the abscisic acid responsiveness	Phytohormone responsiveness
AUR62005629-RA.v1.0	CqSBP04	GARE-motif	cis-acting element involved in the abscisic acid responsiveness	Phytohormone responsiveness
AUR62002563-RA.v1.0	CqSBP05	GARE-motif	cis-acting regulatory element involved in the MeJA-responsiveness	Phytohormone responsiveness
AUR62002563-RA.v1.0	CqSBP05	GARE-motif	gibberellin-responsive element	Phytohormone responsiveness
AUR62002563-RA.v1.0	CqSBP05	GARE-motif	gibberellin-responsive element	Phytohormone responsiveness
AUR62029984-RA.v1.0	CqSBP07	GARE-motif	gibberellin-responsive element	Phytohormone responsiveness

Table S2: Continue

AUR62011728-RA.v1.0	CqSBP13	GARE-motif	cis-acting element involved in the abscisic acid responsiveness	Phytohormone responsiveness
AUR62011728-RA.v1.0	CqSBP13	GARE-motif	cis-acting regulatory element involved in auxin responsiveness	Phytohormone responsiveness
AUR62011728-RA.v1.0	CqSBP13	GARE-motif	auxin-responsive element	Phytohormone responsiveness
AUR62011728-RA.v1.0	CqSBP13	GARE-motif	cis-acting element involved in gibberellin-responsiveness	Phytohormone responsiveness
AUR62035190-RA.v1.0	CqSBP16	GARE-motif	cis-acting regulatory element involved in the MeJA-responsiveness	Phytohormone responsiveness
AUR62003075-RA.v1.0	CqSBP20	GARE-motif	cis-acting regulatory element involved in the MeJA-responsiveness	Phytohormone responsiveness
AUR62007890-RA.v1.0	CqSBP21	GARE-motif	cis-acting regulatory element involved in the MeJA-responsiveness	Phytohormone responsiveness
AUR62042853-RA.v1.0	CqSBP22	GARE-motif	cis-acting regulatory element involved in the MeJA-responsiveness	Phytohormone responsiveness
AUR62042853-RA.v1.0	CqSBP22	GARE-motif	cis-acting regulatory element involved in the MeJA-responsiveness	Phytohormone responsiveness
AUR62042654-RA.v1.0	CqSBP23	GARE-motif	gibberellin-responsive element	Phytohormone responsiveness
AUR62042654-RA.v1.0	CqSBP23	GARE-motif	gibberellin-responsive element	Phytohormone responsiveness
AUR62042654-RA.v1.0	CqSBP23	GARE-motif	gibberellin-responsive element	Phytohormone responsiveness
AUR62002563-RA.v1.0	CqSBP05	P-box	cis-acting element involved in the abscisic acid responsiveness	Phytohormone responsiveness
AUR62002563-RA.v1.0	CqSBP05	P-box	cis-acting regulatory element involved in the MeJA-responsiveness	Phytohormone responsiveness
AUR62029984-RA.v1.0	CqSBP07	P-box	cis-acting regulatory element involved in the MeJA-responsiveness	Phytohormone responsiveness
AUR62019452-RA.v1.0	CqSBP09	P-box	cis-acting element involved in the abscisic acid responsiveness	Phytohormone responsiveness
AUR62032118-RA.v1.0	CqSBP11	P-box	gibberellin-responsive element	Phytohormone responsiveness
AUR62032118-RA.v1.0	CqSBP11	P-box	auxin-responsive element	Phytohormone responsiveness
AUR62032118-RA.v1.0	CqSBP11	P-box	cis-acting element involved in salicylic acid responsiveness	Phytohormone responsiveness
AUR62039662-RA.v1.0	CqSBP12	P-box	cis-acting element involved in the abscisic acid responsiveness	Phytohormone responsiveness
AUR62003075-RA.v1.0	CqSBP20	P-box	gibberellin-responsive element	Phytohormone responsiveness
AUR62003075-RA.v1.0	CqSBP20	P-box	cis-acting element involved in gibberellin-responsiveness	Phytohormone responsiveness
AUR62007890-RA.v1.0	CqSBP21	P-box	cis-acting regulatory element involved in the MeJA-responsiveness	Phytohormone responsiveness
AUR62042853-RA.v1.0	CqSBP22	P-box	gibberellin-responsive element	Phytohormone responsiveness
AUR62007890-RA.v1.0	CqSBP21	SARE	cis-acting element involved in salicylic acid responsiveness	Phytohormone responsiveness
AUR62028919-RA.v1.0	CqSBP03	TATC-box	cis-acting regulatory element involved in auxin responsiveness	Phytohormone responsiveness
AUR62028919-RA.v1.0	CqSBP03	TATC-box	cis-acting regulatory element involved in the MeJA-responsiveness	Phytohormone responsiveness
AUR62005629-RA.v1.0	CqSBP04	TATC-box	cis-acting regulatory element involved in the MeJA-responsiveness	Phytohormone responsiveness
AUR62005629-RA.v1.0	CqSBP04	TATC-box	gibberellin-responsive element	Phytohormone responsiveness
AUR62019452-RA.v1.0	CqSBP09	TATC-box	cis-acting element involved in the abscisic acid responsiveness	Phytohormone responsiveness
AUR62032118-RA.v1.0	CqSBP11	TATC-box	cis-acting regulatory element involved in the MeJA-responsiveness	Phytohormone responsiveness
AUR62035190-RA.v1.0	CqSBP16	TATC-box	gibberellin-responsive element	Phytohormone responsiveness
AUR62035190-RA.v1.0	CqSBP16	TATC-box	cis-acting element involved in salicylic acid responsiveness	Phytohormone responsiveness
AUR62042534-RA.v1.0	CqSBP17	TATC-box	cis-acting regulatory element involved in the MeJA-responsiveness	Phytohormone responsiveness
AUR62042534-RA.v1.0	CqSBP17	TATC-box	cis-acting regulatory element involved in the MeJA-responsiveness	Phytohormone responsiveness
AUR62007890-RA.v1.0	CqSBP21	TATC-box	cis-acting element involved in gibberellin-responsiveness	Phytohormone responsiveness
AUR62013707-RA.v1.0	CqSBP02	TCA-element	gibberellin-responsive element	Phytohormone responsiveness
AUR62029984-RA.v1.0	CqSBP07	TCA-element	cis-acting element involved in salicylic acid responsiveness	Phytohormone responsiveness
AUR62019452-RA.v1.0	CqSBP09	TCA-element	cis-acting element involved in the abscisic acid responsiveness	Phytohormone responsiveness
AUR62012061-RA.v1.0	CqSBP10	TCA-element	cis-acting element involved in the abscisic acid responsiveness	Phytohormone responsiveness
AUR62012061-RA.v1.0	CqSBP10	TCA-element	cis-acting element involved in the abscisic acid responsiveness	Phytohormone responsiveness
AUR62012061-RA.v1.0	CqSBP10	TCA-element	cis-acting element involved in the abscisic acid responsiveness	Phytohormone responsiveness
AUR62012061-RA.v1.0	CqSBP10	TCA-element	cis-acting element involved in the abscisic acid responsiveness	Phytohormone responsiveness
AUR62012061-RA.v1.0	CqSBP10	TCA-element	cis-acting regulatory element involved in auxin responsiveness	Phytohormone responsiveness
AUR62032118-RA.v1.0	CqSBP11	TCA-element	cis-acting regulatory element involved in the MeJA-responsiveness	Phytohormone responsiveness
AUR62032118-RA.v1.0	CqSBP11	TCA-element	cis-acting regulatory element involved in the MeJA-responsiveness	Phytohormone responsiveness
AUR62011728-RA.v1.0	CqSBP13	TCA-element	cis-acting regulatory element involved in auxin responsiveness	Phytohormone responsiveness
AUR62011728-RA.v1.0	CqSBP13	TCA-element	cis-acting element involved in salicylic acid responsiveness	Phytohormone responsiveness
AUR62029416-RA.v1.0	CqSBP14	TCA-element	cis-acting element involved in gibberellin-responsiveness	Phytohormone responsiveness
AUR62003425-RA.v1.0	CqSBP15	TCA-element	cis-acting element involved in salicylic acid responsiveness	Phytohormone responsiveness
AUR62035190-RA.v1.0	CqSBP16	TCA-element	cis-acting regulatory element involved in the MeJA-responsiveness	Phytohormone responsiveness
AUR62035190-RA.v1.0	CqSBP16	TCA-element	cis-acting regulatory element involved in the MeJA-responsiveness	Phytohormone responsiveness
AUR62035190-RA.v1.0	CqSBP16	TCA-element	auxin-responsive element	Phytohormone responsiveness
AUR62035190-RA.v1.0	CqSBP16	TCA-element	cis-acting regulatory element involved in auxin responsiveness	Phytohormone responsiveness
AUR62042534-RA.v1.0	CqSBP17	TCA-element	cis-acting regulatory element involved in the MeJA-responsiveness	Phytohormone responsiveness
AUR62042534-RA.v1.0	CqSBP17	TCA-element	gibberellin-responsive element	Phytohormone responsiveness
AUR62042534-RA.v1.0	CqSBP17	TCA-element	gibberellin-responsive element	Phytohormone responsiveness
AUR62042534-RA.v1.0	CqSBP17	TCA-element	auxin-responsive element	Phytohormone responsiveness
AUR62042534-RA.v1.0	CqSBP17	TCA-element	cis-acting element involved in gibberellin-responsiveness	Phytohormone responsiveness
AUR62042534-RA.v1.0	CqSBP17	TCA-element	cis-acting element involved in salicylic acid responsiveness	Phytohormone responsiveness
AUR62007890-RA.v1.0	CqSBP21	TCA-element	cis-acting element involved in salicylic acid responsiveness	Phytohormone responsiveness
AUR62004146-RA.v1.0	CqSBP01	TGACG-motif	cis-acting regulatory element involved in the MeJA-responsiveness	Phytohormone responsiveness
AUR62004146-RA.v1.0	CqSBP01	TGACG-motif	cis-acting regulatory element involved in the MeJA-responsiveness	Phytohormone responsiveness
AUR62004146-RA.v1.0	CqSBP01	TGACG-motif	cis-acting regulatory element involved in the MeJA-responsiveness	Phytohormone responsiveness
AUR62004146-RA.v1.0	CqSBP01	TGACG-motif	cis-acting regulatory element involved in the MeJA-responsiveness	Phytohormone responsiveness
AUR62004146-RA.v1.0	CqSBP01	TGACG-motif	cis-acting regulatory element involved in the MeJA-responsiveness	Phytohormone responsiveness
AUR62013707-RA.v1.0	CqSBP02	TGACG-motif	cis-acting element involved in the abscisic acid responsiveness	Phytohormone responsiveness
AUR62013707-RA.v1.0	CqSBP02	TGACG-motif	cis-acting element involved in the abscisic acid responsiveness	Phytohormone responsiveness
AUR62013707-RA.v1.0	CqSBP02	TGACG-motif	cis-acting element involved in the abscisic acid responsiveness	Phytohormone responsiveness
AUR62005629-RA.v1.0	CqSBP04	TGACG-motif	cis-acting element involved in the abscisic acid responsiveness	Phytohormone responsiveness
AUR62002563-RA.v1.0	CqSBP05	TGACG-motif	cis-acting element involved in gibberellin-responsiveness	Phytohormone responsiveness
AUR62002563-RA.v1.0	CqSBP05	TGACG-motif	cis-acting element involved in gibberellin-responsiveness	Phytohormone responsiveness
AUR62002563-RA.v1.0	CqSBP05	TGACG-motif	cis-acting element involved in the abscisic acid responsiveness	Phytohormone responsiveness
AUR62029983-RA.v1.0	CqSBP06	TGACG-motif	cis-acting element involved in gibberellin-responsiveness	Phytohormone responsiveness
AUR62029983-RA.v1.0	CqSBP06	TGACG-motif	cis-acting element involved in salicylic acid responsiveness	Phytohormone responsiveness
AUR62029984-RA.v1.0	CqSBP07	TGACG-motif	cis-acting regulatory element involved in the MeJA-responsiveness	Phytohormone responsiveness
AUR62029984-RA.v1.0	CqSBP07	TGACG-motif	cis-acting regulatory element involved in the MeJA-responsiveness	Phytohormone responsiveness
AUR62029984-RA.v1.0	CqSBP07	TGACG-motif	cis-acting regulatory element involved in the MeJA-responsiveness	Phytohormone responsiveness
AUR62019452-RA.v1.0	CqSBP09	TGACG-motif	cis-acting element involved in the abscisic acid responsiveness	Phytohormone responsiveness
AUR62032118-RA.v1.0	CqSBP11	TGACG-motif	gibberellin-responsive element	Phytohormone responsiveness
AUR62039662-RA.v1.0	CqSBP12	TGACG-motif	cis-acting element involved in salicylic acid responsiveness	Phytohormone responsiveness
AUR62011728-RA.v1.0	CqSBP13	TGACG-motif	cis-acting element involved in salicylic acid responsiveness	Phytohormone responsiveness
AUR62011728-RA.v1.0	CqSBP13	TGACG-motif	cis-acting element involved in the abscisic acid responsiveness	Phytohormone responsiveness
AUR62011728-RA.v1.0	CqSBP13	TGACG-motif	cis-acting regulatory element involved in the MeJA-responsiveness	Phytohormone responsiveness
AUR62011728-RA.v1.0	CqSBP13	TGACG-motif	cis-acting regulatory element involved in the MeJA-responsiveness	Phytohormone responsiveness
AUR62003425-RA.v1.0	CqSBP15	TGACG-motif	cis-acting regulatory element involved in the MeJA-responsiveness	Phytohormone responsiveness
AUR62003425-RA.v1.0	CqSBP15	TGACG-motif	cis-acting regulatory element involved in the MeJA-responsiveness	Phytohormone responsiveness
AUR62035190-RA.v1.0	CqSBP16	TGACG-motif	cis-acting element involved in the abscisic acid responsiveness	Phytohormone responsiveness
AUR62035190-RA.v1.0	CqSBP16	TGACG-motif	cis-acting regulatory element involved in the MeJA-responsiveness	Phytohormone responsiveness
AUR62035190-RA.v1.0	CqSBP16	TGACG-motif	cis-acting regulatory element involved in the MeJA-responsiveness	Phytohormone responsiveness
AUR62042534-RA.v1.0	CqSBP17	TGACG-motif	gibberellin-responsive element	Phytohormone responsiveness

