

Full Length Research Paper

***In silico* comparative analysis of EST-SSRs in three cotton genomes**

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In this study, expressed sequence tags- simple sequence repeat (EST-SSRs) were surveyed in three cotton genomes (*Gossypium arboreum*, Ga; *Gossypium raimondii*, Gr and *Gossypium hirsutum*, Gh). The frequency of EST-SSRs was highest in Gr, and motif type for hexanucleotide was obviously abundant in Gr. Trinucleotide repeats were the most abundant motif; AT and AG, AAG and ATC were the most frequent motifs for dinucleotide and trinucleotide, respectively. The repeat number was greatly diverse between the three genomes with the highest variation in Gh. AG and AAG had a high frequency both in homologue groups (HGs) with and without repeat number change between genomes. The range of repeat number change in each HG was wider in Gr-Gh. The annotation of the SSR-ESTs showed that more Gene Ontology (GO) items targeted by SSR-ESTs of Ga and Gr than those of Gh. This study gave us new insights into the difference between the three cotton genomes, which will be more helpful to understand the differentiation and evolution of the three genomes.

Key words: Cotton, simple sequence repeat, expressed sequence tags, motif, gene ontology.

INTRODUCTION

Microsatellites or simple sequence repeats (SSRs) are DNA sequences consisting of tandemly repeated arrays of short (1-6 nucleotides) motifs, which are widespread in both eukaryotic and prokaryotic genomes (Field and Wills, 1996; Tóth et al., 2000). SSRs are abundant across genomes, showing high levels of polymorphism, and are usually considered as evolutionarily neutral DNA sequences. This polymorphism is probably due to slipped-strand mispairing, and simple tandem repeats may be predisposed to further length changes by unequal crossing over and (or) subsequent replication, repair, or recombination errors (Levinson and Gutman, 1987). As a result, microsatellite loci often mutate by insertions or deletions of one or more repeat elements, and the mutation rates generally increase with an increase in the length of the repeats (Wierdl et al., 1997; Xu et al., 2000).

Microsatellite markers were developed for a wide range

of plant species, including many crops. The advantage of microsatellites as molecular markers is that they detect polymorphisms at highly variable loci (Powell et al., 1996; Hedrick, 2001). Furthermore, they are polymerase chain reaction (PCR)-based marker, co-dominant, and distribute throughout the genome. Together, these characteristics make microsatellite loci one of the best genetic markers for mapping purposes (Oliveira et al., 2006).

Microsatellites were developed from both coding and noncoding regions of plant genomes (Temnykh et al., 2001; Morgante et al., 2002). Several resources can be used to search for SSRs, including a variety of DNA libraries such as genomic-enriched for SSRs, bacterial artificial chromosome (BAC) and cDNA libraries, as well as public database, including expressed sequence tags (ESTs) database (Broughton et al., 2003; Li et al., 2004). In recent years, a number of random and targeted gene discovery programs have been initiated for a range of species, and this has led to a dramatic increase in the number of ESTs in public and specific species databases. ESTs database is a fast and efficient way to analyze the transcribed portion of the genome, and now becomes a potentially valuable source for genetic marker development.

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There are over 375,700 cotton ESTs deposited in GenBank (http://www.ncbi.nlm.nih.gov/dbEST/dbEST_summary.html, 1st December, 2010). Among these ESTs, *Gossypium hirsutum* (upland cotton) had the maximum number (268,797) because it is widely planted in the world, followed by *Gossypium raimondii* (63,577), *Gossypium arboreum* (41,768), *Gossypium barbadense* (1,356) and *Gossypium herbaceum* var. *africanum* (247). Except for transcriptome analysis in cotton, these ESTs provide a robust way to develop SSR markers for genetic mapping the cotton genome. Qureshi et al. (2004) developed 84 primers for 133 SSR-containing ESTs from 9,948 sequences of known genes belonging to *G. hirsutum* L. in GenBank. Han et al. (2004) developed 544 EST-SSR primer pairs from 931 ESTs derived from *G. arboreum* fibers at 7 to 10 days post anthesis. After that 489 EST-SSR primer pairs were isolated from 13,505 ESTs which were developed from two cotton fiber/ovule cDNA libraries constructed for upland cotton (Han et al., 2006). Park et al. (2005) developed 1,232 microsatellite markers using 1,557 ESTs-containing SSRs (10 bp) and 5,794 ESTs-containing Complex Sequence Repeats (CSRs) (12 bp) obtained from ~14,000 consensus sequences derived from fiber ESTs generated from the cultivated diploid species *G. arboreum* L. cv AKA8401. Talierco et al. (2006) identified 192 EST-SSR primers from multiple *G. hirsutum* tissues. Wang et al. (2006) developed 1,554 EST-SSRs from 58,906 nonredundant *G. raimondii* EST sequences. Guo et al. (2007) additionally developed 664 *G. hirsutum*-derived EST-SSRs from 12,463 *G. hirsutum* acc. TM-1 sequences and 11,692 *G. hirsutum* cv. Xuzhou142 sequences. Zhang et al. (2007) developed 119 EST-SSRs based on 98 unique ESTs from a cDNA library constructed using developing fibers from *G. barbadense* acc. 3-79. In total, 5,318 EST-SSRs have been developed, accounting for 44.56% of total cotton SSRs (11,938) in the database of cottonmarker (<http://www.cottonmarker.org/Primer.shtml>, 31 December, 2010).

Cotton (*Gossypium* spp.) belongs to the genus *Gossypium* of the family *Malvaceae*, and it is an important cash crop and the second largest source of textile fiber and edible oil throughout the world. The genus *Gossypium* L. comprises about 45 diploid and 5 tetraploid species, and these are assigned to nine genome types on the basis of chromosome pairing affinities: eight diploid genomes (A, B, C, D, E, F, G and K; $2n=2x=26$) and one tetraploid genome (AD; $2n=4x=52$) (Endrizzi et al., 1985; Percival et al., 1999). At the tetraploid level, there are five species, designated (AD)₁ through (AD)₅ for their genome constitutions (Cronn and Wendel, 1998). The allotetraploid species are thought to have formed about 1-2 million years ago (MYA) after a polyploidization event that brought together the genomes of diploids closely related to *G. herbaceum* L. ($2n=2x=26$, A₁ genome) or *G. arboreum* L. ($2n=2x=26$, A₂ genome), and *G. raimondii* L. ($2n=2x=26$, D₅ genome), and they have

been domesticated through extensive human selection (Wendel and Cronn, 2003).

Although the relationship of A, D and AD genome have been clearly defined, the abundantly existing EST sequences of the three genomes may provide an alternative way to study the three genomes. In this study, microsatellites were globally analyzed in ESTs of the three species to reveal their commonness and difference between A, D and AD genome and to discuss its evolution.

MATERIALS AND METHODS

Sources of EST sequences

The assembly EST sequences of *G. arboreum* (Ga), *G. raimondii* (Gr) and *G. hirsutum* (Gh) were downloaded from TIGR (The Institute for Genomic Research) PTAs (Plant Transcript Assemblies) database (<http://plantta.tigr.org>; 15 February, 2010) (Childs et al., 2006). The EST sequences of *G. arboreum* (Release 2) including 4,591 assemblies and 22,292 singletons amounted to 39,157 ESTs in GenBank with 19,283 kb; the EST sequences of *G. raimondii* (Release 2) including 8,665 assemblies and 19,977 singletons amounted to 63,265 ESTs in GenBank with 22,879 kb. The EST sequences of *G. hirsutum* (Release 2) including 24,797 assemblies and 45,870 singletons amounted to 176,521 ESTs in GenBank with 48,609 kb.

Identification of SSRs in ESTs

A windows-based robust SSR pipeline named Serafer developed in our laboratory was used to search SSRs (ftp://ensembl.genomics.org.cn/other/Serafer_1.9.5.zip or http://www.tgjr.org/download/software/Serafer_1.9.5.zip). Serafer takes a FASTA formatted sequence file as an input, and it can produce an Excel file with number of SSRs, sequence name, SSR type, SSR motif, SSR position, repeat length, repeat number, repeat score and the length of the sequence.

In the present study, perfect EST-SSRs were considered to contain motifs of di- to hexanucleotides in size. The minimum repeat unit was defined as 9 for dinucleotides, 6 for trinucleotides, 5 for tetra- and pentanucleotides and 4 for hexanucleotides. These limits were chosen based on earlier studies that investigated plant EST-SSRs (Bérubé et al., 2007).

Compositional analysis of EST-SSRs

Microsatellites were classified by type (example, di- to hexanucleotide) and motif (example, AC, AG, AT, and CG) in Microsoft Excel[®]. What's more, the motifs were classified considering circular permutations and complementarities, example, AG, GA, TC and CT were considered as a single category. The analysis of the occurrence and frequency of EST-SSRs among Ga, Gr and Gh was carried out in Microsoft Excel[®]. Results on repeat type, motif type, repeat number, repeat length and frequency were collected for the three genomes. Frequency of EST-SSR refers to kilo-base pairs of EST sequences containing one SSR.

Identification of homologous SSR-ESTs through blast analysis

Sequences of SSR-ESTs (ESTs containing SSR) were respectively extracted from each database and were assembled into three new

Table 1. Number and frequencies of EST-SSR repeats in three cotton species.

Repeat type	Ga	Gr	Gh
Dinucleotide	183(9.49)	299(13.07)	274(5.64)
Trinucleotide	289(14.99)	499(21.81)	1036(21.31)
Tetranucleotide	32(1.66)	59(2.58)	190(3.91)
Pentanucleotide	10(0.52)	25(1.09)	38(0.78)
Hexanucleotide	90(4.67)	108(4.72)	251(5.16)
Total SSRs	604	990	1789
Total length (Kb)	19,283	22,878.9	48,608.7
Average distance (Kb)	31.93	23.11	27.17

Numbers in parentheses show frequency of repeat unit per 100kb. Ga, *Gossypium arboreum*; Gr, *Gossypium raimondii*; Gh, *Gossypium hirsutum*.

individual databases for Blast analysis. The Blast program MegaBLAST (Altschul et al., 1990) was downloaded from NCBI to identify homologous SSR-ESTs with the criterion for a sequence match based on the E-value threshold of $1e^{-15}$.

Annotation and functional classification of SSR-ESTs

Annotation of gene ontology (GO) terms were performed using Blast2GO (Conesa et al., 2005) with default parameters. Homolog analysis against the NCBI nr protein database was performed using a BLASTX (Altschul et al., 1990) program ($E\text{-value} \leq 1e^{-3}$) and top 20 best BLAST hits were kept. Then, InterProScan (Mulder and Apweiler, 2007) was performed and InterProScan GOs was merged to annotation. The functional categories were simplified by using the Plant GOslim (<http://www.geneontology.org/GO.slims.shtml>). Finally, group 2nd level and multilevel GO terms of the three main categories (biological process, molecular function and cellular component) was obtained and classified.

RESULTS

Comparison of EST-SSRs between the three genomes on the whole

Frequency and distribution of repeat type

There were 604, 990 and 1,789 EST-SSRs present in the EST sequences of Ga, Gr and Gh, respectively (Table S1). The frequency of dinucleotide was higher in Gr than that in Gh, but the number was similar between them; the frequency of trinucleotide was similar between Gr and Gh, but the number was very different (Table 1). The frequency of EST-SSRs was one in 31.93 kb in Ga, 23.11 kb in Gr and 27.17 kb in Gh, respectively. Among all the repeat types, trinucleotide repeats were the most abundant SSR types with up to 21.81 trinucleotide repeat units in 100 kb ESTs (Table 1).

Frequency and distribution of repeat motif

All the di- and trinucleotide motifs (except CG in Gr and Gh) showed different abundance in the three cotton

genomes (Table 2). The most frequent dinucleotide motif was AT in Ga and Gr, whereas AG in Gh. The frequency of AC was low in all three genomes; however, AT was very frequent in Gr, which may be an important characteristics of this genome. For trinucleotide, AAG and ATC were the most frequent motifs in all the three genomes; AAT was also frequent in Gr and Gh.

A total of 9 tetranucleotide motifs, 4 pentanucleotide motifs and 31 hexanucleotide motifs were found in Ga; 21, 20 and 106 in Gr, respectively; 13, 13 and 52 in Gh, respectively. It was obvious that motif type was very abundant in Gr, especially for hexanucleotide. Although the tetra- to hexanucleotide motifs were less in Ga, the AGCCTG was very abundant with 35 ones found. Some tetranucleotide motifs were also very abundant in Gr, such as AAAT, AAAC, AAAG and ATAC. However, no abundant motifs were found to exist in Gh (Table S2).

Repeat number distribution

With an increase in their repeat number, all the perfect repeats detected in the three cotton genomes showed a decrease in their frequency as shown in Figure 1. The three cotton genomes showed the same tendency with a peak at the repeat number of 6, but the frequency was very low in Ga. However, the repeat number was greatly different between the three genomes with more variance in Gh and less in Gr (Figure 1).

To reveal which repeat unit(s) contributes to the variety of repeat number between the three cotton genomes, the major repeat units (di-, tri- and hexanucleotide) were separately counted. Figure 2 shows that di- and hexanucleotide contributed little to the repeat number frequency (Figure 2a and 2c), but dinucleotide contributed a lot to the repeat number variation (Figure 2a). Trinucleotide contributed a lot to the frequencies of repeat number but little to the repeat number variation, and the high frequency of repeat number of 6 was mainly contributed by trinucleotide (Figure 2b). A further exploring of the repeat number of different motifs revealed that the repeat number variation of dinucleotide

Table 2. Frequency of di- and trinucleotide repeats in three cotton species^a.

Repeat type	Motif	Ga	Gr	Gh
Dinucleotide	AT	4.77	8.65	1.05
	AC	0.52	0.87	0.76
	AG	4.10	3.54	3.83
	CG	0.10	0	0
Trinucleotide	AAT	1.76	3.63	2.37
	AAC	0.57	1.49	1.52
	AAG	4.51	6.51	6.03
	ATC	2.85	4.28	4.01
	ACT	0.21	0.48	0.25
	ACC	1.71	1.79	2.47
	ACG	0.41	0.44	0.64
	AGC	1.61	2.01	2.08
	AGG	0.73	0.61	0.88
	CCG	0.62	0.57	1.07

^a Frequency of motif per 100 kb.

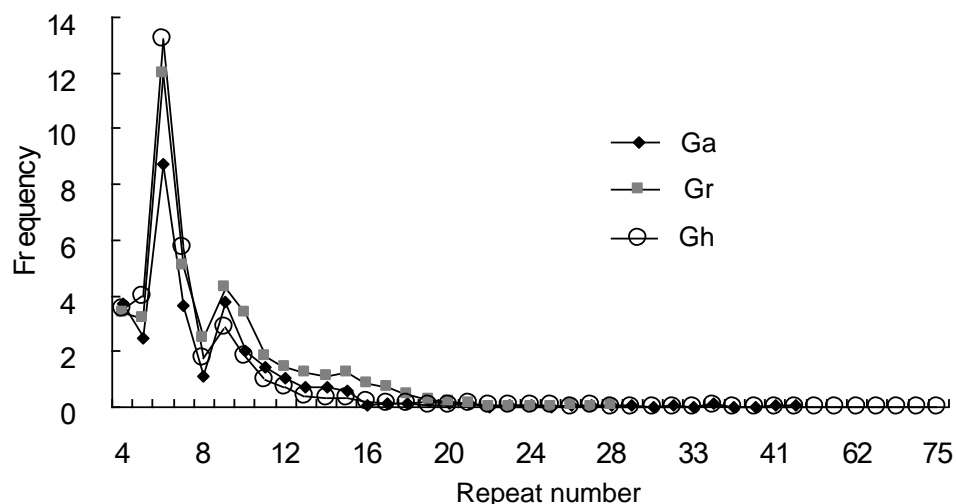


Figure 1. Distribution of the repeat number showed by number/kb in the three cotton species.

was mainly contributed by AG motif in Ga and Gh, and AT in Gr; the frequency of repeat number of 6 was mainly contributed by AAG and ATC motif.

Characteristics of EST-SSRs between A, D and AD genomes by homologous sequences

Homologous SSR-ESTs between A and AD genomes

Blast ($E\text{-value} \leq 1e^{-15}$) analysis was performed to search homologous SSR-ESTs between Ga and Gh, resulting in 196 homologous groups (HG) including 36 dinucleotides, 104 trinucleotides, 12 tetranucleotides and 44 hexa-

nucleotides. In the 195 HGs, one EST of Ga had 1-9 ESTs with an average of 3 of Gh; in the exceptional HG, two Ga sequences with 9 and 10 AT repeats were corresponded to two Gh sequences with 10 and 11 AT repeats. The 196 HGs were divided into three groups: no repeat number change between Ga and Gh with 74 HGs (Group I) (37.8%), more repeat number in Ga than Gh with 31 HGs (Group II) (15.8%) and less repeat number in Ga than Gh with 91 HGs (Group III) (46.4%) (Table S3).

In Group I, all the 5 dinucleotides were AG motif, and ATC and AAG were the most frequent motifs in the trinucleotides. In Group II, the dinucleotides included 1 AC, 3 ATs and 10 AGs; the frequencies of different motifs were not obviously different in the trinucleotides. In Group

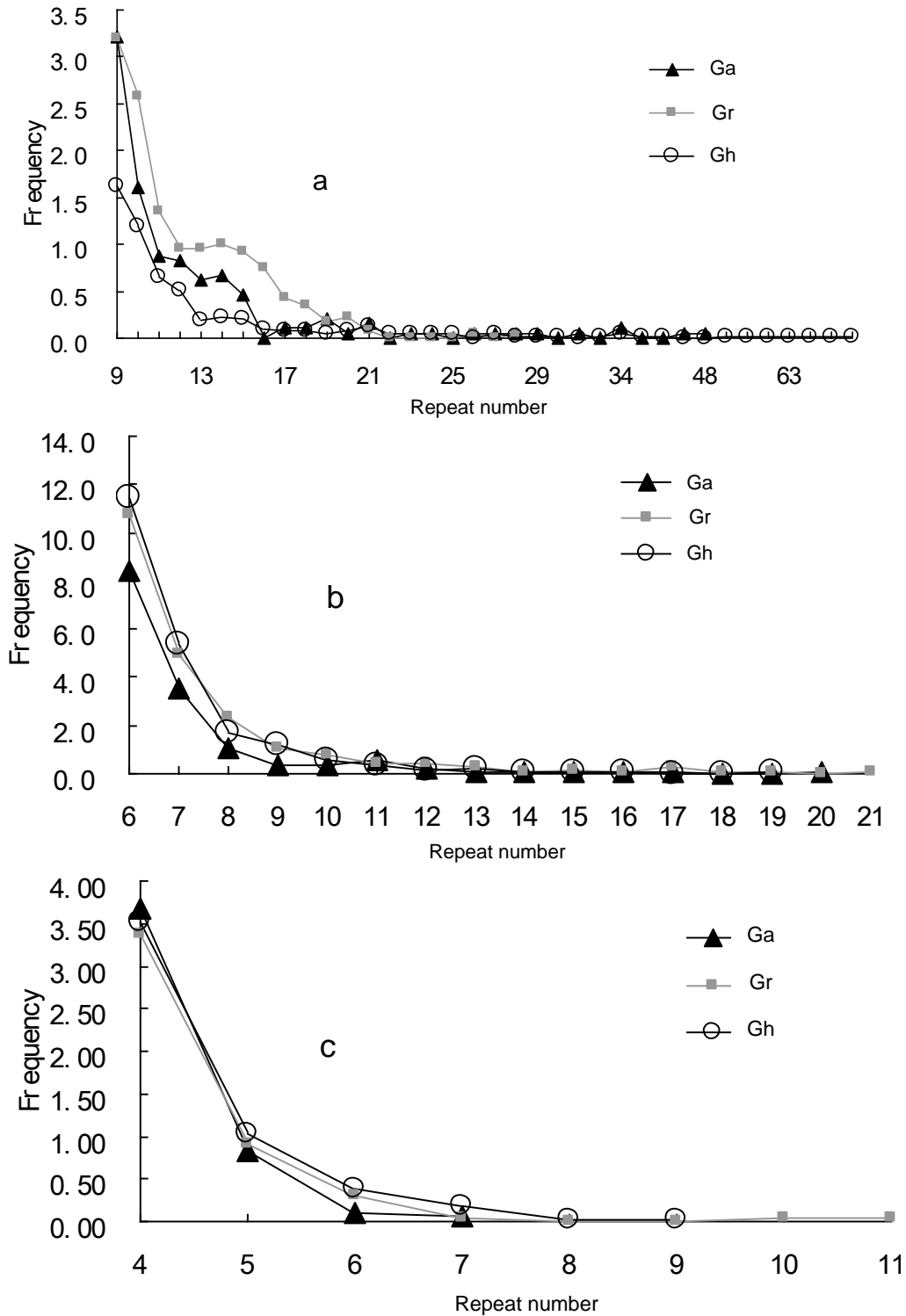


Figure 2. The repeat number of di-, tri- and hexanucleotide between the three cotton species. (a) the repeat number of dinucleotide; (b) the repeat number of trinucleotide; (c) the repeat number of hexanucleotide.

III, the dinucleotides repeats included 4 AGs and 13 ATs, and the most frequent motifs in the trinucleotides repeats were AGC and AAG; among the 35 hexanucleotides, 30

of them were TCAGGC motif (Table S3 and Figure 3a). Because multiple sequences were usually included in one HG and the repeat number varied between

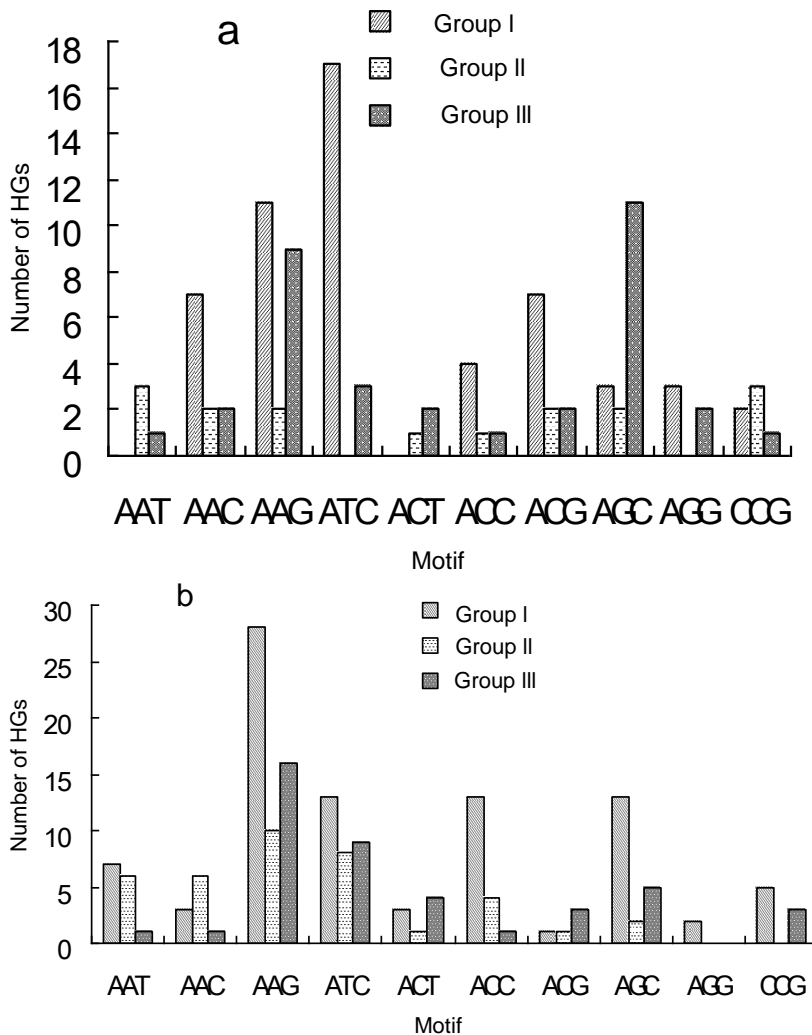


Figure 3. Number of HGs of different trinucleotides motifs in (a) Ga-Gh and (b) Gr-Gh.

sequences, when comparing difference between different genomes, the repeat numbers were averaged. Table 3 shows that the differences of repeat number between Ga and Gh were less than 2 in most HGs.

Homologous SSR-ESTs between D and AD genomes

A total of 249 HGs were identified between Gr and Gh, including 22 dinucleotides, 170 trinucleotides, 15 tetranucleotides, 7 pentanucleotides and 35 hexanucleotides. All the HGs except two HGs had one EST of Gr versus 1-7 ESTs with an average of 1.5 of Gh. In Group I, 123 HGs (49.4%) were included; the 5 dinucleotides included 3 AGs, 1 AT and 1 AC. AAG, ATC, ACC and AGC were the most frequent motifs in the trinucleotides. Among the 12 dinucleotides in Group II, ten of them were AGs and the other two were ACs; the most frequent motif in the

trinucleotides was AAG. In Group III, the dinucleotides included 2 ATs, 2 AGs and 1 AC, and the most frequent motif in the trinucleotides was still AAG (Table S4 and Figure 3b). Compared to the differences of repeated number between Ga and Gh, the differences of repeated number between Gr and Gh were also less than 2 in most HGs, but the range was wider (Table 3).

Homologous SSR-ESTs between A and D genomes

A total of 43 HGs were identified between Ga and Gr including 3 dinucleotides, 33 trinucleotides, 2 tetranucleotides, 3 pentanucleotides and 2 hexanucleotides. One EST of Ga had 1-4 ESTs with an average of 1.4 of Gr in these HGs. The most frequent trinucleotides were ACC and AAG in Group I, ATC in Group II, and only AAG in Group III, respectively. The difference of repeat number

Table 3. HGs with difference in repeat number in Ga-Gh and Gr-Gh.

Repeat number	Number of HGs in Ga-Gh		Number of HGs in Gr-Gh	
	Group II	Group III	Group II	Group III
0~1	20	64	47	41
1~2	3	24	10	13
2~3	2	2	4	1
3~4	6	0	3	2
5	0	0	1	0
6	0	1	1	0
9	0	0	0	3

between Ga and Gr were 1-2 (Table S5).

Homologous SSR-ESTs between A, D and AD genomes

A total of 31 HGs were identified between Ga, Gr and Gh, including 6 dinucleotides, 21 trinucleotides, 2 tetranucleotides and 2 hexanucleotides. The repeat numbers were identical in 6 HGs among the three genomes. Among the HGs with variance in repeat number, all the motifs of dinucleotides were AGs; AAG was the most frequent motif in the trinucleotides (Table S6).

Comparison of functional SSR-ESTs between A, D and AD genomes

Overview of the annotated SSR-ESTs

A total of 585, 937 and 1680 SSR-ESTs of Ga, Gr and Gh were annotated, respectively (level 2). All the SSR-ESTs of the three genomes targeted more 'cellular process', 'metabolic process', 'cell', 'organelle', 'binding' and 'catalytic activity' than other GO items. SSR-ESTs of Ga targeted more 'cellular component organization', 'extra-cellular region' and 'structural molecule activity' than the other two genomes. SSR-ESTs of Gr targeted more 'biological regulation', 'cellular process', 'metabolic process', 'signaling' 'cell', 'organelle' and 'binding' than the other two genomes. SSR-ESTs of Gh targeted less 'cell', 'membrane-enclosed lumen', 'organelle' and 'catalytic activity' than the other two genomes (Table S7 and Figure 4a).

Comparison of the annotated SSR-ESTs of di- and trinucleotides

SSR-ESTs of dinucleotides showed similar GO item distribution compared to all the SSR-ESTs with some

exceptions: SSR-ESTs of Ga targeted more 'cellular component organization', 'developmental process', 'multi-cellular organismal process', 'reproduction' and less 'metabolic process', 'organelle', 'binding', 'catalytic activity', 'structural molecule activity', 'transporter activity'; SSR-ESTs of Gr targeted less 'growth', 'enzyme regular activity'; SSR-ESTs of Gh targeted less 'response to stimulus'. However, SSR-ESTs of trinucleotides showed same GO item distribution as that of all the SSR-ESTs (Figure 4b-c).

Comparison of the annotated EST-SSRs with single motif

Dinucleotide motifs: for ESTs of AC motif, 5 GO items were absent in all three genomes; 5 GO items including 4 of 'biological process' and 1 of 'molecular function' were only present in Gh genome; 'cellular component organization' was only present and 'signaling', 'molecular transducer activity' absent in Ga genome.

For ESTs of AG motif, only 'death' was absent in all three genomes; 'multi-organism process' and 'molecular transducer activity' were also absent in Ga-ESTs, 'structural molecule activity' was absent in Gr-ESTs; 'enzyme regulator activity' was only present in Gh-ESTs. For ESTs of AT motif, 'multi-organism process' and 'structural molecule activity' were only present in Gr-ESTs; 'death' and 'macro-molecular complex' were only absent in Gh-ESTs; 'transporter activity' was also absent in Ga-ESTs (Figure S1).

Trinucleotide motifs: dramatic differences existed in the three genomes, especially for ACG, ACT, AGG and CCG motifs which were rare SSR-ESTs among the trinucleotide motifs. For example, GO items obviously abundant in Gr-ESTs and scarce in Ga-ESTs for ACG motif (Figure S2e). Details of these differences could be seen from Table S7 and Figure S1-2.

DISCUSSION

The frequency, distribution and abundance of SSRs can

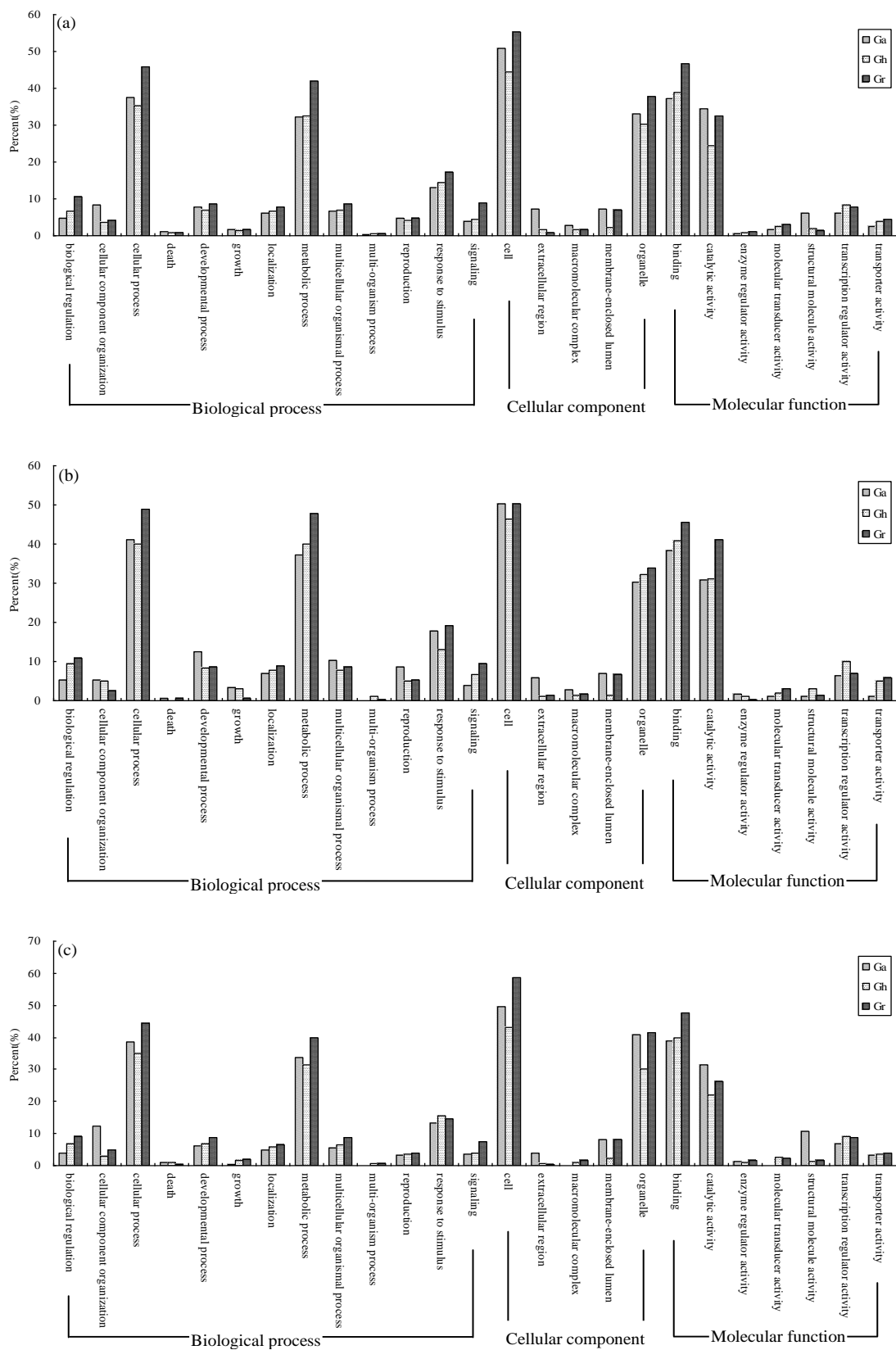


Figure 4. Function classifications of SSR-ESTs. (a).all SSR-ESTs; (b).SSR-ESTs of Dinucleotides; (c).SSR-ESTs of Trinucleotides).

be highly variable depending on the SSR search criteria, the size of the dataset, and the database-mining tools (Varshney et al., 2005). In this study, the criteria described by Bérubé et al. (2007) were taken for identifying perfect SSR repeats, which resulted in a lower frequency compared to the study of Cardle et al. (2000). Although, more EST-SSRs were identified from Gh than Ga and Gr, the average distance (in kb) between SSRs was least in Gr but not in Gh, which indicated that less selection pressure was put on it. It is true for this species because *G. raimondii* (Gr) is a wild cotton species, while *G. arboreum* (Ga) is an Old World cultivated species and *G. hirsutum* (Gh) a New World cultivated species. The obviously high frequency of dinucleotides and the extremely high frequency of AT motif also supported this standpoint: the activity of dinucleotides could increase frame shift mutations; AT dimeric repeats were usually found in the untranslated regions of many species which are more polymorphic than other regions in the genome (Morgante et al., 2002; Jung et al., 2005).

Among all the repeat types, trinucleotide repeats were found to be the most abundant, which is in agreement with previous reports on several crop plants (Cardle et al., 2000; Varshney et al., 2002; Gao et al., 2003; Maia et al., 2009; Victoria et al., 2011) and some partly reports on cotton (Han et al., 2004; Han et al., 2006; Wang et al., 2006; Zhang et al., 2007). The predominance of trinucleotides in ESTs might reflect motifs of repetitive amino-acid sequences (Cardle et al., 2000), and could reduce frame shift mutations (Metzgar et al., 2000). Morgante et al. (2002) also suggested that mutation pressure and positive selection for specific single amino acid stretches are possible reasons for the high frequency of trinucleotide repeats.

In all the four dinucleotide repeats, AT and AG were most common, CG the lowest, and AC also had a low frequency. The rarity of GC/CG repeats seems to be common for all species; however, the most abundant motif in this study was not in accordance with some reports (Cardle et al., 2000; Kantety et al., 2002; Thiel et al., 2003; Jung et al., 2005; Chen et al., 2006). Interestingly, although the Gh derived from the combination of Ga and Gr, AT was very low in Gh among the three genomes which indicated that stronger selection was put on this species during its domestication. The more variance of repeat number in Gh also confirmed this point.