Table S2: Continue

AUR62003075-RA.v1.0	CqSBP20	TGACG-motif	auxin-responsive element	Phytohormone responsiveness
AUR62003075-RA.v1.0	CqSBP20	TGACG-motif	cis-acting element involved in the abscisic acid responsiveness	Phytohormone responsiveness
AUR62003075-RA.v1.0	CqSBP20	TGACG-motif	cis-acting regulatory element involved in the MeJA-responsiveness	Phytohormone responsiveness
AUR62007890-RA.v1.0	CqSBP21	TGACG-motif	cis-acting element involved in the abscisic acid responsiveness	Phytohormone responsiveness
AUR62007890-RA.v1.0	CqSBP21	TGACG-motif	cis-acting element involved in the abscisic acid responsiveness	Phytohormone responsiveness
AUR62007890-RA.v1.0	CqSBP21	TGACG-motif	cis-acting element involved in the abscisic acid responsiveness	Phytohormone responsiveness
AUR62042853-RA.v1.0	CqSBP22	TGACG-motif	cis-acting regulatory element involved in the MeJA-responsiveness	Phytohormone responsiveness
AUR62042853-RA.v1.0	CqSBP22	TGACG-motif	cis-acting regulatory element involved in the MeJA-responsiveness	Phytohormone responsiveness
AUR62042853-RA.v1.0	CqSBP22	TGACG-motif	cis-acting regulatory element involved in the MeJA-responsiveness	Phytohormone responsiveness
AUR62042654-RA.v1.0	CqSBP23	TGACG-motif	cis-acting element involved in the abscisic acid responsiveness	Phytohormone responsiveness
AUR62042654-RA.v1.0	CqSBP23	TGACG-motif	cis-acting element involved in the abscisic acid responsiveness	Phytohormone responsiveness
AUR62042654-RA.v1.0	CqSBP23	TGACG-motif	cis-acting regulatory element involved in the MeJA-responsiveness	Phytohormone responsiveness
AUR62042654-RA.v1.0	CqSBP23	TGACG-motif	cis-acting regulatory element involved in the MeJA-responsiveness	Phytohormone responsiveness
AUR62028919-RA.v1.0	CqSBP03	TGA-element	cis-acting regulatory element involved in auxin responsiveness	Phytohormone responsiveness
AUR62005629-RA.v1.0	CqSBP04	TGA-element	cis-acting regulatory element involved in the MeJA-responsiveness	Phytohormone responsiveness
AUR62029983-RA.v1.0	CqSBP06	TGA-element	auxin-responsive element	Phytohormone responsiveness
AUR62019452-RA.v1.0	CqSBP09	TGA-element	cis-acting element involved in salicylic acid responsiveness	Phytohormone responsiveness
AUR62012061-RA.v1.0	CqSBP10	TGA-element	cis-acting element involved in the abscisic acid responsiveness	Phytohormone responsiveness
AUR62032118-RA.v1.0	CqSBP11	TGA-element	cis-acting regulatory element involved in the MeJA-responsiveness	Phytohormone responsiveness
AUR62039662-RA.v1.0	CqSBP12	TGA-element	cis-acting element involved in salicylic acid responsiveness	Phytohormone responsiveness
AUR62011728-RA.v1.0	CqSBP13	TGA-element	cis-acting regulatory element involved in auxin responsiveness	Phytohormone responsiveness
AUR62005645-RA.v1.0	CqSBP18	TGA-element	cis-acting element involved in gibberellin-responsiveness	Phytohormone responsiveness
AUR62042853-RA.v1.0	CqSBP22	TGA-element	cis-acting element involved in the abscisic acid responsiveness	Phytohormone responsiveness
AUR62004146-RA.v1.0	CqSBP01	ARE	cis-acting regulatory element essential for the anaerobic induction	Tissue-specific expression
AUR62004146-RA.v1.0	CqSBP01	ARE	cis-acting regulatory element essential for the anaerobic induction	Tissue-specific expression
AUR62013707-RA.v1.0	CqSBP02	ARE	cis-acting regulatory element essential for the anaerobic induction	Tissue-specific expression
AUR62028919-RA.v1.0	CqSBP03	ARE	cis-acting regulatory element essential for the anaerobic induction	Tissue-specific expression
AUR62028919-RA.v1.0	CqSBP03	ARE	cis-acting regulatory element essential for the anaerobic induction	Tissue-specific expression
AUR62028919-RA.v1.0	CqSBP03	ARE	cis-acting regulatory element essential for the anaerobic induction	Tissue-specific expression
AUR62028919-RA.v1.0	CqSBP03	ARE	cis-acting regulatory element essential for the anaerobic induction	Tissue-specific expression
AUR62005629-RA.v1.0	CqSBP04	ARE	cis-acting regulatory element essential for the anaerobic induction	Tissue-specific expression
AUR62005629-RA.v1.0	CqSBP04	ARE	cis-acting regulatory element essential for the anaerobic induction	Tissue-specific expression
AUR62002563-RA.v1.0	CqSBP05	ARE	cis-acting regulatory element essential for the anaerobic induction	Tissue-specific expression
AUR62002563-RA.v1.0	CqSBP05	ARE	cis-acting regulatory element essential for the anaerobic induction	Tissue-specific expression
AUR62002563-RA.v1.0	CqSBP05	ARE	cis-acting regulatory element essential for the anaerobic induction	Tissue-specific expression
AUR62002563-RA.v1.0	CqSBP05	ARE	cis-acting regulatory element essential for the anaerobic induction	Tissue-specific expression
AUR62029984-RA.v1.0	CqSBP07	ARE	cis-acting regulatory element essential for the anaerobic induction	Tissue-specific expression
AUR62029984-RA.v1.0	CqSBP07	ARE	cis-acting regulatory element essential for the anaerobic induction	Tissue-specific expression
AUR62029984-RA.v1.0	CqSBP07	ARE	cis-acting regulatory element essential for the anaerobic induction	Tissue-specific expression
AUR62024322-RA.v1.0	CqSBP08	ARE	cis-acting regulatory element essential for the anaerobic induction	Tissue-specific expression
AUR62024322-RA.v1.0	CqSBP08	ARE	cis-acting regulatory element essential for the anaerobic induction	Tissue-specific expression
AUR62024322-RA.v1.0	CqSBP08	ARE	cis-acting regulatory element essential for the anaerobic induction	Tissue-specific expression
AUR62024322-RA.v1.0	CqSBP08	ARE	cis-acting regulatory element essential for the anaerobic induction	Tissue-specific expression
AUR62024322-RA.v1.0	CqSBP08	ARE	cis-acting regulatory element essential for the anaerobic induction	Tissue-specific expression
AUR62012061-RA.v1.0	CqSBP10	ARE	cis-acting regulatory element essential for the anaerobic induction	Tissue-specific expression
AUR62012061-RA.v1.0	CqSBP10	ARE	cis-acting regulatory element essential for the anaerobic induction	Tissue-specific expression
AUR62012061-RA.v1.0	CqSBP10	ARE	cis-acting regulatory element essential for the anaerobic induction	Tissue-specific expression
AUR62012061-RA.v1.0	CqSBP10	ARE	cis-acting regulatory element essential for the anaerobic induction	Tissue-specific expression
AUR62012061-RA.v1.0	CqSBP10	ARE	cis-acting regulatory element essential for the anaerobic induction	Tissue-specific expression
AUR62032118-RA.v1.0	CqSBP11	ARE	cis-acting regulatory element essential for the anaerobic induction	Tissue-specific expression
AUR62032118-RA.v1.0	CqSBP11	ARE	cis-acting regulatory element essential for the anaerobic induction	Tissue-specific expression
AUR62032118-RA.v1.0	CqSBP11	ARE	cis-acting regulatory element essential for the anaerobic induction	Tissue-specific expression
AUR62039662-RA.v1.0	CqSBP12	ARE	cis-acting regulatory element essential for the anaerobic induction	Tissue-specific expression
AUR62039662-RA.v1.0	CqSBP12	ARE	cis-acting regulatory element essential for the anaerobic induction	Tissue-specific expression
AUR62039662-RA.v1.0	CqSBP12	ARE	cis-acting regulatory element essential for the anaerobic induction	Tissue-specific expression
AUR62011728-RA.v1.0	CqSBP13	ARE	cis-acting regulatory element essential for the anaerobic induction	Tissue-specific expression
AUR62011728-RA.v1.0	CqSBP13	ARE	cis-acting regulatory element essential for the anaerobic induction	Tissue-specific expression
AUR62011728-RA.v1.0	CqSBP13	ARE	cis-acting regulatory element essential for the anaerobic induction	Tissue-specific expression
AUR62003425-RA.v1.0	CqSBP15	ARE	cis-acting regulatory element essential for the anaerobic induction	Tissue-specific expression
AUR62003425-RA.v1.0	CqSBP15	ARE	cis-acting regulatory element essential for the anaerobic induction	Tissue-specific expression
AUR62003425-RA.v1.0	CqSBP15	ARE	cis-acting regulatory element essential for the anaerobic induction	Tissue-specific expression
AUR62035190-RA.v1.0	CqSBP16	ARE	cis-acting regulatory element essential for the anaerobic induction	Tissue-specific expression
AUR62035190-RA.v1.0	CqSBP16	ARE	cis-acting regulatory element essential for the anaerobic induction	Tissue-specific expression
AUR62035190-RA.v1.0	CqSBP16	ARE	cis-acting regulatory element essential for the anaerobic induction	Tissue-specific expression
AUR62035190-RA.v1.0	CqSBP16	ARE	cis-acting regulatory element essential for the anaerobic induction	Tissue-specific expression
AUR62035190-RA.v1.0	CqSBP16	ARE	cis-acting regulatory element essential for the anaerobic induction	Tissue-specific expression
AUR62035190-RA.v1.0	CqSBP16	ARE	cis-acting regulatory element essential for the anaerobic induction	Tissue-specific expression
AUR62035190-RA.v1.0	CqSBP16	ARE	cis-acting regulatory element essential for the anaerobic induction	Tissue-specific expression
AUR62035190-RA.v1.0	CqSBP16	ARE	cis-acting regulatory element essential for the anaerobic induction	Tissue-specific expression
AUR62042534-RA.v1.0	CqSBP17	ARE	cis-acting regulatory element essential for the anaerobic induction	Tissue-specific expression
AUR62042534-RA.v1.0	CqSBP17	ARE	cis-acting regulatory element essential for the anaerobic induction	Tissue-specific expression
AUR62042534-RA.v1.0	CqSBP17	ARE	cis-acting regulatory element essential for the anaerobic induction	Tissue-specific expression
AUR62042534-RA.v1.0	CqSBP17	ARE	cis-acting regulatory element essential for the anaerobic induction	Tissue-specific expression
AUR62005645-RA.v1.0	CqSBP18	ARE	cis-acting regulatory element essential for the anaerobic induction	Tissue-specific expression
AUR62005645-RA.v1.0	CqSBP18	ARE	cis-acting regulatory element essential for the anaerobic induction	Tissue-specific expression
AUR62005645-RA.v1.0	CqSBP18	ARE	cis-acting regulatory element essential for the anaerobic induction	Tissue-specific expression
AUR62005645-RA.v1.0	CqSBP18	ARE	cis-acting regulatory element essential for the anaerobic induction	Tissue-specific expression
AUR62005645-RA.v1.0	CqSBP18	ARE	cis-acting regulatory element essential for the anaerobic induction	Tissue-specific expression
AUR62005645-RA.v1.0	CqSBP18	ARE	cis-acting regulatory element essential for the anaerobic induction	Tissue-specific expression
AUR62005645-RA.v1.0	CqSBP18	ARE	cis-acting regulatory element essential for the anaerobic induction	Tissue-specific expression
AUR62028905-RA.v1.0	CqSBP19	ARE	cis-acting regulatory element essential for the anaerobic induction	Tissue-specific expression
AUR62028905-RA.v1.0	CqSBP19	ARE	cis-acting regulatory element essential for the anaerobic induction	Tissue-specific expression
AUR62028905-RA.v1.0	CqSBP19	ARE	cis-acting regulatory element essential for the anaerobic induction	Tissue-specific expression
AUR62028905-RA.v1.0	CqSBP19	ARE	cis-acting regulatory element essential for the anaerobic induction	Tissue-specific expression
AUR62028905-RA.v1.0	CqSBP19	ARE	cis-acting regulatory element essential for the anaerobic induction	Tissue-specific expression
AUR62028905-RA.v1.0	CqSBP19	ARE	cis-acting regulatory element essential for the anaerobic induction	Tissue-specific expression
AUR62003075-RA.v1.0	CqSBP20	ARE	cis-acting regulatory element essential for the anaerobic induction	Tissue-specific expression
AUR62003075-RA.v1.0	CqSBP20	ARE	cis-acting regulatory element essential for the anaerobic induction	Tissue-specific expression
AUR62003075-RA.v1.0	CqSBP20	ARE	cis-acting regulatory element essential for the anaerobic induction	Tissue-specific expression
AUR62003075-RA.v1.0	CqSBP20	ARE	cis-acting regulatory element essential for the anaerobic induction	Tissue-specific expression
AUR62007890-RA.v1.0	CqSBP21	ARE	cis-acting regulatory element essential for the anaerobic induction	Tissue-specific expression

Table S2: Continue

AUR62042853-RA.v1.0	CqSBP22	ARE	cis-acting regulatory element essential for the anaerobic induction	Tissue-specific expression
AUR62042853-RA.v1.0	CqSBP22	ARE	cis-acting regulatory element essential for the anaerobic induction	Tissue-specific expression
AUR62042853-RA.v1.0	CqSBP22	ARE	cis-acting regulatory element essential for the anaerobic induction	Tissue-specific expression
AUR62042853-RA.v1.0	CqSBP22	ARE	cis-acting regulatory element essential for the anaerobic induction	Tissue-specific expression
AUR62042654-RA.v1.0	CqSBP23	ARE	cis-acting regulatory element essential for the anaerobic induction	Tissue-specific expression
AUR62042654-RA.v1.0	CqSBP23	ARE	cis-acting regulatory element essential for the anaerobic induction	Tissue-specific expression
AUR62042654-RA.v1.0	CqSBP23	ARE	cis-acting regulatory element essential for the anaerobic induction	Tissue-specific expression
AUR62042654-RA.v1.0	CqSBP23	ARE	cis-acting regulatory element essential for the anaerobic induction	Tissue-specific expression
AUR62007890-RA.v1.0	CqSBP21	AT-rich sequence	element for maximal elicitor-mediated activation (2copies)	Tissue-specific expression
AUR62007890-RA.v1.0	CqSBP21	AT-rich sequence	element for maximal elicitor-mediated activation (2copies)	Tissue-specific expression
AUR62028919-RA.v1.0	CqSBP03	CAT-box	cis-acting regulatory element related to meristem expression	Tissue-specific expression
AUR62002563-RA.v1.0	CqSBP05	CAT-box	cis-acting regulatory element related to meristem expression	Tissue-specific expression
AUR62002563-RA.v1.0	CqSBP05	CAT-box	cis-acting regulatory element related to meristem expression	Tissue-specific expression
AUR62029984-RA.v1.0	CqSBP07	CAT-box	cis-acting regulatory element related to meristem expression	Tissue-specific expression
AUR62029984-RA.v1.0	CqSBP07	CAT-box	cis-acting regulatory element related to meristem expression	Tissue-specific expression
AUR62029984-RA.v1.0	CqSBP07	CAT-box	cis-acting regulatory element related to meristem expression	Tissue-specific expression
AUR62029984-RA.v1.0	CqSBP07	CAT-box	cis-acting regulatory element related to meristem expression	Tissue-specific expression
AUR62024322-RA.v1.0	CqSBP08	CAT-box	cis-acting regulatory element related to meristem expression	Tissue-specific expression
AUR62019452-RA.v1.0	CqSBP09	CAT-box	cis-acting regulatory element related to meristem expression	Tissue-specific expression
AUR62012061-RA.v1.0	CqSBP10	CAT-box	cis-acting regulatory element related to meristem expression	Tissue-specific expression
AUR62032118-RA.v1.0	CqSBP11	CAT-box	cis-acting regulatory element related to meristem expression	Tissue-specific expression
AUR62039662-RA.v1.0	CqSBP12	CAT-box	cis-acting regulatory element related to meristem expression	Tissue-specific expression
AUR62011728-RA.v1.0	CqSBP13	CAT-box	cis-acting regulatory element related to meristem expression	Tissue-specific expression
AUR62011728-RA.v1.0	CqSBP13	CAT-box	cis-acting regulatory element related to meristem expression	Tissue-specific expression
AUR62011728-RA.v1.0	CqSBP13	CAT-box	cis-acting regulatory element related to meristem expression	Tissue-specific expression
AUR62011728-RA.v1.0	CqSBP13	CAT-box	cis-acting regulatory element related to meristem expression	Tissue-specific expression
AUR62003425-RA.v1.0	CqSBP15	CAT-box	cis-acting regulatory element related to meristem expression	Tissue-specific expression
AUR62003425-RA.v1.0	CqSBP15	CAT-box	cis-acting regulatory element related to meristem expression	Tissue-specific expression
AUR62035190-RA.v1.0	CqSBP16	CAT-box	cis-acting regulatory element related to meristem expression	Tissue-specific expression
AUR62035190-RA.v1.0	CqSBP16	CAT-box	cis-acting regulatory element related to meristem expression	Tissue-specific expression
AUR62035190-RA.v1.0	CqSBP16	CAT-box	cis-acting regulatory element related to meristem expression	Tissue-specific expression
AUR62042534-RA.v1.0	CqSBP17	CAT-box	cis-acting regulatory element related to meristem expression	Tissue-specific expression
AUR62042534-RA.v1.0	CqSBP17	CAT-box	cis-acting regulatory element related to meristem expression	Tissue-specific expression
AUR62042534-RA.v1.0	CqSBP17	CAT-box	cis-acting regulatory element related to meristem expression	Tissue-specific expression
AUR62003075-RA.v1.0	CqSBP20	CAT-box	cis-acting regulatory element related to meristem expression	Tissue-specific expression
AUR62007890-RA.v1.0	CqSBP21	CAT-box	cis-acting regulatory element related to meristem expression	Tissue-specific expression
AUR62042853-RA.v1.0	CqSBP22	CAT-box	cis-acting regulatory element related to meristem expression	Tissue-specific expression
AUR62028919-RA.v1.0	CqSBP03	GC-motif	enhancer-like element involved in anoxic specific inducibility	Tissue-specific expression
AUR62005629-RA.v1.0	CqSBP04	GC-motif	enhancer-like element involved in anoxic specific inducibility	Tissue-specific expression
AUR62019452-RA.v1.0	CqSBP09	GC-motif	enhancer-like element involved in anoxic specific inducibility	Tissue-specific expression
AUR62035190-RA.v1.0	CqSBP16	GC-motif	enhancer-like element involved in anoxic specific inducibility	Tissue-specific expression
AUR62013707-RA.v1.0	CqSBP02	GCN4_motif	cis-regulatory element involved in endosperm expression	Tissue-specific expression
AUR62024322-RA.v1.0	CqSBP08	GCN4_motif	cis-regulatory element involved in endosperm expression	Tissue-specific expression
AUR62024322-RA.v1.0	CqSBP08	GCN4_motif	cis-regulatory element involved in endosperm expression	Tissue-specific expression
AUR62032118-RA.v1.0	CqSBP11	GCN4_motif	cis-regulatory element involved in endosperm expression	Tissue-specific expression
AUR62011728-RA.v1.0	CqSBP13	GCN4_motif	cis-regulatory element involved in endosperm expression	Tissue-specific expression
AUR62029416-RA.v1.0	CqSBP14	GCN4_motif	cis-regulatory element involved in endosperm expression	Tissue-specific expression
AUR62003425-RA.v1.0	CqSBP15	GCN4_motif	cis-regulatory element involved in endosperm expression	Tissue-specific expression
AUR62042853-RA.v1.0	CqSBP22	GCN4_motif	cis-regulatory element involved in endosperm expression	Tissue-specific expression
AUR62013707-RA.v1.0	CqSBP02	HD-Zip 1	element involved in differentiation of the palisade mesophyll cells	Tissue-specific expression
AUR62013707-RA.v1.0	CqSBP02	MBSI	MYB binding site involved in flavonoid biosynthetic genes regulation	Tissue-specific expression
AUR62028919-RA.v1.0	CqSBP03	MBSI	MYB binding site involved in flavonoid biosynthetic genes regulation	Tissue-specific expression
AUR62002563-RA.v1.0	CqSBP05	MBSI	MYB binding site involved in flavonoid biosynthetic genes regulation	Tissue-specific expression
AUR62032118-RA.v1.0	CqSBP11	MBSI	MYB binding site involved in flavonoid biosynthetic genes regulation	Tissue-specific expression
AUR62005645-RA.v1.0	CqSBP18	motif I	cis-acting regulatory element root specific	Tissue-specific expression
AUR62024322-RA.v1.0	CqSBP08	MSA-like	cis-acting element involved in cell cycle regulation	Tissue-specific expression
AUR62011728-RA.v1.0	CqSBP13	MSA-like	cis-acting element involved in cell cycle regulation	Tissue-specific expression
AUR62028919-RA.v1.0	CqSBP03	O2-site	cis-acting regulatory element involved in zein metabolism regulation	Tissue-specific expression
AUR62005629-RA.v1.0	CqSBP04	O2-site	cis-acting regulatory element involved in zein metabolism regulation	Tissue-specific expression
AUR62002563-RA.v1.0	CqSBP05	O2-site	cis-acting regulatory element involved in zein metabolism regulation	Tissue-specific expression
AUR62002563-RA.v1.0	CqSBP05	O2-site	cis-acting regulatory element involved in zein metabolism regulation	Tissue-specific expression
AUR62012061-RA.v1.0	CqSBP10	O2-site	cis-acting regulatory element involved in zein metabolism regulation	Tissue-specific expression
AUR62032118-RA.v1.0	CqSBP11	O2-site	cis-acting regulatory element involved in zein metabolism regulation	Tissue-specific expression
AUR62039662-RA.v1.0	CqSBP12	O2-site	cis-acting regulatory element involved in zein metabolism regulation	Tissue-specific expression
AUR62011728-RA.v1.0	CqSBP13	O2-site	cis-acting regulatory element involved in zein metabolism regulation	Tissue-specific expression
AUR62011728-RA.v1.0	CqSBP13	O2-site	cis-acting regulatory element involved in zein metabolism regulation	Tissue-specific expression
AUR62035190-RA.v1.0	CqSBP16	O2-site	cis-acting regulatory element involved in zein metabolism regulation	Tissue-specific expression
AUR62042534-RA.v1.0	CqSBP17	O2-site	cis-acting regulatory element involved in zein metabolism regulation	Tissue-specific expression
AUR62042534-RA.v1.0	CqSBP17	O2-site	cis-acting regulatory element involved in zein metabolism regulation	Tissue-specific expression
AUR62042654-RA.v1.0	CqSBP23	O2-site	cis-acting regulatory element involved in zein metabolism regulation	Tissue-specific expression
AUR62011728-RA.v1.0	CqSBP13	RY-element	cis-acting regulatory element involved in seed-specific regulation	Tissue-specific expression
AUR62002563-RA.v1.0	CqSBP05	AAAC-motif	light responsive element	Light responsive
AUR62002563-RA.v1.0	CqSBP05	ACE	cis-acting element involved in light responsiveness	Light responsive
AUR62042534-RA.v1.0	CqSBP17	ACE	cis-acting element involved in light responsiveness	Light responsive
AUR62003075-RA.v1.0	CqSBP20	ACE	cis-acting element involved in light responsiveness	Light responsive
AUR62028919-RA.v1.0	CqSBP03	AE-box	part of a module for light response	Light responsive
AUR62028919-RA.v1.0	CqSBP03	AE-box	part of a module for light response	Light responsive
AUR62005629-RA.v1.0	CqSBP04	AE-box	part of a module for light response	Light responsive
AUR62005629-RA.v1.0	CqSBP04	AE-box	part of a module for light response	Light responsive
AUR62002563-RA.v1.0	CqSBP05	AE-box	part of a module for light response	Light responsive
AUR62012061-RA.v1.0	CqSBP10	AE-box	part of a module for light response	Light responsive
AUR62011728-RA.v1.0	CqSBP13	AE-box	part of a module for light response	Light responsive
AUR62003425-RA.v1.0	CqSBP15	AE-box	part of a module for light response	Light responsive
AUR62035190-RA.v1.0	CqSBP16	AE-box	part of a module for light response	Light responsive
AUR62035190-RA.v1.0	CqSBP16	AE-box	part of a module for light response	Light responsive
AUR62005645-RA.v1.0	CqSBP18	AE-box	part of a module for light response	Light responsive
AUR62042853-RA.v1.0	CqSBP22	AE-box	part of a module for light response	Light responsive
AUR62042853-RA.v1.0	CqSBP22	AE-box	part of a module for light response	Light responsive
AUR62042654-RA.v1.0	CqSBP23	AE-box	part of a module for light response	Light responsive
AUR62042534-RA.v1.0	CqSBP17	AT1-motif	part of a light responsive module	Light responsive
AUR62028905-RA.v1.0	CqSBP19	AT1-motif	part of a light responsive module	Light responsive