Among the trinucleotide repeats, AAG was the most frequent motifs in all three genomes, which was the same as some reports on some plants (Cardle et al., 2000; Varshney et al., 2002; Gao et al., 2003; Jung et al., 2005; Kumpatla and Mukhopadhyay, 2005; Aggarwal et al., 2007; Maia et al., 2009; Victoria et al., 2011). Conversely, CCG, the most common motif in monocotyledonous species (Chin et al., 1996; Temnykh et al., 2000; Cordeiro et al., 2001; Morgante et al., 2002; Varshney et

al., 2002), was rare in cotton. It seemed that AAG might be the most abundant EST-SSR motif in dicots. Additionally, ATC was also abundant, which was similar to *Arabidopsis* (Cardle et al., 2000). The similar results between cotton and *Arabidopsis* were rooted from that the Malvaceae and Brassicaceae have diverged from a common ancestor less than 100 million years ago (Bowers et al., 2003), a high level of DNA sequence conservation is expected within protein coding regions (Fulton et al., 2002). However, AAT, ACC and AGC also had a high frequency, but least often in *Arabidopsis* (Cardle et al., 2000). The frequencies of different trinucleotide motifs were different in the three cotton genomes, and no motifs was most frequent in Ga, which is consistent with the fact that this species has been cultivated compared to Gr, but less domesticated compared to Gh.

In the three cotton genomes, the SSR frequency decreased with the increase of repeat number, which had been verified by some other reports (Kumpatla and Mukhopadhyay, 2005; Bérubé et al., 2007). The most frequent repeat number was also similar to the results of Kumpatla and Mukhopadhyay, (2005). However, the range of repeat number was wider than that in pine and spruce (Bérubé et al., 2007). Further survey confirmed that the variance was mainly caused by AG motif of dinucleotide, and the most frequent repeat number by AAG and ATC motif of trinucleotide.

Blast analysis revealed more homologue groups (HGs) in Gr-Gh than in Ga-Gh; however, more subject sequences were in Ga-Gh. Previous studies have proved that Ga is more closed to Gh than Gr (Wendel and Albert, 1992; Zhang et al., 2007; Zhu et al., 2009). Although, more HGs were identified in Gr-Gh, the more subject sequences in HGs of Ga-Gh and the more conserved repeat number change in HGs were the stronger evidence for their relationship. Among all the identified HGs, AG and AAG had a high frequency in all kinds of HGs. These results obtained from this study indicated that AG and AAG motif was an important characteristic of cotton.

The annotated SSR-ESTs showed some differences between the three genomes. The more GO items targeted by SSR-ESTs of Ga and Gr, and the less GO items targeted by SSR-ESTs of Gh indicated that some genes lost their function or were deleted during the polyploidization and domestication. However, the results of single motifs showed that some GO items were only found in SSR-ESTs of Gh, which indicated that non-functional genes in Ga or Gr gained new function in Gh. Because the mutation rate of SSRs is very high which results in the length changes of alleles (Wierdl et al., 1997; Xu et al., 2000), it is possible that some genes gain or loss functions because of the frame shift mutation. The differences of GO items between Ga and Gr could be a reflection of difference between the diploid genomes.

EST-derived SSR has become a novel way for

developing SSRs in many plants, and they have been widely applied in germplasm evaluation, comparative mapping, tagging important traits of interest, and additional map-based cloning of important genes. Some of these EST-SSRs identified in this study have been mapped in our interspecific linkage map derived from *G. hirsutum* and *G. barbadense* (Zhang et al., 2008), and the others are under mapping, which would be helpful in fatherly exploring the mysteries of polyploidy cotton.

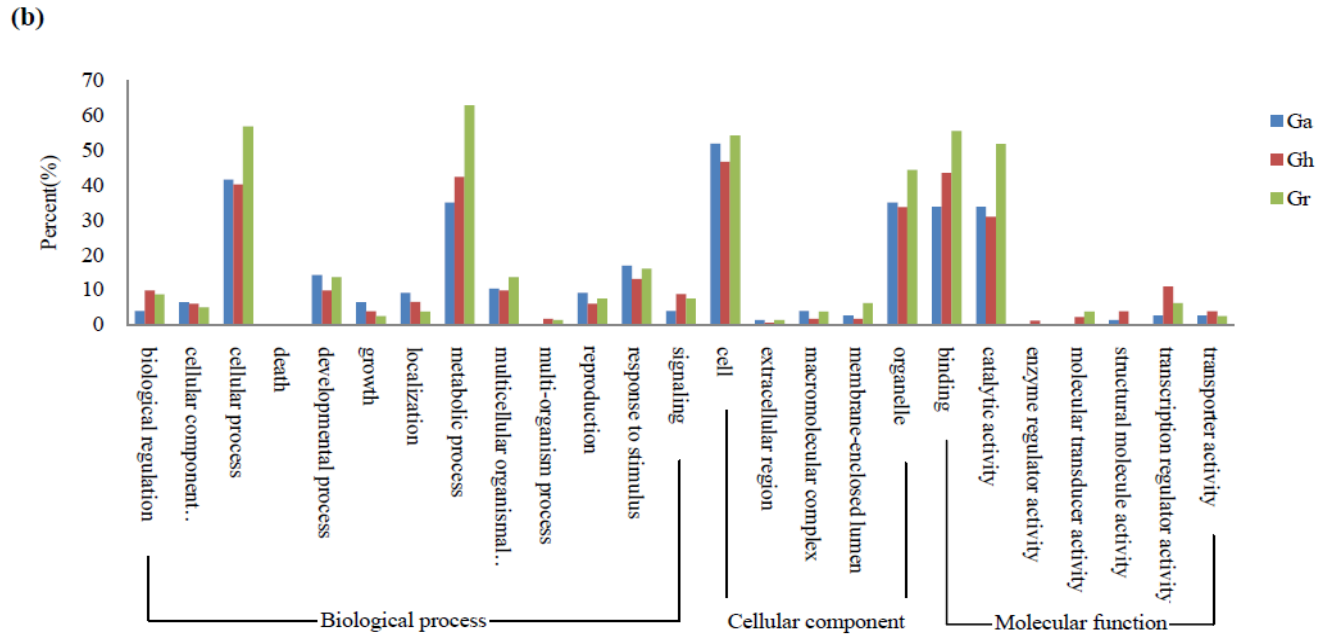
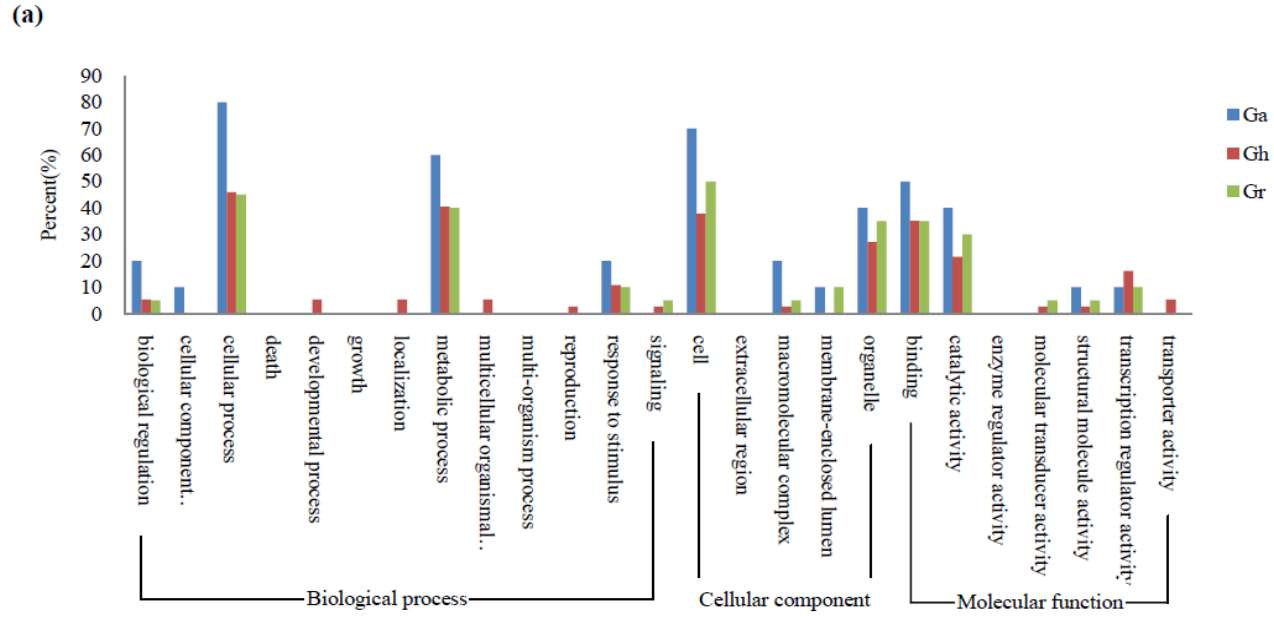
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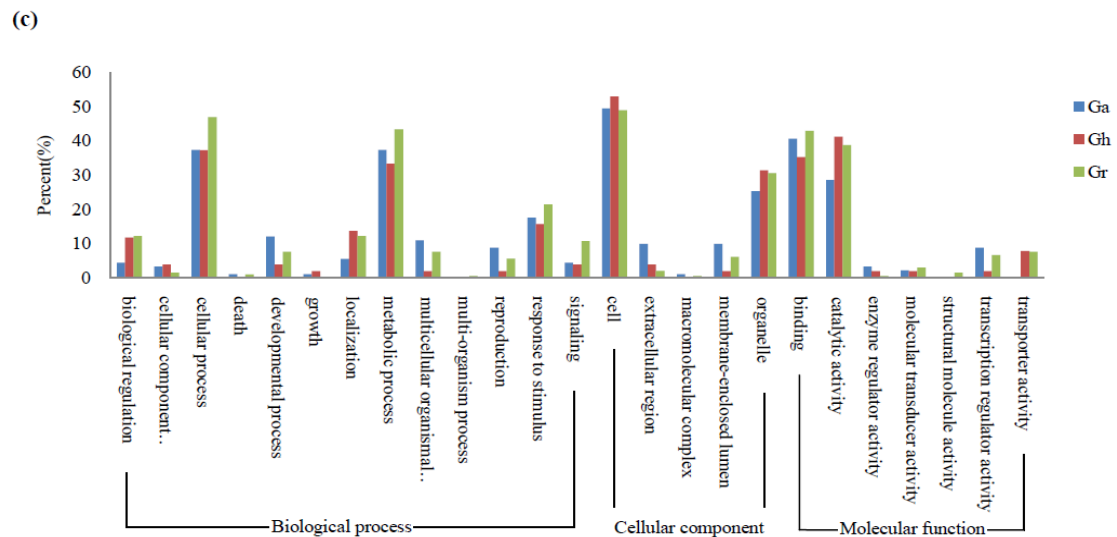
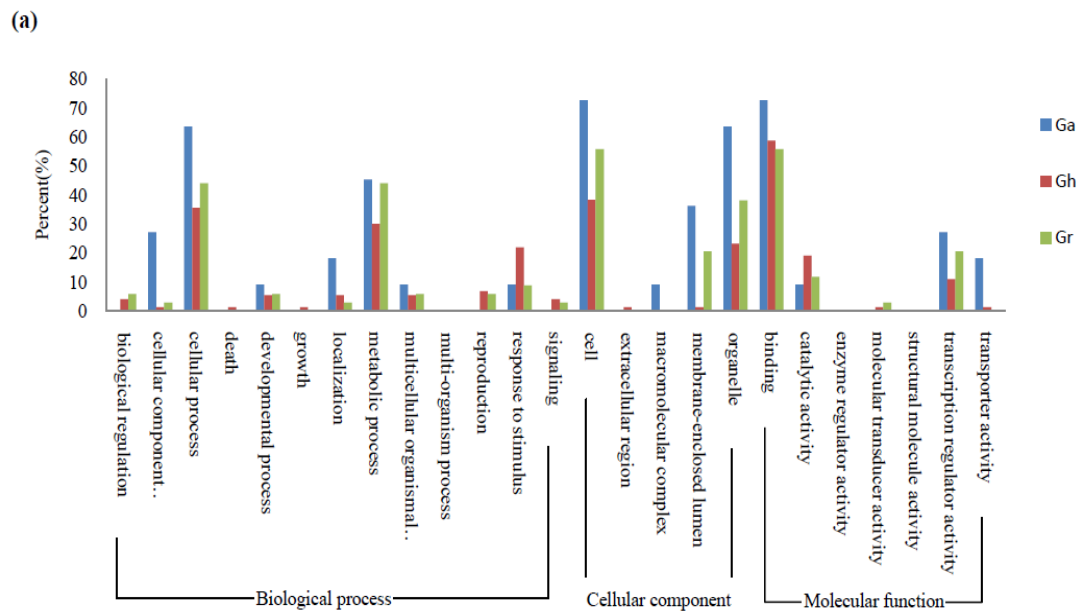
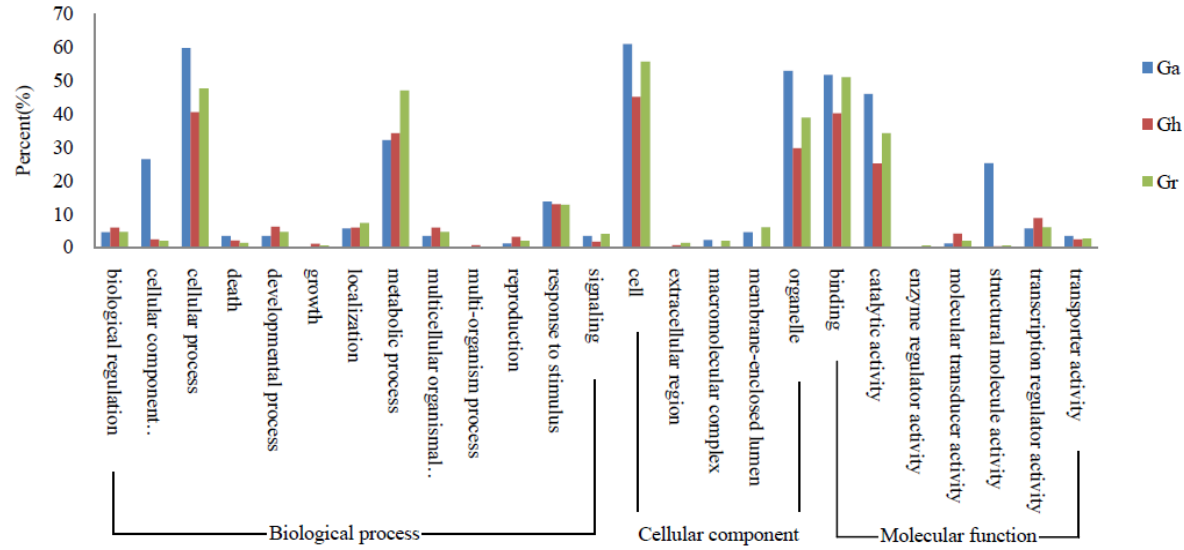


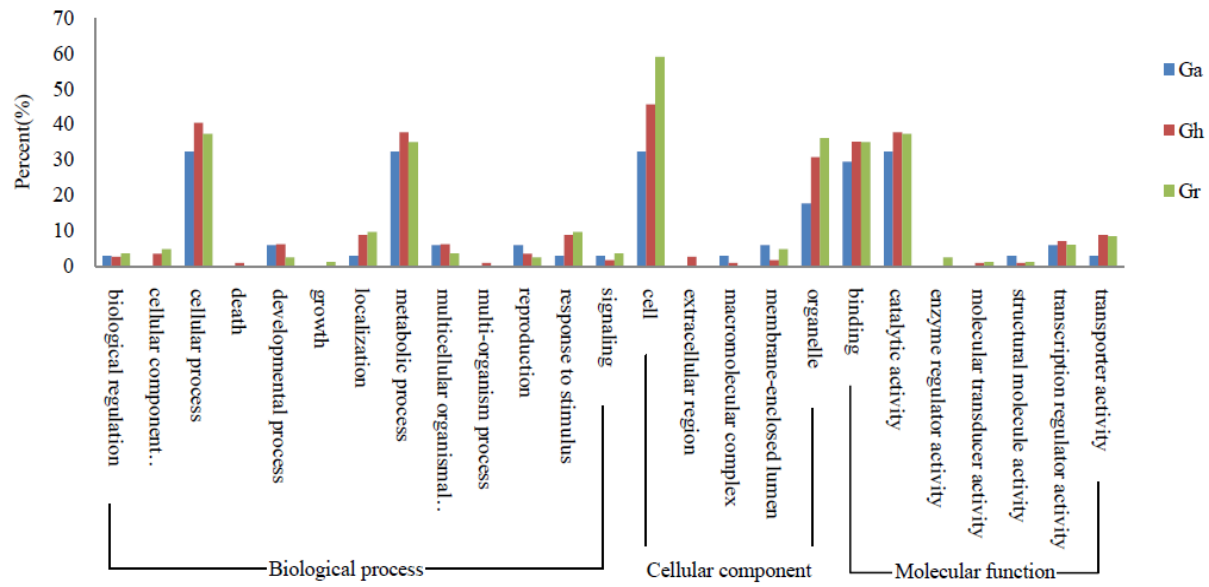
Figure S1. Function classifications of dinucleotides motif SSR-ESTs. (a) AC motif; (b) AG motif; (c) AT motif.

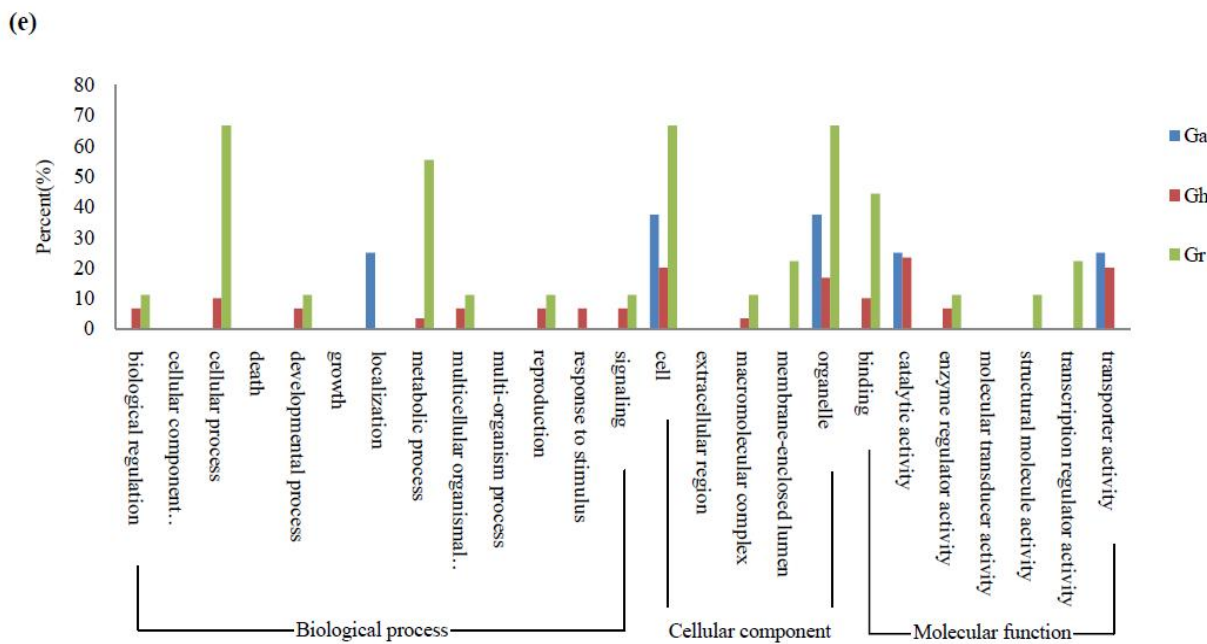
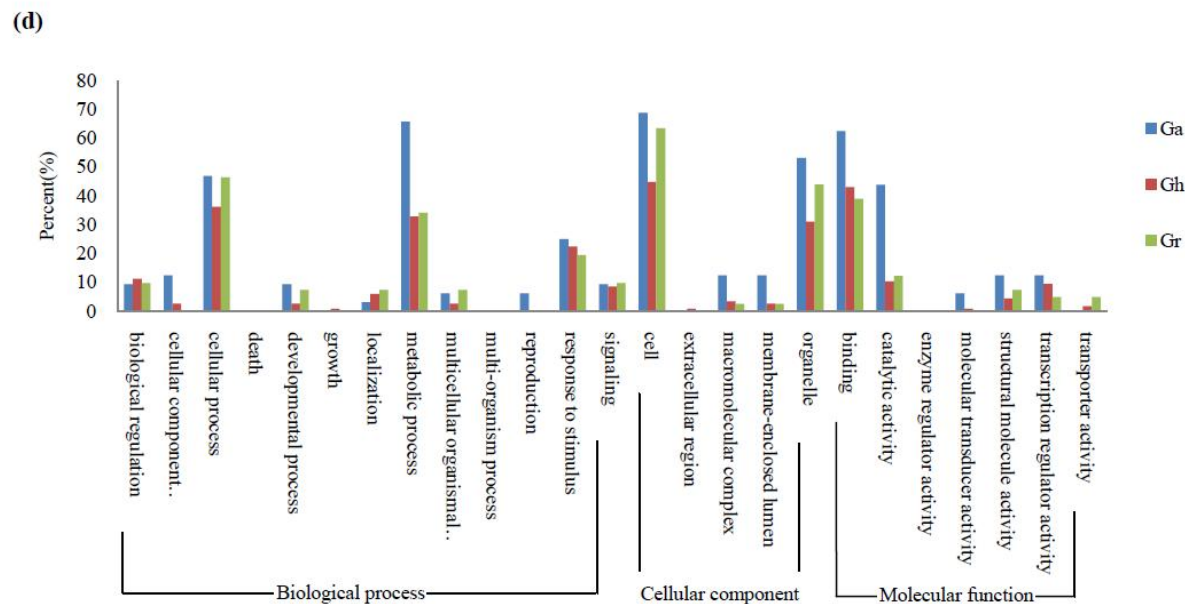


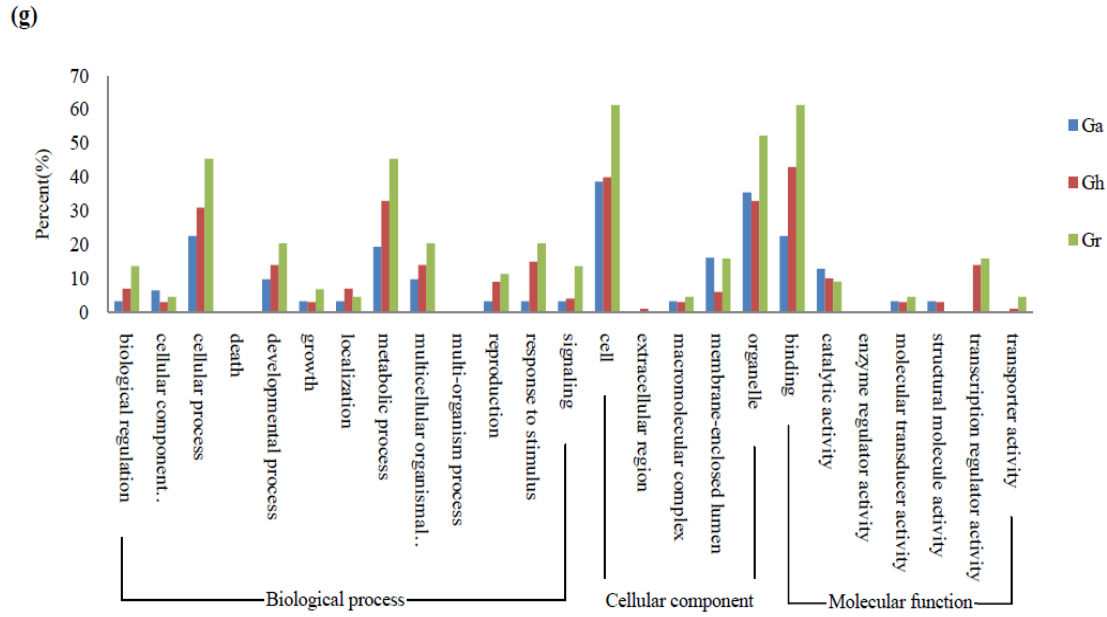
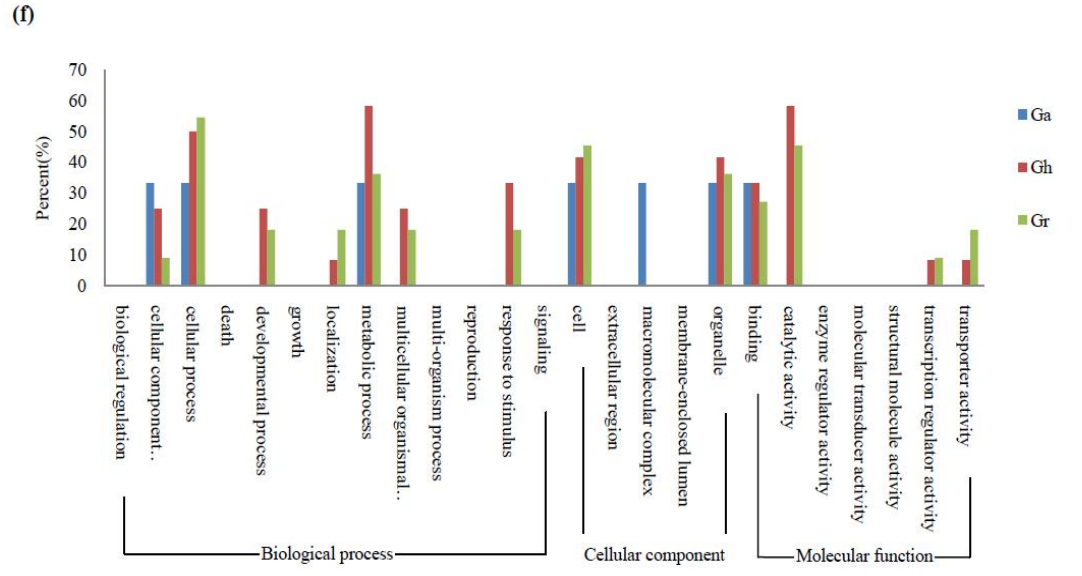
(b)



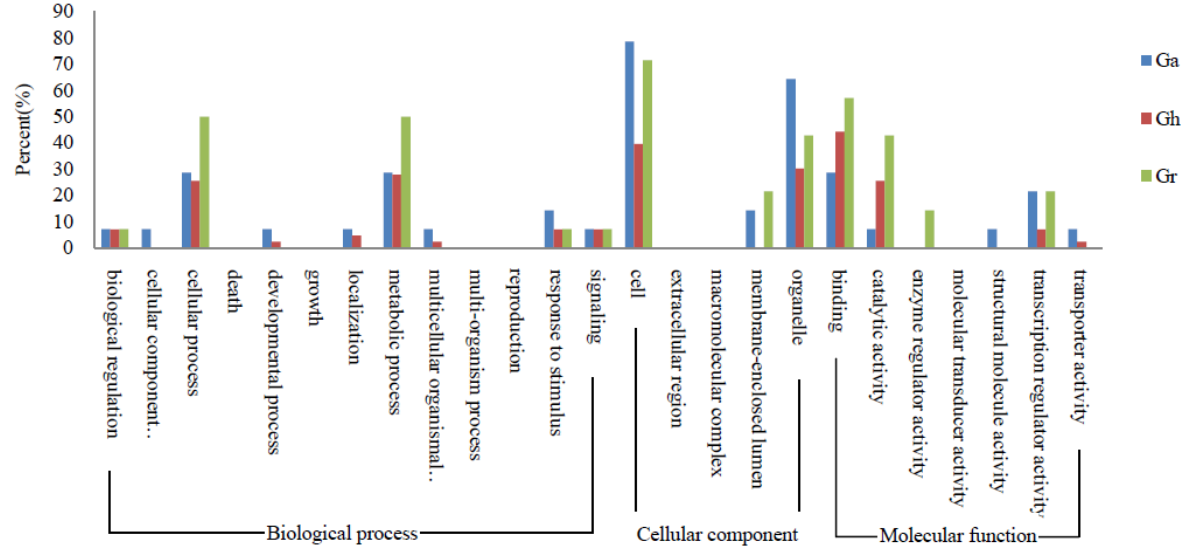
(c)



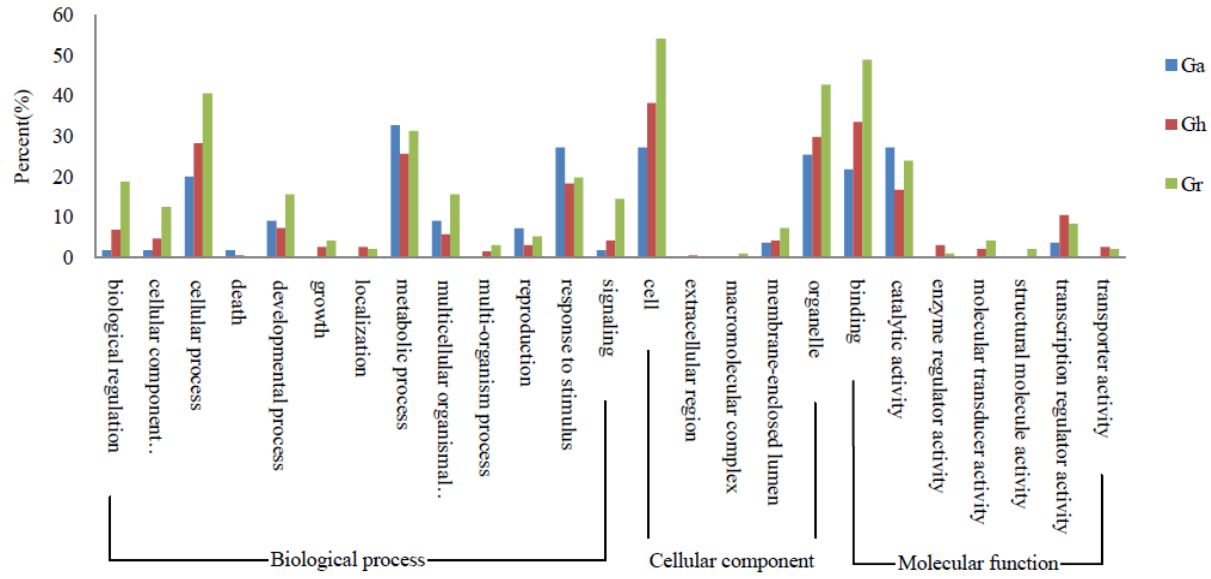




(h)



(i)



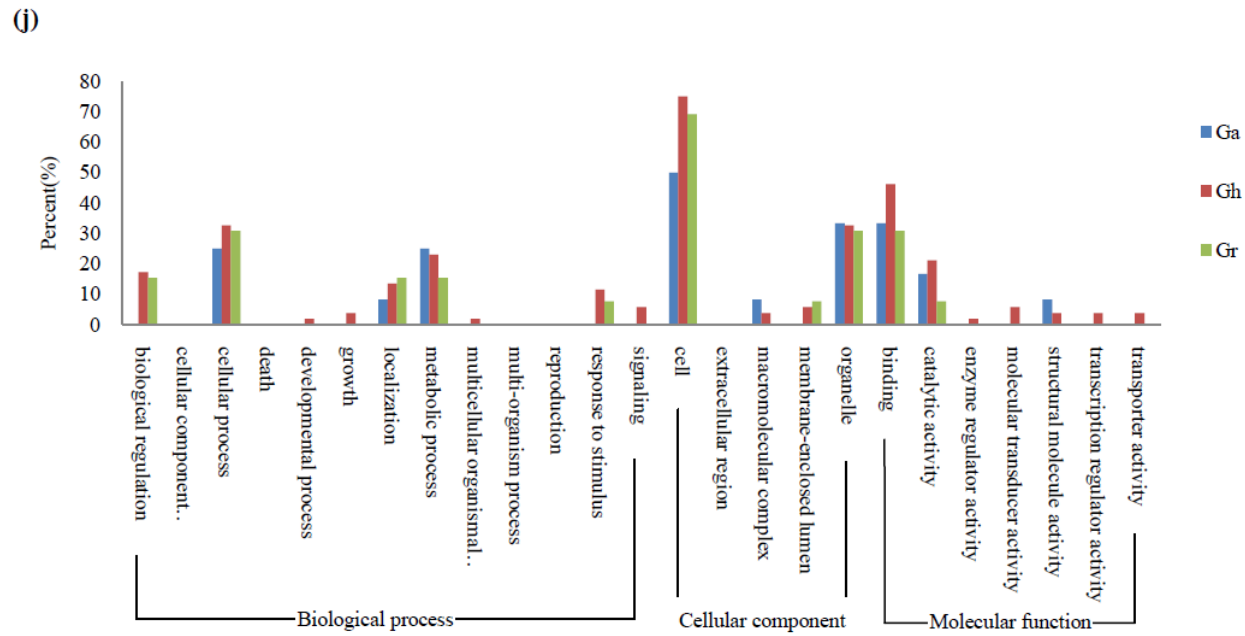


Figure S2. Function classifications of trinucleotides motif SSR-ESTs. (a) AAC motif; (b) AAG motif; (c) AAT motif; (d) ACC motif; (e) ACG motif; (f) ACT motif; (g) AGC motif; (h) AGG motif; (i) ATC motif; (j)CCG motif.

Supplementary Table 1. Contd.

TA4881_29729	2	GA	1198	1217	20	10	GAGAGAGAGAGAGAGAGA
BE052657	2	GA	1	21	20	10	GAGAGAGAGAGAGAGAGAG
BE053217	2	GA	9	64	56	28	GA
BF272810	2	GA	209	251	42	21	GAG
BF274512	2	GA	1	59	58	29	GAG
BF276023	2	GA	702	719	18	9	GAGAGAGAGAGAGAGAGA
BF276490	2	GA	132	168	36	18	GAG
BG440327	2	GA	76	93	18	9	GAGAGAGAGAGAGAGAGA
BG444071	2	GA	1	83	82	41	GA GAGAGAGAGAGAGAGAGAG
BG444077	2	GA	1	96	96	48	GA GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGA
BG445402	2	GA	1	65	64	32	GA G
BG446518	2	GA	295	312	18	9	GAGAGAGAGAGAGAGAGA
BM358395	2	GA	1	29	28	14	GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG
BM358617	2	GA	1	39	38	19	GAG
BM360126	2	GA	8	45	38	19	GA
BQ405858	2	GA	565	582	18	9	GAGAGAGAGAGAGAGAGA
BQ407002	2	GA	3	28	26	13	GAGAGAGAGAGAGAGAGAGAGAGA
AW727558	2	GC	1040	1058	18	9	GCGCGCGCGCGCGCGCGCG
TA6582_29729	2	GT	398	416	18	9	GTGTGTGTGTGTGTGTGTG
TA5092_29729	2	TA	340	358	18	9	TATATATATATATATATAT
TA5674_29729	2	TA	671	693	22	11	TATATATATATATATATATAT
TA5883_29729	2	TA	628	648	20	10	TATATATATATATATATAT
TA5896_29729	2	TA	628	645	18	9	TATATATATATATATA
TA6055_29729	2	TA	551	568	18	9	TATATATATATATATA
TA6309_29729	2	TA	300	328	28	14	TATATATATATATATATATATATAT
TA6558_29729	2	TA	1025	1046	22	11	TATATATATATATATATATA
TA6559_29729	2	TA	429	450	22	11	TATATATATATATATATATA
TA6826_29729	2	TA	541	559	18	9	TATATATATATATATAT
TA7329_29729	2	TA	764	806	42	21	TAT
TA7400_29729	2	TA	1108	1126	18	9	TATATATATATATATATAT
TA7553_29729	2	TA	575	593	18	9	TATATATATATATATATAT
TA7596_29729	2	TA	1007	1024	18	9	TATATATATATATATATA
TA7731_29729	2	TA	575	594	20	10	TATATATATATATATATA
TA7857_29729	2	TA	325	345	20	10	TATATATATATATATATAT
TA7930_29729	2	TA	50	74	24	12	TATATATATATATATATATATAT

Supplementary Table 1. Contd.