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Table S2: Continue

AUR62007890-RA.v1.0	CqSBP21	AT1-motif	part of a light responsive module	Light responsive
AUR62004146-RA.v1.0	CqSBP01	ATC-motif	part of a conserved DNA module involved in light responsiveness	Light responsive
AUR62002563-RA.v1.0	CqSBP05	ATC-motif	part of a conserved DNA module involved in light responsiveness	Light responsive
AUR62029983-RA.v1.0	CqSBP06	ATC-motif	part of a conserved DNA module involved in light responsiveness	Light responsive
AUR62012061-RA.v1.0	CqSBP10	ATC-motif	part of a conserved DNA module involved in light responsiveness	Light responsive
AUR62011728-RA.v1.0	CqSBP13	ATC-motif	part of a conserved DNA module involved in light responsiveness	Light responsive
AUR62042534-RA.v1.0	CqSBP17	ATC-motif	part of a conserved DNA module involved in light responsiveness	Light responsive
AUR62042853-RA.v1.0	CqSBP22	ATC-motif	part of a conserved DNA module involved in light responsiveness	Light responsive
AUR62004146-RA.v1.0	CqSBP01	ATCT-motif	part of a conserved DNA module involved in light responsiveness	Light responsive
AUR62013707-RA.v1.0	CqSBP02	ATCT-motif	part of a conserved DNA module involved in light responsiveness	Light responsive
AUR62029984-RA.v1.0	CqSBP07	ATCT-motif	part of a conserved DNA module involved in light responsiveness	Light responsive
AUR62003425-RA.v1.0	CqSBP15	ATCT-motif	part of a conserved DNA module involved in light responsiveness	Light responsive
AUR62003075-RA.v1.0	CqSBP20	ATCT-motif	part of a conserved DNA module involved in light responsiveness	Light responsive
AUR62007890-RA.v1.0	CqSBP21	ATCT-motif	part of a conserved DNA module involved in light responsiveness	Light responsive
AUR62042654-RA.v1.0	CqSBP23	ATCT-motif	part of a conserved DNA module involved in light responsiveness	Light responsive
AUR62028919-RA.v1.0	CqSBP03	Box 4	part of a conserved DNA module involved in light responsiveness	Light responsive
AUR62005629-RA.v1.0	CqSBP04	Box 4	part of a conserved DNA module involved in light responsiveness	Light responsive
AUR62005629-RA.v1.0	CqSBP04	Box 4	part of a conserved DNA module involved in light responsiveness	Light responsive
AUR62005629-RA.v1.0	CqSBP04	Box 4	part of a conserved DNA module involved in light responsiveness	Light responsive
AUR62029984-RA.v1.0	CqSBP07	Box 4	part of a conserved DNA module involved in light responsiveness	Light responsive
AUR62029984-RA.v1.0	CqSBP07	Box 4	part of a conserved DNA module involved in light responsiveness	Light responsive
AUR62024322-RA.v1.0	CqSBP08	Box 4	part of a conserved DNA module involved in light responsiveness	Light responsive
AUR62024322-RA.v1.0	CqSBP08	Box 4	part of a conserved DNA module involved in light responsiveness	Light responsive
AUR62024322-RA.v1.0	CqSBP08	Box 4	part of a conserved DNA module involved in light responsiveness	Light responsive
AUR62024322-RA.v1.0	CqSBP08	Box 4	part of a conserved DNA module involved in light responsiveness	Light responsive
AUR62019452-RA.v1.0	CqSBP09	Box 4	part of a conserved DNA module involved in light responsiveness	Light responsive
AUR62019452-RA.v1.0	CqSBP09	Box 4	part of a conserved DNA module involved in light responsiveness	Light responsive
AUR62012061-RA.v1.0	CqSBP10	Box 4	part of a conserved DNA module involved in light responsiveness	Light responsive
AUR62012061-RA.v1.0	CqSBP10	Box 4	part of a conserved DNA module involved in light responsiveness	Light responsive
AUR62012061-RA.v1.0	CqSBP10	Box 4	part of a conserved DNA module involved in light responsiveness	Light responsive
AUR62012061-RA.v1.0	CqSBP10	Box 4	part of a conserved DNA module involved in light responsiveness	Light responsive
AUR62012061-RA.v1.0	CqSBP10	Box 4	part of a conserved DNA module involved in light responsiveness	Light responsive
AUR62039662-RA.v1.0	CqSBP12	Box 4	part of a conserved DNA module involved in light responsiveness	Light responsive
AUR62039662-RA.v1.0	CqSBP12	Box 4	part of a conserved DNA module involved in light responsiveness	Light responsive
AUR62011728-RA.v1.0	CqSBP13	Box 4	part of a conserved DNA module involved in light responsiveness	Light responsive
AUR62011728-RA.v1.0	CqSBP13	Box 4	part of a conserved DNA module involved in light responsiveness	Light responsive
AUR62011728-RA.v1.0	CqSBP13	Box 4	part of a conserved DNA module involved in light responsiveness	Light responsive
AUR62029416-RA.v1.0	CqSBP14	Box 4	part of a conserved DNA module involved in light responsiveness	Light responsive
AUR62029416-RA.v1.0	CqSBP14	Box 4	part of a conserved DNA module involved in light responsiveness	Light responsive
AUR62035190-RA.v1.0	CqSBP16	Box 4	part of a conserved DNA module involved in light responsiveness	Light responsive
AUR62042534-RA.v1.0	CqSBP17	Box 4	part of a conserved DNA module involved in light responsiveness	Light responsive
AUR62042534-RA.v1.0	CqSBP17	Box 4	part of a conserved DNA module involved in light responsiveness	Light responsive
AUR62042534-RA.v1.0	CqSBP17	Box 4	part of a conserved DNA module involved in light responsiveness	Light responsive
AUR62042534-RA.v1.0	CqSBP17	Box 4	part of a conserved DNA module involved in light responsiveness	Light responsive
AUR62042534-RA.v1.0	CqSBP17	Box 4	part of a conserved DNA module involved in light responsiveness	Light responsive
AUR62005645-RA.v1.0	CqSBP18	Box 4	part of a conserved DNA module involved in light responsiveness	Light responsive
AUR62005645-RA.v1.0	CqSBP18	Box 4	part of a conserved DNA module involved in light responsiveness	Light responsive
AUR62005645-RA.v1.0	CqSBP18	Box 4	part of a conserved DNA module involved in light responsiveness	Light responsive
AUR62005645-RA.v1.0	CqSBP18	Box 4	part of a conserved DNA module involved in light responsiveness	Light responsive
AUR62028905-RA.v1.0	CqSBP19	Box 4	part of a conserved DNA module involved in light responsiveness	Light responsive
AUR62028905-RA.v1.0	CqSBP19	Box 4	part of a conserved DNA module involved in light responsiveness	Light responsive
AUR62028905-RA.v1.0	CqSBP19	Box 4	part of a conserved DNA module involved in light responsiveness	Light responsive
AUR62028905-RA.v1.0	CqSBP19	Box 4	part of a conserved DNA module involved in light responsiveness	Light responsive
AUR62003075-RA.v1.0	CqSBP20	Box 4	part of a conserved DNA module involved in light responsiveness	Light responsive
AUR62003075-RA.v1.0	CqSBP20	Box 4	part of a conserved DNA module involved in light responsiveness	Light responsive
AUR62003075-RA.v1.0	CqSBP20	Box 4	part of a conserved DNA module involved in light responsiveness	Light responsive
AUR62003075-RA.v1.0	CqSBP20	Box 4	part of a conserved DNA module involved in light responsiveness	Light responsive
AUR62003075-RA.v1.0	CqSBP20	Box 4	part of a conserved DNA module involved in light responsiveness	Light responsive
AUR62003075-RA.v1.0	CqSBP20	Box 4	part of a conserved DNA module involved in light responsiveness	Light responsive
AUR62003075-RA.v1.0	CqSBP20	Box 4	part of a conserved DNA module involved in light responsiveness	Light responsive
AUR62007890-RA.v1.0	CqSBP21	Box 4	part of a conserved DNA module involved in light responsiveness	Light responsive
AUR62007890-RA.v1.0	CqSBP21	Box 4	part of a conserved DNA module involved in light responsiveness	Light responsive
AUR62007890-RA.v1.0	CqSBP21	Box 4	part of a conserved DNA module involved in light responsiveness	Light responsive
AUR62007890-RA.v1.0	CqSBP21	Box 4	part of a conserved DNA module involved in light responsiveness	Light responsive
AUR62007890-RA.v1.0	CqSBP21	Box 4	part of a conserved DNA module involved in light responsiveness	Light responsive
AUR62007890-RA.v1.0	CqSBP21	Box 4	part of a conserved DNA module involved in light responsiveness	Light responsive
AUR62007890-RA.v1.0	CqSBP21	Box 4	part of a conserved DNA module involved in light responsiveness	Light responsive
AUR62007890-RA.v1.0	CqSBP21	Box 4	part of a conserved DNA module involved in light responsiveness	Light responsive
AUR62042853-RA.v1.0	CqSBP22	Box 4	part of a conserved DNA module involved in light responsiveness	Light responsive
AUR62042853-RA.v1.0	CqSBP22	Box 4	part of a conserved DNA module involved in light responsiveness	Light responsive
AUR62042853-RA.v1.0	CqSBP22	Box 4	part of a conserved DNA module involved in light responsiveness	Light responsive
AUR62042654-RA.v1.0	CqSBP23	Box 4	part of a conserved DNA module involved in light responsiveness	Light responsive
AUR62042654-RA.v1.0	CqSBP23	Box 4	part of a conserved DNA module involved in light responsiveness	Light responsive
AUR62042654-RA.v1.0	CqSBP23	Box 4	part of a conserved DNA module involved in light responsiveness	Light responsive
AUR62032118-RA.v1.0	CqSBP11	Box II	part of a light responsive element	Light responsive
AUR62039662-RA.v1.0	CqSBP12	Box II	part of a light responsive element	Light responsive
AUR62011728-RA.v1.0	CqSBP13	Box II	part of a light responsive element	Light responsive
AUR62011728-RA.v1.0	CqSBP13	Box II	part of a light responsive element	Light responsive
AUR62011728-RA.v1.0	CqSBP13	Box II	part of a light responsive element	Light responsive
AUR62005629-RA.v1.0	CqSBP04	chs-CMA1a	part of a light responsive element	Light responsive
AUR62029984-RA.v1.0	CqSBP07	chs-CMA1a	part of a light responsive element	Light responsive
AUR62012061-RA.v1.0	CqSBP10	chs-CMA1a	part of a light responsive element	Light responsive
AUR62032118-RA.v1.0	CqSBP11	chs-CMA1a	part of a light responsive element	Light responsive
AUR62005645-RA.v1.0	CqSBP18	chs-CMA1a	part of a light responsive element	Light responsive
AUR62028905-RA.v1.0	CqSBP19	chs-CMA1a	part of a light responsive element	Light responsive
AUR62013707-RA.v1.0	CqSBP02	chs-CMA2a	part of a light responsive element	Light responsive
AUR62039662-RA.v1.0	CqSBP12	chs-CMA2a	part of a light responsive element	Light responsive
AUR62003075-RA.v1.0	CqSBP20	chs-CMA2a	part of a light responsive element	Light responsive
AUR62002563-RA.v1.0	CqSBP05	GA-motif	part of a light responsive element	Light responsive
AUR62042534-RA.v1.0	CqSBP17	GA-motif	part of a light responsive element	Light responsive
AUR62042534-RA.v1.0	CqSBP17	GA-motif	part of a light responsive element	Light responsive

Table S2: Continue

AUR62042654-RA.v1.0	CqSBP23	GA-motif	part of a light responsive element	Light responsive
AUR62024322-RA.v1.0	CqSBP08	Gap-box	part of a light responsive element	Light responsive
AUR62028919-RA.v1.0	CqSBP03	GATA-motif	part of a light responsive element	Light responsive
AUR62005629-RA.v1.0	CqSBP04	GATA-motif	part of a light responsive element	Light responsive
AUR62002563-RA.v1.0	CqSBP05	GATA-motif	part of a light responsive element	Light responsive
AUR62032118-RA.v1.0	CqSBP11	GATA-motif	part of a light responsive element	Light responsive
AUR62039662-RA.v1.0	CqSBP12	GATA-motif	part of a light responsive element	Light responsive
AUR62039662-RA.v1.0	CqSBP12	GATA-motif	part of a light responsive element	Light responsive
AUR62011728-RA.v1.0	CqSBP13	GATA-motif	part of a light responsive element	Light responsive
AUR62029416-RA.v1.0	CqSBP14	GATA-motif	part of a light responsive element	Light responsive
AUR62029416-RA.v1.0	CqSBP14	GATA-motif	part of a light responsive element	Light responsive
AUR62029416-RA.v1.0	CqSBP14	GATA-motif	part of a light responsive element	Light responsive
AUR62003425-RA.v1.0	CqSBP15	GATA-motif	part of a light responsive element	Light responsive
AUR62035190-RA.v1.0	CqSBP16	GATA-motif	part of a light responsive element	Light responsive
AUR62042534-RA.v1.0	CqSBP17	GATA-motif	part of a light responsive element	Light responsive
AUR62028905-RA.v1.0	CqSBP19	GATA-motif	part of a light responsive element	Light responsive
AUR62003075-RA.v1.0	CqSBP20	GATA-motif	part of a light responsive element	Light responsive
AUR62013707-RA.v1.0	CqSBP02	G-Box	cis-acting regulatory element involved in light responsiveness	Light responsive
AUR62013707-RA.v1.0	CqSBP02	G-box	cis-acting regulatory element involved in light responsiveness	Light responsive
AUR62028919-RA.v1.0	CqSBP03	G-Box	cis-acting regulatory element involved in light responsiveness	Light responsive
AUR62028919-RA.v1.0	CqSBP03	G-box	cis-acting regulatory element involved in light responsiveness	Light responsive
AUR62028919-RA.v1.0	CqSBP03	G-box	cis-acting regulatory element involved in light responsiveness	Light responsive
AUR62005629-RA.v1.0	CqSBP04	G-box	cis-acting regulatory element involved in light responsiveness	Light responsive
AUR62005629-RA.v1.0	CqSBP04	G-box	cis-acting regulatory element involved in light responsiveness	Light responsive
AUR62005629-RA.v1.0	CqSBP04	G-Box	cis-acting regulatory element involved in light responsiveness	Light responsive
AUR62002563-RA.v1.0	CqSBP05	G-box	cis-acting regulatory element involved in light responsiveness	Light responsive
AUR62002563-RA.v1.0	CqSBP05	G-box	cis-acting regulatory element involved in light responsiveness	Light responsive
AUR62002563-RA.v1.0	CqSBP05	G-box	cis-acting regulatory element involved in light responsiveness	Light responsive
AUR62002563-RA.v1.0	CqSBP05	G-box	cis-acting regulatory element involved in light responsiveness	Light responsive
AUR62029984-RA.v1.0	CqSBP07	G-Box	cis-acting regulatory element involved in light responsiveness	Light responsive
AUR62029984-RA.v1.0	CqSBP07	G-box	cis-acting regulatory element involved in light responsiveness	Light responsive
AUR62029984-RA.v1.0	CqSBP07	G-box	cis-acting regulatory element involved in light responsiveness	Light responsive
AUR62029984-RA.v1.0	CqSBP07	G-box	cis-acting regulatory element involved in light responsiveness	Light responsive
AUR62024322-RA.v1.0	CqSBP08	G-Box	cis-acting regulatory element involved in light responsiveness	Light responsive
AUR62019452-RA.v1.0	CqSBP09	G-Box	cis-acting regulatory element involved in light responsiveness	Light responsive
AUR62019452-RA.v1.0	CqSBP09	G-box	cis-acting regulatory element involved in light responsiveness	Light responsive
AUR62019452-RA.v1.0	CqSBP09	G-box	cis-acting regulatory element involved in light responsiveness	Light responsive
AUR62012061-RA.v1.0	CqSBP10	G-Box	cis-acting regulatory element involved in light responsiveness	Light responsive
AUR62032118-RA.v1.0	CqSBP11	G-box	cis-acting regulatory element involved in light responsiveness	Light responsive
AUR62039662-RA.v1.0	CqSBP12	G-box	cis-acting regulatory element involved in light responsiveness	Light responsive
AUR62039662-RA.v1.0	CqSBP12	G-Box	cis-acting regulatory element involved in light responsiveness	Light responsive
AUR62011728-RA.v1.0	CqSBP13	G-box	cis-acting regulatory element involved in light responsiveness	Light responsive
AUR62011728-RA.v1.0	CqSBP13	G-box	cis-acting regulatory element involved in light responsiveness	Light responsive
AUR62011728-RA.v1.0	CqSBP13	G-box	cis-acting regulatory element involved in light responsiveness	Light responsive
AUR62011728-RA.v1.0	CqSBP13	G-box	cis-acting regulatory element involved in light responsiveness	Light responsive
AUR62011728-RA.v1.0	CqSBP13	G-box	cis-acting regulatory element involved in light responsiveness	Light responsive
AUR62011728-RA.v1.0	CqSBP13	G-box	cis-acting regulatory element involved in light responsiveness	Light responsive
AUR62011728-RA.v1.0	CqSBP13	G-box	cis-acting regulatory element involved in light responsiveness	Light responsive
AUR62011728-RA.v1.0	CqSBP13	G-box	cis-acting regulatory element involved in light responsiveness	Light responsive
AUR62011728-RA.v1.0	CqSBP13	G-box	cis-acting regulatory element involved in light responsiveness	Light responsive
AUR62011728-RA.v1.0	CqSBP13	G-box	cis-acting regulatory element involved in light responsiveness	Light responsive
AUR62011728-RA.v1.0	CqSBP13	G-box	cis-acting regulatory element involved in light responsiveness	Light responsive
AUR62011728-RA.v1.0	CqSBP13	G-box	cis-acting regulatory element involved in light responsiveness	Light responsive
AUR62011728-RA.v1.0	CqSBP13	G-Box	cis-acting regulatory element involved in light responsiveness	Light responsive
AUR62011728-RA.v1.0	CqSBP13	G-Box	cis-acting regulatory element involved in light responsiveness	Light responsive
AUR62011728-RA.v1.0	CqSBP13	G-Box	cis-acting regulatory element involved in light responsiveness	Light responsive
AUR62011728-RA.v1.0	CqSBP13	G-Box	cis-acting regulatory element involved in light responsiveness	Light responsive
AUR62029416-RA.v1.0	CqSBP14	G-box	cis-acting regulatory element involved in light responsiveness	Light responsive
AUR62029416-RA.v1.0	CqSBP14	G-box	cis-acting regulatory element involved in light responsiveness	Light responsive
AUR62029416-RA.v1.0	CqSBP14	G-box	cis-acting regulatory element involved in light responsiveness	Light responsive
AUR62029416-RA.v1.0	CqSBP14	G-box	cis-acting regulatory element involved in light responsiveness	Light responsive
AUR62003425-RA.v1.0	CqSBP15	G-box	cis-acting regulatory element involved in light responsiveness	Light responsive
AUR62003425-RA.v1.0	CqSBP15	G-box	cis-acting regulatory element involved in light responsiveness	Light responsive
AUR62042534-RA.v1.0	CqSBP17	G-box	cis-acting regulatory element involved in light responsiveness	Light responsive
AUR62042534-RA.v1.0	CqSBP17	G-box	cis-acting regulatory element involved in light responsiveness	Light responsive
AUR62042534-RA.v1.0	CqSBP17	G-box	cis-acting regulatory element involved in light responsiveness	Light responsive
AUR62042534-RA.v1.0	CqSBP17	G-Box	cis-acting regulatory element involved in light responsiveness	Light responsive
AUR62042534-RA.v1.0	CqSBP17	G-Box	cis-acting regulatory element involved in light responsiveness	Light responsive
AUR62028905-RA.v1.0	CqSBP19	G-Box	cis-acting regulatory element involved in light responsiveness	Light responsive
AUR62028905-RA.v1.0	CqSBP19	G-box	cis-acting regulatory element involved in light responsiveness	Light responsive
AUR62003075-RA.v1.0	CqSBP20	G-box	cis-acting regulatory element involved in light responsiveness	Light responsive
AUR62003075-RA.v1.0	CqSBP20	G-box	cis-acting regulatory element involved in light responsiveness	Light responsive
AUR62003075-RA.v1.0	CqSBP20	G-box	cis-acting regulatory element involved in light responsiveness	Light responsive
AUR62003075-RA.v1.0	CqSBP20	G-Box	cis-acting regulatory element involved in light responsiveness	Light responsive
AUR62003075-RA.v1.0	CqSBP20	G-Box	cis-acting regulatory element involved in light responsiveness	Light responsive
AUR62003075-RA.v1.0	CqSBP20	G-Box	cis-acting regulatory element involved in light responsiveness	Light responsive
AUR62007890-RA.v1.0	CqSBP21	G-box	cis-acting regulatory element involved in light responsiveness	Light responsive
AUR62007890-RA.v1.0	CqSBP21	G-Box	cis-acting regulatory element involved in light responsiveness	Light responsive
AUR62042853-RA.v1.0	CqSBP22	G-Box	cis-acting regulatory element involved in light responsiveness	Light responsive
AUR62042853-RA.v1.0	CqSBP22	G-box	cis-acting regulatory element involved in light responsiveness	Light responsive
AUR62042853-RA.v1.0	CqSBP22	G-box	cis-acting regulatory element involved in light responsiveness	Light responsive
AUR62042853-RA.v1.0	CqSBP22	G-box	cis-acting regulatory element involved in light responsiveness	Light responsive
AUR62042654-RA.v1.0	CqSBP23	G-box	cis-acting regulatory element involved in light responsiveness	Light responsive
AUR62042654-RA.v1.0	CqSBP23	G-box	cis-acting regulatory element involved in light responsiveness	Light responsive
AUR62042654-RA.v1.0	CqSBP23	G-box	cis-acting regulatory element involved in light responsiveness	Light responsive
AUR62042654-RA.v1.0	CqSBP23	G-box	cis-acting regulatory element involved in light responsiveness	Light responsive
AUR62042654-RA.v1.0	CqSBP23	G-Box	cis-acting regulatory element involved in light responsiveness	Light responsive
AUR62042654-RA.v1.0	CqSBP23	G-Box	cis-acting regulatory element involved in light responsiveness	Light responsive
AUR62042654-RA.v1.0	CqSBP23	G-Box	cis-acting regulatory element involved in light responsiveness	Light responsive
AUR62042654-RA.v1.0	CqSBP23	G-Box	cis-acting regulatory element involved in light responsiveness	Light responsive
AUR62004146-RA.v1.0	CqSBP01	GT1-motif	light responsive element	Light responsive