TA8217_29729	2	TA	153	173	20	10	TATATATATATATATATAT
TA8382_29729	2	TA	667	684	18	9	TATATATATATATATATA
TA8392_29729	2	TA	268	286	18	9	TATATATATATATATATAT
TA8913_29729	2	TA	560	578	18	9	TATATATATATATATATAT
BE052625	2	TA	205	223	18	9	TATATATATATATATATAT
BE053700	2	TA	357	377	20	10	TATATATATATATATATAT
BE054013	2	TA	381	411	30	15	TATATATATATATATATATATATATAT
BE054303	2	TA	142	160	18	9	TATATATATATATATATAT
BE054872	2	TA	266	284	18	9	TATATATATATATATATAT
BE055619	2	TA	345	363	18	9	TATATATATATATATATAT
BF268601	2	TA	246	270	24	12	TATATATATATATATATATATAT
BF268682	2	TA	530	551	22	11	TATATATATATATATATATA
BF270944	2	TA	60	79	20	10	TATATATATATATATATA
BF276865	2	TA	343	364	22	11	TATATATATATATATATATA
BF276973	2	TA	369	387	18	9	TATATATATATATATATAT
BG441636	2	TA	344	362	18	9	TATATATATATATATATAT
BG442302	2	TA	311	329	18	9	TATATATATATATATATAT
BG443157	2	TA	346	364	18	9	TATATATATATATATATAT
BG444416	2	TA	212	230	18	9	TATATATATATATATATAT
BG444964	2	TA	287	305	18	9	TATATATATATATATATAT
BG445759	2	TA	191	214	24	12	TATATATATATATATATATATA
BQ402139	2	TA	456	475	20	10	TATATATATATATATATA
BQ405728	2	TA	590	614	24	12	TATATATATATATATATATATAT
BQ407767	2	TA	116	134	18	9	TATATATATATATATATAT
BQ408241	2	TA	597	620	24	12	TATATATATATATATATATATA
BQ410148	2	TA	467	487	20	10	TATATATATATATATATAT
BQ412586	2	TA	59	76	18	9	TATATATATATATATA
BQ413236	2	TA	510	546	36	18	TATATATATATATATATATATATATATATATAT
BQ413280	2	TA	446	466	20	10	TATATATATATATATATAT
BQ414241	2	TA	535	575	40	20	TATATATATATATATATATATATATATATATATATAT
BQ414392	2	TA	504	528	24	12	TATATATATATATATATATATAT
BQ414409	2	TA	594	616	22	11	TATATATATATATATATATAT
BQ415692	2	TA	8	36	28	14	TATATATATATATATATATATATAT
BQ416174	2	TA	533	557	24	12	TATATATATATATATATATATAT
TA4987_29729	2	TC	358	385	28	14	TCTCTCTCTCTCTCTCTCTCTC
TA5977_29729	2	TC	41	58	18	9	TCTCTCTCTCTCTCTC
TA7156_29729	2	TC	3	31	28	14	TCTCTCTCTCTCTCTCTCTCTCT

Supplementary Table 1. Contd.

TA7299_29729	2	TC	15	33	18	9	TCTCTCTCTCTCTCTCT
TA8009_29729	2	TC	118	135	18	9	TCTCTCTCTCTCTCTCTC
TA8184_29729	2	TC	46	64	18	9	TCTCTCTCTCTCTCTCT
TA8562_29729	2	TC	1	21	20	10	TCTCTCTCTCTCTCTCT
AW731151	2	TC	252	272	20	10	TCTCTCTCTCTCTCTCT
BE053003	2	TC	1	24	24	12	TCTCTCTCTCTCTCTCTCTC
BE053023	2	TC	325	342	18	9	TCTCTCTCTCTCTCTCTC
BF268139	2	TC	72	101	30	15	TCTCTCTCTCTCTCTCTCTCTCTC
BF268191	2	TC	1	30	30	15	TCTCTCTCTCTCTCTCTCTCTCTC
BF268204	2	TC	10	38	28	14	TCTCTCTCTCTCTCTCTCTCTCT
BF270284	2	TC	49	67	18	9	TCTCTCTCTCTCTCTCT
BF271444	2	TC	16	40	24	12	TCTCTCTCTCTCTCTCTCTCT
BF271486	2	TC	16	40	24	12	TCTCTCTCTCTCTCTCTCTCT
BF271488	2	TC	16	40	24	12	TCTCTCTCTCTCTCTCTCTCT
BF272117	2	TC	520	546	26	13	TCTCTCTCTCTCTCTCTCTCTCT
BF272287	2	TC	31	57	26	13	TCTCTCTCTCTCTCTCTCTCTCT
BG440412	2	TC	16	36	20	10	TCTCTCTCTCTCTCTCTCT
BG440825	2	TC	1	34	34	17	TCTCTCTCTCTCTCTCTCTCTCTCTCTC
BG442970	2	TC	98	146	48	24	TCT
BG443314	2	TC	47	73	26	13	TCTCTCTCTCTCTCTCTCTCTCT
BG444045	2	TC	52	69	18	9	TCTCTCTCTCTCTCTCTC
BG445733	2	TC	604	621	18	9	TCTCTCTCTCTCTCTCTC
BG446768	2	TC	76	95	20	10	TCTCTCTCTCTCTCTCTCTC
BM359473	2	TC	44	70	26	13	TCTCTCTCTCTCTCTCTCTCTCT
BQ402652	2	TC	370	389	20	10	TCTCTCTCTCTCTCTCTCTC
BQ402783	2	TC	11	41	30	15	TCTCTCTCTCTCTCTCTCTCTCTCTCT
BQ403786	2	TC	91	121	30	15	TCTCTCTCTCTCTCTCTCTCTCTCTCT
BQ405745	2	TC	1	19	18	9	TCTCTCTCTCTCTCTCT
BQ405963	2	TC	5	24	20	10	TCTCTCTCTCTCTCTCTCTC
BQ406414	2	TC	1	18	18	9	TCTCTCTCTCTCTCTCTC
BQ409912	2	TC	200	221	22	11	TCTCTCTCTCTCTCTCTCTC
TA8998_29729	2	TG	948	966	18	9	TGTGTGTGTGTGTGTGTGT
BQ409179	2	TG	592	610	18	9	TGTGTGTGTGTGTGTGTGT
TA6479_29729	3	AAC	589	607	18	6	AACAACAACAACAACAACA
TA6818_29729	3	AAG	44	66	21	7	AAGAAGAAGAAGAAGAAGAAGAA
TA8763_29729	3	AAG	253	284	30	10	AAGAAGAAGAAGAAGAAGAAGAAGAA
BF270051	3	AAG	322	344	21	7	AAGAAGAAGAAGAAGAAGAA
BF274071	3	AAG	323	346	24	8	AAGAAGAAGAAGAAGAAGAAG

Supplementary Table 1. Contd.

BF276199	3	AAG	18	38	21	7	AAGAAGAAGAAGAAGAAG
BF276717	3	AAG	18	35	18	6	AAGAAGAAGAAGAAGAAG
BM360670	3	AAG	35	52	18	6	AAGAAGAAGAAGAAGAAG
BQ402652	3	AAG	523	540	18	6	AAGAAGAAGAAGAAGAAG
TA5627_29729	3	AAT	386	432	45	15	AATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATA
BF269744	3	AAT	510	531	21	7	AATAATAATAATAATAATA
BF272815	3	AAT	248	268	21	7	AATAATAATAATAATAAT
BM359991	3	AAT	3	21	18	6	AATAATAATAATAATA
BQ409090	3	AAT	68	88	21	7	AATAATAATAATAATAAT
TA9317_29729	3	ACA	526	551	24	8	ACAACAACAACAACAACAACAAC
TA5263_29729	3	ACC	66	83	18	6	ACCACCACCACCACCACC
TA8615_29729	3	ACC	174	193	18	6	ACCACCACCACCACCACC
BE052321	3	ACC	21	38	18	6	ACCACCACCACCACCACC
BE054357	3	ACC	394	411	18	6	ACCACCACCACCACCACC
BE055367	3	ACC	1	18	18	6	ACCACCACCACCACCACC
BG440558	3	ACC	10	27	18	6	ACCACCACCACCACCACC
BG443450	3	ACC	30	47	18	6	ACCACCACCACCACCACC
BM360664	3	ACC	55	72	18	6	ACCACCACCACCACCACC
BQ403357	3	ACC	1	19	18	6	ACCACCACCACCACCACC
BQ407239	3	ACT	254	275	21	7	ACTACTACTACTACTACTACTA
BG444624	3	AGA	464	481	18	6	AGAAGAAGAAGAAGAAGA
TA5416_29729	3	AGC	478	500	21	7	AGCAGCAGCAGCAGCAGCAGCAG
BE054201	3	AGC	478	500	21	7	AGCAGCAGCAGCAGCAGCAGCAG
BE055322	3	AGC	473	495	21	7	AGCAGCAGCAGCAGCAGCAGCAG
BF277776	3	AGC	314	333	18	6	AGCAGCAGCAGCAGCAGCAG
BG441547	3	AGC	333	355	21	7	AGCAGCAGCAGCAGCAGCAGCAG
BG441749	3	AGC	462	484	21	7	AGCAGCAGCAGCAGCAGCAGCAG
BG442685	3	AGC	443	465	21	7	AGCAGCAGCAGCAGCAGCAGCAG
BG443059	3	AGC	111	133	21	7	AGCAGCAGCAGCAGCAGCAGCAG
BG443578	3	AGC	401	423	21	7	AGCAGCAGCAGCAGCAGCAGCAG
BM359805	3	AGC	376	398	21	7	AGCAGCAGCAGCAGCAGCAGCAG
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BQ402549	3	AGG	244	264	21	7	AGGAGGAGGAGGAGGAGGAGG
TA8270_29729	3	AGT	182	199	18	6	AGTAGTAGTAGTAGTAGT
AW728773	3	AGT	107	135	27	9	AGTAGTAGTAGTAGTAGTAGTAGTAG
AW728773	3	AGT	137	162	24	8	AGTAGTAGTAGTAGTAGTAGTAGTAG
TA7230_29729	3	ATA	482	500	18	6	ATAATAATAATAATAATA

Supplementary Table 1. Contd.

BQ406809	3	CAC	17	38	21	7	CACCACCACCACCACCACC
BQ407414	3	CAC	138	156	18	6	CACCACCACCACCACCACC
BQ407429	3	CAC	495	514	18	6	CACCACCACCACCACCACCA
BQ410306	3	CAC	343	362	18	6	CACCACCACCACCACCACCA
TA6708_29729	3	CAG	19	51	33	11	CAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG
TA9237_29729	3	CAG	9	31	21	7	CAGCAGCAGCAGCAGCAGCAGCA
BF269259	3	CAG	173	195	21	7	CAGCAGCAGCAGCAGCAGCAGCA
BF276122	3	CAG	441	458	18	6	CAGCAGCAGCAGCAGCAG
BG443126	3	CAG	158	175	18	6	CAGCAGCAGCAGCAGCAG
BG446140	3	CAG	249	266	18	6	CAGCAGCAGCAGCAGCAG
BM359410	3	CAG	156	173	18	6	CAGCAGCAGCAGCAGCAG
BQ406334	3	CAG	476	498	21	7	CAGCAGCAGCAGCAGCAGCAGCA
BQ406746	3	CAG	257	279	21	7	CAGCAGCAGCAGCAGCAGCAGCA
BQ413346	3	CAG	569	586	18	6	CAGCAGCAGCAGCAGCAG
TA5303_29729	3	CAT	123	142	18	6	CATCATCATCATCATCATCA
TA7168_29729	3	CAT	496	514	18	6	CATCATCATCATCATCATC
AW726061	3	CAT	131	150	18	6	CATCATCATCATCATCATCA
BE052471	3	CAT	238	256	18	6	CATCATCATCATCATCATC
BE053330	3	CAT	107	126	18	6	CATCATCATCATCATCATCA
BF275536	3	CAT	195	216	21	7	CATCATCATCATCATCATC
BF275537	3	CAT	9	28	18	6	CATCATCATCATCATCATCA
BF275563	3	CAT	13	35	21	7	CATCATCATCATCATCATCA
BG441669	3	CAT	90	109	18	6	CATCATCATCATCATCATCA
BG442727	3	CAT	81	100	18	6	CATCATCATCATCATCATCA
BG442903	3	CAT	111	130	18	6	CATCATCATCATCATCATCA
BG445378	3	CAT	399	418	18	6	CATCATCATCATCATCATCA
BQ410319	3	CAT	178	196	18	6	CATCATCATCATCATCATC
BQ410999	3	CAT	461	479	18	6	CATCATCATCATCATCATC
BQ411009	3	CAT	412	431	18	6	CATCATCATCATCATCATCA
BQ411446	3	CAT	271	293	21	7	CATCATCATCATCATCATCA
BQ412920	3	CAT	61	80	18	6	CATCATCATCATCATCATCA
BQ413309	3	CAT	465	482	18	6	CATCATCATCATCATCAT
BQ413494	3	CAT	98	122	24	8	CATCATCATCATCATCATCATC
BQ415559	3	CAT	470	489	18	6	CATCATCATCATCATCATCA
BF276058	3	CCA	55	75	21	7	CCACCACCACCACCACCACCA
BG443488	3	CCA	56	76	21	7	CCACCACCACCACCACCACCA
BQ403357	3	CCA	371	388	18	6	CCACCACCACCACCACCA

Supplementary Table 1. Contd.

BF276313	3	TGC	56	73	18	6	TGCTGCTGCTGCTGCTGC
BG442229	3	TGC	266	283	18	6	TGCTGCTGCTGCTGCTGC
BQ401914	3	TGC	117	134	18	6	TGCTGCTGCTGCTGCTGC
BF271971	3	TGG	233	256	24	8	TGGTGGTGGTGGTGGTGGTGG
BE052575	3	TGT	556	573	18	6	TGTTGTTGTTGTTGTTGT
TA5476_29729	3	TTA	886	935	48	16	TTATTATTATTATTATTATTATTATTATTATTATTATTATTATTATTATTATTATT
TA5626_29729	3	TTA	458	476	18	6	TTATTATTATTATTATTATT
TA5985_29729	3	TTA	1483	1501	18	6	TTATTATTATTATTATTATT
TA7034_29729	3	TTA	541	558	18	6	TTATTATTATTATTATTATT
BF276846	3	TTA	668	705	36	12	TTATTATTATTATTATTATTATTATTATTATTATTATTATTATTATT
BF276847	3	TTA	661	698	36	12	TTATTATTATTATTATTATTATTATTATTATTATTATTATTATTATT
BG444301	3	TTA	520	539	18	6	TTATTATTATTATTATTATT
BQ405592	3	TTA	20	53	33	11	TTATTATTATTATTATTATTATTATTATTATTATTATTATTATTATT
BQ413644	3	TTA	25	43	18	6	TTATTATTATTATTATTATT
BQ415860	3	TTA	484	518	33	11	TTATTATTATTATTATTATTATTATTATTATTATTATTATTATTATT
TA4858_29729	3	TTC	18	37	18	6	TTCTTCTTCTTCTTCTTCTT
TA4859_29729	3	TTC	30	49	18	6	TTCTTCTTCTTCTTCTTCTT
TA5246_29729	3	TTC	691	708	18	6	TTCTTCTTCTTCTTCTTC
TA6371_29729	3	TTC	32	61	30	10	TTCTTCTTCTTCTTCTTCTTCTTCTTCTTC
TA6739_29729	3	TTC	176	193	18	6	TTCTTCTTCTTCTTCTTC
TA6740_29729	3	TTC	219	236	18	6	TTCTTCTTCTTCTTCTTC
TA7048_29729	3	TTC	101	121	21	7	TTCTTCTTCTTCTTCTTCTTC
TA7486_29729	3	TTC	44	64	21	7	TTCTTCTTCTTCTTCTTCTTC
TA9370_29729	3	TTC	209	226	18	6	TTCTTCTTCTTCTTCTTC
BE051955	3	TTC	24	43	18	6	TTCTTCTTCTTCTTCTTCTT
BE052040	3	TTC	18	37	18	6	TTCTTCTTCTTCTTCTTCTT
BE052859	3	TTC	30	49	18	6	TTCTTCTTCTTCTTCTTCTT
BE052916	3	TTC	123	141	18	6	TTCTTCTTCTTCTTCTTCTT
BE053214	3	TTC	86	105	18	6	TTCTTCTTCTTCTTCTTCTT
BE053742	3	TTC	15	34	18	6	TTCTTCTTCTTCTTCTTCTT
BE054092	3	TTC	15	34	18	6	TTCTTCTTCTTCTTCTTCTT
BE054356	3	TTC	35	54	18	6	TTCTTCTTCTTCTTCTTCTT
BE055134	3	TTC	15	35	21	7	TTCTTCTTCTTCTTCTTCTTC
BE055541	3	TTC	30	49	18	6	TTCTTCTTCTTCTTCTTCTT
BF277771	3	TTC	98	118	21	7	TTCTTCTTCTTCTTCTTCTTC
BG440000	3	TTC	32	51	18	6	TTCTTCTTCTTCTTCTTCTT
BG440223	3	TTC	15	34	18	6	TTCTTCTTCTTCTTCTTCTT
BG440502	3	TTC	3	22	18	6	TTCTTCTTCTTCTTCTTCTT

Supplementary Table 1. Contd.

BG440440	4	TAAA	21	42	20	5	TAAATAAATAAATAAATA
BG447194	4	TAAT	356	376	20	5	TAATTAATTAATTAATTAATT
TA8897_29729	4	TATG	421	456	36	9	TATGTATGTATGTATGTATGTATGTATGTATG
BE053131	4	TATG	337	359	20	5	TATGTATGTATGTATGTATGTAT
BM357948	4	TATG	642	664	20	5	TATGTATGTATGTATGTATGTAT
BM358426	4	TATG	538	565	28	7	TATGTATGTATGTATGTATGTATGTATG
BQ414527	4	TATT	9	29	20	5	TATTTATTTATTTATTTATTT
BG439886	4	TGTA	616	635	20	5	TGTATGTATGTATGTATGTATGTA
BF272588	4	TTCT	16	37	20	5	TTCTTTCTTTCTTTCTTTCTTT
TA5862_29729	4	TTTA	455	477	20	5	TTTATTTATTTATTTATTTATTT
BQ409148	4	TTTC	130	156	24	6	TTTCTTTCTTTCTTTCTTTCTTTCTTT
BQ402637	4	TTTG	484	506	20	5	TTTGTTTGTTTGTTTGTTTGTTT
BF271164	5	AGAAA	44	68	25	5	AGAAAAGAAAAGAAAAGAAAAGAAA
TA7673_29729	5	AGAAG	68	93	25	5	AGAAGAGAAGAGAAGAGAAGAGAAGA
BG444055	5	AGAGA	20	53	30	6	AGAGAAGAGAAGAGAAGAGAAGAGAAGAGAG
BQ412345	5	CAAAC	72	96	25	5	CAAACCAAACCAAACCAAACCAAAC
BF276655	5	TCCCC	64	90	25	5	TCCCCTCCCCTCCCCTCCCCTCCCCTC
BF276803	5	TCTAA	24	51	25	5	TCTAATCTAATCTAATCTAATCTAATCT
BF274421	5	TCTTT	445	470	25	5	TCTTTTCTTTTCTTTTCTTTTCTTTT
TA7484_29729	5	TTCTT	34	61	25	5	TTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT
BG445274	5	TTTCT	72	97	25	5	TTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTT
TA7930_29729	5	TTTTC	330	354	25	5	TTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT
BE052504	6	AAAAAT	1	24	24	4	AAAAATAAAAAATAAAAAATAAAAAAT
BF278842	6	AAAAAT	44	73	30	5	AAAAATAAAAAATAAAAAATAAAAAATAAAAAAT
BG447357	6	AAAAAT	453	477	24	4	AAAAATAAAAAATAAAAAATAAAAAATA
BQ408211	6	AAGCTC	35	59	24	4	AAGCTCAAGCTCAAGCTCAAGCTCA
BG440787	6	AAGGCA	48	80	30	5	AAGGCAAAGGCAAAGGCAAAGGCAAAGGCAAAG
BF272140	6	CAACAG	291	317	24	4	CAACAGCAACAGCAACAGCAACAGCAA
BG440800	6	CACAGG	201	228	24	4	CACAGGCACAGGCACAGGCACAGGCACA
TA5668_29729	6	CACTCT	107	131	24	4	CACTCTCACTCTCACTCTCACTCTC
TA9237_29729	6	CAGCAA	336	360	24	4	CAGCAACAGCAACAGCAACAGCAAC
BG444074	6	CAGGCA	132	166	30	5	CAGGCACAGGCACAGGCACAGGCACAGGCACAGGC
BM358018	6	CCACAG	15	47	30	5	CCACAGCCACAGCCACAGCCACAGCCACAGCCA
TA6665_29729	6	CCCCAA	91	119	24	4	CCCCAACCCCAACCCCAACCCCAACCCCA
BE052870	6	CCCCAA	212	240	24	4	CCCCAACCCCAACCCCAACCCCAACCCCA
BE054108	6	CCCCAA	64	92	24	4	CCCCAACCCCAACCCCAACCCCAACCCCA
BF277774	6	CCCCTC	40	64	24	4	CCCCTCCCCTCCCCTCCCCTCCCCTCC

Supplementary Table 1. Contd.

BE053289	6	CCCTTC	234	263	30	5	CCCTTCCCCTTCCCCTTCCCCTTCCCCTTC
BE054387	6	CCCTTT	140	169	30	5	CCCTTTCCCTTTCCCTTTCCCTTTCCCTTT
BQ414792	6	CCGAGA	364	410	42	7	CCGAGACCGAGACCGAGACCGAGACCGAGACCGAGACCGAGACCGAG
TA8669_29729	6	CCTCCA	42	66	24	4	CCTCCACCTCCACCTCCACCTCCAC
BQ402121	6	CGGCTC	458	488	30	5	CGGCTCCGGCTCCGGCTCCGGCTCCGGCTCC
BQ414131	6	CGGCTC	453	483	30	5	CGGCTCCGGCTCCGGCTCCGGCTCCGGCTCC
TA5668_29729	6	CTCTCA	139	163	24	4	CTCTCACTCTCACTCTCACTCTCAC
BF270137	6	CTCTCC	97	126	30	5	CTCTCCCTCTCCCTCTCCCTCTCCCTCTCC
BQ404244	6	CTGCCT	84	108	24	4	CTGCCTCTGCCTCTGCCTCTGCCTC
BE054746	6	CTTCCC	209	233	24	4	CTTCCCCTTCCCCTTCCCCTTCCCCTTCCC
BG445180	6	CTTCCC	212	236	24	4	CTTCCCCTTCCCCTTCCCCTTCCCCTTCCC
BF275274	6	GAAGAT	478	504	24	4	GAAGATGAAGATGAAGATGAAGATGAA
BG446849	6	GAAGAT	460	487	24	4	GAAGATGAAGATGAAGATGAAGATGAAG
BQ409057	6	GAGGAA	522	545	24	4	GAGGAAGAGGAAGAGGAAGAGGAA
TA8901_29729	6	GAGTCC	23	49	24	4	GAGTCCGAGTCCGAGTCCGAGTCCGAG
BG445177	6	GATAGG	276	301	24	4	GATAGGGATAGGGATAGGGATAGGGGA
BG445815	6	GATAGG	561	586	24	4	GATAGGGATAGGGATAGGGATAGGGGA
BQ414273	6	GATGGG	381	404	24	4	GATGGGGATGGGGATGGGGATGGG
BQ402465	6	GCCACA	561	585	24	4	GCCACAGCCACAGCCACAGCCACAG
TA4949_29729	6	GCTCAT	329	354	24	4	GCTCATGCTCATGCTCATGCTCATGC
BF272793	6	GCTCCT	60	95	36	6	GCTCCTGCTCCTGCTCCTGCTCCTGCTCCT
BM359711	6	GGAAGA	260	286	24	4	GGAAGAGGAAGAGGAAGAGGAAGAGGA
BQ402120	6	GGAGCC	588	611	24	4	GGAGCCGGAGCCGGAGCCGGAGCC
TA9009_29729	6	GGCTTC	144	173	30	5	GGCTTCGGCTTCGGCTTCGGCTTCGGCTTC
TA6589_29729	6	TATTTT	395	419	24	4	TATTTTATTTTATTTTATTTTATTTT
BG440224	6	TCAAGC	259	288	30	5	TCAAGCTCAAGCTCAAGCTCAAGCTCAAGC
BG440896	6	TCAAGC	267	296	30	5	TCAAGCTCAAGCTCAAGCTCAAGCTCAAGC
TA4950_29729	6	TCAGGC	267	293	24	4	TCAGGCTCAGGCTCAGGCTCAGGCTCA
BE052527	6	TCAGGC	183	209	24	4	TCAGGCTCAGGCTCAGGCTCAGGCTCA
BE052669	6	TCAGGC	256	282	24	4	TCAGGCTCAGGCTCAGGCTCAGGCTCA
BE052760	6	TCAGGC	260	286	24	4	TCAGGCTCAGGCTCAGGCTCAGGCTCA
BE053088	6	TCAGGC	215	241	24	4	TCAGGCTCAGGCTCAGGCTCAGGCTCA
BE053587	6	TCAGGC	215	241	24	4	TCAGGCTCAGGCTCAGGCTCAGGCTCA
BE053730	6	TCAGGC	261	287	24	4	TCAGGCTCAGGCTCAGGCTCAGGCTCA
BE053966	6	TCAGGC	266	292	24	4	TCAGGCTCAGGCTCAGGCTCAGGCTCA
BE054144	6	TCAGGC	262	288	24	4	TCAGGCTCAGGCTCAGGCTCAGGCTCA
BE054522	6	TCAGGC	266	292	24	4	TCAGGCTCAGGCTCAGGCTCAGGCTCA

Supplementary Table 1. Contd.

BE054976	6	TCAGGC	229	255	24	4	TCAGGCTCAGGCTCAGGCTCAGGCTCA
BE055230	6	TCAGGC	256	282	24	4	TCAGGCTCAGGCTCAGGCTCAGGCTCA
BE055232	6	TCAGGC	265	291	24	4	TCAGGCTCAGGCTCAGGCTCAGGCTCA
BE055623	6	TCAGGC	265	291	24	4	TCAGGCTCAGGCTCAGGCTCAGGCTCA
BE055624	6	TCAGGC	265	291	24	4	TCAGGCTCAGGCTCAGGCTCAGGCTCA
BE055626	6	TCAGGC	261	287	24	4	TCAGGCTCAGGCTCAGGCTCAGGCTCA
BF272413	6	TCAGGC	274	300	24	4	TCAGGCTCAGGCTCAGGCTCAGGCTCA
BG440521	6	TCAGGC	257	283	24	4	TCAGGCTCAGGCTCAGGCTCAGGCTCA
BG441211	6	TCAGGC	242	268	24	4	TCAGGCTCAGGCTCAGGCTCAGGCTCA
BG442797	6	TCAGGC	241	267	24	4	TCAGGCTCAGGCTCAGGCTCAGGCTCA
BG443565	6	TCAGGC	309	335	24	4	TCAGGCTCAGGCTCAGGCTCAGGCTCA
BG443843	6	TCAGGC	257	283	24	4	TCAGGCTCAGGCTCAGGCTCAGGCTCA
BG443923	6	TCAGGC	258	284	24	4	TCAGGCTCAGGCTCAGGCTCAGGCTCA
BG444074	6	TCAGGC	167	192	24	4	TCAGGCTCAGGCTCAGGCTCAGGCTC
BG444093	6	TCAGGC	243	269	24	4	TCAGGCTCAGGCTCAGGCTCAGGCTCA
BG444468	6	TCAGGC	258	284	24	4	TCAGGCTCAGGCTCAGGCTCAGGCTCA
BG444500	6	TCAGGC	121	147	24	4	TCAGGCTCAGGCTCAGGCTCAGGCTCA
BG444556	6	TCAGGC	2	28	24	4	TCAGGCTCAGGCTCAGGCTCAGGCTCA
BG444921	6	TCAGGC	265	291	24	4	TCAGGCTCAGGCTCAGGCTCAGGCTCA
BG444937	6	TCAGGC	257	283	24	4	TCAGGCTCAGGCTCAGGCTCAGGCTCA
BG445036	6	TCAGGC	267	293	24	4	TCAGGCTCAGGCTCAGGCTCAGGCTCA
BG445128	6	TCAGGC	257	283	24	4	TCAGGCTCAGGCTCAGGCTCAGGCTCA
BG445281	6	TCAGGC	242	268	24	4	TCAGGCTCAGGCTCAGGCTCAGGCTCA
BG446067	6	TCAGGC	266	292	24	4	TCAGGCTCAGGCTCAGGCTCAGGCTCA
TA6451_29729	6	TCCTCT	236	268	30	5	TCCTCTTCCTCTTCCTCTTCCTCTTCCTCTTC
BG442199	6	TCTTCG	184	224	36	6	TCTTCGTCCTTCGTCCTTCGTCCTTCGTCCTTCGTCCTTC
BQ410449	6	TCTTTT	94	118	24	4	TCTTTTTCTTTTTCTTTTTCTTTTT
BF279254	6	TGCAAT	78	106	24	4	TGCAATTGCAATTGCAATTGCAATTGCAA
TA4888_29729	6	TGGCTG	694	726	30	5	TGGCTGTGGCTGTGGCTGTGGCTGTGGCTGTGG
BQ409453	6	TGGCTG	513	545	30	5	TGGCTGTGGCTGTGGCTGTGGCTGTGGCTGTGG
BQ415466	6	TGGCTG	548	580	30	5	TGGCTGTGGCTGTGGCTGTGGCTGTGGCTGTGG
TA5994_29729	6	TGTGAG	29	54	24	4	TGTGAGTGTGAGTGTGAGTGTGAGTG
BG441253	6	TGTGAG	25	50	24	4	TGTGAGTGTGAGTGTGAGTGTGAGTG
BM358740	6	TGTGAG	25	50	24	4	TGTGAGTGTGAGTGTGAGTGTGAGTG
BG446247	6	TTTCCT	48	73	24	4	TTTCCTTTTCCTTTTCCTTTTCCTTT
TA9299_29729	6	TTTTGG	450	476	24	4	TTTTGGTTTTGGTTTTGGTTTTGGTTT
BF270158	6	TTTTTC	162	185	24	4	TTTTTCTTTTCTTTTTCTTTTTC

Supplementary Table 2.

Repeat unit	Motif	Ga	Gr	Gh
Tetranucleotide	AAAT	10	52	5
	AAAC	2	22	4
	AAAG	2	31	11
	AATT	2	7	6
	AATC	1	3	1
	AATG		3	2
	AACC	1	1	
	AAGC		1	
	AAGG		2	2
	ATAC	9	39	17
	ATAG		5	3
	ATCC		4	3
	ATGC		2	2
	ACAG		2	2
	ACTC		4	
	ACCT		1	
	AGCT		1	
	AGCC	1	2	1
	AGCG		2	
	AGGC		5	
AGGG	4	1		
Pentanucleotide	AAAAT		4	2
	AAAAC		2	1
	AAAAG	5	3	1
	AAATC		4	
	AAACC	1	2	3
	AAAGC			1
	AATAT		1	1
	AATAC		2	
	AATCT	1		
	AACTC		1	3
	AACTG		1	
	AACCT		1	
	AACCC		3	
	AACCG		3	

Supplementary Table 2.

	AAGAG	2	4	8
	ATACC			1
	ATACT			1
	ATATC		1	
	ATAGC		1	1
	ATCTC		1	
	ATGCC			1
	ACAGT		1	
	ACCAG			1
	ACCTC		1	
	AGCCT		1	
	AGGGG	1	1	
Hexanucleotide	AAAAAT	4	3	6
	AAAAAC		3	
	AAAAAG	2	4	5
	AAAATT		4	
	AAAATC		1	1
	AAAATG		1	5
	AAAAGG	1		2
	AAAACC	1	6	1
	AAATAT		1	
	AAATAC		1	
	AAATTT		1	
	AAATTG		1	
	AAATCC		3	
	AAATGG		2	
	AAATGG			1
	AAAGGG	1		2
AAAGGC	1			
AAACAG		1		
AAACCC		3		
AAAGAC		1		
AAAGAG		2		
AAAGCC		1		
AAAGGC		9		
AAAGGG		2		

Supplementary Table 2.

AATTCC	1	
AATTGC	1	1
AATCAT	1	
AATCAG	1	
AATCCC	2	1
AATGAG	3	1
AATGTG		3
AATGGC	2	6
AATGGG	3	1
AACAAG	1	1
AACATG	1	
AACATC		2
AACACT	1	
AACAGC	2	8 2
AACTCC	3	1
AACTCG		1
AACTGG	1	
AACCAC		1
AACCAG	1	
AACCTC	8	1
AAC CCT	2	3
AACCCC	3	4
AACGCC	1	1
AACGGC	1	
AAGATG	2	6 1
AAGACG	1	1
AAGAGG	3	8 3
AAGCAC	1	
AAGCAG	1	1
AAGCTC	3	1
AAGCTG	1	
AAGCCT	1	
AAGCCG	1	
AAGGAG	7	1
AAGGTG	5	2
AAGGCC		2
AAGGGC	1	

Supplementary Table 2. Contd.

AAGGGG	3	2
ATATAC	6	5
ATATAG	2	1
ATAGAC	1	
ATAGCC	1	
ATAGGG	2	1 1
ATCACC	4	3
ATCACG	1	
ATCAGC	3	3
ATCTCC	3	
ATCCTC	2	
ATCCCC	1	2
ATCCGC	2	
ATCGCC	2	
ATCGGC	1	
ATGACC	4	
ATGAGC	1	1
ATGCCC	4	2
ACACTC	3	
ACACGC	1	
ACAGTG	2	
ACAGCC	5	2 2
ACAGGC	2	1
ACAGGG	1	
ACTCTC	2	3 1
ACTCCT		1
ACTCGG	1	1
ACTGCT	1	
ACTGGT	1	1
ACCAGC	5	
ACCAGG	1	
ACCTCC	1	3 2
ACCTCG	2	
ACCCTC	1	
ACCCCC	1	
ACCCCG		1
ACCGAG	1	1

Supplementary Table 2. Contd.

ACCGCC	4	2
ACGCTC	1	
ACGCC	1	
ACGCCG	1	1
ACGGAG	2	
ACGGGC	1	1
AGAGCG	1	
AGAGGC	1	
AGAGGG	1	3 3
AGCAGG	1	7 8
AGCTCC	2	1
AGCTGC	1	1
AGCCTC	3	
AGCCTG	35	14
AGCCGG	3	
AGCCCC	1	2
AGCGGC	1	
AGCGGG	1	2
AGGCCG	2	
AGGCGC	1	
AGGCGG	5	4
AGGGGC	2	
AGGGGG	1	
CCCGGG		1

Supplementary Table 2.

Group I							
HG	Sequence ID	Period Size	Period	Rep. Length	Copy Num.	Blast Strand	Species
1	BQ403493 Putative ubiquitin-conjugating enzyme [Oryza sativa (japonica cultivar-group)]	2	AG	18	9	Plus	Gossypium_arboreum
	DR044194 Putative ubiquitin-conjugating enzyme [Populus canadensis (Carolina poplar)]	2	AG	18	9	Plus	Gossypium_hirsutum
	TA22106_3635 Putative ubiquitin-conjugating enzyme [Oryza sativa (japonica cultivar-group)]	2	AG	18	9	Plus	Gossypium_hirsutum
2	BQ404091 Putative ubiquitin-conjugating enzyme [Oryza sativa (japonica cultivar-group)]	2	AG	18	9	Plus	Gossypium_arboreum
	DR044194 Putative ubiquitin-conjugating enzyme [Populus canadensis (Carolina poplar)]	2	AG	18	9	Plus	Gossypium_hirsutum

Supplementary Table 3. Contd.

	TA22106_3635 Putative ubiquitin-conjugating enzyme [<i>Oryza sativa</i> (japonica cultivar-group)]	2	AG	18	9	Plus	Gossypium_hirsutum
3	BQ410390 Putative ubiquitin-conjugating enzyme [<i>Oryza sativa</i> (japonica cultivar-group)]	2	AG	18	9	Plus	Gossypium_arboreum
	DR044194 Putative ubiquitin-conjugating enzyme [<i>Populus canadensis</i> (Carolina poplar)]	2	AG	18	9	Plus	Gossypium_hirsutum
	TA22106_3635 Putative ubiquitin-conjugating enzyme [<i>Oryza sativa</i> (japonica cultivar-group)]	2	AG	18	9	Plus	Gossypium_hirsutum
4	TA5984_29729 Putative ubiquitin carrier protein UBC7 [<i>Oryza sativa</i> (japonica cultivar-group)]	2	CT	18	9	Plus	Gossypium_arboreum
	AI726604 Putative ubiquitin carrier protein UBC7 [<i>Oryza sativa</i> (japonica cultivar-group)]	2	CT	18	9	Plus	Gossypium_hirsutum
5	BG446518 Sucrose transporter [<i>Malus domestica</i> (Apple) (<i>Malus sylvestris</i>)]	2	GA	18	9	Plus	Gossypium_arboreum
	TA31646_3635 Putative sucrose carrier [<i>Ricinus communis</i> (Castor bean)]	2	GA	18	9	Plus	Gossypium_hirsutum
6	BF270051	3	AAG	21	7	Plus	Gossypium_arboreum
	TA26991_3635 RNA polymerase II transcriptional coactivator KELP [<i>Arabidopsis thaliana</i> (Mouse-ear cress)]	3	AAG	21	7	Plus	Gossypium_hirsutum
	DR455976	3	AAG	21	7	Plus	Gossypium_hirsutum
7	BQ402652 Eukaryotic translation initiation factor 2 subunit beta [<i>Triticum aestivum</i> (Wheat)]	3	AAG	18	6	Plus	Gossypium_arboreum
	TA28888_3635 Eukaryotic translation initiation factor 2 beta subunit-like [<i>Solanum tuberosum</i> (Potato)]	3	AAG	18	6	Plus	Gossypium_hirsutum
8	BM360670	3	AAG	18	6	Plus	Gossypium_arboreum
	TA41661_3635 Hypothetical protein [<i>Medicago truncatula</i> (Barrel medic)]	3	AAG	18	6	Plus	Gossypium_hirsutum
9	TA8615_29729	3	ACC	18	6	Plus	Gossypium_arboreum
	TA20920_3635 Heavy metal transport/detoxification protein; Harpin-induced 1 [<i>Medicago truncatula</i> (Barrel medic)]	3	ACC	18	6	Plus	Gossypium_hirsutum
10	BG444624	3	AGA	18	6	Plus	Gossypium_arboreum
	TA23448_3635 Adenylate translocator (Brittle-1)-like protein [<i>Arabidopsis thaliana</i> (Mouse-ear cress)]	3	AGA	18	6	Plus	Gossypium_hirsutum
11	BM359324 GRF1-interacting factor 1 [<i>Arabidopsis thaliana</i> (Mouse-ear cress)]	3	CAA	18	6	Plus	Gossypium_arboreum
	DT555999 GRF1-interacting factor 1 [<i>Arabidopsis thaliana</i> (Mouse-ear cress)]	3	CAA	18	6	Plus	Gossypium_hirsutum
12	BQ407429 Similarity to N-acetyltransferase [<i>Arabidopsis thaliana</i> (Mouse-ear cress)]	3	CAC	18	6	Plus	Gossypium_arboreum
	TA20324_3635 Similarity to N-acetyltransferase [<i>Arabidopsis thaliana</i> (Mouse-ear cress)]	3	CAC	18	6	Plus	Gossypium_hirsutum
13	BQ404164 Similarity to N-acetyltransferase [<i>Arabidopsis thaliana</i> (Mouse-ear cress)]	3	CAC	18	6	Plus	Gossypium_arboreum
	TA20324_3635 Similarity to N-acetyltransferase [<i>Arabidopsis thaliana</i> (Mouse-ear cress)]	3	CAC	18	6	Plus	Gossypium_hirsutum

Supplementary Table 3. Contd.

14	BQ410306 Similarity to N-acetyltransferase [Arabidopsis thaliana (Mouse-ear cress)]	3	CAC	18	6	Plus	Gossypium_arboreum
	TA20324_3635 Similarity to N-acetyltransferase [Arabidopsis thaliana (Mouse-ear cress)]	3	CAC	18	6	Plus	Gossypium_hirsutum
15	BQ407414	3	CAC	18	6	Plus	Gossypium_arboreum
	DW242818	3	CAC	18	6	Plus	Gossypium_hirsutum
	DW242818	3	CAC	18	6	Plus	Gossypium_hirsutum
	DW242818	3	CAC	18	6	Plus	Gossypium_hirsutum
16	BF276122	3	CAG	18	6	Plus	Gossypium_arboreum
	DW244622	3	CAG	18	6	Plus	Gossypium_hirsutum
	TA21810_3635	3	CAG	18	6	Plus	Gossypium_hirsutum
	TA21808_3635	3	CAG	18	6	Plus	Gossypium_hirsutum
17	BM359410	3	CAG	18	6	Plus	Gossypium_arboreum
	DW244622	3	CAG	18	6	Plus	Gossypium_hirsutum
	TA21808_3635	3	CAG	18	6	Plus	Gossypium_hirsutum
	TA21810_3635	3	CAG	18	6	Plus	Gossypium_hirsutum
18	BG443126	3	CAG	18	6	Plus	Gossypium_arboreum
	DW244622	3	CAG	18	6	Plus	Gossypium_hirsutum
	TA21808_3635	3	CAG	18	6	Plus	Gossypium_hirsutum
	TA21810_3635	3	CAG	18	6	Plus	Gossypium_hirsutum
19	BQ414418	3	ATG	18	6	Plus	Gossypium_arboreum
	TA41967_3635	3	CAT	18	6	Minus	Gossypium_hirsutum
20	BG445378 Hypothetical protein [Cleome spinosa]	3	CAT	18	6	Plus	Gossypium_arboreum
	DR458947 Hypothetical protein [Cleome spinosa]	3	CAT	18	6	Plus	Gossypium_hirsutum
21	BE053330 Cysteine proteinase [Gossypium hirsutum (Upland cotton)]	3	CAT	18	6	Plus	Gossypium_arboreum
	TA21017_3635 Cysteine proteinase [Gossypium hirsutum (Upland cotton)]	3	CAT	18	6	Plus	Gossypium_hirsutum
22	BQ412920	3	CAT	18	6	Plus	Gossypium_arboreum
	DW514597	3	TGA	18	6	Minus	Gossypium_hirsutum
23	BG442727 Cysteine proteinase [Gossypium hirsutum (Upland cotton)]	3	CAT	18	6	Plus	Gossypium_arboreum
	TA21017_3635 Cysteine proteinase [Gossypium hirsutum (Upland cotton)]	3	CAT	18	6	Plus	Gossypium_hirsutum

Supplementary Table 3. Contd.

24	BQ411009 Hypothetical protein [Cleome spinosa]	3	CAT	18	6	Plus	Gossypium_arboreum
	DR458947 Hypothetical protein [Cleome spinosa]	3	CAT	18	6	Plus	Gossypium_hirsutum
25	BG442903 Cysteine proteinase [Gossypium hirsutum (Upland cotton)]	3	CAT	18	6	Plus	Gossypium_arboreum
	TA21017_3635 Cysteine proteinase [Gossypium hirsutum (Upland cotton)]	3	CAT	18	6	Plus	Gossypium_hirsutum
26	BE052471	3	CAT	18	6	Plus	Gossypium_arboreum
	TA33369_3635	3	CAT	18	6	Plus	Gossypium_hirsutum
27	BQ410999	3	CAT	18	6	Plus	Gossypium_arboreum
	DR453293	3	GAT	18	6	Minus	Gossypium_hirsutum
	DT052017	3	CAT	18	6	Plus	Gossypium_hirsutum
28	BG441669 Cysteine proteinase [Gossypium hirsutum (Upland cotton)]	3	CAT	18	6	Plus	Gossypium_arboreum
	TA21017_3635 Cysteine proteinase [Gossypium hirsutum (Upland cotton)]	3	CAT	18	6	Plus	Gossypium_hirsutum
29	AW726061	3	CAT	18	6	Plus	Gossypium_arboreum
	TA21017_3635 Cysteine proteinase [Gossypium hirsutum (Upland cotton)]	3	CAT	18	6	Plus	Gossypium_hirsutum
30	BQ410319 Elicitor inducible protein [Nicotiana tabacum (Common tobacco)]	3	CAT	18	6	Plus	Gossypium_arboreum
	TA22715_3635 F9F8.20 protein [Arabidopsis thaliana (Mouse-ear cress)]	3	CAT	18	6	Plus	Gossypium_hirsutum
	DW514790	3	CAT	18	6	Plus	Gossypium_hirsutum
31	TA7168_29729 Wound-induced protein 1 [Solanum tuberosum (Potato)]	3	CAT	18	6	Plus	Gossypium_arboreum
	DW514790	3	CAT	18	6	Plus	Gossypium_hirsutum
	TA22715_3635 F9F8.20 protein [Arabidopsis thaliana (Mouse-ear cress)]	3	CAT	18	6	Plus	Gossypium_hirsutum
32	TA5303_29729 Cysteine proteinase [Gossypium hirsutum (Upland cotton)]	3	CAT	18	6	Plus	Gossypium_arboreum
	TA21017_3635 Cysteine proteinase [Gossypium hirsutum (Upland cotton)]	3	CAT	18	6	Plus	Gossypium_hirsutum
33	BQ403789 RAR1 [Arabidopsis thaliana (Mouse-ear cress)]	3	CCA	21	7	Plus	Gossypium_arboreum
	DN800615 RAR1 [Arabidopsis thaliana (Mouse-ear cress)]	3	CCA	21	7	Plus	Gossypium_hirsutum
	TA23709_3635 Putative Rar1 protein [Solanum demissum (Wild potato)]	3	CCA	21	7	Plus	Gossypium_hirsutum
34	BG443488 Putative Rar1 protein [Solanum demissum (Wild potato)]	3	CCA	21	7	Plus	Gossypium_arboreum
	DN800615 RAR1 [Arabidopsis thaliana (Mouse-ear cress)]	3	CCA	21	7	Plus	Gossypium_hirsutum

Supplementary Table 3. Contd.

	TA23709_3635 Putative Rar1 protein [Solanum demissum (Wild potato)]	3	CCA	21	7	Plus	Gossypium_hirsutum
35	BF276058 Putative Rar1 protein [Solanum demissum (Wild potato)]	3	CCA	21	7	Plus	Gossypium_arboreum
	DN800615 RAR1 [Arabidopsis thaliana (Mouse-ear cress)]	3	CCA	21	7	Plus	Gossypium_hirsutum
	TA23709_3635 Putative Rar1 protein [Solanum demissum (Wild potato)]	3	CCA	21	7	Plus	Gossypium_hirsutum
36	BQ406649	3	CCA	18	6	Plus	Gossypium_arboreum
	TA20324_3635 Similarity to N-acetyltransferase [Arabidopsis thaliana (Mouse-ear cress)]	3	CAC	18	6	Plus	Gossypium_hirsutum
37	BE052283 Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:K14A3 [Arabidopsis thaliana (Mouse-ear cress)]	3	CTT	18	6	Plus	Gossypium_arboreum
	DW496704 Hypothetical protein [Brassica oleracea (Wild cabbage)]	3	CTT	18	6	Plus	Gossypium_hirsutum
38	TA7685_29729 Non-green plastid inner envelope membrane protein precursor [Brassica oleracea (Wild cabbage)]	3	CTT	21	7	Plus	Gossypium_arboreum
	TA24688_3635 Putative non-green plastid inner envelope membrane protein [Arabidopsis thaliana (Mouse-ear cress)]	3	CTT	21	7	Plus	Gossypium_hirsutum
39	BE054572 Calnexin [Glycine max (Soybean)]	3	GAA	21	7	Plus	Gossypium_arboreum
	TA22700_3635 Calnexin [Glycine max (Soybean)]	3	GAA	21	7	Plus	Gossypium_hirsutum
40	BG446521 Hypothetical protein T16K5.150 [Arabidopsis thaliana (Mouse-ear cress)]	3	GAC	18	6	Plus	Gossypium_arboreum
	DT546230	3	GAC	18	6	Plus	Gossypium_hirsutum
	TA23939_3635 Predicted protein [Arabidopsis thaliana (Mouse-ear cress)]	3	GAC	18	6	Plus	Gossypium_hirsutum
41	BG446506 Predicted protein [Arabidopsis thaliana (Mouse-ear cress)]	3	GAC	18	6	Plus	Gossypium_arboreum
	DT546230	3	GAC	18	6	Plus	Gossypium_hirsutum
	TA23939_3635 Predicted protein [Arabidopsis thaliana (Mouse-ear cress)]	3	GAC	18	6	Plus	Gossypium_hirsutum
42	BG442800 AT5g64160/MHJ24_14 [Arabidopsis thaliana (Mouse-ear cress)]	3	GAC	18	6	Plus	Gossypium_arboreum
	TA34306_3635 AT5g64160/MHJ24_14 [Arabidopsis thaliana (Mouse-ear cress)]	3	GAC	18	6	Plus	Gossypium_hirsutum
43	BQ401418 Hypothetical protein OJ1288_G09.18 [Oryza sativa (japonica cultivar-group)]	3	GAC	18	6	Plus	Gossypium_arboreum
	TA34306_3635 AT5g64160/MHJ24_14 [Arabidopsis thaliana (Mouse-ear cress)]	3	GAC	18	6	Plus	Gossypium_hirsutum
44	BQ406180 F2D10.15 [Arabidopsis thaliana (Mouse-ear cress)]	3	GAC	18	6	Plus	Gossypium_arboreum
	DT562604 F2D10.15 [Arabidopsis thaliana (Mouse-ear cress)]	3	GAC	18	6	Plus	Gossypium_hirsutum
	TA33154_3635 Hypothetical protein P0489D11.5 [Oryza sativa (japonica cultivar-group)]	3	GAC	18	6	Plus	Gossypium_hirsutum
45	BQ411879	3	GAC	18	6	Plus	Gossypium_arboreum

Supplementary Table 3. Contd.

	TA34306_3635 AT5g64160/MHJ24_14 [Arabidopsis thaliana (Mouse-ear cress)]	3	GAC	18	6	Plus	Gossypium_hirsutum
46	BM359245 Putative tumor differentially expressed protein 1 [Oryza sativa (japonica cultivar-group)]	3	GAG	18	6	Plus	Gossypium_arboreum
	TA22207_3635 T24D18.26 protein [Arabidopsis thaliana (Mouse-ear cress)]	3	GAG	18	6	Plus	Gossypium_hirsutum
47	BQ402314 T24D18.26 protein [Arabidopsis thaliana (Mouse-ear cress)]	3	GAG	18	6	Plus	Gossypium_arboreum
	TA22207_3635 T24D18.26 protein [Arabidopsis thaliana (Mouse-ear cress)]	3	GAG	18	6	Plus	Gossypium_hirsutum
48	CB066413 Putative tumor differentially expressed protein 1 [Oryza sativa (japonica cultivar-group)]	3	GAG	18	6	Plus	Gossypium_arboreum
	TA22207_3635 T24D18.26 protein [Arabidopsis thaliana (Mouse-ear cress)]	3	GAG	18	6	Plus	Gossypium_hirsutum
49	BQ410998	3	GAT	18	6	Plus	Gossypium_arboreum
	DR453293	3	GAT	18	6	Plus	Gossypium_hirsutum
50	BG445086	3	GAT	18	6	Plus	Gossypium_arboreum
	DT555558 Gb AAF36750.1 [Arabidopsis thaliana (Mouse-ear cress)]	3	GAT	18	6	Plus	Gossypium_hirsutum
	TA31218_3635 Gb AAF36750.1 [Arabidopsis thaliana (Mouse-ear cress)]	3	GAT	18	6	Plus	Gossypium_hirsutum
51	BF270416 BZIP protein BZO2H2 [Arabidopsis thaliana (Mouse-ear cress)]	3	GAT	18	6	Plus	Gossypium_arboreum
	TA26195_3635	3	GAT	18	6	Plus	Gossypium_hirsutum
52	BF276904 Putative 7-transmembrane G-protein-coupled receptor [Solanum chacoense (Chaco potato)]	3	GGC	18	6	Plus	Gossypium_arboreum
	TA33755_3635 Putative 7-transmembrane G-protein-coupled receptor [Solanum chacoense (Chaco potato)]	3	GGC	18	6	Plus	Gossypium_hirsutum
53	BG443893	3	GGC	18	6	Plus	Gossypium_arboreum
	TA28715_3635	3	GCC	18	6	Minus	Gossypium_hirsutum
54	BM359726	3	TCT	18	6	Plus	Gossypium_arboreum
	DT460417 Homeodomain protein Hfi22 [Nicotiana tabacum (Common tobacco)]	3	GAA	18	6	Minus	Gossypium_hirsutum
55	TA8283_29729 Hypothetical protein [Medicago truncatula (Barrel medic)]	3	TCT	18	6	Plus	Gossypium_arboreum
	TA32679_3635 Hypothetical protein [Medicago truncatula (Barrel medic)]	3	TCT	18	6	Plus	Gossypium_hirsutum
56	BG442229 Von Willebrand factor, type A; Ubiquitin interacting motif [Medicago truncatula (Barrel medic)]	3	TGC	18	6	Plus	Gossypium_arboreum
	TA22965_3635 Von Willebrand factor, type A; Ubiquitin interacting motif [Medicago truncatula (Barrel medic)]	3	TGC	18	6	Plus	Gossypium_hirsutum
	DT571041 Von Willebrand factor, type A; Ubiquitin interacting motif [Medicago truncatula (Barrel medic)]	3	TGC	18	6	Plus	Gossypium_hirsutum

Supplementary Table 3. Contd.

57	TA5246_29729 Fatty acid elongase [<i>Persea americana</i> (Avocado)]	3	TTC	18	6	Plus	<i>Gossypium_ arboreum</i>
	DN799958 Fatty acid elongase [<i>Persea americana</i> (Avocado)]	3	TTC	18	6	Plus	<i>Gossypium_ hirsutum</i>
	DT466005 Fatty acid elongase [<i>Persea americana</i> (Avocado)]	3	TTC	18	6	Plus	<i>Gossypium_ hirsutum</i>
	TA20571_3635 Putative fatty acid elongase [<i>Zea mays</i> (Maize)]	3	TTC	18	6	Plus	<i>Gossypium_ hirsutum</i>
	TA20576_3635 Putative beta-ketoacyl-CoA synthase [<i>Oryza sativa</i> (<i>japonica</i> cultivar-group)]	3	TTC	18	6	Plus	<i>Gossypium_ hirsutum</i>
58	TA9370_29729 Fatty acid elongase [<i>Persea americana</i> (Avocado)]	3	TTC	18	6	Plus	<i>Gossypium_ arboreum</i>
	DN799958 Fatty acid elongase [<i>Persea americana</i> (Avocado)]	3	TTC	18	6	Plus	<i>Gossypium_ hirsutum</i>
	TA20571_3635 Putative fatty acid elongase [<i>Zea mays</i> (Maize)]	3	TTC	18	6	Plus	<i>Gossypium_ hirsutum</i>
	DT466005 Fatty acid elongase [<i>Persea americana</i> (Avocado)]	3	TTC	18	6	Plus	<i>Gossypium_ hirsutum</i>
	TA20576_3635 Putative beta-ketoacyl-CoA synthase [<i>Oryza sativa</i> (<i>japonica</i> cultivar-group)]	3	TTC	18	6	Plus	<i>Gossypium_ hirsutum</i>
59	BF274447	3	TTG	18	6	Plus	<i>Gossypium_ arboreum</i>
	TA28224_3635 Cyclin-like F-box [<i>Medicago truncatula</i> (Barrel medic)]	3	TTG	18	6	Plus	<i>Gossypium_ hirsutum</i>
	DT573761 Cyclin-like F-box [<i>Medicago truncatula</i> (Barrel medic)]	3	TTG	18	6	Plus	<i>Gossypium_ hirsutum</i>
60	BQ405038 Hypothetical protein T5J17.10 [<i>Arabidopsis thaliana</i> (Mouse-ear cress)]	4	AATT	20	5	Plus	<i>Gossypium_ arboreum</i>
	DW235242	4	AATT	20	5	Plus	<i>Gossypium_ hirsutum</i>
	DV850022 Hypothetical protein [<i>Medicago truncatula</i> (Barrel medic)]	4	AATT	20	5	Plus	<i>Gossypium_ hirsutum</i>
61	BQ407187 Putative 1-aminocyclopropane-1-carboxylate deaminase [<i>Oryza sativa</i> (<i>japonica</i> cultivar-group)]	4	ACAT	36	9	Plus	<i>Gossypium_ arboreum</i>
	TA28634_3635 Putative 1-aminocyclopropane-1-carboxylate deaminase [<i>Oryza sativa</i> (<i>japonica</i> cultivar-group)]	4	ACAT	36	9	Plus	<i>Gossypium_ hirsutum</i>
62	BQ415843 Putative 1-aminocyclopropane-1-carboxylate deaminase [<i>Oryza sativa</i> (<i>japonica</i> cultivar-group)]	4	ACAT	36	9	Plus	<i>Gossypium_ arboreum</i>
	TA28634_3635 Putative 1-aminocyclopropane-1-carboxylate deaminase [<i>Oryza sativa</i> (<i>japonica</i> cultivar-group)]	4	ACAT	36	9	Plus	<i>Gossypium_ hirsutum</i>
63	BQ414500 F11A17.2 protein [<i>Arabidopsis thaliana</i> (Mouse-ear cress)]	4	ACAT	36	9	Plus	<i>Gossypium_ arboreum</i>
	TA28634_3635 Putative 1-aminocyclopropane-1-carboxylate deaminase [<i>Oryza sativa</i> (<i>japonica</i> cultivar-group)]	4	ACAT	36	9	Plus	<i>Gossypium_ hirsutum</i>
64	BF278325 Copper chaperone [<i>Populus alba</i> x <i>Populus tremula</i> var. <i>glandulosa</i>]	4	ATTG	24	6	Plus	<i>Gossypium_ arboreum</i>
	TA28375_3635 Copper chaperone [<i>Populus alba</i> x <i>Populus tremula</i> var. <i>glandulosa</i>]	4	ATTG	24	6	Plus	<i>Gossypium_ hirsutum</i>
	DW499145 Copper chaperone [<i>Populus alba</i> x <i>Populus tremula</i> var. <i>glandulosa</i>]	4	ATTG	24	6	Plus	<i>Gossypium_ hirsutum</i>
65	BM357948 Mitogen-activated protein kinase [<i>Euphorbia esula</i> (Leafy spurge)]	4	TATG	20	5	Plus	<i>Gossypium_ arboreum</i>
	TA23495_3635 Mitogen-activated protein kinase 1 [<i>Lycopersicon esculentum</i> (Tomato)]	4	TATG	20	5	Plus	<i>Gossypium_ hirsutum</i>

Supplementary Table 3. Contd.

66	TA8669_29729 Putative CDP-diacylglycerol--glycerol-3-phosphate 3- phosphatidyltransferase [Arabidopsis thaliana (Mouse-ear cress)]	6	CCTCCA	24	4	Plus	Gossypium_arboreum
	TA31034_3635 Putative CDP-diacylglycerol--glycerol-3-phosphate 3- phosphatidyltransferase [Arabidopsis thaliana (Mouse-ear cress)]	6	CCTCCA	24	4	Plus	Gossypium_hirsutum
67	BF275274 GT-like trihelix DNA-binding protein, putative [Arabidopsis thaliana (Mouse-ear cress)]	6	GAAGAT	24	4	Plus	Gossypium_arboreum
	DR459252	6	GAAGAT	24	4	Plus	Gossypium_hirsutum
68	BG446849 GT-like trihelix DNA-binding protein, putative [Arabidopsis thaliana (Mouse-ear cress)]	6	GAAGAT	24	4	Plus	Gossypium_arboreum
	DR459252	6	GAAGAT	24	4	Plus	Gossypium_hirsutum
69	BG445177	6	GATAGG	24	4	Plus	Gossypium_arboreum
	TA37112_3635 Zinc finger, RING-type; RINGv [Medicago truncatula (Barrel medic)]	6	GATAGG	24	4	Plus	Gossypium_hirsutum
70	BG445815 T5A14.7 protein [Arabidopsis thaliana (Mouse-ear cress)]	6	GATAGG	24	4	Plus	Gossypium_arboreum
	TA37112_3635 Zinc finger, RING-type; RINGv [Medicago truncatula (Barrel medic)]	6	GATAGG	24	4	Plus	Gossypium_hirsutum
71	BM359711 Hypothetical protein T8M16_190 [Arabidopsis thaliana (Mouse-ear cress)]	6	GGAAGA	24	4	Plus	Gossypium_arboreum
	TA34184_3635 RNA-binding protein AKIP1-like [Solanum tuberosum (Potato)]	6	GGAAGA	24	4	Plus	Gossypium_hirsutum
72	BG444556 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	24	4	Plus	Gossypium_arboreum
	TA20231_3635 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	24	4	Plus	Gossypium_hirsutum
	DR044175 Fb35 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	24	4	Plus	Gossypium_hirsutum
	DR044185 Fb35 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	24	4	Plus	Gossypium_hirsutum
	TA20267_3635 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	24	4	Plus	Gossypium_hirsutum
	DR044210 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	24	4	Plus	Gossypium_hirsutum
73	BF279254	6	TGCAAT	24	4	Plus	Gossypium_arboreum
	TA44674_3635 Protein At3g56830 [Arabidopsis thaliana (Mouse-ear cress)]	6	CAATTG	24	4	Plus	Gossypium_hirsutum
74	TA9299_29729 Predicted protein [Populus alba x Populus tremula]	6	TTTTGG	24	4	Plus	Gossypium_arboreum
	TA40993_3635 Predicted protein [Populus alba x Populus tremula]	6	TGTTT	24	4	Plus	Gossypium_hirsutum
Group II							
HG	Sequence ID	Period Size	Period	Rep. Length	Copy Num.	Blast Strand	Species
1	BG441478 Thioredoxin domain-containing protein 9 homolog [Arabidopsis thaliana (Mouse-ear cress)]	2	AC	20	10	Plus	Gossypium_arboreum

Supplementary Table 3. Contd.

	TA29754_3635 Putative ATP binding protein associated with cell differentiation; Protein 1-4 [Oryza sativa (japonica cultivar-group)]	2	AC	18	9	Plus	Gossypium_hirsutum
2	TA6183_29729 Eukaryotic translation initiation factor 3 subunit 12 [Oryza sativa (Rice)]	2	AT	26	13	Plus	Gossypium_arboreum
	TA23639_3635 Eukaryotic translation initiation factor 3 subunit 12 [Oryza sativa (Rice)]	2	AT	24	12	Plus	Gossypium_hirsutum
3	BF272268 OSJNBb0039L24.7 protein [Oryza sativa (japonica cultivar-group)]	2	CT	30	15	Plus	Gossypium_arboreum
	DR458537 Putative LIM domain protein PLIM-2 [Oryza sativa (japonica cultivar-group)]	2	CT	22	11	Plus	Gossypium_hirsutum
	AI054962 Putative LIM domain protein PLIM-2 [Oryza sativa (japonica cultivar-group)]	2	CT	22	11	Plus	Gossypium_hirsutum
4	TA5890_29729 LIM-domain SF3 protein [Nicotiana tabacum (Common tobacco)]	2	CT	30	15	Plus	Gossypium_arboreum
	DR458537 Putative LIM domain protein PLIM-2 [Oryza sativa (japonica cultivar-group)]	2	CT	22	11	Plus	Gossypium_hirsutum
	AI054962 Putative LIM domain protein PLIM-2 [Oryza sativa (japonica cultivar-group)]	2	CT	22	11	Plus	Gossypium_hirsutum
5	BG445759	2	TA	24	12	Plus	Gossypium_arboreum
	DT548108	2	TA	18	9	Plus	Gossypium_hirsutum
6	TA6309_29729 E-class P450, group I [Medicago truncatula (Barrel medic)]	2	TA	28	14	Plus	Gossypium_arboreum
	TA23514_3635 E-class P450, group I [Medicago truncatula (Barrel medic)]	2	TA	26	13	Plus	Gossypium_hirsutum
7	BM359473 F20N2.15 [Arabidopsis thaliana (Mouse-ear cress)]	2	TC	26	13	Plus	Gossypium_arboreum
	DR456327 BTB/POZ; TRAF-like [Medicago truncatula (Barrel medic)]	2	TC	18	9	Plus	Gossypium_hirsutum
8	BG443314 F20N2.15 [Arabidopsis thaliana (Mouse-ear cress)]	2	TC	26	13	Plus	Gossypium_arboreum
	DR456327 BTB/POZ; TRAF-like [Medicago truncatula (Barrel medic)]	2	TC	18	9	Plus	Gossypium_hirsutum
9	BF272117 Gb AAF02129.1 [Arabidopsis thaliana (Mouse-ear cress)]	2	TC	26	13	Plus	Gossypium_arboreum
	DT051614 Gb AAF02129.1 [Arabidopsis thaliana (Mouse-ear cress)]	2	TC	24	12	Plus	Gossypium_hirsutum
10	TA7156_29729 Hypothetical protein [Medicago truncatula (Barrel medic)]	2	TC	28	14	Plus	Gossypium_arboreum
	DN802296	2	CT	20	10	Plus	Gossypium_hirsutum
	TA35543_3635 Hypothetical protein [Medicago truncatula (Barrel medic)]	2	TC	22	11	Plus	Gossypium_hirsutum
11	BG446768 T16O11.17 protein [Arabidopsis thaliana (Mouse-ear cress)]	2	TC	20	10	Plus	Gossypium_arboreum
	TA24594_3635 Hypothetical protein [Medicago truncatula (Barrel medic)]	2	TC	18	9	Plus	Gossypium_hirsutum
12	BF268204	2	TC	28	14	Plus	Gossypium_arboreum

Supplementary Table 3. Contd.

	DN802296	2	CT	20	10	Plus	Gossypium_hirsutum
	TA35543_3635 Hypothetical protein [Medicago truncatula (Barrel medic)]	2	TC	22	11	Plus	Gossypium_hirsutum
13	BE052113	2	CT	26	13	Plus	Gossypium_arboreum
	TA30762_3635 Targeting protein for Xklp2 containing protein, expressed [Oryza sativa (japonica cultivar-group)]	2	TC	22	11	Plus	Gossypium_hirsutum
14	BF272287 Hypothetical protein At3g56480/T5P19_130 [Arabidopsis thaliana (Mouse-ear cress)]	2	TC	26	13	Plus	Gossypium_arboreum
	TA33492_3635 Hypothetical protein At3g56480/T5P19_130 [Arabidopsis thaliana (Mouse-ear cress)]	2	TC	20	10	Plus	Gossypium_hirsutum
	DR044137	2	TC	22	11	Plus	Gossypium_hirsutum
15	BF274071 RNA polymerase II transcriptional coactivator KELP [Arabidopsis thaliana (Mouse-ear cress)]	3	AAG	24	8	Plus	Gossypium_arboreum
	DR455976	3	AAG	21	7	Plus	Gossypium_hirsutum
	TA26990_3635 RNA polymerase II transcriptional coactivator KELP [Arabidopsis thaliana (Mouse-ear cress)]	3	AAG	21	7	Plus	Gossypium_hirsutum
	TA26991_3635 RNA polymerase II transcriptional coactivator KELP [Arabidopsis thaliana (Mouse-ear cress)]	3	AAG	21	7	Plus	Gossypium_hirsutum
16	BF269744 Putative epoxide hydrolase [Arabidopsis thaliana (Mouse-ear cress)]	3	AAT	21	7	Plus	Gossypium_arboreum
	TA41918_3635 Soluble epoxide hydrolase [Citrus jambhiri (rough lemon)]	3	AAT	18	6	Plus	Gossypium_hirsutum
17	TA8375_29729 Sucrose synthase [Gossypium hirsutum (Upland cotton)]	3	ATA	39	13	Plus	Gossypium_arboreum
	TA23143_3635 Sucrose synthase [Gossypium hirsutum (Upland cotton)]	3	ATA	30	10	Plus	Gossypium_hirsutum
18	BQ408202 Hypothetical protein At3g26700/MLJ15_10 [Arabidopsis thaliana (Mouse-ear cress)]	3	ATT	21	7	Plus	Gossypium_arboreum
	DR457741 Protein kinase-like protein [Cicer arietinum (Chickpea) (Garbanzo)]	3	ATT	18	6	Plus	Gossypium_hirsutum
	DT462889 Hypothetical protein At3g26700/MLJ15_10 [Arabidopsis thaliana (Mouse-ear cress)]	3	ATT	21	7	Plus	Gossypium_hirsutum
19	BF269259	3	CAG	21	7	Plus	Gossypium_arboreum
	TA37795_3635	3	TGC	18	6	Minus	Gossypium_hirsutum
20	BF270454 Nascent polypeptide-associated complex NAC; UBA-like [Medicago truncatula (Barrel medic)]	3	GAC	21	7	Plus	Gossypium_arboreum
	AI731240 Nascent polypeptide-associated complex NAC; UBA-like [Medicago truncatula (Barrel medic)]	3	GAC	18	6	Plus	Gossypium_hirsutum
	DR457661 Nascent polypeptide-associated complex subunit alpha-like protein 5 [Arabidopsis thaliana (Mouse-ear cress)]	3	GAC	18	6	Plus	Gossypium_hirsutum
	DN779978	3	GAC	18	6	Plus	Gossypium_hirsutum
	CD485985 Nascent polypeptide-associated complex subunit alpha-like protein 5 [Arabidopsis thaliana (Mouse-ear cress)]	3	GAC	18	6	Plus	Gossypium_hirsutum
	AI730170 Nascent polypeptide-associated complex subunit alpha-like protein 5 [Arabidopsis thaliana (Mouse-ear cress)]	3	GAC	21	7	Plus	Gossypium_hirsutum
	DR044193 Nascent polypeptide-associated complex subunit alpha-like protein 5 [Arabidopsis thaliana (Mouse-ear cress)]	3	GAC	21	7	Plus	Gossypium_hirsutum
	TA22487_3635 Nascent polypeptide-associated complex NAC; UBA-like [Medicago truncatula (Barrel medic)]	3	GAC	21	7	Plus	Gossypium_hirsutum

Supplementary Table 3. Contd.