Table S2: Continue

.AUR62004146-RA.v1.0	CqSBP01	GT1-motif	light responsive element	Light responsive
AUR62013707-RA.v1.0	CqSBP02	GT1-motif	light responsive element	Light responsive
AUR62028919-RA.v1.0	CqSBP03	GT1-motif	light responsive element	Light responsive
AUR62028919-RA.v1.0	CqSBP03	GT1-motif	light responsive element	Light responsive
AUR62028919-RA.v1.0	CqSBP03	GT1-motif	light responsive element	Light responsive
AUR62028919-RA.v1.0	CqSBP03	GT1-motif	light responsive element	Light responsive
AUR62028919-RA.v1.0	CqSBP03	GT1-motif	light responsive element	Light responsive
AUR62028919-RA.v1.0	CqSBP03	GT1-motif	light responsive element	Light responsive
AUR62028919-RA.v1.0	CqSBP03	GT1-motif	light responsive element	Light responsive
AUR62005629-RA.v1.0	CqSBP04	GT1-motif	light responsive element	Light responsive
AUR62005629-RA.v1.0	CqSBP04	GT1-motif	light responsive element	Light responsive
AUR62005629-RA.v1.0	CqSBP04	GT1-motif	light responsive element	Light responsive
AUR62005629-RA.v1.0	CqSBP04	GT1-motif	light responsive element	Light responsive
AUR62005629-RA.v1.0	CqSBP04	GT1-motif	light responsive element	Light responsive
AUR62005629-RA.v1.0	CqSBP04	GT1-motif	light responsive element	Light responsive
AUR62005629-RA.v1.0	CqSBP04	GT1-motif	light responsive element	Light responsive
AUR62029983-RA.v1.0	CqSBP06	GT1-motif	light responsive element	Light responsive
AUR62029983-RA.v1.0	CqSBP06	GT1-motif	light responsive element	Light responsive
AUR62024322-RA.v1.0	CqSBP08	GT1-motif	light responsive element	Light responsive
AUR62024322-RA.v1.0	CqSBP08	GT1-motif	light responsive element	Light responsive
AUR62024322-RA.v1.0	CqSBP08	GT1-motif	light responsive element	Light responsive
AUR62019452-RA.v1.0	CqSBP09	GT1-motif	light responsive element	Light responsive
AUR62032118-RA.v1.0	CqSBP11	GT1-motif	light responsive element	Light responsive
AUR62032118-RA.v1.0	CqSBP11	GT1-motif	light responsive element	Light responsive
AUR62032118-RA.v1.0	CqSBP11	GT1-motif	light responsive element	Light responsive
AUR62032118-RA.v1.0	CqSBP11	GT1-motif	light responsive element	Light responsive
AUR62032118-RA.v1.0	CqSBP11	GT1-motif	light responsive element	Light responsive
AUR62039662-RA.v1.0	CqSBP12	GT1-motif	light responsive element	Light responsive
AUR62039662-RA.v1.0	CqSBP12	GT1-motif	light responsive element	Light responsive
AUR62039662-RA.v1.0	CqSBP12	GT1-motif	light responsive element	Light responsive
AUR62039662-RA.v1.0	CqSBP12	GT1-motif	light responsive element	Light responsive
AUR62035190-RA.v1.0	CqSBP16	GT1-motif	light responsive element	Light responsive
AUR62035190-RA.v1.0	CqSBP16	GT1-motif	light responsive element	Light responsive
AUR62042534-RA.v1.0	CqSBP17	GT1-motif	light responsive element	Light responsive
AUR62042534-RA.v1.0	CqSBP17	GT1-motif	light responsive element	Light responsive
AUR62042534-RA.v1.0	CqSBP17	GT1-motif	light responsive element	Light responsive
AUR62005645-RA.v1.0	CqSBP18	GT1-motif	light responsive element	Light responsive
AUR62028905-RA.v1.0	CqSBP19	GT1-motif	light responsive element	Light responsive
AUR62003075-RA.v1.0	CqSBP20	GT1-motif	light responsive element	Light responsive
AUR62003075-RA.v1.0	CqSBP20	GT1-motif	light responsive element	Light responsive
AUR62003075-RA.v1.0	CqSBP20	GT1-motif	light responsive element	Light responsive
AUR62003075-RA.v1.0	CqSBP20	GT1-motif	light responsive element	Light responsive
AUR62003075-RA.v1.0	CqSBP20	GT1-motif	light responsive element	Light responsive
AUR62007890-RA.v1.0	CqSBP21	GT1-motif	light responsive element	Light responsive
AUR62007890-RA.v1.0	CqSBP21	GT1-motif	light responsive element	Light responsive
AUR62007890-RA.v1.0	CqSBP21	GT1-motif	light responsive element	Light responsive
AUR62007890-RA.v1.0	CqSBP21	GT1-motif	light responsive element	Light responsive
AUR62042853-RA.v1.0	CqSBP22	GT1-motif	light responsive element	Light responsive
AUR62042853-RA.v1.0	CqSBP22	GT1-motif	light responsive element	Light responsive
AUR62042654-RA.v1.0	CqSBP23	GT1-motif	light responsive element	Light responsive
AUR62005629-RA.v1.0	CqSBP04	GTGGC-motif	part of a light responsive element	Light responsive
AUR62012061-RA.v1.0	CqSBP10	GTGGC-motif	part of a light responsive element	Light responsive
AUR62032118-RA.v1.0	CqSBP11	GTGGC-motif	part of a light responsive element	Light responsive
AUR62042853-RA.v1.0	CqSBP22	GTGGC-motif	part of a light responsive element	Light responsive
AUR62042654-RA.v1.0	CqSBP23	GTGGC-motif	part of a light responsive element	Light responsive
AUR62004146-RA.v1.0	CqSBP01	I-box	part of a light responsive element	Light responsive
AUR62004146-RA.v1.0	CqSBP01	I-box	part of a light responsive element	Light responsive
AUR62013707-RA.v1.0	CqSBP02	I-box	part of a light responsive element	Light responsive
AUR62002563-RA.v1.0	CqSBP05	I-box	part of a light responsive element	Light responsive
AUR62029983-RA.v1.0	CqSBP06	I-box	part of a light responsive element	Light responsive
AUR62029984-RA.v1.0	CqSBP07	I-box	part of a light responsive element	Light responsive
AUR62029984-RA.v1.0	CqSBP07	I-box	part of a light responsive element	Light responsive
AUR62029984-RA.v1.0	CqSBP07	I-box	part of a light responsive element	Light responsive
AUR62032118-RA.v1.0	CqSBP11	I-box	part of a light responsive element	Light responsive
AUR62032118-RA.v1.0	CqSBP11	I-box	part of a light responsive element	Light responsive
AUR62032118-RA.v1.0	CqSBP11	I-box	part of a light responsive element	Light responsive
AUR62039662-RA.v1.0	CqSBP12	I-box	part of a light responsive element	Light responsive
AUR62039662-RA.v1.0	CqSBP12	I-box	part of a light responsive element	Light responsive
AUR62003075-RA.v1.0	CqSBP20	I-box	part of a light responsive element	Light responsive
AUR62007890-RA.v1.0	CqSBP21	I-box	part of a light responsive element	Light responsive
AUR62042654-RA.v1.0	CqSBP23	I-box	part of a light responsive element	Light responsive
AUR62032118-RA.v1.0	CqSBP11	LAMP-element	part of a light responsive element	Light responsive
AUR62032118-RA.v1.0	CqSBP11	LAMP-element	part of a light responsive element	Light responsive
AUR62039662-RA.v1.0	CqSBP12	LAMP-element	part of a light responsive element	Light responsive
AUR62003075-RA.v1.0	CqSBP20	LAMP-element	part of a light responsive element	Light responsive
AUR62007890-RA.v1.0	CqSBP21	LAMP-element	part of a light responsive element	Light responsive
AUR62005629-RA.v1.0	CqSBP04	MRE	MYB binding site involved in light responsiveness	Light responsive
AUR62002563-RA.v1.0	CqSBP05	MRE	MYB binding site involved in light responsiveness	Light responsive
AUR62012061-RA.v1.0	CqSBP10	MRE	MYB binding site involved in light responsiveness	Light responsive
AUR62032118-RA.v1.0	CqSBP11	MRE	MYB binding site involved in light responsiveness	Light responsive
AUR62011728-RA.v1.0	CqSBP13	MRE	MYB binding site involved in light responsiveness	Light responsive
AUR62035190-RA.v1.0	CqSBP16	MRE	MYB binding site involved in light responsiveness	Light responsive
AUR62035190-RA.v1.0	CqSBP16	MRE	MYB binding site involved in light responsiveness	Light responsive
AUR62042534-RA.v1.0	CqSBP17	MRE	MYB binding site involved in light responsiveness	Light responsive
AUR62003075-RA.v1.0	CqSBP20	MRE	MYB binding site involved in light responsiveness	Light responsive
AUR62007890-RA.v1.0	CqSBP21	MRE	MYB binding site involved in light responsiveness	Light responsive
AUR62004146-RA.v1.0	CqSBP01	Sp1	light responsive element	Light responsive
AUR62004146-RA.v1.0	CqSBP01	Sp1	light responsive element	Light responsive
AUR62013707-RA.v1.0	CqSBP02	Sp1	light responsive element	Light responsive
AUR62019452-RA.v1.0	CqSBP09	Sp1	light responsive element	Light responsive
AUR62042853-RA.v1.0	CqSBP22	Sp1	light responsive element	Light responsive