21	BE053470 Nascent polypeptide associated complex alpha chain [<i>Oryza sativa</i> (japonica cultivar-group)]	3	GAC	21	7	Plus	Gossypium_arboreum
	AI731240 Nascent polypeptide-associated complex NAC; UBA-like [<i>Medicago truncatula</i> (Barrel medic)]	3	GAC	18	6	Plus	Gossypium_hirsutum
	DR457661 Nascent polypeptide-associated complex subunit alpha-like protein 5 [<i>Arabidopsis thaliana</i> (Mouse-ear cress)]	3	GAC	18	6	Plus	Gossypium_hirsutum
	DN779978	3	GAC	18	6	Plus	Gossypium_hirsutum
	CD485985 Nascent polypeptide-associated complex subunit alpha-like protein 5 [<i>Arabidopsis thaliana</i> (Mouse-ear cress)]	3	GAC	18	6	Plus	Gossypium_hirsutum
	AI730170 Nascent polypeptide-associated complex subunit alpha-like protein 5 [<i>Arabidopsis thaliana</i> (Mouse-ear cress)]	3	GAC	21	7	Plus	Gossypium_hirsutum
	DR044193 Nascent polypeptide-associated complex subunit alpha-like protein 5 [<i>Arabidopsis thaliana</i> (Mouse-ear cress)]	3	GAC	21	7	Plus	Gossypium_hirsutum
	TA22487_3635 Nascent polypeptide-associated complex NAC; UBA-like [<i>Medicago truncatula</i> (Barrel medic)]	3	GAC	21	7	Plus	Gossypium_hirsutum
22	BG440543	3	GCC	21	7	Plus	Gossypium_arboreum
	TA27320_3635 F10K1.20 protein [<i>Arabidopsis thaliana</i> (Mouse-ear cress)]	3	GCC	18	6	Plus	Gossypium_hirsutum
23	BM358391 Hypothetical protein P0015C02.10 [<i>Oryza sativa</i> (japonica cultivar-group)]	3	GCC	21	7	Plus	Gossypium_arboreum
	TA27320_3635 F10K1.20 protein [<i>Arabidopsis thaliana</i> (Mouse-ear cress)]	3	GCC	18	6	Plus	Gossypium_hirsutum
24	BG445086	3	GGC	21	7	Plus	Gossypium_arboreum
	DT555558 Gb AAF36750.1 [<i>Arabidopsis thaliana</i> (Mouse-ear cress)]	3	GGC	18	6	Plus	Gossypium_hirsutum
	TA31218_3635 Gb AAF36750.1 [<i>Arabidopsis thaliana</i> (Mouse-ear cress)]	3	GCG	24	8	Plus	Gossypium_hirsutum
25	BQ405592 unknown protein [<i>Arabidopsis thaliana</i>]	3	GTG	21	7	Plus	Gossypium_arboreum
	TA38018_3635 unknown protein [<i>Arabidopsis thaliana</i>]	3	GTG	18	6	Plus	Gossypium_hirsutum
26	BQ415371	3	GTT	24	8	Plus	Gossypium_arboreum
	TA22290_3635 Myb, DNA-binding [<i>Medicago truncatula</i> (Barrel medic)]	3	CAA	21	7	Minus	Gossypium_hirsutum
27	CK640498 Late embryogenesis-like protein [<i>Prunus armeniaca</i> (Apricot)]	3	TGA	24	8	Plus	Gossypium_arboreum
	AJ513319 Late embryogenesis-like protein [<i>Prunus armeniaca</i> (Apricot)]	3	TGA	21	7	Plus	Gossypium_hirsutum
	DT047070	3	TCA	21	7	Minus	Gossypium_hirsutum
	TA20630_3635 Late embryogenesis-like protein [<i>Prunus armeniaca</i> (Apricot)]	3	TGA	21	7	Plus	Gossypium_hirsutum
	DW225975 Late embryogenesis-like protein [<i>Prunus armeniaca</i> (Apricot)]	3	GAT	21	7	Plus	Gossypium_hirsutum
	DW499141 Late embryogenesis-like protein [<i>Prunus armeniaca</i> (Apricot)]	3	TGA	21	7	Plus	Gossypium_hirsutum
	TA42103_3635	3	TGA	24	8	Plus	Gossypium_hirsutum
	CO493420 Late embryogenesis-like protein [<i>Prunus armeniaca</i> (Apricot)]	3	TGA	24	8	Plus	Gossypium_hirsutum
28	TA6371_29729 T7I23.17 protein [<i>Arabidopsis thaliana</i> (Mouse-ear cress)]	3	TTC	30	10	Plus	Gossypium_arboreum
	TA25576_3635 T7I23.17 protein [<i>Arabidopsis thaliana</i> (Mouse-ear cress)]	3	TTC	27	9	Plus	Gossypium_hirsutum

Supplementary Table 3. Contd.

29	BQ402724	3	CAA	21	7	Plus	Gossypium_ arboreum
	AI055346 Helicase, C-terminal [Medicago truncatula (Barrel medic)]	3	CAA	18	6	Plus	Gossypium_hirsutum
	TA27181_3635 DEAD-box ATP-dependent RNA helicase 8 [Arabidopsis thaliana (Mouse-ear cress)]	3	CAA	18	6	Plus	Gossypium_hirsutum
30	TA6708_29729	3	CAG	33	11	Plus	Gossypium_ arboreum
	TA22510_3635	3	CAG	27	9	Plus	Gossypium_hirsutum
31	BQ411825 Phospholipase D delta isoform 1a [Gossypium hirsutum (Upland cotton)]	4	GTAT	40	10	Plus	Gossypium_ arboreum
	TA20281_3635 Phospholipase D delta isoform 1a [Gossypium hirsutum (Upland cotton)]	4	TGTA	28	7	Plus	Gossypium_hirsutum
	TA20264_3635 Phospholipase D delta isoform 1a [Gossypium hirsutum (Upland cotton)]	4	TGTA	40	10	Plus	Gossypium_hirsutum
	TA20247_3635 Phospholipase D delta isoform 1a [Gossypium hirsutum (Upland cotton)]	4	TGTA	40	10	Plus	Gossypium_hirsutum
Group III							
HG	Sequence ID	Period Size	Period	Rep. Length	Copy Num.	Blast Strand	Species
1	TA6910_29729	2	AG	18	9	Plus	Gossypium_ arboreum
	DR462523	2	TC	18	9	Minus	Gossypium_hirsutum
	DT571123	2	TC	24	12	Minus	Gossypium_hirsutum
2	BQ407993	2	AG	18	9	Plus	Gossypium_ arboreum
	DR462523	2	TC	18	9	Minus	Gossypium_hirsutum
	DT571123	2	TC	24	12	Minus	Gossypium_hirsutum
3	TA7299_29729 F6l1.14 protein [Arabidopsis thaliana (Mouse-ear cress)]	2	AT	18	9	Plus	Gossypium_ arboreum
	TA44152_3635 F6l1.14 protein [Arabidopsis thaliana (Mouse-ear cress)]	2	AT	22	11	Plus	Gossypium_hirsutum
4	BF270284 Pentaxin [Medicago truncatula (Barrel medic)]	2	AT	18	9	Plus	Gossypium_ arboreum
	TA44152_3635 F6l1.14 protein [Arabidopsis thaliana (Mouse-ear cress)]	2	AT	22	11	Plus	Gossypium_hirsutum
5	BG440327	2	GA	18	9	Plus	Gossypium_ arboreum
	TA34307_3635 Gb AAC24081.1 [Arabidopsis thaliana (Mouse-ear cress)]	2	AG	30	15	Plus	Gossypium_hirsutum
	DT574307 Gb AAC24081.1 [Arabidopsis thaliana (Mouse-ear cress)]	2	AG	30	15	Plus	Gossypium_hirsutum
6	BG444416	2	TA	18	9	Plus	Gossypium_ arboreum
	TA21656_3635 Snakin-1 [Solanum tuberosum (Potato)]	2	AT	18	9	Plus	Gossypium_hirsutum
	DT049695 Snakin-1 [Solanum tuberosum (Potato)]	2	AT	18	9	Plus	Gossypium_hirsutum

Supplementary Table 3. Contd.

	DT049714 Snakin-1 [Solanum tuberosum (Potato)]	2	AT	18	9	Plus	Gossypium_hirsutum
	DT053439 Snakin-1 [Solanum tuberosum (Potato)]	2	AT	20	10	Plus	Gossypium_hirsutum
	DT053492 Snakin-1 [Solanum tuberosum (Potato)]	2	AT	20	10	Plus	Gossypium_hirsutum
	DT053135 Snakin-1 [Solanum tuberosum (Potato)]	2	AT	20	10	Plus	Gossypium_hirsutum
	DT053298 Snakin-1 [Solanum tuberosum (Potato)]	2	AT	20	10	Plus	Gossypium_hirsutum
7	BE054872 Snakin-1 [Solanum tuberosum (Potato)]	2	TA	18	9	Plus	Gossypium_arboreum
	TA21656_3635 Snakin-1 [Solanum tuberosum (Potato)]	2	AT	18	9	Plus	Gossypium_hirsutum
	DT049695 Snakin-1 [Solanum tuberosum (Potato)]	2	AT	18	9	Plus	Gossypium_hirsutum
	DT049714 Snakin-1 [Solanum tuberosum (Potato)]	2	AT	18	9	Plus	Gossypium_hirsutum
	DT053439 Snakin-1 [Solanum tuberosum (Potato)]	2	AT	20	10	Plus	Gossypium_hirsutum
	DT053492 Snakin-1 [Solanum tuberosum (Potato)]	2	AT	20	10	Plus	Gossypium_hirsutum
	DT053298 Snakin-1 [Solanum tuberosum (Potato)]	2	AT	20	10	Plus	Gossypium_hirsutum
	DT053135 Snakin-1 [Solanum tuberosum (Potato)]	2	AT	20	10	Plus	Gossypium_hirsutum
8	BG444964 Snakin-1 [Solanum tuberosum (Potato)]	2	TA	18	9	Plus	Gossypium_arboreum
	TA21656_3635 Snakin-1 [Solanum tuberosum (Potato)]	2	AT	18	9	Plus	Gossypium_hirsutum
	DT049695 Snakin-1 [Solanum tuberosum (Potato)]	2	AT	18	9	Plus	Gossypium_hirsutum
	DT049714 Snakin-1 [Solanum tuberosum (Potato)]	2	AT	18	9	Plus	Gossypium_hirsutum
	DT053439 Snakin-1 [Solanum tuberosum (Potato)]	2	AT	20	10	Plus	Gossypium_hirsutum
	DT053135 Snakin-1 [Solanum tuberosum (Potato)]	2	AT	20	10	Plus	Gossypium_hirsutum
	DT053298 Snakin-1 [Solanum tuberosum (Potato)]	2	AT	20	10	Plus	Gossypium_hirsutum
	DT053492 Snakin-1 [Solanum tuberosum (Potato)]	2	AT	20	10	Plus	Gossypium_hirsutum
9	BE055619	2	TA	18	9	Plus	Gossypium_arboreum
	TA21656_3635 Snakin-1 [Solanum tuberosum (Potato)]	2	AT	18	9	Plus	Gossypium_hirsutum
	DT049714 Snakin-1 [Solanum tuberosum (Potato)]	2	AT	18	9	Plus	Gossypium_hirsutum
	DT049695 Snakin-1 [Solanum tuberosum (Potato)]	2	AT	18	9	Plus	Gossypium_hirsutum
	DT053298 Snakin-1 [Solanum tuberosum (Potato)]	2	AT	20	10	Plus	Gossypium_hirsutum
	DT053492 Snakin-1 [Solanum tuberosum (Potato)]	2	AT	20	10	Plus	Gossypium_hirsutum
	DT053439 Snakin-1 [Solanum tuberosum (Potato)]	2	AT	20	10	Plus	Gossypium_hirsutum
	DT053135 Snakin-1 [Solanum tuberosum (Potato)]	2	AT	20	10	Plus	Gossypium_hirsutum
10	BG443157 Snakin-1 [Solanum tuberosum (Potato)]	2	TA	18	9	Plus	Gossypium_arboreum
	TA21656_3635 Snakin-1 [Solanum tuberosum (Potato)]	2	AT	18	9	Plus	Gossypium_hirsutum
	DT049695 Snakin-1 [Solanum tuberosum (Potato)]	2	AT	18	9	Plus	Gossypium_hirsutum
	DT049714 Snakin-1 [Solanum tuberosum (Potato)]	2	AT	18	9	Plus	Gossypium_hirsutum
	DT053439 Snakin-1 [Solanum tuberosum (Potato)]	2	AT	20	10	Plus	Gossypium_hirsutum
	DT053298 Snakin-1 [Solanum tuberosum (Potato)]	2	AT	20	10	Plus	Gossypium_hirsutum

Supplementary Table 3. Contd.

	DT053492 Snakin-1 [Solanum tuberosum (Potato)]	2	AT	20	10	Plus	Gossypium_hirsutum
	DT053135 Snakin-1 [Solanum tuberosum (Potato)]	2	AT	20	10	Plus	Gossypium_hirsutum
11	BG441636 Snakin-1 [Solanum tuberosum (Potato)]	2	TA	18	9	Plus	Gossypium_arboreum
	TA21656_3635 Snakin-1 [Solanum tuberosum (Potato)]	2	AT	18	9	Plus	Gossypium_hirsutum
	DT049714 Snakin-1 [Solanum tuberosum (Potato)]	2	AT	18	9	Plus	Gossypium_hirsutum
	DT049695 Snakin-1 [Solanum tuberosum (Potato)]	2	AT	18	9	Plus	Gossypium_hirsutum
	DT053298 Snakin-1 [Solanum tuberosum (Potato)]	2	AT	20	10	Plus	Gossypium_hirsutum
	DT053492 Snakin-1 [Solanum tuberosum (Potato)]	2	AT	20	10	Plus	Gossypium_hirsutum
	DT053439 Snakin-1 [Solanum tuberosum (Potato)]	2	AT	20	10	Plus	Gossypium_hirsutum
	DT053135 Snakin-1 [Solanum tuberosum (Potato)]	2	AT	20	10	Plus	Gossypium_hirsutum
12	TA5092_29729 Snakin-1 [Solanum tuberosum (Potato)]	2	TA	18	9	Plus	Gossypium_arboreum
	TA21656_3635 Snakin-1 [Solanum tuberosum (Potato)]	2	AT	18	9	Plus	Gossypium_hirsutum
	DT049695 Snakin-1 [Solanum tuberosum (Potato)]	2	AT	18	9	Plus	Gossypium_hirsutum
	DT049714 Snakin-1 [Solanum tuberosum (Potato)]	2	AT	18	9	Plus	Gossypium_hirsutum
	DT053439 Snakin-1 [Solanum tuberosum (Potato)]	2	AT	20	10	Plus	Gossypium_hirsutum
	DT053492 Snakin-1 [Solanum tuberosum (Potato)]	2	AT	20	10	Plus	Gossypium_hirsutum
	DT053298 Snakin-1 [Solanum tuberosum (Potato)]	2	AT	20	10	Plus	Gossypium_hirsutum
	DT053135 Snakin-1 [Solanum tuberosum (Potato)]	2	AT	20	10	Plus	Gossypium_hirsutum
13	BQ407767	2	TA	18	9	Plus	Gossypium_arboreum
	DT049714 Snakin-1 [Solanum tuberosum (Potato)]	2	AT	18	9	Plus	Gossypium_hirsutum
	TA21656_3635 Snakin-1 [Solanum tuberosum (Potato)]	2	AT	18	9	Plus	Gossypium_hirsutum
	DT053439 Snakin-1 [Solanum tuberosum (Potato)]	2	AT	20	10	Plus	Gossypium_hirsutum
14	TA7596_29729 Hypothetical protein F12A12.60 [Arabidopsis thaliana (Mouse-ear cress)]	2	TA	18	9	Plus	Gossypium_arboreum
	TA7596_29729 Hypothetical protein F12A12.60 [Arabidopsis thaliana (Mouse-ear cress)]	2	AT	20	10	Plus	Gossypium_arboreum
	DR463781	2	TA	20	10	Plus	Gossypium_hirsutum
	DT456861	2	TA	22	11	Minus	Gossypium_hirsutum
15	TA6055_29729 CAMP response element binding (CREB) protein [Medicago truncatula (Barrel medic)]	2	TA	18	9	Plus	Gossypium_arboreum
	DR463833 CAMP response element binding (CREB) protein [Medicago truncatula (Barrel medic)]	2	TA	22	11	Plus	Gossypium_hirsutum
	DT049066 BZIP transcription factor ATB2 [Glycine max (Soybean)]	2	TA	22	11	Plus	Gossypium_hirsutum
16	BQ412586	2	TA	18	9	Plus	Gossypium_arboreum
	DR463781	2	TA	20	10	Minus	Gossypium_hirsutum

Supplementary Table 3. Contd.

	DT456861	2	TA	22	11	Plus	Gossypium_hirsutum
17	BF270284 Pentaxin [<i>Medicago truncatula</i> (Barrel medic)]	2	TC	18	9	Plus	Gossypium_arboreum
	TA44152_3635 F6I1.14 protein [<i>Arabidopsis thaliana</i> (Mouse-ear cress)]	2	TC	22	11	Plus	Gossypium_hirsutum
18	TA6479_29729 MYB transcription factor [<i>Cucumis sativus</i> (Cucumber)]	3	AAC	18	6	Plus	Gossypium_arboreum
	TA42751_3635	3	AAC	18	6	Plus	Gossypium_hirsutum
	DW008269 MYB transcription factor [<i>Cucumis sativus</i> (Cucumber)]	3	AAC	21	7	Plus	Gossypium_hirsutum
19	TA6818_29729 T1N6.1 protein [<i>Arabidopsis thaliana</i> (Mouse-ear cress)]	3	AAG	21	7	Plus	Gossypium_arboreum
	AI731713 T1N6.1 protein [<i>Arabidopsis thaliana</i> (Mouse-ear cress)]	3	AAG	24	8	Plus	Gossypium_hirsutum
20	BF276199 Putative early nodule-specific-like protein ENOD8 [<i>Oryza sativa</i> (japonica cultivar-group)]	3	AAG	21	7	Plus	Gossypium_arboreum
	TA35757_3635 Putative early nodule-specific-like protein ENOD8 [<i>Oryza sativa</i> (japonica cultivar-group)]	3	AAG	24	8	Plus	Gossypium_hirsutum
21	TA5263_29729 Cytochrome c1, heme protein, mitochondrial precursor [<i>Solanum tuberosum</i> (Potato)]	3	ACC	18	6	Plus	Gossypium_arboreum
	TA24730_3635 Putative ubiquinol-cytochrome-c reductase cytochrome c1 [<i>Oryza sativa</i> (japonica cultivar-group)]	3	ACC	24	8	Plus	Gossypium_hirsutum
22	BE055322	3	AGC	21	7	Plus	Gossypium_arboreum
	TA21426_3635	3	AGC	27	9	Plus	Gossypium_hirsutum
23	BE054201	3	AGC	21	7	Plus	Gossypium_arboreum
	TA21426_3635	3	AGC	27	9	Plus	Gossypium_hirsutum
24	BG441749	3	AGC	21	7	Plus	Gossypium_arboreum
	TA21426_3635	3	AGC	27	9	Plus	Gossypium_hirsutum
25	BM359805	3	AGC	21	7	Plus	Gossypium_arboreum
	TA21426_3635	3	AGC	27	9	Plus	Gossypium_hirsutum
26	BG443578	3	AGC	21	7	Plus	Gossypium_arboreum
	TA21426_3635	3	AGC	27	9	Plus	Gossypium_hirsutum
27	BG443059	3	AGC	21	7	Plus	Gossypium_arboreum
	TA21426_3635	3	AGC	27	9	Plus	Gossypium_hirsutum
28	BG441547	3	AGC	21	7	Plus	Gossypium_arboreum

Supplementary Table 3. Contd.

	TA21426_3635	3	AGC	27	9	Plus	Gossypium_hirsutum
29	BG442685	3	AGC	21	7	Plus	Gossypium_arboreum
	TA21426_3635	3	AGC	27	9	Plus	Gossypium_hirsutum
30	TA5416_29729	3	AGC	21	7	Plus	Gossypium_arboreum
	TA21426_3635	3	AGC	27	9	Plus	Gossypium_hirsutum
31	BF270534	3	CAC	18	6	Plus	Gossypium_arboreum
	DT050816	3	TGG	21	7	Minus	Gossypium_hirsutum
32	BG446140	3	CAG	18	6	Plus	Gossypium_arboreum
	TA21426_3635	3	AGC	27	9	Plus	Gossypium_hirsutum
33	BE055500 MYC2 [Catharanthus roseus (Rosy periwinkle) (Madagascar periwinkle)]	3	CTC	18	6	Plus	Gossypium_arboreum
	TA21503_3635	3	CTC	21	7	Plus	Gossypium_hirsutum
34	BF276934 Hypothetical protein At2g44300 [Arabidopsis thaliana (Mouse-ear cress)]	3	CTG	18	6	Plus	Gossypium_arboreum
	DR462320 Hypothetical protein At2g44300 [Arabidopsis thaliana (Mouse-ear cress)]	3	CTG	21	7	Plus	Gossypium_hirsutum
35	BF275766 T7123.17 protein [Arabidopsis thaliana (Mouse-ear cress)]	3	CTT	24	8	Plus	Gossypium_arboreum
	TA25576_3635 T7123.17 protein [Arabidopsis thaliana (Mouse-ear cress)]	3	TTC	27	9	Plus	Gossypium_hirsutum
36	BQ405354 Ultraviolet-B-repressible protein [Gossypium hirsutum (Upland cotton)]	3	CTT	21	7	Plus	Gossypium_arboreum
	TA39593_3635 Ultraviolet-B-repressible protein [Gossypium hirsutum (Upland cotton)]	3	CTT	24	8	Plus	Gossypium_hirsutum
37	BF270826 Hypothetical protein T20N10_200 [Arabidopsis thaliana (Mouse-ear cress)]	3	GAA	21	7	Plus	Gossypium_arboreum
	DW476508	3	TCT	21	7	Minus	Gossypium_hirsutum
	DW476507	3	GAA	21	7	Plus	Gossypium_hirsutum
	TA28486_3635 Hypothetical protein T20N10_200 [Arabidopsis thaliana (Mouse-ear cress)]	3	AGA	39	13	Plus	Gossypium_hirsutum
38	BQ407920 Auxin and ethylene responsive GH3-like protein [Capsicum chinense (Scotch bonnet) (Bonnet pepper)]	3	GAT	18	6	Plus	Gossypium_arboreum
	DW505072 Auxin and ethylene responsive GH3-like protein [Capsicum chinense (Scotch bonnet) (Bonnet pepper)]	3	GAT	18	6	Plus	Gossypium_hirsutum
	DT054325 Probable indole-3-acetic acid-amido synthetase GH3.1 [Arabidopsis thaliana (Mouse-ear cress)]	3	GAT	21	7	Plus	Gossypium_hirsutum
	TA21526_3635 Nt-gh3 deduced protein [Nicotiana tabacum (Common tobacco)]	3	GAT	21	7	Plus	Gossypium_hirsutum
39	TA7199_29729 Auxin and ethylene responsive GH3-like protein [Capsicum chinense (Scotch bonnet) (Bonnet pepper)]	3	GAT	18	6	Plus	Gossypium_arboreum

Supplementary Table 3. Contd.

	DW505072 Auxin and ethylene responsive GH3-like protein [<i>Capsicum chinense</i> (Scotch bonnet) (Bonnet pepper)]	3	GAT	18	6	Plus	<i>Gossypium_hirsutum</i>
	DT054325 Probable indole-3-acetic acid-amido synthetase GH3.1 [<i>Arabidopsis thaliana</i> (Mouse-ear cress)]	3	GAT	21	7	Plus	<i>Gossypium_hirsutum</i>
	TA21526_3635 Nt-gh3 deduced protein [<i>Nicotiana tabacum</i> (Common tobacco)]	3	GAT	21	7	Plus	<i>Gossypium_hirsutum</i>
40	TA8195_29729 Phospho-2-dehydro-3-deoxyheptonate aldolase 2, chloroplast precursor [<i>Arabidopsis thaliana</i> (Mouse-ear cress)]	3	GCG	18	6	Plus	<i>Gossypium_arboreum</i>
	TA32414_3635 Phospho-2-dehydro-3-deoxyheptonate aldolase 2, chloroplast precursor [<i>Arabidopsis thaliana</i> (Mouse-ear cress)]	3	GCG	24	8	Plus	<i>Gossypium_hirsutum</i>
41	BM359886 Cleft lip and palate associated transmembrane protein-like [<i>Arabidopsis thaliana</i> (Mouse-ear cress)]	3	GGA	21	7	Plus	<i>Gossypium_arboreum</i>
	TA28051_3635 Cleft lip and palate associated transmembrane protein-like [<i>Arabidopsis thaliana</i> (Mouse-ear cress)]	3	GGA	24	8	Plus	<i>Gossypium_hirsutum</i>
	DT559190 Cleft lip and palate associated transmembrane protein-like [<i>Arabidopsis thaliana</i> (Mouse-ear cress)]	3	GGA	27	9	Plus	<i>Gossypium_hirsutum</i>
42	BF278307 Putative RING zinc finger protein-like protein [<i>Thellungiella halophila</i> (Salt cress)]	3	TCA	21	7	Plus	<i>Gossypium_arboreum</i>
	TA23903_3635 RING-H2 finger protein [<i>Poncirus trifoliata</i> (Hardy orange)]	3	TCA	24	8	Plus	<i>Gossypium_hirsutum</i>
43	BQ404554 Copper/zinc superoxide dismutase, putative [<i>Medicago truncatula</i> (Barrel medic)]	3	TCT	18	6	Plus	<i>Gossypium_arboreum</i>
	DT567072 Cu/Zn-superoxide dismutase copper chaperone precursor [<i>Glycine max</i> (Soybean)]	3	TCT	18	6	Plus	<i>Gossypium_hirsutum</i>
	TA23380_3635 Cu/Zn-superoxide dismutase copper chaperone precursor [<i>Glycine max</i> (Soybean)]	3	TCT	21	7	Plus	<i>Gossypium_hirsutum</i>
44	BG444426	3	TCT	24	8	Plus	<i>Gossypium_arboreum</i>
	TA21780_3635 At5g06390 [<i>Arabidopsis thaliana</i> (Mouse-ear cress)]	3	TCT	27	9	Plus	<i>Gossypium_hirsutum</i>
	DR044171 Gb AAF02137.1 [<i>Arabidopsis thaliana</i> (Mouse-ear cress)]	3	TCT	27	9	Plus	<i>Gossypium_hirsutum</i>
	TA21781_3635 Gb AAF02137.1 [<i>Arabidopsis thaliana</i> (Mouse-ear cress)]	3	TCT	27	9	Plus	<i>Gossypium_hirsutum</i>
45	TA5514_29729 Salt tolerance protein [<i>Sesuvium portulacastrum</i> (Shoreline sea purslane)]	3	TGA	18	6	Plus	<i>Gossypium_arboreum</i>
	AJ513319 Late embryogenesis-like protein [<i>Prunus armeniaca</i> (Apricot)]	3	TGA	21	7	Plus	<i>Gossypium_hirsutum</i>
	DW225975 Late embryogenesis-like protein [<i>Prunus armeniaca</i> (Apricot)]	3	GAT	21	7	Plus	<i>Gossypium_hirsutum</i>
	TA20630_3635 Late embryogenesis-like protein [<i>Prunus armeniaca</i> (Apricot)]	3	TGA	21	7	Plus	<i>Gossypium_hirsutum</i>
	DW499141 Late embryogenesis-like protein [<i>Prunus armeniaca</i> (Apricot)]	3	TGA	21	7	Plus	<i>Gossypium_hirsutum</i>
	DT047070	3	TCA	21	7	Minus	<i>Gossypium_hirsutum</i>
	CO493420 Late embryogenesis-like protein [<i>Prunus armeniaca</i> (Apricot)]	3	TGA	24	8	Plus	<i>Gossypium_hirsutum</i>
46	BQ410493 Late embryogenesis-like protein [<i>Prunus armeniaca</i> (Apricot)]	3	TGA	18	6	Plus	<i>Gossypium_arboreum</i>
	TA42103_3635	3	TGA	24	8	Plus	<i>Gossypium_hirsutum</i>
47	TA5823_29729 Histone deacetylase 2a [<i>Solanum chacoense</i> (Chaco potato)]	3	TGC	18	6	Plus	<i>Gossypium_arboreum</i>
	TA22749_3635	3	TGC	18	6	Plus	<i>Gossypium_hirsutum</i>

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	DW514526 Histone deacetylase 2a [Solanum chacoense (Chaco potato)]	3	TGC	18	6	Plus	Gossypium_hirsutum
	TA22748_3635	3	TGC	18	6	Plus	Gossypium_hirsutum
	TA22750_3635 Histone deacetylase 2a [Solanum chacoense (Chaco potato)]	3	GCT	21	7	Plus	Gossypium_hirsutum
48	BF270691 Histone deacetylase 2a [Solanum chacoense (Chaco potato)]	3	TGC	18	6	Plus	Gossypium_arboreum
	TA22749_3635	3	TGC	18	6	Plus	Gossypium_hirsutum
	DW514526 Histone deacetylase 2a [Solanum chacoense (Chaco potato)]	3	TGC	18	6	Plus	Gossypium_hirsutum
	TA22748_3635	3	TGC	18	6	Plus	Gossypium_hirsutum
	TA22750_3635 Histone deacetylase 2a [Solanum chacoense (Chaco potato)]	3	GCT	21	7	Plus	Gossypium_hirsutum
49	TA5985_29729 Protein At3g63460 [Arabidopsis thaliana (Mouse-ear cress)]	3	TTA	18	6	Plus	Gossypium_arboreum
	TA26634_3635	3	TAA	18	6	Minus	Gossypium_hirsutum
	TA26636_3635	3	ATA	21	7	Minus	Gossypium_hirsutum
	TA26635_3635 Protein At3g63460 [Arabidopsis thaliana (Mouse-ear cress)]	3	TTA	21	7	Plus	Gossypium_hirsutum
50	TA7048_29729 Hypothetical protein [Medicago truncatula (Barrel medic)]	3	TTC	21	7	Plus	Gossypium_arboreum
	DR459816 Hypothetical protein [Medicago truncatula (Barrel medic)]	3	TTC	27	9	Plus	Gossypium_hirsutum
	TA26423_3635 Hypothetical protein [Medicago truncatula (Barrel medic)]	3	TTC	27	9	Plus	Gossypium_hirsutum
51	BQ404857 Hypothetical protein [Medicago truncatula (Barrel medic)]	3	TTC	21	7	Plus	Gossypium_arboreum
	DR459816 Hypothetical protein [Medicago truncatula (Barrel medic)]	3	TTC	27	9	Plus	Gossypium_hirsutum
	TA26423_3635 Hypothetical protein [Medicago truncatula (Barrel medic)]	3	TTC	27	9	Plus	Gossypium_hirsutum
52	TA6604_29729	4	ATTT	20	5	Plus	Gossypium_arboreum
	TA33749_3635 Rapid alkalization factor 2 [Solanum chacoense (Chaco potato)]	4	ATTT	20	5	Plus	Gossypium_hirsutum
	DT559940 Rapid alkalization factor 2 [Solanum chacoense (Chaco potato)]	4	ATTT	24	6	Plus	Gossypium_hirsutum
53	BF268634 Rapid alkalization factor 2 [Solanum chacoense (Chaco potato)]	4	ATTT	20	5	Plus	Gossypium_arboreum
	TA33749_3635 Rapid alkalization factor 2 [Solanum chacoense (Chaco potato)]	4	ATTT	20	5	Plus	Gossypium_hirsutum
	DT559940 Rapid alkalization factor 2 [Solanum chacoense (Chaco potato)]	4	ATTT	24	6	Plus	Gossypium_hirsutum
54	BG439886 Hypothetical protein [Medicago truncatula (Barrel medic)]	4	TGTA	20	5	Plus	Gossypium_arboreum
	TA31088_3635 Hypothetical protein [Medicago truncatula (Barrel medic)]	4	TGTA	24	6	Plus	Gossypium_hirsutum
55	BF272588 1-aminocyclopropane-1-carboxylate synthase [Momordica charantia (Bitter gourd) (Balsam pear)]	4	TTCT	20	5	Plus	Gossypium_arboreum
	TA23441_3635 1-aminocyclopropane-1-carboxylate synthase ACS6 [Gossypium hirsutum (Upland cotton)]	4	TTCT	24	6	Plus	Gossypium_hirsutum

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56	BQ402637 Hypothetical protein F7A10.9 [Arabidopsis thaliana (Mouse-ear cress)]	4	TTTG	20	5	Plus	Gossypium_arboreum
	DW496475 Hypothetical protein F7A10.9 [Arabidopsis thaliana (Mouse-ear cress)]	4	TTTG	24	6	Plus	Gossypium_hirsutum
	TA29538_3635 Hypothetical protein F7A10.9 [Arabidopsis thaliana (Mouse-ear cress)]	4	TTTG	24	6	Plus	Gossypium_hirsutum
57	BQ408211 Protein At5g14170 [Arabidopsis thaliana (Mouse-ear cress)]	6	AAGCTC	24	4	Plus	Gossypium_arboreum
	DR453420	6	AAGCTC	30	5	Plus	Gossypium_hirsutum
58	BG440787 YT521-B-like protein [Medicago truncatula (Barrel medic)]	6	AAGGCA	30	5	Plus	Gossypium_arboreum
	DT554707 YT521-B-like protein [Medicago truncatula (Barrel medic)]	6	AAGGCA	36	6	Plus	Gossypium_hirsutum
59	BE054108	6	CCCCAA	24	4	Plus	Gossypium_arboreum
	TA25871_3635	6	CCCCAA	36	6	Plus	Gossypium_hirsutum
60	TA6665_29729	6	CCCCAA	24	4	Plus	Gossypium_arboreum
	TA25871_3635	6	CCCCAA	36	6	Plus	Gossypium_hirsutum
	TA25870_3635	6	ACCCCA	48	8	Plus	Gossypium_hirsutum
61	BG444093 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	24	4	Plus	Gossypium_arboreum
	TA20267_3635 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	24	4	Plus	Gossypium_hirsutum
	TA20221_3635 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	24	4	Plus	Gossypium_hirsutum
	TA20231_3635 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	24	4	Plus	Gossypium_hirsutum
	DR044175 Fb35 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	24	4	Plus	Gossypium_hirsutum
	DR044185 Fb35 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	24	4	Plus	Gossypium_hirsutum
	DR044205 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	30	5	Plus	Gossypium_hirsutum
	CO499609 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	30	5	Plus	Gossypium_hirsutum
	TA20273_3635 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	30	5	Plus	Gossypium_hirsutum
	DT569706 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	30	5	Plus	Gossypium_hirsutum
62	BG444468 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	24	4	Plus	Gossypium_arboreum
	DR044210 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	24	4	Plus	Gossypium_hirsutum
	DR044175 Fb35 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	24	4	Plus	Gossypium_hirsutum
	TA20221_3635 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	24	4	Plus	Gossypium_hirsutum
	TA20231_3635 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	24	4	Plus	Gossypium_hirsutum
	TA20267_3635 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	24	4	Plus	Gossypium_hirsutum
	DT569706 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	30	5	Plus	Gossypium_hirsutum
	CO499609 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	30	5	Plus	Gossypium_hirsutum
	DR044205 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	30	5	Plus	Gossypium_hirsutum

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	TA20273_3635 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	30	5	Plus	Gossypium_hirsutum
63	BG444074 At5g57100 [Arabidopsis thaliana (Mouse-ear cress)]	6	TCAGGC	24	4	Plus	Gossypium_arboreum
	DT571165 At5g57100 [Arabidopsis thaliana (Mouse-ear cress)]	6	CAGGCT	30	5	Plus	Gossypium_hirsutum
64	BG443843 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	24	4	Plus	Gossypium_arboreum
	DR044210 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	24	4	Plus	Gossypium_hirsutum
	TA20221_3635 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	24	4	Plus	Gossypium_hirsutum
	TA20231_3635 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	24	4	Plus	Gossypium_hirsutum
	TA20267_3635 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	24	4	Plus	Gossypium_hirsutum
	DR044175 Fb35 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	24	4	Plus	Gossypium_hirsutum
	DR044205 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	30	5	Plus	Gossypium_hirsutum
	CO499609 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	30	5	Plus	Gossypium_hirsutum
	DT569706 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	30	5	Plus	Gossypium_hirsutum
	TA20273_3635 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	30	5	Plus	Gossypium_hirsutum
65	BG443923 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	24	4	Plus	Gossypium_arboreum
	TA20267_3635 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	24	4	Plus	Gossypium_hirsutum
	TA20221_3635 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	24	4	Plus	Gossypium_hirsutum
	TA20231_3635 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	24	4	Plus	Gossypium_hirsutum
	DR044175 Fb35 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	24	4	Plus	Gossypium_hirsutum
	DR044185 Fb35 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	24	4	Plus	Gossypium_hirsutum
	DR044205 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	30	5	Plus	Gossypium_hirsutum
	CO499609 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	30	5	Plus	Gossypium_hirsutum
	TA20273_3635 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	30	5	Plus	Gossypium_hirsutum
	DT569706 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	30	5	Plus	Gossypium_hirsutum
66	BG444500 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	24	4	Plus	Gossypium_arboreum
	DR044210 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	24	4	Plus	Gossypium_hirsutum
	DR044175 Fb35 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	24	4	Plus	Gossypium_hirsutum
	TA20221_3635 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	24	4	Plus	Gossypium_hirsutum
	TA20231_3635 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	24	4	Plus	Gossypium_hirsutum
	TA20267_3635 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	24	4	Plus	Gossypium_hirsutum
	TA20273_3635 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	30	5	Plus	Gossypium_hirsutum
	CO499609 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	30	5	Plus	Gossypium_hirsutum
	DR044205 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	30	5	Plus	Gossypium_hirsutum
	DT569706 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	30	5	Plus	Gossypium_hirsutum

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67	BG445128 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	24	4	Plus	Gossypium_arboreum
	DR044210 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	24	4	Plus	Gossypium_hirsutum
	DR044175 Fb35 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	24	4	Plus	Gossypium_hirsutum
	TA20221_3635 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	24	4	Plus	Gossypium_hirsutum
	TA20231_3635 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	24	4	Plus	Gossypium_hirsutum
	TA20267_3635 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	24	4	Plus	Gossypium_hirsutum
	DT569706 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	30	5	Plus	Gossypium_hirsutum
	DR044205 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	30	5	Plus	Gossypium_hirsutum
	CO499609 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	30	5	Plus	Gossypium_hirsutum
	TA20273_3635 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	30	5	Plus	Gossypium_hirsutum
68	BG445281 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	24	4	Plus	Gossypium_arboreum
	TA20221_3635 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	24	4	Plus	Gossypium_hirsutum
	DR044185 Fb35 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	24	4	Plus	Gossypium_hirsutum
	TA20231_3635 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	24	4	Plus	Gossypium_hirsutum
	DR044210 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	24	4	Plus	Gossypium_hirsutum
	TA20267_3635 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	24	4	Plus	Gossypium_hirsutum
	TA20273_3635 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	30	5	Plus	Gossypium_hirsutum
	CO499609 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	30	5	Plus	Gossypium_hirsutum
	DR044205 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	30	5	Plus	Gossypium_hirsutum
	DT569706 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	30	5	Plus	Gossypium_hirsutum
69	BG446067 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	24	4	Plus	Gossypium_arboreum
	DR044210 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	24	4	Plus	Gossypium_hirsutum
	TA20221_3635 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	24	4	Plus	Gossypium_hirsutum
	TA20231_3635 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	24	4	Plus	Gossypium_hirsutum
	TA20267_3635 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	24	4	Plus	Gossypium_hirsutum
	DR044175 Fb35 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	24	4	Plus	Gossypium_hirsutum
	DR044205 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	30	5	Plus	Gossypium_hirsutum
	CO499609 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	30	5	Plus	Gossypium_hirsutum
	DT569706 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	30	5	Plus	Gossypium_hirsutum
	TA20273_3635 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	30	5	Plus	Gossypium_hirsutum
70	BG443565 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	24	4	Plus	Gossypium_arboreum
	TA20267_3635 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	24	4	Plus	Gossypium_hirsutum
	TA20231_3635 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	24	4	Plus	Gossypium_hirsutum

Supplementary Table 3. Contd.

	DR044175 Fb35 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	24	4	Plus	Gossypium_hirsutum
	TA20221_3635 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	24	4	Plus	Gossypium_hirsutum
	CO499609 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	30	5	Plus	Gossypium_hirsutum
	DR044205 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	30	5	Plus	Gossypium_hirsutum
	DT569706 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	30	5	Plus	Gossypium_hirsutum
	TA20273_3635 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	30	5	Plus	Gossypium_hirsutum
71	BG445036 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	24	4	Plus	Gossypium_arboreum
	TA20221_3635 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	24	4	Plus	Gossypium_hirsutum
	DR044175 Fb35 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	24	4	Plus	Gossypium_hirsutum
	TA20231_3635 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	24	4	Plus	Gossypium_hirsutum
	DR044210 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	24	4	Plus	Gossypium_hirsutum
	TA20267_3635 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	24	4	Plus	Gossypium_hirsutum
	DT569706 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	30	5	Plus	Gossypium_hirsutum
	CO499609 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	30	5	Plus	Gossypium_hirsutum
	DR044205 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	30	5	Plus	Gossypium_hirsutum
	TA20273_3635 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	30	5	Plus	Gossypium_hirsutum
72	BG444921 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	24	4	Plus	Gossypium_arboreum
	DR044210 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	24	4	Plus	Gossypium_hirsutum
	DR044175 Fb35 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	24	4	Plus	Gossypium_hirsutum
	TA20221_3635 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	24	4	Plus	Gossypium_hirsutum
	TA20231_3635 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	24	4	Plus	Gossypium_hirsutum
	TA20267_3635 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	24	4	Plus	Gossypium_hirsutum
	DT569706 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	30	5	Plus	Gossypium_hirsutum
	DR044205 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	30	5	Plus	Gossypium_hirsutum
	CO499609 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	30	5	Plus	Gossypium_hirsutum
	TA20273_3635 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	30	5	Plus	Gossypium_hirsutum
73	BG444937 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	24	4	Plus	Gossypium_arboreum
	DR044210 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	24	4	Plus	Gossypium_hirsutum
	DR044175 Fb35 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	24	4	Plus	Gossypium_hirsutum
	TA20221_3635 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	24	4	Plus	Gossypium_hirsutum
	TA20231_3635 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	24	4	Plus	Gossypium_hirsutum
	TA20267_3635 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	24	4	Plus	Gossypium_hirsutum
	DT569706 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	30	5	Plus	Gossypium_hirsutum
	CO499609 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	30	5	Plus	Gossypium_hirsutum

Supplementary Table 3. Contd.

	DR044205 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	30	5	Plus	Gossypium_hirsutum
	TA20273_3635 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	30	5	Plus	Gossypium_hirsutum
74	BG440521 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	24	4	Plus	Gossypium_arboreum
	DR044210 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	24	4	Plus	Gossypium_hirsutum
	DR044175 Fb35 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	24	4	Plus	Gossypium_hirsutum
	TA20221_3635 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	24	4	Plus	Gossypium_hirsutum
	TA20231_3635 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	24	4	Plus	Gossypium_hirsutum
	TA20267_3635 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	24	4	Plus	Gossypium_hirsutum
	DT569706 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	30	5	Plus	Gossypium_hirsutum
	CO499609 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	30	5	Plus	Gossypium_hirsutum
	DR044205 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	30	5	Plus	Gossypium_hirsutum
	TA20273_3635 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	30	5	Plus	Gossypium_hirsutum
75	BE054522 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	24	4	Plus	Gossypium_arboreum
	DR044210 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	24	4	Plus	Gossypium_hirsutum
	DR044175 Fb35 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	24	4	Plus	Gossypium_hirsutum
	TA20221_3635 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	24	4	Plus	Gossypium_hirsutum
	TA20231_3635 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	24	4	Plus	Gossypium_hirsutum
	TA20267_3635 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	24	4	Plus	Gossypium_hirsutum
	DT569706 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	30	5	Plus	Gossypium_hirsutum
	DR044205 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	30	5	Plus	Gossypium_hirsutum
	CO499609 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	30	5	Plus	Gossypium_hirsutum
	TA20273_3635 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	30	5	Plus	Gossypium_hirsutum
76	BE054651 E6-1 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	24	4	Plus	Gossypium_arboreum
	DR044210 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	24	4	Plus	Gossypium_hirsutum
	TA20221_3635 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	24	4	Plus	Gossypium_hirsutum
	TA20231_3635 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	24	4	Plus	Gossypium_hirsutum
	TA20267_3635 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	24	4	Plus	Gossypium_hirsutum
	DR044175 Fb35 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	24	4	Plus	Gossypium_hirsutum
	DR044205 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	30	5	Plus	Gossypium_hirsutum
	CO499609 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	30	5	Plus	Gossypium_hirsutum
	DT569706 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	30	5	Plus	Gossypium_hirsutum
	TA20273_3635 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	30	5	Plus	Gossypium_hirsutum
77	BE054976 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	24	4	Plus	Gossypium_arboreum

Supplementary Table 3. Contd.

	DR044210 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	24	4	Plus	Gossypium_hirsutum
	DR044175 Fb35 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	24	4	Plus	Gossypium_hirsutum
	TA20221_3635 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	24	4	Plus	Gossypium_hirsutum
	TA20231_3635 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	24	4	Plus	Gossypium_hirsutum
	TA20267_3635 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	24	4	Plus	Gossypium_hirsutum
	TA20273_3635 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	30	5	Plus	Gossypium_hirsutum
	CO499609 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	30	5	Plus	Gossypium_hirsutum
	DR044205 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	30	5	Plus	Gossypium_hirsutum
	DT569706 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	30	5	Plus	Gossypium_hirsutum
78	BE054144 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	24	4	Plus	Gossypium_arboreum
	DR044210 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	24	4	Plus	Gossypium_hirsutum
	DR044175 Fb35 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	24	4	Plus	Gossypium_hirsutum
	TA20221_3635 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	24	4	Plus	Gossypium_hirsutum
	TA20231_3635 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	24	4	Plus	Gossypium_hirsutum
	TA20267_3635 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	24	4	Plus	Gossypium_hirsutum
	DT569706 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	30	5	Plus	Gossypium_hirsutum
	DR044205 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	30	5	Plus	Gossypium_hirsutum
	CO499609 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	30	5	Plus	Gossypium_hirsutum
	TA20273_3635 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	30	5	Plus	Gossypium_hirsutum
79	BE053966 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	24	4	Plus	Gossypium_arboreum
	DR044210 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	24	4	Plus	Gossypium_hirsutum
	TA20221_3635 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	24	4	Plus	Gossypium_hirsutum
	TA20267_3635 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	24	4	Plus	Gossypium_hirsutum
	DR044175 Fb35 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	24	4	Plus	Gossypium_hirsutum
	TA20231_3635 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	24	4	Plus	Gossypium_hirsutum
	DR044205 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	30	5	Plus	Gossypium_hirsutum
	DT569706 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	30	5	Plus	Gossypium_hirsutum
	CO499609 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	30	5	Plus	Gossypium_hirsutum
	TA20273_3635 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	30	5	Plus	Gossypium_hirsutum
80	BE052527 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	24	4	Plus	Gossypium_arboreum
	DR044210 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	24	4	Plus	Gossypium_hirsutum
	DR044175 Fb35 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	24	4	Plus	Gossypium_hirsutum
	TA20221_3635 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	24	4	Plus	Gossypium_hirsutum
	TA20231_3635 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	24	4	Plus	Gossypium_hirsutum

Supplementary Table 3. Contd.

	TA20267_3635 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	24	4	Plus	Gossypium_hirsutum
	TA20273_3635 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	30	5	Plus	Gossypium_hirsutum
	CO499609 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	30	5	Plus	Gossypium_hirsutum
	DT569706 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	30	5	Plus	Gossypium_hirsutum
	DR044205 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	30	5	Plus	Gossypium_hirsutum
81	BE053587 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	24	4	Plus	Gossypium_arboreum
	TA20267_3635 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	24	4	Plus	Gossypium_hirsutum
	TA20221_3635 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	24	4	Plus	Gossypium_hirsutum
	TA20231_3635 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	24	4	Plus	Gossypium_hirsutum
	DR044175 Fb35 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	24	4	Plus	Gossypium_hirsutum
	DR044185 Fb35 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	24	4	Plus	Gossypium_hirsutum
	DR044205 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	30	5	Plus	Gossypium_hirsutum
	CO499609 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	30	5	Plus	Gossypium_hirsutum
	DT569706 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	30	5	Plus	Gossypium_hirsutum
	TA20273_3635 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	30	5	Plus	Gossypium_hirsutum
82	BE053730 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	24	4	Plus	Gossypium_arboreum
	DR044210 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	24	4	Plus	Gossypium_hirsutum
	DR044175 Fb35 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	24	4	Plus	Gossypium_hirsutum
	TA20221_3635 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	24	4	Plus	Gossypium_hirsutum
	TA20231_3635 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	24	4	Plus	Gossypium_hirsutum
	TA20267_3635 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	24	4	Plus	Gossypium_hirsutum
	DT569706 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	30	5	Plus	Gossypium_hirsutum
	DR044205 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	30	5	Plus	Gossypium_hirsutum
	CO499609 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	30	5	Plus	Gossypium_hirsutum
	TA20273_3635 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	30	5	Plus	Gossypium_hirsutum
83	BG442797 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	24	4	Plus	Gossypium_arboreum
	TA20267_3635 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	24	4	Plus	Gossypium_hirsutum
	TA20221_3635 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	24	4	Plus	Gossypium_hirsutum
	TA20231_3635 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	24	4	Plus	Gossypium_hirsutum
	DR044175 Fb35 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	24	4	Plus	Gossypium_hirsutum
	DR044185 Fb35 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	24	4	Plus	Gossypium_hirsutum
	DR044205 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	30	5	Plus	Gossypium_hirsutum
	CO499609 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	30	5	Plus	Gossypium_hirsutum
	DT569706 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	30	5	Plus	Gossypium_hirsutum

Supplementary Table 3. Contd.

	TA20273_3635 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	30	5	Plus	Gossypium_hirsutum
84	BE055230 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	24	4	Plus	Gossypium_arboreum
	DR044210 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	24	4	Plus	Gossypium_hirsutum
	DR044175 Fb35 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	24	4	Plus	Gossypium_hirsutum
	TA20221_3635 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	24	4	Plus	Gossypium_hirsutum
	TA20231_3635 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	24	4	Plus	Gossypium_hirsutum
	TA20267_3635 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	24	4	Plus	Gossypium_hirsutum
	DT569706 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	30	5	Plus	Gossypium_hirsutum
	CO499609 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	30	5	Plus	Gossypium_hirsutum
	DR044205 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	30	5	Plus	Gossypium_hirsutum
	TA20273_3635 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	30	5	Plus	Gossypium_hirsutum
85	TA4950_29729 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	24	4	Plus	Gossypium_arboreum
	TA20221_3635 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	24	4	Plus	Gossypium_hirsutum
	TA20267_3635 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	24	4	Plus	Gossypium_hirsutum
	DR044210 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	24	4	Plus	Gossypium_hirsutum
	DR044185 Fb35 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	24	4	Plus	Gossypium_hirsutum
	TA20231_3635 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	24	4	Plus	Gossypium_hirsutum
	CO499609 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	30	5	Plus	Gossypium_hirsutum
	DT569706 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	30	5	Plus	Gossypium_hirsutum
	TA20273_3635 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	30	5	Plus	Gossypium_hirsutum
	DR044205 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	30	5	Plus	Gossypium_hirsutum
6	BG441211 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	24	4	Plus	Gossypium_arboreum
	TA20267_3635 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	24	4	Plus	Gossypium_hirsutum
	TA20221_3635 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	24	4	Plus	Gossypium_hirsutum
	TA20231_3635 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	24	4	Plus	Gossypium_hirsutum
	DR044175 Fb35 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	24	4	Plus	Gossypium_hirsutum
	DR044185 Fb35 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	24	4	Plus	Gossypium_hirsutum
	DR044205 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	30	5	Plus	Gossypium_hirsutum
	CO499609 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	30	5	Plus	Gossypium_hirsutum
	DT569706 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	30	5	Plus	Gossypium_hirsutum
	TA20273_3635 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	30	5	Plus	Gossypium_hirsutum
87	BE055232 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	24	4	Plus	Gossypium_arboreum
	DR044210 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	24	4	Plus	Gossypium_hirsutum

Supplementary Table 3. Contd.

	DR044205 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	30	5	Plus	Gossypium_hirsutum
	TA20273_3635 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	30	5	Plus	Gossypium_hirsutum
91	BE055624 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	24	4	Plus	Gossypium_arboreum
	DR044210 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	24	4	Plus	Gossypium_hirsutum
	DR044175 Fb35 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	24	4	Plus	Gossypium_hirsutum
	TA20221_3635 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	24	4	Plus	Gossypium_hirsutum
	TA20231_3635 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	24	4	Plus	Gossypium_hirsutum
	TA20267_3635 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	24	4	Plus	Gossypium_hirsutum
	DT569706 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	30	5	Plus	Gossypium_hirsutum
	CO499609 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	30	5	Plus	Gossypium_hirsutum
	DR044205 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	30	5	Plus	Gossypium_hirsutum
	TA20273_3635 Protein E6 [Gossypium hirsutum (Upland cotton)]	6	TCAGGC	30	5	Plus	Gossypium_hirsutum

Supplementary Table 4.

Group I							
HG	Sequence ID	Period Size	Period	Rep. Length	Copy Num.	Blast Strand	Species
1	TA16319_29730 Emb CAB87904.1 [Arabidopsis thaliana (Mouse-ear cress)]	2	AG	24	12	Plus	Gossypium_raimondii
	AI731677 Emb CAB87904.1 [Arabidopsis thaliana (Mouse-ear cress)]	2	AG	24	12	Plus	Gossypium_hirsutum
	TA22041_3635 Hypothetical protein At3g26935 [Arabidopsis thaliana (Mouse-ear cress)]	2	AG	24	12	Plus	Gossypium_hirsutum
2	CO118048 Hypothetical protein At3g22280 [Arabidopsis thaliana (Mouse-ear cress)]	2	AT	20	10	Plus	Gossypium_raimondii
	DT047324	2	TA	20	10	Minus	Gossypium_hirsutum
3	TA9835_29730 F-box protein-like [Oryza sativa (japonica cultivar-group)]	2	CT	20	10	Plus	Gossypium_raimondii
	TA25552_3635 F-box protein-like [Oryza sativa (japonica cultivar-group)]	2	CT	20	10	Plus	Gossypium_hirsutum
	TA25551_3635 T3H13.1 protein [Arabidopsis thaliana (Mouse-ear cress)]	2	CT	20	10	Plus	Gossypium_hirsutum
4	TA30762_3635 Targeting protein for Xklp2 containing protein, expressed [Oryza sativa (japonica cultivar-group)]	2	TC	22	11	Plus	Gossypium_hirsutum
	TA12822_29730	2	CT	22	11	Plus	Gossypium_raimondii
5	CO079094 Hypothetical protein [Solanum tuberosum (Potato)]	2	TG	20	10	Plus	Gossypium_raimondii
	TA25279_3635 Hypothetical protein [Solanum tuberosum (Potato)]	2	TG	20	10	Plus	Gossypium_hirsutum

Supplementary Table 4. Contd.

6	CO088220 Eukaryotic translation initiation factor 2 subunit beta [<i>Triticum aestivum</i> (Wheat)]	3	AAG	18	6	Plus	<i>Gossypium_raimondii</i>
	TA28888_3635 Eukaryotic translation initiation factor 2 beta subunit-like [<i>Solanum tuberosum</i> (Potato)]	3	AAG	18	6	Plus	<i>Gossypium_hirsutum</i>
7	CO084206	3	AAG	18	6	Plus	<i>Gossypium_raimondii</i>
	TA39376_3635 Hypothetical protein At4g35530 [<i>Arabidopsis thaliana</i> (Mouse-ear cress)]	3	AAG	18	6	Plus	<i>Gossypium_hirsutum</i>
8	TA14327_29730 Eukaryotic translation initiation factor 2 beta subunit-like [<i>Solanum tuberosum</i> (Potato)]	3	AAG	18	6	Plus	<i>Gossypium_raimondii</i>
	TA28888_3635 Eukaryotic translation initiation factor 2 beta subunit-like [<i>Solanum tuberosum</i> (Potato)]	3	AAG	18	6	Plus	<i>Gossypium_hirsutum</i>
9	TA10994_29730 DNA repair helicase XPB2 [<i>Arabidopsis thaliana</i> (Mouse-ear cress)]	3	AAG	18	6	Plus	<i>Gossypium_raimondii</i>
	CO495668 DNA repair helicase XPB1 [<i>Arabidopsis thaliana</i> (Mouse-ear cress)]	3	AAG	18	6	Plus	<i>Gossypium_hirsutum</i>
10	TA12940_29730 Esterase/lipase/thioesterase; Peptidase S9B, dipeptidylpeptidase IV N- terminal [<i>Medicago truncatula</i> (Barrel medic)]	3	AAT	18	6	Plus	<i>Gossypium_raimondii</i>
	DW506950 Putative dipeptidyl peptidase IV [<i>Oryza sativa</i> (japonica cultivar-group)]	3	AAT	18	6	Plus	<i>Gossypium_hirsutum</i>
11	TA10917_29730 T7N9.15 [<i>Arabidopsis thaliana</i> (Mouse-ear cress)]	3	ACC	27	9	Plus	<i>Gossypium_raimondii</i>
	TA23937_3635 T7N9.15 [<i>Arabidopsis thaliana</i> (Mouse-ear cress)]	3	ACC	27	9	Plus	<i>Gossypium_hirsutum</i>
12	TA16260_29730 Putative membrane transporter [<i>Arabidopsis thaliana</i> (Mouse-ear cress)]	3	ACC	18	6	Plus	<i>Gossypium_raimondii</i>
	TA21124_3635 Putative membrane transporter [<i>Arabidopsis thaliana</i> (Mouse-ear cress)]	3	ACC	18	6	Plus	<i>Gossypium_hirsutum</i>
13	TA13654_29730 SNF1 related protein kinase [<i>Arabidopsis thaliana</i> (Mouse-ear cress)]	3	ACC	18	6	Plus	<i>Gossypium_raimondii</i>
	TA32113_3635 SNF1 related protein kinase [<i>Arabidopsis thaliana</i> (Mouse-ear cress)]	3	ACC	18	6	Plus	<i>Gossypium_hirsutum</i>
14	CO096690 Hypothetical protein [<i>Arabidopsis thaliana</i> (Mouse-ear cress)]	3	ACC	18	6	Plus	<i>Gossypium_raimondii</i>
	TA31238_3635 Hypothetical protein [<i>Arabidopsis thaliana</i> (Mouse-ear cress)]	3	ACC	18	6	Plus	<i>Gossypium_hirsutum</i>
15	TA13896_29730 Contains similarity to ethylene responsive element binding factor [<i>Arabidopsis thaliana</i> (Mouse-ear cress)]	3	AGA	18	6	Plus	<i>Gossypium_raimondii</i>
	TA25013_3635 Ethylene-responsive transcription factor 5 [<i>Nicotiana tabacum</i> (Common tobacco)]	3	AGA	18	6	Plus	<i>Gossypium_hirsutum</i>
16	CO074836 TCP transcription factor [<i>Medicago truncatula</i> (Barrel medic)]	3	AGA	18	6	Plus	<i>Gossypium_raimondii</i>
	TA25064_3635 TCP transcription factor [<i>Medicago truncatula</i> (Barrel medic)]	3	AGA	18	6	Plus	<i>Gossypium_hirsutum</i>
17	TA12812_29730	3	AGA	18	6	Plus	<i>Gossypium_raimondii</i>
	DW235030	3	CTT	18	6	Minus	<i>Gossypium_hirsutum</i>
	TA22163_3635	3	CTT	18	6	Minus	<i>Gossypium_hirsutum</i>

Supplementary Table 4. Contd.

18	TA10286_29730 Gamma hydroxybutyrate dehydrogenase-like protein [Oryza sativa (japonica cultivar-group)]	3	AGA	18	6	Plus	Gossypium_raimondii
	DN804214 Gamma hydroxybutyrate dehydrogenase [Arabidopsis thaliana (Mouse-ear cress)]	3	AGA	18	6	Plus	Gossypium_hirsutum
19	CO117125 Telomere binding protein TBP1 [Nicotiana glutinosa (Tobacco)]	3	AGC	18	6	Plus	Gossypium_raimondii
	TA34162_3635 Telomere repeat-binding protein homolog [Arabidopsis thaliana (Mouse-ear cress)]	3	AGC	18	6	Plus	Gossypium_hirsutum
20	TA12177_29730 Telomere binding protein TBP1 [Nicotiana glutinosa (Tobacco)]	3	AGC	18	6	Plus	Gossypium_raimondii
	TA34162_3635 Telomere repeat-binding protein homolog [Arabidopsis thaliana (Mouse-ear cress)]	3	AGC	18	6	Plus	Gossypium_hirsutum
21	CO122920 Hypothetical protein P0456E05.23 [Oryza sativa (japonica cultivar-group)]	3	ATC	18	6	Plus	Gossypium_raimondii
	DR459558	3	TGA	18	6	Minus	Gossypium_hirsutum
22	CO128050 Hypothetical protein P0456E05.23 [Oryza sativa (japonica cultivar-group)]	3	ATC	18	6	Plus	Gossypium_raimondii
	DR459558	3	TGA	18	6	Minus	Gossypium_hirsutum
23	CO094728 Hypothetical protein T8G24.9 [Arabidopsis thaliana (Mouse-ear cress)]	3	ATG	18	6	Plus	Gossypium_raimondii
	DT553753 Hypothetical protein T8G24.9 [Arabidopsis thaliana (Mouse-ear cress)]	3	ATG	18	6	Plus	Gossypium_hirsutum
24	DR455003	3	ATT	18	6	Plus	Gossypium_hirsutum
	CO107954	3	ATT	18	6	Plus	Gossypium_raimondii
25	DR455003	3	ATT	18	6	Plus	Gossypium_hirsutum
	TA10229_29730	3	ATT	18	6	Plus	Gossypium_raimondii
26	CO100998	3	ATT	18	6	Plus	Gossypium_raimondii
	DR455003	3	ATT	18	6	Plus	Gossypium_hirsutum
27	TA13997_29730 Hypothetical protein F23E12.210 [Arabidopsis thaliana (Mouse-ear cress)]	3	CAA	18	6	Plus	Gossypium_raimondii
	DW504741 Hypothetical protein F23E12.210 [Arabidopsis thaliana (Mouse-ear cress)]	3	CAA	18	6	Plus	Gossypium_hirsutum
28	CO075719 F28L1.7 protein [Arabidopsis thaliana (Mouse-ear cress)]	3	CAA	18	6	Plus	Gossypium_raimondii
	TA21684_3635	3	CAA	18	6	Plus	Gossypium_hirsutum
	DN802943 F28L1.7 protein [Arabidopsis thaliana (Mouse-ear cress)]	3	CAA	18	6	Plus	Gossypium_hirsutum
	TA21681_3635	3	CAA	18	6	Plus	Gossypium_hirsutum
29	TA11100_29730	3	CAA	18	6	Plus	Gossypium_raimondii
	DN780342	3	TTG	18	6	Minus	Gossypium_hirsutum

Supplementary Table 4. Contd.

	TA25295_3635 Putative zinc finger protein ID1 [<i>Oryza sativa</i> (japonica cultivar-group)]	3	CAA	18	6	Plus	<i>Gossypium_hirsutum</i>
30	CO117165 Mutant <i>cinnata</i> [<i>Antirrhinum majus</i> (Garden snapdragon)]	3	CAC	18	6	Plus	<i>Gossypium_raidmondii</i>
	TA35391_3635 Mutant <i>cinnata</i> [<i>Antirrhinum majus</i> (Garden snapdragon)]	3	CAC	18	6	Plus	<i>Gossypium_hirsutum</i>
31	TA12798_29730 Transcriptional factor B3; Auxin response factor; Aux/IAA_ARF_dimerisation [<i>Medicago truncatula</i> (Barrel medic)]	3	CAG	18	6	Plus	<i>Gossypium_raidmondii</i>
	TA43550_3635	3	CAG	18	6	Plus	<i>Gossypium_hirsutum</i>
32	CO127350 Hypothetical protein Z97340.18 [<i>Arabidopsis thaliana</i> (Mouse-ear cress)]	3	CAG	18	6	Plus	<i>Gossypium_raidmondii</i>
	TA30296_3635 Hypothetical protein Z97340.18 [<i>Arabidopsis thaliana</i> (Mouse-ear cress)]	3	CAG	18	6	Plus	<i>Gossypium_hirsutum</i>
33	CO099987 Hypothetical protein Z97340.18 [<i>Arabidopsis thaliana</i> (Mouse-ear cress)]	3	CAG	18	6	Plus	<i>Gossypium_raidmondii</i>
	TA30296_3635 Hypothetical protein Z97340.18 [<i>Arabidopsis thaliana</i> (Mouse-ear cress)]	3	CAG	18	6	Plus	<i>Gossypium_hirsutum</i>
34	TA12116_29730 At3g04070 [<i>Arabidopsis thaliana</i> (Mouse-ear cress)]	3	CAG	18	6	Plus	<i>Gossypium_raidmondii</i>
	CD485949	3	CAG	18	6	Plus	<i>Gossypium_hirsutum</i>
35	TA14299_29730 Eukaryotic transcription factor, DNA-binding [<i>Medicago truncatula</i> (Barrel medic)]	3	CAT	18	6	Plus	<i>Gossypium_raidmondii</i>
	TA41967_3635	3	CAT	18	6	Plus	<i>Gossypium_hirsutum</i>
36	TA9645_29730 Auxin-regulated protein [<i>Populus tremula</i> x <i>Populus tremuloides</i>]	3	CAT	21	7	Plus	<i>Gossypium_raidmondii</i>
	DW511571	3	CAT	21	7	Plus	<i>Gossypium_hirsutum</i>
37	CO121268 Nt-iaa28 deduced protein [<i>Nicotiana tabacum</i> (Common tobacco)]	3	CAT	21	7	Plus	<i>Gossypium_raidmondii</i>
	DW511571	3	CAT	21	7	Plus	<i>Gossypium_hirsutum</i>
38	TA11701_29730 HyPRP1 [<i>Gossypium hirsutum</i> (Upland cotton)]	3	CCA	21	7	Plus	<i>Gossypium_raidmondii</i>
	TA21454_3635 HyPRP1 [<i>Gossypium hirsutum</i> (Upland cotton)]	3	CCA	21	7	Plus	<i>Gossypium_hirsutum</i>
39	CO092245 RAR1 [<i>Arabidopsis thaliana</i> (Mouse-ear cress)]	3	CCA	21	7	Plus	<i>Gossypium_raidmondii</i>
	DN800615 RAR1 [<i>Arabidopsis thaliana</i> (Mouse-ear cress)]	3	CCA	21	7	Plus	<i>Gossypium_hirsutum</i>
	TA23709_3635 Putative Rar1 protein [<i>Solanum demissum</i> (Wild potato)]	3	CCA	21	7	Plus	<i>Gossypium_hirsutum</i>
40	CO088421 HyPRP1 [<i>Gossypium hirsutum</i> (Upland cotton)]	3	CCA	21	7	Plus	<i>Gossypium_raidmondii</i>
	TA21454_3635 HyPRP1 [<i>Gossypium hirsutum</i> (Upland cotton)]	3	CCA	21	7	Plus	<i>Gossypium_hirsutum</i>
41	TA10530_29730 ATPF3 [<i>Arabidopsis thaliana</i> (Mouse-ear cress)]	3	CCG	21	7	Plus	<i>Gossypium_raidmondii</i>

Supplementary Table 4. Contd.

	DT570547 Hypothetical protein At5g63530 [Arabidopsis thaliana (Mouse-ear cress)]	3	CCG	21	7	Plus	Gossypium_hirsutum
	DT560725 OSJNBa0053B21.14 protein [Oryza sativa (japonica cultivar-group)]	3	CCG	21	7	Plus	Gossypium_hirsutum
	DT548104 ATFP3 [Arabidopsis thaliana (Mouse-ear cress)]	3	CCG	21	7	Plus	Gossypium_hirsutum
	TA21278_3635 Hypothetical protein At5g50740 [Arabidopsis thaliana (Mouse-ear cress)]	3	CCG	21	7	Plus	Gossypium_hirsutum
42	CO074297 OSJNBa0053B21.14 protein [Oryza sativa (japonica cultivar-group)]	3	CCG	21	7	Plus	Gossypium_raidmondii
	DT548104 ATFP3 [Arabidopsis thaliana (Mouse-ear cress)]	3	CCG	21	7	Plus	Gossypium_hirsutum
	DT570547 Hypothetical protein At5g63530 [Arabidopsis thaliana (Mouse-ear cress)]	3	CCG	21	7	Plus	Gossypium_hirsutum
	TA21278_3635 Hypothetical protein At5g50740 [Arabidopsis thaliana (Mouse-ear cress)]	3	CCG	21	7	Plus	Gossypium_hirsutum
	DT560725 OSJNBa0053B21.14 protein [Oryza sativa (japonica cultivar-group)]	3	CCG	21	7	Plus	Gossypium_hirsutum
43	CO096636	3	CCG	18	6	Plus	Gossypium_raidmondii
	TA21684_3635	3	CGG	18	6	Minus	Gossypium_hirsutum
44	CO074836 TCP transcription factor [Medicago truncatula (Barrel medic)]	3	CGA	18	6	Plus	Gossypium_raidmondii
	DR454446	3	CGA	18	6	Plus	Gossypium_hirsutum
	TA25064_3635 TCP transcription factor [Medicago truncatula (Barrel medic)]	3	CGA	18	6	Plus	Gossypium_hirsutum
45	CO075719 F28L1.7 protein [Arabidopsis thaliana (Mouse-ear cress)]	3	CGG	18	6	Plus	Gossypium_raidmondii
	DN758979	3	CGG	18	6	Plus	Gossypium_hirsutum
	TA21683_3635 Protein At5g19090 [Arabidopsis thaliana (Mouse-ear cress)]	3	CGG	18	6	Plus	Gossypium_hirsutum
	TA21684_3635	3	CGG	18	6	Plus	Gossypium_hirsutum
	TA21681_3635	3	CGG	18	6	Plus	Gossypium_hirsutum
46	TA17138_29730 MYC2 [Catharanthus roseus (Rosy periwinkle) (Madagascar periwinkle)]	3	CTC	21	7	Plus	Gossypium_raidmondii
	TA21503_3635	3	CTC	21	7	Plus	Gossypium_hirsutum
47	CO125521 Hypothetical protein F18O22_180 [Arabidopsis thaliana (Mouse-ear cress)]	3	CTT	24	8	Plus	Gossypium_raidmondii
	AI731904 Hypothetical protein F18O22_180 [Arabidopsis thaliana (Mouse-ear cress)]	3	CTT	24	8	Plus	Gossypium_hirsutum
48	TA12795_29730 Putative exoglucanase [Oryza sativa (Rice)]	3	CTT	21	7	Plus	Gossypium_raidmondii
	TA36696_3635 T15F16.6 protein [Arabidopsis thaliana (Mouse-ear cress)]	3	GAA	21	7	Minus	Gossypium_hirsutum
49	TA10320_29730 Glutamate-1-semialdehyde 2,1-aminomutase 2, chloroplast precursor [Arabidopsis thaliana (Mouse-ear cress)]	3	CTT	18	6	Plus	Gossypium_raidmondii
	TA30107_3635 Glutamate-1-semialdehyde 2,1-aminomutase 2, chloroplast precursor [Arabidopsis thaliana (Mouse-ear cress)]	3	CTT	18	6	Plus	Gossypium_hirsutum
50	CO111000	3	CTT	18	6	Plus	Gossypium_raidmondii

Supplementary Table 4. Contd.