Table S2: Continue

AUR62042654-RA.v1.0	CqSBP23	Sp1	light responsive element	Light responsive
AUR62042654-RA.v1.0	CqSBP23	Sp1	light responsive element	Light responsive
AUR62013707-RA.v1.0	CqSBP02	TCCC-motif	part of a light responsive element	Light responsive
AUR62019452-RA.v1.0	CqSBP09	TCCC-motif	part of a light responsive element	Light responsive
AUR62019452-RA.v1.0	CqSBP09	TCCC-motif	part of a light responsive element	Light responsive
AUR62011728-RA.v1.0	CqSBP13	TCCC-motif	part of a light responsive element	Light responsive
AUR62029416-RA.v1.0	CqSBP14	TCCC-motif	part of a light responsive element	Light responsive
AUR62003425-RA.v1.0	CqSBP15	TCCC-motif	part of a light responsive element	Light responsive
AUR62003425-RA.v1.0	CqSBP15	TCCC-motif	part of a light responsive element	Light responsive
AUR62005645-RA.v1.0	CqSBP18	TCCC-motif	part of a light responsive element	Light responsive
AUR62005645-RA.v1.0	CqSBP18	TCCC-motif	part of a light responsive element	Light responsive
AUR62028905-RA.v1.0	CqSBP19	TCCC-motif	part of a light responsive element	Light responsive
AUR62028905-RA.v1.0	CqSBP19	TCCC-motif	part of a light responsive element	Light responsive
AUR62042853-RA.v1.0	CqSBP22	TCCC-motif	part of a light responsive element	Light responsive
AUR62013707-RA.v1.0	CqSBP02	TCT-motif	part of a light responsive element	Light responsive
AUR62013707-RA.v1.0	CqSBP02	TCT-motif	part of a light responsive element	Light responsive
AUR62013707-RA.v1.0	CqSBP02	TCT-motif	part of a light responsive element	Light responsive
AUR62028919-RA.v1.0	CqSBP03	TCT-motif	part of a light responsive element	Light responsive
AUR62005629-RA.v1.0	CqSBP04	TCT-motif	part of a light responsive element	Light responsive
AUR62029984-RA.v1.0	CqSBP07	TCT-motif	part of a light responsive element	Light responsive
AUR62024322-RA.v1.0	CqSBP08	TCT-motif	part of a light responsive element	Light responsive
AUR62019452-RA.v1.0	CqSBP09	TCT-motif	part of a light responsive element	Light responsive
AUR62019452-RA.v1.0	CqSBP09	TCT-motif	part of a light responsive element	Light responsive
AUR62012061-RA.v1.0	CqSBP10	TCT-motif	part of a light responsive element	Light responsive
AUR62032118-RA.v1.0	CqSBP11	TCT-motif	part of a light responsive element	Light responsive
AUR62032118-RA.v1.0	CqSBP11	TCT-motif	part of a light responsive element	Light responsive
AUR62039662-RA.v1.0	CqSBP12	TCT-motif	part of a light responsive element	Light responsive
AUR62039662-RA.v1.0	CqSBP12	TCT-motif	part of a light responsive element	Light responsive
AUR62011728-RA.v1.0	CqSBP13	TCT-motif	part of a light responsive element	Light responsive
AUR62029416-RA.v1.0	CqSBP14	TCT-motif	part of a light responsive element	Light responsive
AUR62029416-RA.v1.0	CqSBP14	TCT-motif	part of a light responsive element	Light responsive
AUR62003425-RA.v1.0	CqSBP15	TCT-motif	part of a light responsive element	Light responsive
AUR62003425-RA.v1.0	CqSBP15	TCT-motif	part of a light responsive element	Light responsive
AUR62035190-RA.v1.0	CqSBP16	TCT-motif	part of a light responsive element	Light responsive
AUR62035190-RA.v1.0	CqSBP16	TCT-motif	part of a light responsive element	Light responsive
AUR62042534-RA.v1.0	CqSBP17	TCT-motif	part of a light responsive element	Light responsive
AUR62042534-RA.v1.0	CqSBP17	TCT-motif	part of a light responsive element	Light responsive
AUR62005645-RA.v1.0	CqSBP18	TCT-motif	part of a light responsive element	Light responsive
AUR62005645-RA.v1.0	CqSBP18	TCT-motif	part of a light responsive element	Light responsive
AUR62028905-RA.v1.0	CqSBP19	TCT-motif	part of a light responsive element	Light responsive
AUR62028905-RA.v1.0	CqSBP19	TCT-motif	part of a light responsive element	Light responsive
AUR62007890-RA.v1.0	CqSBP21	TCT-motif	part of a light responsive element	Light responsive
AUR62007890-RA.v1.0	CqSBP21	TCT-motif	part of a light responsive element	Light responsive
AUR62007890-RA.v1.0	CqSBP21	TCT-motif	part of a light responsive element	Light responsive
AUR62042654-RA.v1.0	CqSBP23	TCT-motif	part of a light responsive element	Light responsive
AUR62002563-RA.v1.0	CqSBP05	AACA_motif	involved in endosperm-specific negative expression	Stress responsiveess
AUR62029984-RA.v1.0	CqSBP07	AACA_motif	involved in endosperm-specific negative expression	Stress responsivenes
AUR62003425-RA.v1.0	CqSBP15	DRE	cis-acting element involved in dehydration, low-temp, salt stresses	Stress responsiveness
AUR62028919-RA.v1.0	CqSBP03	LTR	cis-acting element involved in low-temperature responsiveness	Stress responsiveness
AUR62028919-RA.v1.0	CqSBP03	LTR	cis-acting element involved in low-temperature responsiveness	Stress responsiveness
AUR62005629-RA.v1.0	CqSBP04	LTR	cis-acting element involved in low-temperature responsiveness	Stress responsiveness
AUR62002563-RA.v1.0	CqSBP05	LTR	cis-acting element involved in low-temperature responsiveness	Stress responsiveness
AUR62002563-RA.v1.0	CqSBP05	LTR	cis-acting element involved in low-temperature responsiveness	Stress responsiveness
AUR62024322-RA.v1.0	CqSBP08	LTR	cis-acting element involved in low-temperature responsiveness	Stress responsiveness
AUR62024322-RA.v1.0	CqSBP08	LTR	cis-acting element involved in low-temperature responsiveness	Stress responsiveness
AUR62024322-RA.v1.0	CqSBP08	LTR	cis-acting element involved in low-temperature responsiveness	Stress responsiveness
AUR62024322-RA.v1.0	CqSBP08	LTR	cis-acting element involved in low-temperature responsiveness	Stress responsiveness
AUR62024322-RA.v1.0	CqSBP08	LTR	cis-acting element involved in low-temperature responsiveness	Stress responsiveness
AUR62019452-RA.v1.0	CqSBP09	LTR	cis-acting element involved in low-temperature responsiveness	Stress responsiveness
AUR62039662-RA.v1.0	CqSBP12	LTR	cis-acting element involved in low-temperature responsiveness	Stress responsiveness
AUR62011728-RA.v1.0	CqSBP13	LTR	cis-acting element involved in low-temperature responsiveness	Stress responsiveness
AUR62011728-RA.v1.0	CqSBP13	LTR	cis-acting element involved in low-temperature responsiveness	Stress responsiveness
AUR62011728-RA.v1.0	CqSBP13	LTR	cis-acting element involved in low-temperature responsiveness	Stress responsiveness
AUR62029416-RA.v1.0	CqSBP14	LTR	cis-acting element involved in low-temperature responsiveness	Stress responsiveness
AUR62003425-RA.v1.0	CqSBP15	LTR	cis-acting element involved in low-temperature responsiveness	Stress responsiveness
AUR62042853-RA.v1.0	CqSBP22	LTR	cis-acting element involved in low-temperature responsiveness	Stress responsiveness
AUR62042853-RA.v1.0	CqSBP22	LTR	cis-acting element involved in low-temperature responsiveness	Stress responsiveness
AUR62042853-RA.v1.0	CqSBP22	LTR	cis-acting element involved in low-temperature responsiveness	Stress responsiveness
AUR62042654-RA.v1.0	CqSBP23	LTR	cis-acting element involved in low-temperature responsiveness	Stress responsiveness
AUR62042654-RA.v1.0	CqSBP23	LTR	cis-acting element involved in low-temperature responsiveness	Stress responsiveness
AUR62013707-RA.v1.0	CqSBP02	MBS	MYB binding site involved in drought-inducibility	Stress responsiveness
AUR62028919-RA.v1.0	CqSBP03	MBS	MYB binding site involved in drought-inducibility	Stress responsiveness
AUR62028919-RA.v1.0	CqSBP03	MBS	MYB binding site involved in drought-inducibility	Stress responsiveness
AUR62005629-RA.v1.0	CqSBP04	MBS	MYB binding site involved in drought-inducibility	Stress responsiveness
AUR62005629-RA.v1.0	CqSBP04	MBS	MYB binding site involved in drought-inducibility	Stress responsiveness
AUR62005629-RA.v1.0	CqSBP04	MBS	MYB binding site involved in drought-inducibility	Stress responsiveness
AUR62002563-RA.v1.0	CqSBP05	MBS	MYB binding site involved in drought-inducibility	Stress responsiveness
AUR62002563-RA.v1.0	CqSBP05	MBS	MYB binding site involved in drought-inducibility	Stress responsiveness
AUR62002563-RA.v1.0	CqSBP05	MBS	MYB binding site involved in drought-inducibility	Stress responsiveness
AUR62029984-RA.v1.0	CqSBP07	MBS	MYB binding site involved in drought-inducibility	Stress responsiveness
AUR62029984-RA.v1.0	CqSBP07	MBS	MYB binding site involved in drought-inducibility	Stress responsiveness
AUR62029984-RA.v1.0	CqSBP07	MBS	MYB binding site involved in drought-inducibility	Stress responsiveness
AUR62024322-RA.v1.0	CqSBP08	MBS	MYB binding site involved in drought-inducibility	Stress responsiveness
AUR62024322-RA.v1.0	CqSBP08	MBS	MYB binding site involved in drought-inducibility	Stress responsiveness
AUR62019452-RA.v1.0	CqSBP09	MBS	MYB binding site involved in drought-inducibility	Stress responsiveness
AUR62012061-RA.v1.0	CqSBP10	MBS	MYB binding site involved in drought-inducibility	Stress responsiveness
AUR62012061-RA.v1.0	CqSBP10	MBS	MYB binding site involved in drought-inducibility	Stress responsiveness
AUR62012061-RA.v1.0	CqSBP10	MBS	MYB binding site involved in drought-inducibility	Stress responsiveness
AUR62012061-RA.v1.0	CqSBP10	MBS	MYB binding site involved in drought-inducibility	Stress responsiveness
AUR62032118-RA.v1.0	CqSBP11	MBS	MYB binding site involved in drought-inducibility	Stress responsiveness
AUR62011728-RA.v1.0	CqSBP13	MBS	MYB binding site involved in drought-inducibility	Stress responsiveness

Table S2: Continue

AUR62011728-RA.v1.0	CqSBP13	MBS	MYB binding site involved in drought-inducibility	Stress responsiveness
AUR62011728-RA.v1.0	CqSBP13	MBS	MYB binding site involved in drought-inducibility	Stress responsiveness
AUR62029416-RA.v1.0	CqSBP14	MBS	MYB binding site involved in drought-inducibility	Stress responsiveness
AUR62003425-RA.v1.0	CqSBP15	MBS	MYB binding site involved in drought-inducibility	Stress responsiveness
AUR62035190-RA.v1.0	CqSBP16	MBS	MYB binding site involved in drought-inducibility	Stress responsiveness
AUR62035190-RA.v1.0	CqSBP16	MBS	MYB binding site involved in drought-inducibility	Stress responsiveness
AUR62035190-RA.v1.0	CqSBP16	MBS	MYB binding site involved in drought-inducibility	Stress responsiveness
AUR62035190-RA.v1.0	CqSBP16	MBS	MYB binding site involved in drought-inducibility	Stress responsiveness
AUR62042534-RA.v1.0	CqSBP17	MBS	MYB binding site involved in drought-inducibility	Stress responsiveness
AUR62042534-RA.v1.0	CqSBP17	MBS	MYB binding site involved in drought-inducibility	Stress responsiveness
AUR62042534-RA.v1.0	CqSBP17	MBS	MYB binding site involved in drought-inducibility	Stress responsiveness
AUR62042534-RA.v1.0	CqSBP17	MBS	MYB binding site involved in drought-inducibility	Stress responsiveness
AUR62005645-RA.v1.0	CqSBP18	MBS	MYB binding site involved in drought-inducibility	Stress responsiveness
AUR62003075-RA.v1.0	CqSBP20	MBS	MYB binding site involved in drought-inducibility	Stress responsiveness
AUR62003075-RA.v1.0	CqSBP20	MBS	MYB binding site involved in drought-inducibility	Stress responsiveness
AUR62003075-RA.v1.0	CqSBP20	MBS	MYB binding site involved in drought-inducibility	Stress responsiveness
AUR62003075-RA.v1.0	CqSBP20	MBS	MYB binding site involved in drought-inducibility	Stress responsiveness
AUR62007890-RA.v1.0	CqSBP21	MBS	MYB binding site involved in drought-inducibility	Stress responsiveness
AUR62042853-RA.v1.0	CqSBP22	MBS	MYB binding site involved in drought-inducibility	Stress responsiveness
AUR62042654-RA.v1.0	CqSBP23	MBS	MYB binding site involved in drought-inducibility	Stress responsiveness
AUR62004146-RA.v1.0	CqSBP01	TC-rich repeats	cis-acting element involved in defense and stress responsiveness	Stress responsiveness
AUR62013707-RA.v1.0	CqSBP02	TC-rich repeats	cis-acting element involved in defense and stress responsiveness	Stress responsiveness
AUR62028919-RA.v1.0	CqSBP03	TC-rich repeats	cis-acting element involved in defense and stress responsiveness	Stress responsiveness
AUR62002563-RA.v1.0	CqSBP05	TC-rich repeats	cis-acting element involved in defense and stress responsiveness	Stress responsiveness
AUR62002563-RA.v1.0	CqSBP05	TC-rich repeats	cis-acting element involved in defense and stress responsiveness	Stress responsiveness
AUR62002563-RA.v1.0	CqSBP05	TC-rich repeats	cis-acting element involved in defense and stress responsiveness	Stress responsiveness
AUR62002563-RA.v1.0	CqSBP05	TC-rich repeats	cis-acting element involved in defense and stress responsiveness	Stress responsiveness
AUR62029983-RA.v1.0	CqSBP06	TC-rich repeats	cis-acting element involved in defense and stress responsiveness	Stress responsiveness
AUR62029983-RA.v1.0	CqSBP06	TC-rich repeats	cis-acting element involved in defense and stress responsiveness	Stress responsiveness
AUR62029983-RA.v1.0	CqSBP06	TC-rich repeats	cis-acting element involved in defense and stress responsiveness	Stress responsiveness
AUR62029984-RA.v1.0	CqSBP07	TC-rich repeats	cis-acting element involved in defense and stress responsiveness	Stress responsiveness
AUR62029984-RA.v1.0	CqSBP07	TC-rich repeats	cis-acting element involved in defense and stress responsiveness	Stress responsiveness
AUR62024322-RA.v1.0	CqSBP08	TC-rich repeats	cis-acting element involved in defense and stress responsiveness	Stress responsiveness
AUR62024322-RA.v1.0	CqSBP08	TC-rich repeats	cis-acting element involved in defense and stress responsiveness	Stress responsiveness
AUR62012061-RA.v1.0	CqSBP10	TC-rich repeats	cis-acting element involved in defense and stress responsiveness	Stress responsiveness
AUR62012061-RA.v1.0	CqSBP10	TC-rich repeats	cis-acting element involved in defense and stress responsiveness	Stress responsiveness
AUR62012061-RA.v1.0	CqSBP10	TC-rich repeats	cis-acting element involved in defense and stress responsiveness	Stress responsiveness
AUR62032118-RA.v1.0	CqSBP11	TC-rich repeats	cis-acting element involved in defense and stress responsiveness	Stress responsiveness
AUR62032118-RA.v1.0	CqSBP11	TC-rich repeats	cis-acting element involved in defense and stress responsiveness	Stress responsiveness
AUR62032118-RA.v1.0	CqSBP11	TC-rich repeats	cis-acting element involved in defense and stress responsiveness	Stress responsiveness
AUR62039662-RA.v1.0	CqSBP12	TC-rich repeats	cis-acting element involved in defense and stress responsiveness	Stress responsiveness
AUR62039662-RA.v1.0	CqSBP12	TC-rich repeats	cis-acting element involved in defense and stress responsiveness	Stress responsiveness
AUR62039662-RA.v1.0	CqSBP12	TC-rich repeats	cis-acting element involved in defense and stress responsiveness	Stress responsiveness
AUR62003425-RA.v1.0	CqSBP15	TC-rich repeats	cis-acting element involved in defense and stress responsiveness	Stress responsiveness
AUR62005645-RA.v1.0	CqSBP18	TC-rich repeats	cis-acting element involved in defense and stress responsiveness	Stress responsiveness
AUR62028905-RA.v1.0	CqSBP19	TC-rich repeats	cis-acting element involved in defense and stress responsiveness	Stress responsiveness
AUR62003075-RA.v1.0	CqSBP20	TC-rich repeats	cis-acting element involved in defense and stress responsiveness	Stress responsiveness
AUR62042534-RA.v1.0	CqSBP17	WUN-motif	wound-responsive element	Stress responsiveness
AUR62005645-RA.v1.0	CqSBP18	WUN-motif	wound-responsive element	Stress responsiveness
AUR62003075-RA.v1.0	CqSBP20	WUN-motif	wound-responsive element	Stress responsiveness
AUR62007890-RA.v1.0	CqSBP21	WUN-motif	wound-responsive element	eStress responsiveness

Table S3: The values of 23 CqSBP genes in tissues and treatments downloaded from NCBI