	DW235030	3	CTT	18	6	Plus	Gossypium_hirsutum
	TA22163_3635	3	CTT	18	6	Plus	Gossypium_hirsutum
51	CO080640 Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:K14A3 [Arabidopsis thaliana (Mouse-ear cress)]	3	CTT	18	6	Plus	Gossypium_raidmondii
	DW496704 Hypothetical protein [Brassica oleracea (Wild cabbage)]	3	CTT	18	6	Plus	Gossypium_hirsutum
52	TA10526_29730 Hypothetical protein F10M23.360 [Arabidopsis thaliana (Mouse-ear cress)]	3	CTT	18	6	Plus	Gossypium_raidmondii
	DT048210 AT4g27020/F10M23_360 [Arabidopsis thaliana (Mouse-ear cress)]	3	CTT	18	6	Plus	Gossypium_hirsutum
53	CO121921	3	CTT	18	6	Plus	Gossypium_raidmondii
	DT047343	3	CTT	18	6	Plus	Gossypium_hirsutum
54	CO098330 GATA transcription factor 14 [Arabidopsis thaliana (Mouse-ear cress)]	3	GAA	18	6	Plus	Gossypium_raidmondii
	TA23453_3635 GATA transcription factor 14 [Arabidopsis thaliana (Mouse-ear cress)]	3	GAA	18	6	Plus	Gossypium_hirsutum
	DT572945	3	GAA	18	6	Plus	Gossypium_hirsutum
	TA23455_3635 Hypothetical protein [Thellungiella halophila (Salt cress)]	3	GAA	18	6	Plus	Gossypium_hirsutum
55	TA11396_29730 GATA transcription factor 14 [Arabidopsis thaliana (Mouse-ear cress)]	3	GAA	18	6	Plus	Gossypium_raidmondii
	DT572945	3	GAA	18	6	Plus	Gossypium_hirsutum
	TA23455_3635 Hypothetical protein [Thellungiella halophila (Salt cress)]	3	GAA	18	6	Plus	Gossypium_hirsutum
	TA23453_3635 GATA transcription factor 14 [Arabidopsis thaliana (Mouse-ear cress)]	3	GAA	18	6	Plus	Gossypium_hirsutum
	TA23454_3635	3	TTC	18	6	Minus	Gossypium_hirsutum
56	CO113948 Hypothetical protein [Arabidopsis thaliana (Mouse-ear cress)]	3	GAA	18	6	Plus	Gossypium_raidmondii
	DR456101	3	GAA	18	6	Plus	Gossypium_hirsutum
	TA43955_3635 Hypothetical protein [Arabidopsis thaliana (Mouse-ear cress)]	3	GAA	18	6	Plus	Gossypium_hirsutum
	TA36873_3635 Hypothetical protein [Arabidopsis thaliana (Mouse-ear cress)]	3	GAA	18	6	Plus	Gossypium_hirsutum
57	TA9687_29730 Protein At5g20190 [Arabidopsis thaliana (Mouse-ear cress)]	3	GAA	24	8	Plus	Gossypium_raidmondii
	DN758687 Protein At5g20190 [Arabidopsis thaliana (Mouse-ear cress)]	3	GAA	24	8	Plus	Gossypium_hirsutum
58	CO126475 Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:K14A3 [Arabidopsis thaliana (Mouse-ear cress)]	3	GAG	21	7	Plus	Gossypium_raidmondii
	TA25142_3635 Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:K14A3 [Arabidopsis thaliana (Mouse-ear cress)]	3	GAG	21	7	Plus	Gossypium_hirsutum
	DT569099 Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:K14A3 [Arabidopsis thaliana (Mouse-ear cress)]	3	GAG	21	7	Plus	Gossypium_hirsutum
59	TA15485_29730 Hypothetical protein At3g20260 [Arabidopsis thaliana (Mouse-ear cress)]	3	GAT	18	6	Plus	Gossypium_raidmondii
	DT555558 Gb AAF36750.1 [Arabidopsis thaliana (Mouse-ear cress)]	3	GAT	18	6	Plus	Gossypium_hirsutum

Supplementary Table 4. Contd.

	TA31218_3635 Gb AAF36750.1 [Arabidopsis thaliana (Mouse-ear cress)]	3	GAT	18	6	Plus	Gossypium_hirsutum
60	TA16069_29730 GTP1/OBG [Medicago truncatula (Barrel medic)]	3	GAT	18	6	Plus	Gossypium_raismondii
	DW230589 GTP1/OBG [Medicago truncatula (Barrel medic)]	3	GAT	18	6	Plus	Gossypium_hirsutum
61	TA15021_29730 Emb CAA16573.1 [Arabidopsis thaliana (Mouse-ear cress)]	3	GAT	18	6	Plus	Gossypium_raismondii
	TA44028_3635 Hypothetical protein F10N7.30 [Arabidopsis thaliana (Mouse-ear cress)]	3	GAT	18	6	Plus	Gossypium_hirsutum
62	TA10905_29730 Rieske [2Fe-2S] domain, putative [Oryza sativa (japonica cultivar-group)]	3	GCA	18	6	Plus	Gossypium_raismondii
	DW499682 Rieske [2Fe-2S] domain, putative [Oryza sativa (japonica cultivar-group)]	3	GCA	18	6	Plus	Gossypium_hirsutum
63	CO074381 Amino acid/polyamine transporter II [Medicago truncatula (Barrel medic)]	3	GCA	18	6	Plus	Gossypium_raismondii
	TA44554_3635	3	GCA	18	6	Plus	Gossypium_hirsutum
64	CO074960 Rieske [2Fe-2S] domain, putative [Oryza sativa (japonica cultivar-group)]	3	GCA	18	6	Plus	Gossypium_raismondii
	DW499682 Rieske [2Fe-2S] domain, putative [Oryza sativa (japonica cultivar-group)]	3	GCA	18	6	Plus	Gossypium_hirsutum
65	CO105377 Predicted protein [Populus alba x Populus tremula]	3	GCT	18	6	Plus	Gossypium_raismondii
	TA33856_3635 Predicted protein [Populus alba x Populus tremula]	3	GCT	18	6	Plus	Gossypium_hirsutum
66	CO085114 Cleft lip and palate associated transmembrane protein-like [Arabidopsis thaliana (Mouse-ear cress)]	3	GGA	24	8	Plus	Gossypium_raismondii
	TA28051_3635 Cleft lip and palate associated transmembrane protein-like [Arabidopsis thaliana (Mouse-ear cress)]	3	GGA	24	8	Plus	Gossypium_hirsutum
67	TA12379_29730 Pre-mRNA splicing factor [Oryza sativa (Rice)]	3	GGC	21	7	Plus	Gossypium_raismondii
	TA35576_3635 Pre-mRNA splicing factor [Oryza sativa (Rice)]	3	GGC	21	7	Plus	Gossypium_hirsutum
68	TA11455_29730 50S ribosomal protein L5, chloroplast precursor [Arabidopsis thaliana (Mouse-ear cress)]	3	GGT	18	6	Plus	Gossypium_raismondii
	TA25745_3635 50S ribosomal protein L5, chloroplast precursor [Arabidopsis thaliana (Mouse-ear cress)]	3	GGT	18	6	Plus	Gossypium_hirsutum
69	TA10731_29730 unknown protein [Arabidopsis thaliana]	3	GTG	18	6	Plus	Gossypium_raismondii
	TA38018_3635 unknown protein [Arabidopsis thaliana]	3	GTG	18	6	Plus	Gossypium_hirsutum
70	TA10656_29730 Endo-1,4-beta-glucanase precursor [Lycopersicon esculentum (Tomato)]	3	TAC	18	6	Plus	Gossypium_raismondii
	AI055507 Endo-1,4-beta-glucanase [Glycine max (Soybean)]	3	TAC	18	6	Plus	Gossypium_hirsutum
	TA23759_3635 Endo-1,4-beta-glucanase precursor [Lycopersicon esculentum (Tomato)]	3	TAC	18	6	Plus	Gossypium_hirsutum
71	TA12398_29730 Patellin-3 [Arabidopsis thaliana (Mouse-ear cress)]	3	TAC	18	6	Plus	Gossypium_raismondii

Supplementary Table 4. Contd.

	TA24577_3635 Putative cytosolic factor [<i>Trifolium pratense</i> (Red clover)]	3	TAC	18	6	Plus	<i>Gossypium_hirsutum</i>
72	TA10655_29730 Endoglucanase 17 precursor [<i>Arabidopsis thaliana</i> (Mouse-ear cress)]	3	TAC	18	6	Plus	<i>Gossypium_raidmondii</i>
	AI055507 Endo-1,4-beta-glucanase [<i>Glycine max</i> (Soybean)]	3	TAC	18	6	Plus	<i>Gossypium_hirsutum</i>
	TA23759_3635 Endo-1,4-beta-glucanase precursor [<i>Lycopersicon esculentum</i> (Tomato)]	3	TAC	18	6	Plus	<i>Gossypium_hirsutum</i>
73	TA15027_29730 Hypothetical protein [<i>Cicer arietinum</i> (Chickpea) (Garbanzo)]	3	TAT	18	6	Plus	<i>Gossypium_raidmondii</i>
	TA26727_3635 Hypothetical protein [<i>Cicer arietinum</i> (Chickpea) (Garbanzo)]	3	TAT	18	6	Plus	<i>Gossypium_hirsutum</i>
74	TA13070_29730 unknown protein [<i>Arabidopsis thaliana</i>]	3	TAT	18	6	Plus	<i>Gossypium_raidmondii</i>
	TA28431_3635 unknown protein [<i>Arabidopsis thaliana</i>]	3	TAT	18	6	Plus	<i>Gossypium_hirsutum</i>
75	CO096513 F10G19.3 protein [<i>Arabidopsis thaliana</i> (Mouse-ear cress)]	3	TCC	18	6	Plus	<i>Gossypium_raidmondii</i>
	TA42124_3635 F10G19.3 protein [<i>Arabidopsis thaliana</i> (Mouse-ear cress)]	3	TCC	18	6	Plus	<i>Gossypium_hirsutum</i>
76	TA42124_3635 F10G19.3 protein [<i>Arabidopsis thaliana</i> (Mouse-ear cress)]	3	TCC	18	6	Plus	<i>Gossypium_hirsutum</i>
	CO116088 F10G19.3 protein [<i>Arabidopsis thaliana</i> (Mouse-ear cress)]	3	TCC	18	6	Plus	<i>Gossypium_raidmondii</i>
77	CO079404	3	TCT	18	6	Plus	<i>Gossypium_raidmondii</i>
	DT047343	3	CTT	18	6	Plus	<i>Gossypium_hirsutum</i>
78	TA11358_29730 Hypothetical protein MED24.18 [<i>Arabidopsis thaliana</i> (Mouse-ear cress)]	3	TCT	21	7	Plus	<i>Gossypium_raidmondii</i>
	TA34299_3635 Hypothetical protein MED24.18 [<i>Arabidopsis thaliana</i> (Mouse-ear cress)]	3	TCT	21	7	Plus	<i>Gossypium_hirsutum</i>
79	TA13968_29730 At2g20670/F23N11.1 [<i>Arabidopsis thaliana</i> (Mouse-ear cress)]	3	TGA	27	9	Plus	<i>Gossypium_raidmondii</i>
	DT572217 Hypothetical protein F8B4.180 [<i>Arabidopsis thaliana</i> (Mouse-ear cress)]	3	TGA	27	9	Plus	<i>Gossypium_hirsutum</i>
80	TA15848_29730 Hypothetical protein F28P22.14 [<i>Arabidopsis thaliana</i> (Mouse-ear cress)]	3	TGA	18	6	Plus	<i>Gossypium_raidmondii</i>
	DT549381	3	TGA	18	6	Plus	<i>Gossypium_hirsutum</i>
81	TA11085_29730 6b-interacting protein 1-like [<i>Oryza sativa</i> (japonica cultivar-group)]	3	TGA	18	6	Plus	<i>Gossypium_raidmondii</i>
	DR458359	3	TGA	18	6	Plus	<i>Gossypium_hirsutum</i>
82	CO131026 Protein At2g27110 [<i>Arabidopsis thaliana</i> (Mouse-ear cress)]	3	TGA	18	6	Plus	<i>Gossypium_raidmondii</i>
	DW519866 Protein At2g27110 [<i>Arabidopsis thaliana</i> (Mouse-ear cress)]	3	TGA	18	6	Plus	<i>Gossypium_hirsutum</i>
	TA42826_3635 Protein At2g27110 [<i>Arabidopsis thaliana</i> (Mouse-ear cress)]	3	TGA	18	6	Plus	<i>Gossypium_hirsutum</i>

Supplementary Table 4. Contd.

83	CO105343 Von Willebrand factor, type A; Ubiquitin interacting motif [Medicago truncatula (Barrel medic)]	3	TGC	18	6	Plus	Gossypium_raidmondii
	DT571041 Von Willebrand factor, type A; Ubiquitin interacting motif [Medicago truncatula (Barrel medic)]	3	TGC	18	6	Plus	Gossypium_hirsutum
	TA22965_3635 Von Willebrand factor, type A; Ubiquitin interacting motif [Medicago truncatula (Barrel medic)]	3	TGC	18	6	Plus	Gossypium_hirsutum
84	TA12115_29730	3	TGC	18	6	Plus	Gossypium_raidmondii
	CD485949	3	CAG	18	6	Minus	Gossypium_hirsutum
85	CO088783 Von Willebrand factor, type A; Ubiquitin interacting motif [Medicago truncatula (Barrel medic)]	3	TGC	18	6	Plus	Gossypium_raidmondii
	DT571041 Von Willebrand factor, type A; Ubiquitin interacting motif [Medicago truncatula (Barrel medic)]	3	TGC	18	6	Plus	Gossypium_hirsutum
	TA22965_3635 Von Willebrand factor, type A; Ubiquitin interacting motif [Medicago truncatula (Barrel medic)]	3	TGC	18	6	Plus	Gossypium_hirsutum
86	TA14161_29730 Probable WRKY transcription factor 48 [Arabidopsis thaliana (Mouse-ear cress)]	3	TGG	18	6	Plus	Gossypium_raidmondii
	TA40466_3635	3	TGG	18	6	Plus	Gossypium_hirsutum
87	TA9645_29730 Auxin-regulated protein [Populus tremula x Populus tremuloides]	3	TGG	21	7	Plus	Gossypium_raidmondii
	CD486500 Auxin-regulated protein [Populus tremula x Populus tremuloides]	3	TGG	21	7	Plus	Gossypium_hirsutum
	TA24844_3635 Auxin-regulated protein [Populus tremula x Populus tremuloides]	3	TGG	21	7	Plus	Gossypium_hirsutum
88	CO100284 Aux/IAA protein [Populus tremula x Populus tremuloides]	3	TGG	18	6	Plus	Gossypium_raidmondii
	DW480781 Auxin-responsive protein IAA11 [Arabidopsis thaliana (Mouse-ear cress)]	3	TGG	18	6	Plus	Gossypium_hirsutum
	DW488302	3	ACC	18	6	Minus	Gossypium_hirsutum
	DW488301	3	TGG	18	6	Plus	Gossypium_hirsutum
	TA26814_3635 Auxin-responsive protein IAA11 [Arabidopsis thaliana (Mouse-ear cress)]	3	TGG	18	6	Plus	Gossypium_hirsutum
89	CO083872 Putative cytosolic factor [Trifolium pratense (Red clover)]	3	TTA	18	6	Plus	Gossypium_raidmondii
	TA26727_3635 Hypothetical protein [Cicer arietinum (Chickpea) (Garbanzo)]	3	TAT	18	6	Plus	Gossypium_hirsutum
90	CO089818 Hypothetical protein [Arabidopsis thaliana (Mouse-ear cress)]	3	TTC	18	6	Plus	Gossypium_raidmondii
	TA28845_3635 At5g37660 [Arabidopsis thaliana (Mouse-ear cress)]	3	TTC	18	6	Plus	Gossypium_hirsutum
91	CO082594 Nucellin-like protein [Arabidopsis thaliana (Mouse-ear cress)]	3	TTC	18	6	Plus	Gossypium_raidmondii
	TA43902_3635 Nucellin-like protein [Arabidopsis thaliana (Mouse-ear cress)]	3	TTC	18	6	Plus	Gossypium_hirsutum
92	CO070235	3	TTC	21	7	Plus	Gossypium_raidmondii
	TA39369_3635 Inducer of CBF expression 1 protein [Capsella bursa-pastoris (Shepherd's purse)]	3	TTC	21	7	Plus	Gossypium_hirsutum

Supplementary Table 4. Contd.

93	TA16995_29730 2-C-methyl-D-erythritol 2,4-cyclodiphosphate synthase, chloroplast precursor [Arabidopsis thaliana (Mouse-ear cress)]	3	TTC	21	7	Plus	Gossypium_raidmondii
	AI731296 2-C-methyl-D-erythritol 2,4-cyclodiphosphate synthase, chloroplast precursor [Arabidopsis thaliana (Mouse-ear cress)]	3	TTC	21	7	Plus	Gossypium_hirsutum
	TA28796_3635 2-C-methyl-D-erythritol 2,4-cyclodiphosphate synthase, chloroplast precursor [Arabidopsis thaliana (Mouse-ear cress)]	3	TTC	21	7	Plus	Gossypium_hirsutum
94	TA12750_29730 Polypyrimidine tract-binding protein 1-like [Oryza sativa (japonica cultivar-group)]	4	ATCT	24	6	Plus	Gossypium_raidmondii
	TA34023_3635 Polypyrimidine tract-binding protein 1-like [Oryza sativa (japonica cultivar-group)]	4	ATCT	24	6	Plus	Gossypium_hirsutum
95	TA9530_29730 Chromosome 10 SCAF12030, whole genome shotgun sequence [Tetraodon nigroviridis (Green puffer)]	4	ATGA	20	5	Plus	Gossypium_raidmondii
	TA22504_3635 Chromosome 10 SCAF12030, whole genome shotgun sequence [Tetraodon nigroviridis (Green puffer)]	4	ATGA	20	5	Plus	Gossypium_hirsutum
86	TA11291_29730	4	CATA	24	6	Plus	Gossypium_raidmondii
	TA24344_3635 Dual specificity phosphatase, catalytic domain, putative [Medicago truncatula (Barrel medic)]	4	GTAT	24	6	Minus	Gossypium_hirsutum
97	TA14342_29730 Putative MYB family transcription factor [Arabidopsis thaliana (Mouse-ear cress)]	4	TATG	20	5	Plus	Gossypium_raidmondii
	DW511541	4	TATG	20	5	Plus	Gossypium_hirsutum
98	TA14305_29730 Mitogen-activated protein kinase 1 [Lycopersicon esculentum (Tomato)]	4	TATG	20	5	Plus	Gossypium_raidmondii
	TA23495_3635 Mitogen-activated protein kinase 1 [Lycopersicon esculentum (Tomato)]	4	TATG	20	5	Plus	Gossypium_hirsutum
99	TA16726_29730 Mitogen-activated protein kinase 2 [Lycopersicon esculentum (Tomato)]	4	TATG	20	5	Plus	Gossypium_raidmondii
	TA23495_3635 Mitogen-activated protein kinase 1 [Lycopersicon esculentum (Tomato)]	4	TATG	20	5	Plus	Gossypium_hirsutum
100	TA9059_29730 Root phototropism protein 2 [Arabidopsis thaliana (Mouse-ear cress)]	4	TTGT	20	5	Plus	Gossypium_raidmondii
	CA993380 Phototropic response-like protein [Malus domestica (Apple) (Malus sylvestris)]	4	TTGT	20	5	Plus	Gossypium_hirsutum
101	TA9210_29730 antiporter/ glucose-6-phosphate transporter [Arabidopsis thaliana]	5	AAACC	25	5	Plus	Gossypium_raidmondii
	TA28118_3635 antiporter/ glucose-6-phosphate transporter [Arabidopsis thaliana]	5	AAACC	25	5	Plus	Gossypium_hirsutum
102	TA10662_29730 Expressed protein [Arabidopsis thaliana (Mouse-ear cress)]	5	ATGCT	25	5	Plus	Gossypium_raidmondii
	TA25857_3635 Expressed protein [Arabidopsis thaliana (Mouse-ear cress)]	5	ATGCT	25	5	Plus	Gossypium_hirsutum
103	CO102286 F2D10.13 [Arabidopsis thaliana (Mouse-ear cress)]	5	GAAGA	25	5	Plus	Gossypium_raidmondii
	TA26724_3635 F2D10.13 [Arabidopsis thaliana (Mouse-ear cress)]	5	GAAGA	25	5	Plus	Gossypium_hirsutum
104	TA11200_29730 Eukaryotic peptide chain release factor subunit 1-3 [Arabidopsis thaliana (Mouse-ear cress)]	5	GTTTG	25	5	Plus	Gossypium_raidmondii
	TA22251_3635 Putative eukaryotic peptide chain release factor subunit 1-3 [Oryza sativa (japonica cultivar-group)]	5	GTTTG	25	5	Plus	Gossypium_hirsutum

Supplementary Table 4. Contd.

105	TA10378_29730 Hypothetical protein At1g70160 [Arabidopsis thaliana (Mouse-ear cress)]	6	AATCC C	24	4	Plus	Gossypium_raimondii
	DT559035 Hypothetical protein At1g70160 [Arabidopsis thaliana (Mouse-ear cress)]	6	CAATC C	24	4	Plus	Gossypium_hirsutum
	TA23974_3635 Hypothetical protein At1g70160 [Arabidopsis thaliana (Mouse-ear cress)]	6	CAATC C	24	4	Plus	Gossypium_hirsutum
106	TA9618_29730 Hypothetical protein [Arabidopsis thaliana (Mouse-ear cress)]	6	ACCAA A	30	5	Plus	Gossypium_raimondii
	DT564564	6	ACCAA A	30	5	Plus	Gossypium_hirsutum
	DT556816	6	ACCAA A	30	5	Plus	Gossypium_hirsutum
	DT558262	6	ACCAA A	30	5	Plus	Gossypium_hirsutum
	TA24430_3635 Hypothetical protein [Arabidopsis thaliana (Mouse-ear cress)]	6	ACCAA A	30	5	Plus	Gossypium_hirsutum
107	TA9545_29730 Alpha-1,4 glucan phosphorylase L isozyme, chloroplast precursor [Vicia faba (Broad bean)]	6	AGAAG C	24	4	Plus	Gossypium_raimondii
	TA28987_3635 Alpha-1,4 glucan phosphorylase L isozyme, chloroplast precursor [Vicia faba (Broad bean)]	6	AGAAG C	24	4	Plus	Gossypium_hirsutum
108	CO105571	6	CAACG C	24	4	Plus	Gossypium_raimondii
	TA34092_3635 Hypothetical protein [Arabidopsis thaliana (Mouse-ear cress)]	6	CCAAC G	24	4	Plus	Gossypium_hirsutum
109	TA11832_29730 Hypothetical protein At4g32600 [Arabidopsis thaliana (Mouse-ear cress)]	6	CCAGC T	24	4	Plus	Gossypium_raimondii
	DW512264	6	CCAGC T	24	4	Plus	Gossypium_hirsutum
110	CO114031 unknown protein [Arabidopsis thaliana]	6	CCAGT A	24	4	Plus	Gossypium_raimondii
	TA25756_3635 unknown protein [Arabidopsis thaliana]	6	CCAGT A	24	4	Plus	Gossypium_hirsutum

Supplementary Table 4. Contd.

111	CO118091	6	CCCAT G	24	4	Plus	Gossypium_raimondii
	TA24455_3635 Hypothetical protein At2g43170 [Arabidopsis thaliana (Mouse-ear cress)]	6	GCATG G	24	4	Minus	Gossypium_hirsutum
112	DT555662 At1g14000/F7A19_9 [Arabidopsis thaliana (Mouse-ear cress)]	6	CCGAC G	24	4	Plus	Gossypium_hirsutum
	TA16508_29730 At1g14000/F7A19_9 [Arabidopsis thaliana (Mouse-ear cress)]	6	GCCGA C	24	4	Plus	Gossypium_raimondii
113	TA17036_29730 MYB transcription factor MYB127 [Glycine max (Soybean)]	6	CCTCT C	30	5	Plus	Gossypium_raimondii
	DR041738 MYB transcription factor MYB127 [Glycine max (Soybean)]	6	CCTCT C	30	5	Plus	Gossypium_hirsutum
114	CO071668 MYB transcription factor MYB127 [Glycine max (Soybean)]	6	CCTCT C	30	5	Plus	Gossypium_raimondii
	DR041738 MYB transcription factor MYB127 [Glycine max (Soybean)]	6	CCTCT C	30	5	Plus	Gossypium_hirsutum
115	TA12532_29730 Putative ABC transporter ATPase; 10053-12032 [Arabidopsis thaliana (Mouse-ear cress)]	6	CCTCT C	24	4	Plus	Gossypium_raimondii
	TA25929_3635 Putative ABC transporter ATPase; 10053-12032 [Arabidopsis thaliana (Mouse-ear cress)]	6	CCTCT C	24	4	Plus	Gossypium_hirsutum
116	CO093803 Timing of CAB expression 1 protein [Castanea sativa (Sweet chestnut)]	6	CGGGA G	24	4	Plus	Gossypium_raimondii
	TA26774_3635 Two-component response regulator-like PRR37 [Oryza sativa (Rice)]	6	GAGCG G	24	4	Plus	Gossypium_hirsutum
117	TA13748_29730 Tubby; Di-trans-poly-cis-decaprenylcistransferase; Cyclin-like F- box [Medicago truncatula (Barrel medic)]	6	GGCG GA	24	4	Plus	Gossypium_raimondii
	AI732056 F12M16.22 [Arabidopsis thaliana (Mouse-ear cress)]	6	GGCG GA	24	4	Plus	Gossypium_hirsutum
118	TA10515_29730 Fructose-1,6-bisphosphatase [Pisum sativum (Garden pea)]	6	TCTCA C	30	5	Plus	Gossypium_raimondii
	DW483497 Fructose-1,6-bisphosphatase [Pisum sativum (Garden pea)]	6	TCTCA C	30	5	Plus	Gossypium_hirsutum

Supplementary Table 4. Contd.

119	TA9736_29730 Transcription factor DRE-binding factor 2 [Gossypium hirsutum (Upland cotton)]	6	TCTCC T	24	4	Plus	Gossypium_raimondii
	DV848960 Transcription factor DRE-binding factor 2 [Gossypium hirsutum (Upland cotton)]	6	TCTCC T	24	4	Plus	Gossypium_hirsutum
	DT465897	6	TCTCC T	24	4	Plus	Gossypium_hirsutum
	DT572833	6	TCTCC T	24	4	Plus	Gossypium_hirsutum
	TA22759_3635 Transcription factor DRE-binding factor 2 [Gossypium hirsutum (Upland cotton)]	6	TCTCC T	24	4	Plus	Gossypium_hirsutum
120	TA13949_29730 Plastid ribosomal protein L19, putative [Brassica oleracea (Wild cabbage)]	6	TGAAG G	24	4	Plus	Gossypium_raimondii
	DR455677 Plastid ribosomal protein L19, putative [Brassica oleracea (Wild cabbage)]	6	TGAAG G	24	4	Plus	Gossypium_hirsutum
	CO499248 Plastid ribosomal protein L19, putative [Brassica oleracea (Wild cabbage)]	6	TGAAG G	24	4	Plus	Gossypium_hirsutum
121	TA15877_29730 At1g26300/F28B23_4 [Arabidopsis thaliana (Mouse-ear cress)]	6	TGATG C	24	4	Plus	Gossypium_raimondii
	TA28020_3635 At1g26300/F28B23_4 [Arabidopsis thaliana (Mouse-ear cress)]	6	TGATG C	24	4	Plus	Gossypium_hirsutum
122	CO126735 Protein kinase [Arabidopsis thaliana (Mouse-ear cress)]	6	TGGTG A	24	4	Plus	Gossypium_raimondii
	DW489261 Protein kinase [Arabidopsis thaliana (Mouse-ear cress)]	6	TGGTG A	24	4	Plus	Gossypium_hirsutum
123	TA13723_29730 Protein kinase [Arabidopsis thaliana (Mouse-ear cress)]	6	TGGTG A	24	4	Plus	Gossypium_raimondii
	DW489261 Protein kinase [Arabidopsis thaliana (Mouse-ear cress)]	6	TGGTG A	24	4	Plus	Gossypium_hirsutum
Group II							
HG	Sequence ID	Period Size	Period	Rep. Length	Copy Num.	Blast Strand	Species
1	CO074722 Gb AAC24081.1 [Arabidopsis thaliana (Mouse-ear cress)]	2	AG	34	17	Plus	Gossypium_raimondii
	TA34307_3635 Gb AAC24081.1 [Arabidopsis thaliana (Mouse-ear cress)]	2	AG	30	15	Plus	Gossypium_hirsutum
	DT574307 Gb AAC24081.1 [Arabidopsis thaliana (Mouse-ear cress)]	2	AG	30	15	Plus	Gossypium_hirsutum

Supplementary Table 4. Contd.

2	TA14574_29730 IRE homolog; protein kinase-like protein [Arabidopsis thaliana (Mouse-ear cress)]	2	AG	26	13	Plus	Gossypium_raidmondii
	CO498746 IRE homolog; protein kinase-like protein [Arabidopsis thaliana (Mouse-ear cress)]	2	AG	20	10	Plus	Gossypium_hirsutum
3	TA10286_29730 Gamma hydroxybutyrate dehydrogenase-like protein [Oryza sativa (japonica cultivar-group)]	2	AG	28	14	Plus	Gossypium_raidmondii
	DN804214 Gamma hydroxybutyrate dehydrogenase [Arabidopsis thaliana (Mouse-ear cress)]	2	AG	26	13	Plus	Gossypium_hirsutum
4	TA15654_29730 Hypothetical protein F23E12.210 [Arabidopsis thaliana (Mouse-ear cress)]	2	CA	22	11	Plus	Gossypium_raidmondii
	TA38621_3635 Hypothetical protein F23E12.210 [Arabidopsis thaliana (Mouse-ear cress)]	2	CA	18	9	Plus	Gossypium_hirsutum
5	TA11234_29730 Putative fasciclin-like arabinogalactan protein FLA2 [Trifolium pratense (Red clover)]	2	CA	30	15	Plus	Gossypium_raidmondii
	TA21226_3635 Putative fasciclin-like arabinogalactan protein [Salicornia europaea (Common glasswort)]	2	CA	20	10	Plus	Gossypium_hirsutum
6	CO114663 Arabidopsis thaliana gl1 homolog [Arabidopsis thaliana (Mouse-ear cress)]	2	CT	28	14	Plus	Gossypium_raidmondii
	DT049270 Hypothetical protein [Medicago truncatula (Barrel medic)]	2	TC	20	10	Plus	Gossypium_hirsutum
7	CO081596 NAM-like protein [Arabidopsis thaliana (Mouse-ear cress)]	2	CT	22	11	Plus	Gossypium_raidmondii
	TA22929_3635 NAM-like protein [Arabidopsis thaliana (Mouse-ear cress)]	2	CT	18	9	Plus	Gossypium_hirsutum
	DT527598 Unknown protein [Lycopersicon esculentum (Tomato)]	2	CT	20	10	Plus	Gossypium_hirsutum
8	TA9287_29730 Arabidopsis thaliana gl1 homolog [Arabidopsis thaliana (Mouse-ear cress)]	2	CT	28	14	Plus	Gossypium_raidmondii
	DT049270 Hypothetical protein [Medicago truncatula (Barrel medic)]	2	TC	20	10	Plus	Gossypium_hirsutum
9	TA13307_29730 Hypothetical protein [Medicago truncatula (Barrel medic)]	2	CT	26	13	Plus	Gossypium_raidmondii
	DN802296	2	CT	20	10	Plus	Gossypium_hirsutum
10	TA14305_29730 Mitogen-activated protein kinase 1 [Lycopersicon esculentum (Tomato)]	2	TC	40	20	Plus	Gossypium_raidmondii
	CA993935 Mitogen-activated protein kinase 1 [Lycopersicon esculentum (Tomato)]	2	TC	38	19	Plus	Gossypium_hirsutum
11	CO086021	2	TC	22	11	Plus	Gossypium_raidmondii
	DR044199 Hypothetical protein OSJNBa0014O06.1 [Oryza sativa (japonica cultivar-group)]	2	TC	18	9	Plus	Gossypium_hirsutum
	TA31302_3635	2	TC	18	9	Plus	Gossypium_hirsutum
12	CO094396 Hypothetical protein OSJNBa0014O06.1 [Oryza sativa (japonica cultivar-group)]	2	TC	22	11	Plus	Gossypium_raidmondii
	DR044199 Hypothetical protein OSJNBa0014O06.1 [Oryza sativa (japonica cultivar-group)]	2	TC	18	9	Plus	Gossypium_hirsutum
	TA31302_3635	2	TC	18	9	Plus	Gossypium_hirsutum

Supplementary Table 4. Contd.

13	CO109699 Zinc finger protein [Pimpinella brachycarpa]	3	AAC	21	7	Plus	Gossypium_raidmondii
	TA21928_3635 SPF1 protein [Ipomoea batatas (Sweet potato) (Batate)]	3	AAC	18	6	Plus	Gossypium_hirsutum
14	TA13731_29730 Protein phosphatase-2C-like protein [Arabidopsis thaliana (Mouse-ear cress)]	3	AAG	21	7	Plus	Gossypium_raidmondii
	DW513876	3	AAG	18	6	Plus	Gossypium_hirsutum
	DW513876	3	AAG	18	6	Plus	Gossypium_hirsutum
15	CO129071 Putative C2H2-type zinc finger protein [Arabidopsis thaliana (Mouse-ear cress)]	3	ACA	24	8	Plus	Gossypium_raidmondii
	DN804675	3	ACA	21	7	Plus	Gossypium_hirsutum
16	TA9550_29730	3	ACC	21	7	Plus	Gossypium_raidmondii
	TA42267_3635	3	TGG	18	6	Minus	Gossypium_hirsutum
	TA29583_3635	3	ACC	18	6	Plus	Gossypium_hirsutum
17	CO116035 Adenylate translocator (Brittle-1)-like protein [Arabidopsis thaliana (Mouse-ear cress)]	3	AGA	21	7	Plus	Gossypium_raidmondii
	TA23448_3635 Adenylate translocator (Brittle-1)-like protein [Arabidopsis thaliana (Mouse-ear cress)]	3	AGA	18	6	Plus	Gossypium_hirsutum
18	CO129567 Adenylate translocator (Brittle-1)-like protein [Arabidopsis thaliana (Mouse-ear cress)]	3	AGA	21	7	Plus	Gossypium_raidmondii
	TA23448_3635 Adenylate translocator (Brittle-1)-like protein [Arabidopsis thaliana (Mouse-ear cress)]	3	AGA	18	6	Plus	Gossypium_hirsutum
19	CO103751 Hypothetical protein At2g17970 [Arabidopsis thaliana (Mouse-ear cress)]	3	AGA	21	7	Plus	Gossypium_raidmondii
	DT566790 Hypothetical protein At2g17970 [Arabidopsis thaliana (Mouse-ear cress)]	3	AGA	18	6	Plus	Gossypium_hirsutum
20	TA10409_29730 Hly-III related proteins [Medicago truncatula (Barrel medic)]	3	ATC	45	15	Plus	Gossypium_raidmondii
	TA37119_3635 Hly-III related proteins [Medicago truncatula (Barrel medic)]	3	ATC	42	14	Plus	Gossypium_hirsutum
21	TA14749_29730 Hypothetical protein T16K5.250 [Arabidopsis thaliana (Mouse-ear cress)]	3	ATG	39	13	Plus	Gossypium_raidmondii
	DT555093 Hypothetical protein T16K5.250 [Arabidopsis thaliana (Mouse-ear cress)]	3	ATG	21	7	Plus	Gossypium_hirsutum
	TA28739_3635 Hypothetical protein T16K5.250 [Arabidopsis thaliana (Mouse-ear cress)]	3	ATG	21	7	Plus	Gossypium_hirsutum
22	TA8867_29730 Wound-responsive protein, putative [Arabidopsis thaliana (Mouse-ear cress)]	3	ATT	36	12	Plus	Gossypium_raidmondii
	TA27626_3635 Wound-responsive protein, putative [Arabidopsis thaliana (Mouse-ear cress)]	3	ATT	30	10	Plus	Gossypium_hirsutum
23	CO080595 Putative calcium-dependent protein kinase [Oryza sativa (japonica cultivar-group)]	3	CAA	21	7	Plus	Gossypium_raidmondii
	TA41417_3635	3	CAA	18	6	Plus	Gossypium_hirsutum
24	CO097102 Putative zinc finger protein [Oryza sativa (japonica cultivar-group)]	3	CAA	24	8	Plus	Gossypium_raidmondii

Supplementary Table 4. Contd.