	Target -id	Apical immature meristems	Flowers and Leaves seeds	Petioles	Stems	Inflores- Internode	Dry Seedling	Sweet cences	Bitter Leaves	Flowers of white bitter seeds	Fruit of white bitter quinoa	Fruit of white sweet Root quinoa	Flowers of yellow Root _CK	Roo t quinoa	Root CK	Root dry	Shoot heat	Shoot low P	Shoot salt	Shoot CK	Shoot_ dry	target heat	low_P	Shoot salt quinoa
AUR62007890-RA	CqSBP01	78.66500	135.40300	1.129150	3.824560	5.4562700	0.2864907	176.6300000	1.1351990	0.0000000	76.838850	0.0347996	15.2694500	0.00000000	0.0400	0.1600	0.1733	0.0000	0.000	2.0833	0.7767	0.8233	1.7167	1.3067
AUR62042654-RA	CqSBP02	131.54400	140.11200	2.258290	2.124760	2.1862467	0.0987913	166.7316700	0.3427617	0.0000000	79.906950	0.1136216	41.2893500	0.00000000	0.0667	0.3667	0.0000	0.2667	0.180	1.8733	0.6733	0.6967	2.5600	1.9400
AUR62042534-RA	CqSBP03	24.48460	7.17386	19.768400	26.746400	7.2992433	3.7205700	23.6259330	3.0235433	2.7888567	14.509450	2.7679000	5.3246600	2.71547000	9.8000	9.2667	3.4300	3.9267	9.420	8.2067	7.2633	4.4400	3.4100	4.7200
AUR62005645-RA	CqSBP04	25.62590	8.07060	26.326100	35.847200	8.6872233	3.8647200	21.1688000	6.2553300	3.3676600	14.067400	2.2991350	7.0293700	3.26153500	10.1367	8.4000	4.3833	5.0233	5.790	7.7600	9.7833	5.1800	3.4467	5.1033
AUR62012061-RA	CqSBP05	11.24930	11.21400	5.312860	4.005210	9.1881900	16.0137000	19.9961670	7.4707033	6.1066000	10.642280	4.2259400	5.2088900	2.60385000	9.1733	8.5900	5.9767	6.7300	7.590	5.0267	4.4467	4.4633	2.0067	3.0067
AUR62039662-RA	CqSBP06	14.92020	21.46620	7.640500	8.977780	19.4009000	18.9389670	26.6316670	9.9848267	11.5305000	11.923770	9.2303600	7.5758750	5.72922500	15.6633	17.1833	12.6600	12.5967	13.200	8.1200	8.0700	7.1767	4.5000	6.1800
AUR62032118-RA	CqSBP07	13.61630	14.62360	6.011420	7.541070	9.7400200	5.1924367	14.0570330	3.5163400	4.0081600	5.574935	2.7379400	3.6053250	2.01005500	6.3167	5.9300	4.3633	3.9167	4.965	4.2567	4.5400	3.9467	2.2567	3.1633
AUR62029416-RA	CqSBP08	16.46010	8.70123	8.981330	45.330600	5.8982100	1.0244877	14.9386000	2.5778533	1.8779967	6.924145	2.2251300	3.0356850	1.92918000	6.3567	5.5733	2.4900	3.8133	5.300	3.4567	2.5300	2.0367	1.3533	2.0467
AUR62042853-RA	CqSBP09	102.34900	10.62120	2.566530	10.401300	0.7535243	0.1701577	102.3263300	0.8189217	0.0917827	14.490335	0.1719060	2.3971390	0.02153865	0.0733	0.4067	0.3167	0.1167	0.165	0.4233	0.0800	0.0667	0.6533	0.5200
AUR62011728-RA	CqSBP10	16.05280	7.27735	12.165700	38.749500	8.2111433	0.6339850	16.8274670	2.3739733	1.7907000	5.121495	1.7346850	3.7489450	1.62107500	5.1833	4.2567	1.7067	2.0800	6.135	2.8167	2.9100	1.3967	1.6167	1.6667
AUR62013707-RA	CqSBP11	3.26202	2.59903	1.677390	2.885220	3.6530533	0.9870560	4.4392367	1.7663243	0.8497220	3.171905	0.8547160	1.6781150	0.53842650	2.2700	1.7700	1.5233	1.4867	1.450	2.0633	1.5300	1.6267	0.7833	0.8300
AUR62004146-RA	CqSBP12	1.74041	2.76921	1.134360	3.066170	2.2660700	0.4950700	3.2277100	0.6929287	0.6107097	2.104490	0.6288830	1.2108015	0.73726650	2.2567	1.2067	0.8733	0.8467	1.885	0.9533	1.0067	1.0367	0.7233	0.5733
AUR62003075-RA	CqSBP13	28.73190	35.77380	15.517700	25.108200	77.6002330	19.4338670	61.9760670	27.4250670	16.8407670	20.878150	11.3378500	14.2294500	9.71000500	20.2367	23.7333	18.3733	16.0833	16.135	8.4267	9.5133	8.3767	5.7700	6.4000
AUR62002563-RA	CqSBP14	6.58920	3.83065	0.764839	0.000000	0.1350913	0.0866362	5.1428500	0.0699240	0.1290969	0.866140	0.1400965	1.0540570	0.05219440	0.0700	0.1967	0.0767	0.0833	0.435	0.3333	0.2033	0.1867	0.3767	0.4467
AUR62019452-RA	CqSBP15	10.38230	6.76256	0.379782	0.280813	1.2342360	0.1514275	9.8985167	0.7209787	0.4630793	1.954910	0.4478350	1.7825650	0.17496415	0.1867	0.1233	0.2100	0.2433	0.165	0.5100	0.2233	0.3200	1.4700	0.2500
AUR62035190-RA	CqSBP16	20.19570	37.03290	5.891910	7.439300	30.7641330	19.2191330	40.6415670	12.6192670	8.5895700	13.962200	9.3883850	8.6573950	6.16438000	19.0700	19.1933	14.6700	13.4167	11.935	10.8967	11.7200	11.2900	6.9867	7.8900
AUR62029984-RA	CqSBP17	7.68047	15.38210	1.912550	3.087540	12.6389000	9.9451233	14.3731000	4.2228600	4.1533467	5.539235	4.9147050	3.6128350	3.25472000	6.3400	6.2367	5.6233	4.7967	3.280	3.9667	3.6500	4.1000	2.1000	2.6933
AUR62003425-RA	CqSBP18	17.19160	4.17463	1.602390	3.253860	3.0035567	0.1150800	10.2165430	0.5815967	0.2083273	9.787075	0.4523660	2.2924900	0.05067710	0.9567	0.5133	0.4567	0.6167	0.485	1.2367	0.5500	0.5467	0.4800	0.2400
AUR62028905-RA	CqSBP19	28.21750	9.46023	4.255500	7.380460	9.8514200	0.4243373	28.7020670	1.9448533	0.5018077	4.728375	0.5122200	2.4849750	0.28619550	1.0333	1.1033	0.5367	0.8367	0.805	0.8067	0.3233	0.2800	0.5200	0.2633
AUR62029983-RA	CqSBP20	7.04899	12.43550	5.241110	8.087000	11.7500930	0.2865193	18.9039330	6.9702500	0.7460977	5.656710	1.0954700	2.9542750	0.76448750	2.7967	2.1800	1.0367	1.2667	3.425	0.9800	2.2700	0.8000	0.9400	1.3100
AUR62024322-RA	CqSBP21	8.35569	11.77400	7.784450	6.043630	12.8464170	0.2051437	17.9289330	7.2883100	0.5886260	3.369550	0.6018885	2.4162400	0.37000000	2.1433	1.5800	0.7233	1.0967	2.420	1.2700	1.5700	0.7267	0.8667	1.1733
AUR62005629-RA	CqSBP22	6.10170	9.50345	3.576100	3.694220	8.8519233	11.3352330	8.3136967	5.0180033	10.0247730	5.392785	6.3323650	3.7412350	6.61164000	8.8733	8.9167	7.8300	6.4700	4.710	3.8200	4.1833	3.5667	1.6833	1.8033
AUR62028919-RA	CqSBP23	5.74651	7.83340	4.192300	2.571560	7.9130467	10.0869570	7.9156133	3.8711967	5.4600400	5.407615	5.2448800	3.2217650	4.96547500	8.0967	7.5533	6.4100	5.8933	4.915	2.8800	2.9033	2.5267	1.5200	1.7667

Table S4: The primer designed for qRT-PCR

	F	R	Size
CqSBP01	GCACTTACTTCTCCGCCGATGATG	ATGACGACGGTGGTAATGCTTAGC	146
CqSBP02	TACTTCTCCGCCGATGATGACCTC	ATGACGACGGTGGTAATGCTTAGC	141
CqSBP03	GGTGTGCCGTCTGATGTCTTCC	AATGGTTAAGTGCGGGAGGTTCTG	148
CqSBP04	GGTGTGCCGTCTGATGTCTTCC	AATGGTTAAGTGCGGGAGGTTCTG	148
CqSBP05	CCTGATGTTACTGGCTCCAATGGG	TGTGCTGTCTCGGGCGTTTTC	141
CqSBP06	GGCAAAGGGGTGTATGCTGGTATC	TACGAGGAGCTGCTGGAGGTAATG	91
CqSBP07	CTCCTTCACACTGCCGTCCAAAG	GCTGCTGGGTGATTCATCTGAGAC	111
CqSBP08	ACTCCCGTCTCCCAGTGTAATGC	TGGCACACCATCTGAACCACAAC	120
CqSBP09	GTGGAGATGGAGGAGATGGAGGAG	CCTTATGACGGCGGTGGTAACG	120
CqSBP10	ACTCCCGTCTCCCAGTGTAATGC	GGCCAAGTCCCAAATGACCAGATG	142

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Table S4: Continue

CqSBP11	CTTGGCTCTTTTGGACGCAACATC	TTACAGGGTGACATCCAGGCATTG	140
CqSBP12	TCCGCGAAAGATTACCACAAGAGG	AATGGAACCTGCTACACTGCTGAC	115
CqSBP13	AGGGAAAGGGACCATTGGGAGAC	CAGACCTTGTGACGCCTGTGATAG	143
CqSBP14	GGCTTCTTCGTCTTCTCCTTCACC	CCTTATGGCGGCGATGATATTCCC	149
CqSBP15	GGCTTCTTCGTCGTCTCCTTCAC	CCTTATGGCGGCGATGATATTCCC	149
CqSBP16	TCGGCTTCGTCTGGGTAGTCTTC	AGGAGGGCTGCTGCTCTTCG	106
CqSBP17	CATCACCAACAGCAACAGCAACAC	ACTACCCAGACGAAGCCGATCAG	138
CqSBP18	CAGGCTTACAGAGGCAGACAGTTC	GAGAGCACGATCCGAGTCAATCAC	96
CqSBP19	GTGATTGACTCGGATCGTGCTCTC	AGGGCTCGGATGATGGAAGGTAC	123
CqSBP20	AGCGGCATAAGGTCTGTGATGTTC	AGCAGAAAGACGCCTACGACAAC	149
CqSBP21	AGCGGCATAAGGTCTGTGATGTTC	AGCAGAAAGACGCCTACGACAAC	149
CqSBP22	TGTGCTAATGCTACCTCGGTTGTG	CAGACTTCCTTCGCCGCCTATTG	103
CqSBP23	GCGGAGGAGGAGGAAGAAGAGAC	GGCACCTGACACTTCGCTACAC	86

Table S5: Relative expression of 23 genes by qRT-PCR

	0h	2h	4h	8h	12h
CqSBP01	1.000	4.994	18.090	4.455	65.793
CqSBP02	1.000	3.533	40.601	3.267	70.534
CqSBP03	1.000	0.463	0.635	0.892	1.229
CqSBP04	1.000	0.362	3.054	0.552	1.195
CqSBP05	1.000	0.385	1.860	0.279	2.261
CqSBP06	1.000	0.460	1.230	0.330	3.650
CqSBP07	1.000	0.308	1.483	0.592	2.874
CqSBP08	1.000	0.234	1.833	0.600	5.300
CqSBP09	1.000	0.800	1.800	1.200	0.311
CqSBP10	1.000	0.158	0.938	0.310	0.589
CqSBP11	1.000	0.152	0.596	0.120	0.109
CqSBP12	1.000	1.782	18.072	1.196	2.904
CqSBP13	1.000	1.717	29.790	20.376	78.124
CqSBP14	1.000	0.224	1.759	2.266	1.094
CqSBP15	1.000	0.025	0.258	0.117	0.121
CqSBP16	1.000	0.380	5.099	1.036	8.973
CqSBP17	1.000	0.209	1.607	0.363	1.409
CqSBP18	1.000	0.221	0.506	0.401	0.664
CqSBP19	1.000	0.232	0.496	0.561	0.430
CqSBP20	1.000	0.123	1.556	0.156	0.473
CqSBP21	1.000	0.178	4.758	1.336	4.338
CqSBP22	1.000	0.312	1.357	0.389	3.088
CqSBP23	1.000	0.624	5.803	0.327	1.019