	TA21598_3635 Zinc finger DNA-binding protein [Catharanthus roseus (Rosy periwinkle) (Madagascar periwinkle)]	3	CAA	21	7	Plus	Gossypium_hirsutum
	TA21596_3635 Cys2/His2-type zinc finger protein, putative [Arabidopsis thaliana (Mouse-ear cress)]	3	CAA	21	7	Plus	Gossypium_hirsutum
25	TA13961_29730 Zinc finger DNA-binding protein [Catharanthus roseus (Rosy periwinkle) (Madagascar periwinkle)]	3	CAA	24	8	Plus	Gossypium_raidmondii
	TA21596_3635 Cys2/His2-type zinc finger protein, putative [Arabidopsis thaliana (Mouse-ear cress)]	3	CAA	21	7	Plus	Gossypium_hirsutum
	TA21598_3635 Zinc finger DNA-binding protein [Catharanthus roseus (Rosy periwinkle) (Madagascar periwinkle)]	3	CAA	21	7	Plus	Gossypium_hirsutum
26	TA10131_29730 Squamosa promoter binding protein-homologue 3 [Antirrhinum majus (Garden snapdragon)]	3	CCA	24	8	Plus	Gossypium_raidmondii
	DT569996	3	CCA	18	6	Plus	Gossypium_hirsutum
	TA34843_3635	3	CCA	24	8	Plus	Gossypium_hirsutum
27	CO115407 Squamosa promoter binding protein-homologue 3 [Antirrhinum majus (Garden snapdragon)]	3	CCA	24	8	Plus	Gossypium_raidmondii
	DT569996	3	CCA	18	6	Plus	Gossypium_hirsutum
	TA34843_3635	3	CCA	24	8	Plus	Gossypium_hirsutum
28	CO125017	3	CCA	24	8	Plus	Gossypium_raidmondii
	DT569996	3	CCA	18	6	Plus	Gossypium_hirsutum
	TA34843_3635	3	CCA	24	8	Plus	Gossypium_hirsutum
29	TA11642_29730	3	CTT	24	8	Plus	Gossypium_raidmondii
	DT458545	3	CTT	21	7	Plus	Gossypium_hirsutum
30	TA8814_29730 F22K20.9 protein [Arabidopsis thaliana (Mouse-ear cress)]	3	GAA	30	10	Plus	Gossypium_raidmondii
	DW486618	3	GAA	18	6	Plus	Gossypium_hirsutum
	DW486619	3	TTC	18	6	Minus	Gossypium_hirsutum
31	TA9084_29730 Calnexin [Glycine max (Soybean)]	3	GAA	27	9	Plus	Gossypium_raidmondii
	TA22700_3635 Calnexin [Glycine max (Soybean)]	3	GAA	21	7	Plus	Gossypium_hirsutum
32	CO087702	3	GAC	21	7	Plus	Gossypium_raidmondii
	DT455649	3	GAC	18	6	Plus	Gossypium_hirsutum
33	CO118175	3	GAT	21	7	Plus	Gossypium_raidmondii
	TA24244_3635	3	GAT	18	6	Plus	Gossypium_hirsutum
34	CO081152	3	GAT	21	7	Plus	Gossypium_raidmondii
	TA24244_3635	3	GAT	18	6	Plus	Gossypium_hirsutum

Supplementary Table 4. Contd.

35	TA12772_29730 Hypothetical protein [Medicago truncatula (Barrel medic)]	3	GAT	21	7	Plus	Gossypium_raidmondii
	TA24244_3635	3	GAT	18	6	Plus	Gossypium_hirsutum
36	TA10501_29730 RNA recognition motif family protein, expressed [Oryza sativa (japonica cultivar-group)]	3	GAT	21	7	Plus	Gossypium_raidmondii
	DW232867 RNA recognition motif family protein, expressed [Oryza sativa (japonica cultivar-group)]	3	GAT	18	6	Plus	Gossypium_hirsutum
	DW489296 Hypothetical protein At2g37340 [Arabidopsis thaliana (Mouse-ear cress)]	3	GAT	18	6	Plus	Gossypium_hirsutum
	TA20824_3635 RNA recognition motif family protein, expressed [Oryza sativa (japonica cultivar-group)]	3	GAT	18	6	Plus	Gossypium_hirsutum
37	CO111128	3	GCA	27	9	Plus	Gossypium_raidmondii
	DT565265	3	GCA	18	6	Plus	Gossypium_hirsutum
	DT463674 Auxin response factor 8 [Arabidopsis thaliana (Mouse-ear cress)]	3	GCA	27	9	Plus	Gossypium_hirsutum
38	TA9639_29730 Unnamed protein product-related [Medicago truncatula (Barrel medic)]	3	GCT	24	8	Plus	Gossypium_raidmondii
	TA22416_3635 Translation initiation factor 3 [Oryza sativa (Rice)]	3	GCT	18	6	Plus	Gossypium_hirsutum
	TA22417_3635	3	GCT	18	6	Plus	Gossypium_hirsutum
	DN762148	3	GCT	24	8	Plus	Gossypium_hirsutum
39	CO126702 9G8-like SR protein [Arabidopsis thaliana (Mouse-ear cress)]	3	GGT	21	7	Plus	Gossypium_raidmondii
	DR458655 Putative RSZp22 splicing factor [Arabidopsis thaliana (Mouse-ear cress)]	3	GGT	18	6	Plus	Gossypium_hirsutum
40	CO128109	3	TCA	21	7	Plus	Gossypium_raidmondii
	DW514675 Protein SCAR4 [Arabidopsis thaliana (Mouse-ear cress)]	3	TGA	18	6	Minus	Gossypium_hirsutum
	DT047243	3	TCA	21	7	Plus	Gossypium_hirsutum
41	TA15947_29730	3	TGA	21	7	Plus	Gossypium_raidmondii
	TA27337_3635	3	TGA	18	6	Plus	Gossypium_hirsutum
42	TA16375_29730 Cytochrome b5 [Olea europaea (Common olive)]	3	TGT	21	7	Plus	Gossypium_raidmondii
	TA36324_3635 Cytochrome b5 [Olea europaea (Common olive)]	3	TGT	18	6	Plus	Gossypium_hirsutum
43	TA9599_29730 Glutamine synthetase cytosolic isozyme 1 [Vitis vinifera (Grape)]	3	TTA	21	7	Plus	Gossypium_raidmondii
	TA21971_3635 Glutamine synthetase (EC 6.3.1.2) (Glutamate--ammonia ligase) (GS(1)) [Alnus glutinosa (Alder)]	3	TTA	18	6	Plus	Gossypium_hirsutum
44	CO102079 Putative serine protease-like protein [Arabidopsis thaliana (Mouse-ear cress)]	3	TTA	27	9	Plus	Gossypium_raidmondii
	TA23671_3635 Putative serine protease-like protein [Arabidopsis thaliana (Mouse-ear cress)]	3	TTA	21	7	Plus	Gossypium_hirsutum

Supplementary Table 4. Contd.

45	TA17231_29730 Protein At3g63460 [Arabidopsis thaliana (Mouse-ear cress)]	3	TTA	21	7	Plus	Gossypium_aimondii
	TA26634_3635	3	TAA	18	6	Minus	Gossypium_hirsutum
	TA26635_3635 Protein At3g63460 [Arabidopsis thaliana (Mouse-ear cress)]	3	TTA	21	7	Plus	Gossypium_hirsutum
	TA26636_3635	3	ATA	21	7	Minus	Gossypium_hirsutum
46	TA9513_29730 Putative serine protease-like protein [Arabidopsis thaliana (Mouse-ear cress)]	3	TTA	27	9	Plus	Gossypium_aimondii
	TA23671_3635 Putative serine protease-like protein [Arabidopsis thaliana (Mouse-ear cress)]	3	TTA	21	7	Plus	Gossypium_hirsutum
47	CO089244 Ser/Thr protein kinase [Lotus japonicus]	3	TTA	36	12	Plus	Gossypium_aimondii
	TA41161_3635 Ser/Thr protein kinase [Lotus japonicus]	3	TTA	33	11	Plus	Gossypium_hirsutum
48	TA15579_29730 TCP transcription factor [Medicago truncatula (Barrel medic)]	3	TTC	21	7	Plus	Gossypium_aimondii
	TA27906_3635 TCP transcription factor [Medicago truncatula (Barrel medic)]	3	TTC	18	6	Plus	Gossypium_hirsutum
49	CO117323 Adenylate kinase, chloroplast, putative, expressed [Oryza sativa (japonica cultivar-group)]	3	TTC	21	7	Plus	Gossypium_aimondii
	TA42874_3635 Probable adenylate kinase 1, chloroplast precursor [Arabidopsis thaliana (Mouse-ear cress)]	3	TTC	18	6	Plus	Gossypium_hirsutum
50	CO115391 F7F22.5 [Arabidopsis thaliana (Mouse-ear cress)]	3	TTC	24	8	Plus	Gossypium_aimondii
	DT552155 unknown protein [Arabidopsis thaliana]	3	CTT	21	7	Plus	Gossypium_hirsutum
	TA35637_3635 F7F22.5 [Arabidopsis thaliana (Mouse-ear cress)]	3	TTC	24	8	Plus	Gossypium_hirsutum
51	TA10229_29730	3	GTA	27	9	Plus	Gossypium_aimondii
	TA34896_3635 Protein At4g19110 [Arabidopsis thaliana (Mouse-ear cress)]	3	CTA	18	6	Minus	Gossypium_hirsutum
52	CO084206	4	AAAG	36	9	Plus	Gossypium_aimondii
	TA39376_3635 Hypothetical protein At4g35530 [Arabidopsis thaliana (Mouse-ear cress)]	4	AAAG	24	6	Plus	Gossypium_hirsutum
53	CO102888 Hypothetical protein T5J17.10 [Arabidopsis thaliana (Mouse-ear cress)]	4	AATT	24	6	Plus	Gossypium_aimondii
	DW235242	4	AATT	20	5	Plus	Gossypium_hirsutum
	DV850022 Hypothetical protein [Medicago truncatula (Barrel medic)]	4	AATT	20	5	Plus	Gossypium_hirsutum
54	CO078485 Hypothetical protein [Medicago truncatula (Barrel medic)]	4	AATT	24	6	Plus	Gossypium_aimondii
	DW235242	4	AATT	20	5	Plus	Gossypium_hirsutum
	DV850022 Hypothetical protein [Medicago truncatula (Barrel medic)]	4	AATT	20	5	Plus	Gossypium_hirsutum
55	TA11144_29730 NAM-like protein [Prunus persica (Peach)]	4	ATAC	24	6	Plus	Gossypium_aimondii
	TA29199_3635	4	ATAC	20	5	Plus	Gossypium_hirsutum

Supplementary Table 4. Contd.

56	CO092319 Branched-chain-amino-acid aminotransferase 3, chloroplast precursor [Arabidopsis thaliana (Mouse-ear cress)]	5	GTTGA	30	6	Plus	Gossypium_raimondii
	TA25329_3635 Branched-chain-amino-acid aminotransferase 3, chloroplast precursor [Arabidopsis thaliana (Mouse-ear cress)]	5	GTTGA	25	5	Plus	Gossypium_hirsutum
57	TA11688_29730 Branched-chain-amino-acid aminotransferase 3, chloroplast precursor [Arabidopsis thaliana (Mouse-ear cress)]	5	GTTGA	30	6	Plus	Gossypium_raimondii
	TA25329_3635 Branched-chain-amino-acid aminotransferase 3, chloroplast precursor [Arabidopsis thaliana (Mouse-ear cress)]	5	GTTGA	25	5	Plus	Gossypium_hirsutum
58	CO078229 Branched-chain-amino-acid aminotransferase 3, chloroplast precursor [Arabidopsis thaliana (Mouse-ear cress)]	5	GTTGA	30	6	Plus	Gossypium_raimondii
	TA25329_3635 Branched-chain-amino-acid aminotransferase 3, chloroplast precursor [Arabidopsis thaliana (Mouse-ear cress)]	5	GTTGA	25	5	Plus	Gossypium_hirsutum
59	CO105097 Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MY113 [Arabidopsis thaliana (Mouse-ear cress)]	6	AAATG G	30	5	Plus	Gossypium_raimondii
	TA22883_3635 ZF-HD homeobox protein [Flaveria bidentis (Coastalplain yellowtops)]	6	ATGGA A	24	4	Plus	Gossypium_hirsutum
	DW224844 Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MY113 [Arabidopsis thaliana (Mouse-ear cress)]	6	ATGGA A	24	4	Plus	Gossypium_hirsutum
60	TA14584_29730	6	AACCT C	30	5	Plus	Gossypium_raimondii
	AI726550	6	AACCT C	24	4	Plus	Gossypium_hirsutum
61	CO085294 Granule bound starch synthase II precursor [Manihot esculenta (Cassava) (Manioc)]	6	AAGAT G	30	5	Plus	Gossypium_raimondii
	TA40470_3635	6	AAGAT G	24	4	Plus	Gossypium_hirsutum
62	CO097080 Hypothetical protein [Medicago truncatula (Barrel medic)]	6	AATGA G	36	6	Plus	Gossypium_raimondii
	TA25429_3635	6	AATGA G	30	5	Plus	Gossypium_hirsutum
	DW228127	6	AATGA G	36	6	Plus	Gossypium_hirsutum
	TA25430_3635 Hypothetical protein [Medicago truncatula (Barrel medic)]	6	AATGA G	36	6	Plus	Gossypium_hirsutum
63	TA14464_29730 SWAP/Surp; Ubiquitin [Medicago truncatula (Barrel medic)]	6	CAGCT G	30	5	Plus	Gossypium_raimondii

Supplementary Table 4. Contd.

	DT571043 SWAP/Supr; Ubiquitin [Medicago truncatula (Barrel medic)]	6	CAGCT G	24	4	Plus	Gossypium_hirsutum
64	TA9415_29730 Two-component response regulator-like APRR7 [Arabidopsis thaliana (Mouse-ear cress)]	6	GAGCG G	30	5	Plus	Gossypium_raidmondii
	TA26774_3635 Two-component response regulator-like PRR37 [Oryza sativa (Rice)]	6	GAGCG G	24	4	Plus	Gossypium_hirsutum
65	TA11166_29730 Zinc finger, RING-type; RINGv [Medicago truncatula (Barrel medic)]	6	GATAG G	30	5	Plus	Gossypium_raidmondii
	TA37112_3635 Zinc finger, RING-type; RINGv [Medicago truncatula (Barrel medic)]	6	GATAG G	24	4	Plus	Gossypium_hirsutum
66	TA17050_29730 Unknown protein [Nicotiana plumbaginifolia (Leadwort-leaved tobacco)]	6	TATATC	30	5	Plus	Gossypium_raidmondii
	TA28109_3635 ARIADNE-like protein ARI7 [Arabidopsis thaliana (Mouse-ear cress)]	6	TATATC	24	4	Plus	Gossypium_hirsutum
Group III							
HG	Sequence ID	Period Size	Period	Rep. Length	Copy Num.	Blast Strand	Species
1	TA9287_29730 Arabidopsis thaliana gl1 homolog [Arabidopsis thaliana (Mouse-ear cress)]	2	AT	20	10	Plus	Gossypium_raidmondii
	DT049270 Hypothetical protein [Medicago truncatula (Barrel medic)]	2	AT	24	12	Plus	Gossypium_hirsutum
2	CO114663 Arabidopsis thaliana gl1 homolog [Arabidopsis thaliana (Mouse-ear cress)]	2	AT	20	10	Plus	Gossypium_raidmondii
	DT049270 Hypothetical protein [Medicago truncatula (Barrel medic)]	2	AT	24	12	Plus	Gossypium_hirsutum
3	TA11468_29730 Hypothetical protein T11111.9 [Arabidopsis thaliana (Mouse-ear cress)]	2	CT	20	10	Plus	Gossypium_raidmondii
	TA23603_3635 Hypothetical protein T11111.9 [Arabidopsis thaliana (Mouse-ear cress)]	2	TC	22	11	Plus	Gossypium_hirsutum
4	CO096573 T2K10.11 protein [Arabidopsis thaliana (Mouse-ear cress)]	2	TC	20	10	Plus	Gossypium_raidmondii
	TA24566_3635 T2K10.11 protein [Arabidopsis thaliana (Mouse-ear cress)]	2	TC	22	11	Plus	Gossypium_hirsutum
5	CO113228	2	TG	20	10	Plus	Gossypium_raidmondii
	TA20238_3635	2	TG	28	14	Plus	Gossypium_hirsutum
6	CO092723	3	ACG	18	6	Plus	Gossypium_raidmondii
	DT562671	3	CGA	24	8	Plus	Gossypium_hirsutum
	DR044179	3	GAC	24	8	Plus	Gossypium_hirsutum

Supplementary Table 4. Contd.

	DR044172	3	GAC	27	9	Plus	Gossypium_hirsutum
7	CO121631	3	AGC	18	6	Plus	Gossypium_raidmondii
	TA22417_3635	3	GCT	18	6	Minus	Gossypium_hirsutum
	DN762148	3	GCT	24	8	Minus	Gossypium_hirsutum
8	TA14807_29730 Hypothetical protein [Medicago truncatula (Barrel medic)]	3	CAA	18	6	Plus	Gossypium_raidmondii
	AI729014 Hypothetical protein [Medicago truncatula (Barrel medic)]	3	CAA	21	7	Plus	Gossypium_hirsutum
	TA31876_3635 Hypothetical protein [Medicago truncatula (Barrel medic)]	3	CAA	21	7	Plus	Gossypium_hirsutum
9	TA16121_29730	3	CAG	18	6	Plus	Gossypium_raidmondii
	DR457648	3	CAG	24	8	Plus	Gossypium_hirsutum
10	TA16599_29730	3	CAG	24	8	Plus	Gossypium_raidmondii
	TA22510_3635	3	CAG	27	9	Plus	Gossypium_hirsutum
11	TA11781_29730 Hypothetical protein OSJNBa0003O19.4 [Oryza sativa (Rice)]	3	CGT	21	7	Plus	Gossypium_raidmondii
	DR463779 Zinc finger Glo3-like protein [Medicago sativa (Alfalfa)]	3	CGT	27	9	Plus	Gossypium_hirsutum
	AI727625 Hypothetical protein At4g17885 [Arabidopsis thaliana (Mouse-ear cress)]	3	CGT	27	9	Plus	Gossypium_hirsutum
13	TA9638_29730 Eukaryotic translation initiation factor 3 subunit 10 [Arabidopsis thaliana (Mouse-ear cress)]	3	CTG	18	6	Plus	Gossypium_raidmondii
	TA22416_3635 Translation initiation factor 3 [Oryza sativa (Rice)]	3	GCT	18	6	Plus	Gossypium_hirsutum
	TA22417_3635	3	GCT	18	6	Plus	Gossypium_hirsutum
	DN762148	3	GCT	24	8	Plus	Gossypium_hirsutum
14	TA13992_29730 Biotin/lipoyl attachment [Medicago truncatula (Barrel medic)]	3	CTT	18	6	Plus	Gossypium_raidmondii
	TA24677_3635 Biotin/lipoyl attachment [Medicago truncatula (Barrel medic)]	3	CTT	21	7	Plus	Gossypium_hirsutum
	DW518702 Biotin/lipoyl attachment [Medicago truncatula (Barrel medic)]	3	CTT	21	7	Plus	Gossypium_hirsutum
	TA24676_3635	3	CTT	24	8	Plus	Gossypium_hirsutum
15	TA14710_29730 Ultraviolet-B-repressible protein [Gossypium hirsutum (Upland cotton)]	3	CTT	21	7	Plus	Gossypium_raidmondii
	TA39593_3635 Ultraviolet-B-repressible protein [Gossypium hirsutum (Upland cotton)]	3	CTT	24	8	Plus	Gossypium_hirsutum
16	TA11488_29730 Nucleosome/chromatin assembly factor group A [Zea mays (Maize)]	3	GAA	18	6	Plus	Gossypium_raidmondii
	TA32508_3635 NAP1Ps [Pisum sativum (Garden pea)]	3	GAA	18	6	Plus	Gossypium_hirsutum
	TA32507_3635 Putative nucleosome assembly protein [Oryza sativa (japonica cultivar-group)]	3	GAA	21	7	Plus	Gossypium_hirsutum

Supplementary Table 4. Contd.

17	CO082472	3	AAG	18	6	Plus	Gossypium_raidondii
	DN760252	3	GAA	21	7	Plus	Gossypium_hirsutum
	DT526895	3	AAG	18	6	Plus	Gossypium_hirsutum
	TA34933_3635	3	AAG	18	6	Plus	Gossypium_hirsutum
	TA34933_3635	3	AGA	18	6	Plus	Gossypium_hirsutum
18	CO130189	3	GAC	18	6	Plus	Gossypium_raidondii
	DT562671	3	GAC	18	6	Plus	Gossypium_hirsutum
	DR044179	3	GAC	24	8	Plus	Gossypium_hirsutum
	DT562671	3	CGA	24	8	Plus	Gossypium_hirsutum
	CO130189	3	GAC	24	8	Plus	Gossypium_raidondii
	DR044172	3	GAC	27	9	Plus	Gossypium_hirsutum
19	CO090142 F6A14.10 protein [Arabidopsis thaliana (Mouse-ear cress)]	3	GAT	18	6	Plus	Gossypium_raidondii
	TA25557_3635 Putative SET protein, phosphatase 2A inhibitor; 76220-74135 [Arabidopsis thaliana (Mouse-ear cress)]	3	GAT	45	15	Plus	Gossypium_hirsutum
20	CO076869 Late embryogenesis-like protein [Prunus armeniaca (Apricot)]	3	GAT	18	6	Plus	Gossypium_raidondii
	DW225975 Late embryogenesis-like protein [Prunus armeniaca (Apricot)]	3	GAT	21	7	Plus	Gossypium_hirsutum
	DW499141 Late embryogenesis-like protein [Prunus armeniaca (Apricot)]	3	TGA	21	7	Plus	Gossypium_hirsutum
	TA20630_3635 Late embryogenesis-like protein [Prunus armeniaca (Apricot)]	3	TGA	21	7	Plus	Gossypium_hirsutum
21	CO093670	3	GAT	24	8	Plus	Gossypium_raidondii
	TA33834_3635	3	GAT	27	9	Plus	Gossypium_hirsutum
22	CO086193 Putative SET protein, phosphatase 2A inhibitor; 76220-74135 [Arabidopsis thaliana (Mouse-ear cress)]	3	GAT	18	6	Plus	Gossypium_raidondii
	TA25557_3635 Putative SET protein, phosphatase 2A inhibitor; 76220-74135 [Arabidopsis thaliana (Mouse-ear cress)]	3	GAT	45	15	Plus	Gossypium_hirsutum
23	CO097964 Emb CAB81597.1 [Arabidopsis thaliana (Mouse-ear cress)]	3	GAT	18	6	Plus	Gossypium_raidondii
	TA34412_3635 Emb CAB81597.1 [Arabidopsis thaliana (Mouse-ear cress)]	3	GAT	21	7	Plus	Gossypium_hirsutum
24	TA9239_29730 F6A14.10 protein [Arabidopsis thaliana (Mouse-ear cress)]	3	GAT	18	6	Plus	Gossypium_raidondii
	TA25557_3635 Putative SET protein, phosphatase 2A inhibitor; 76220-74135 [Arabidopsis thaliana (Mouse-ear cress)]	3	GAT	45	15	Plus	Gossypium_hirsutum
25	CO120982 Type-B response regulator [Catharanthus roseus (Rosy periwinkle) (Madagascar periwinkle)]	3	GCA	21	7	Plus	Gossypium_raidondii
	DT548587 Type-B response regulator [Catharanthus roseus (Rosy periwinkle) (Madagascar periwinkle)]	3	GCA	24	8	Plus	Gossypium_hirsutum
26	CO113411 At2g36630/F1O11.26 [Arabidopsis thaliana (Mouse-ear cress)]	3	GCC	18	6	Plus	Gossypium_raidondii

Supplementary Table 4. Contd.

	DW482895		3	CGC	21	7	Minus	Gossypium_hirsutum
	DW482894		3	GGC	21	7	Plus	Gossypium_hirsutum
27	TA9284_29730 At2g36630/F1O11.26 [Arabidopsis thaliana (Mouse-ear cress)]		3	GGC	18	6	Plus	Gossypium_raimondii
	DW482895		3	CGC	21	7	Minus	Gossypium_hirsutum
	DW482894		3	GGC	21	7	Plus	Gossypium_hirsutum
28	CO071933 At2g36630/F1O11.26 [Arabidopsis thaliana (Mouse-ear cress)]		3	GGC	18	6	Plus	Gossypium_raimondii
	DW482895		3	CGC	21	7	Minus	Gossypium_hirsutum
	DW482894		3	GGC	21	7	Plus	Gossypium_hirsutum
29	TA10085_29730		3	TCA	21	7	Plus	Gossypium_raimondii
	TA31716_3635		3	TCA	24	8	Plus	Gossypium_hirsutum
30	TA17016_29730		3	TCA	21	7	Plus	Gossypium_raimondii
	TA28467_3635 Putative bHLH transcription factor [Arabidopsis thaliana (Mouse-ear cress)]		3	CAT	18	6	Plus	Gossypium_hirsutum
	TA28466_3635		3	CAT	18	6	Plus	Gossypium_hirsutum
	TA17016_29730		3	CAT	21	7	Plus	Gossypium_raimondii
	TA28466_3635		3	CAT	27	9	Plus	Gossypium_hirsutum
31	CO116980		3	TCA	18	6	Plus	Gossypium_raimondii
	DT549374		3	TCA	24	8	Plus	Gossypium_hirsutum
32	CO128567 Putative arabinogalactan-protein [Oryza sativa (japonica cultivar-group)]		3	TCT	21	7	Plus	Gossypium_raimondii
	DR044171 Gb AAF02137.1 [Arabidopsis thaliana (Mouse-ear cress)]		3	TCT	27	9	Plus	Gossypium_hirsutum
	TA21781_3635 Gb AAF02137.1 [Arabidopsis thaliana (Mouse-ear cress)]		3	TCT	27	9	Plus	Gossypium_hirsutum
	TA21780_3635 At5g06390 [Arabidopsis thaliana (Mouse-ear cress)]		3	TCT	27	9	Plus	Gossypium_hirsutum
33	TA11292_29730 Hypothetical protein At2g35680; T20F21.13 [Arabidopsis thaliana (Mouse-ear cress)]		3	TCT	21	7	Plus	Gossypium_raimondii
	TA24343_3635 Hypothetical protein At2g35680; T20F21.13 [Arabidopsis thaliana (Mouse-ear cress)]		3	TCT	24	8	Plus	Gossypium_hirsutum
34	CO085995 Putative PTEN-like phosphatase [Oryza sativa (japonica cultivar-group)]		3	TCT	21	7	Plus	Gossypium_raimondii
	TA24343_3635 Hypothetical protein At2g35680; T20F21.13 [Arabidopsis thaliana (Mouse-ear cress)]		3	TCT	24	8	Plus	Gossypium_hirsutum
35	CO095090 Putative PTEN-like phosphatase [Oryza sativa (japonica cultivar-group)]		3	TCT	21	7	Plus	Gossypium_raimondii
	TA24343_3635 Hypothetical protein At2g35680; T20F21.13 [Arabidopsis thaliana (Mouse-ear cress)]		3	TCT	24	8	Plus	Gossypium_hirsutum

Supplementary Table 4. Contd.

36	TA12487_29730 Putative leucine-rich repeat disease resistance protein [Arabidopsis thaliana (Mouse-ear cress)]	3	TCT	21	7	Plus	Gossypium_aimondii
	TA35487_3635 Putative leucine-rich repeat disease resistance protein [Arabidopsis thaliana (Mouse-ear cress)]	3	TCT	24	8	Plus	Gossypium_hirsutum
37	CO125503 Late embryogenesis-like protein [Prunus armeniaca (Apricot)]	3	TGA	18	6	Plus	Gossypium_aimondii
	DT047070	3	TCA	21	7	Minus	Gossypium_hirsutum
	AJ513319 Late embryogenesis-like protein [Prunus armeniaca (Apricot)]	3	TGA	21	7	Plus	Gossypium_hirsutum
	DW499141 Late embryogenesis-like protein [Prunus armeniaca (Apricot)]	3	TGA	21	7	Plus	Gossypium_hirsutum
	TA20630_3635 Late embryogenesis-like protein [Prunus armeniaca (Apricot)]	3	TGA	21	7	Plus	Gossypium_hirsutum
38	CO123383 Salt tolerance protein [Sesuvium portulacastrum (Shoreline sea purslane)]	3	TGA	21	7	Plus	Gossypium_aimondii
	DT047070	3	TCA	21	7	Minus	Gossypium_hirsutum
	TA20630_3635 Late embryogenesis-like protein [Prunus armeniaca (Apricot)]	3	TGA	21	7	Plus	Gossypium_hirsutum
	AJ513319 Late embryogenesis-like protein [Prunus armeniaca (Apricot)]	3	TGA	21	7	Plus	Gossypium_hirsutum
	DW499141 Late embryogenesis-like protein [Prunus armeniaca (Apricot)]	3	TGA	21	7	Plus	Gossypium_hirsutum
	DW225975 Late embryogenesis-like protein [Prunus armeniaca (Apricot)]	3	GAT	21	7	Plus	Gossypium_hirsutum
	TA42103_3635	3	TGA	24	8	Plus	Gossypium_hirsutum
	CO493420 Late embryogenesis-like protein [Prunus armeniaca (Apricot)]	3	TGA	24	8	Plus	Gossypium_hirsutum
39	TA9193_29730 Salt tolerance protein [Sesuvium portulacastrum (Shoreline sea purslane)]	3	TGA	21	7	Plus	Gossypium_aimondii
	AJ513319 Late embryogenesis-like protein [Prunus armeniaca (Apricot)]	3	TGA	21	7	Plus	Gossypium_hirsutum
	DT047070	3	TCA	21	7	Minus	Gossypium_hirsutum
	TA20630_3635 Late embryogenesis-like protein [Prunus armeniaca (Apricot)]	3	TGA	21	7	Plus	Gossypium_hirsutum
	DW225975 Late embryogenesis-like protein [Prunus armeniaca (Apricot)]	3	GAT	21	7	Plus	Gossypium_hirsutum
	DW499141 Late embryogenesis-like protein [Prunus armeniaca (Apricot)]	3	TGA	21	7	Plus	Gossypium_hirsutum
	TA42103_3635	3	TGA	24	8	Plus	Gossypium_hirsutum
	CO493420 Late embryogenesis-like protein [Prunus armeniaca (Apricot)]	3	TGA	24	8	Plus	Gossypium_hirsutum
40	TA10749_29730 Phloroglucinol O-methyltransferase [Rosa chinensis var. spontanea]	3	TGA	21	7	Plus	Gossypium_aimondii
	TA35930_3635 Phloroglucinol O-methyltransferase [Rosa chinensis var. spontanea]	3	TGA	21	7	Plus	Gossypium_hirsutum
	DT048525	3	TCA	24	8	Minus	Gossypium_hirsutum
41	TA9659_29730 MADS box protein GHMADS-1 [Gossypium hirsutum (Upland cotton)]	3	TTA	18	6	Plus	Gossypium_aimondii
	DR457971	3	AAT	18	6	Minus	Gossypium_hirsutum
	DW231765 MADS box protein GHMADS-1 [Gossypium hirsutum (Upland cotton)]	3	TTA	18	6	Plus	Gossypium_hirsutum
	DT048252 MADS box protein GHMADS-1 [Gossypium hirsutum (Upland cotton)]	3	TTA	18	6	Plus	Gossypium_hirsutum
	DT457922 MADS box protein GHMADS-1 [Gossypium hirsutum (Upland cotton)]	3	TTA	21	7	Plus	Gossypium_hirsutum
	TA24540_3635 MADS box protein GHMADS-1 [Gossypium hirsutum (Upland cotton)]	3	TTA	21	7	Plus	Gossypium_hirsutum

Supplementary Table 4. Contd.

42	TA13626_29730 Hypothetical protein [Medicago truncatula (Barrel medic)]	3	TTC	21	7	Plus	Gossypium_raidmondii
	DR459816 Hypothetical protein [Medicago truncatula (Barrel medic)]	3	TTC	27	9	Plus	Gossypium_hirsutum
	TA26423_3635 Hypothetical protein [Medicago truncatula (Barrel medic)]	3	TTC	27	9	Plus	Gossypium_hirsutum
43	TA13856_29730 Thylakoid lumenal protein-like [Oryza sativa (japonica cultivar-group)]	3	TTC	18	6	Plus	Gossypium_raidmondii
	TA26484_3635 Thylakoid lumenal protein-like [Oryza sativa (japonica cultivar-group)]	3	TTC	18	6	Plus	Gossypium_hirsutum
	DN803954 Hypothetical protein At1g12250 [Arabidopsis thaliana (Mouse-ear cress)]	3	TTC	21	7	Plus	Gossypium_hirsutum
44	TA14465_29730 Acid phosphatase-like protein [Arabidopsis thaliana (Mouse-ear cress)]	3	TTC	24	8	Plus	Gossypium_raidmondii
	AI054761	3	TTC	27	9	Plus	Gossypium_hirsutum
45	CO105461 CBL-interacting serine/threonine-protein kinase 11 [Arabidopsis thaliana (Mouse-ear cress)]	3	TTC	18	6	Plus	Gossypium_raidmondii
	TA42588_3635 CBL-interacting serine/threonine-protein kinase 11 [Arabidopsis thaliana (Mouse-ear cress)]	3	TTC	24	8	Plus	Gossypium_hirsutum
46	CO074478 Thylakoid lumenal protein-like [Oryza sativa (japonica cultivar-group)]	3	TTC	18	6	Plus	Gossypium_raidmondii
	TA26484_3635 Thylakoid lumenal protein-like [Oryza sativa (japonica cultivar-group)]	3	TTC	18	6	Plus	Gossypium_hirsutum
	DN803954 Hypothetical protein At1g12250 [Arabidopsis thaliana (Mouse-ear cress)]	3	TTC	21	7	Plus	Gossypium_hirsutum
47	CO123080	3	TTC	18	6	Plus	Gossypium_raidmondii
	DN802775	3	TTC	21	7	Plus	Gossypium_hirsutum
48	CO069614 Acid phosphatase 1 precursor (EC 3.1.3.2) (Apase-1(1)) [Lycopersicon esculentum (Tomato)]	3	TTC	24	8	Plus	Gossypium_raidmondii
	AI054761	3	TTC	27	9	Plus	Gossypium_hirsutum
49	TA13320_29730	4	GACA	20	5	Plus	Gossypium_raidmondii
	TA28576_3635	4	GACA	24	6	Plus	Gossypium_hirsutum
50	CO075206	4	GATA	20	5	Plus	Gossypium_raidmondii
	TA26759_3635	4	TATC	24	6	Minus	Gossypium_hirsutum
51	TA12438_29730	3	TGG	21	7	Plus	Gossypium_raidmondii
	TA22248_3635	3	CAC	39	13	Minus	Gossypium_hirsutum
	TA22249_3635	3	CAC	18	6	Minus	Gossypium_hirsutum
	DN801177	3	CAC	39	13	Minus	Gossypium_hirsutum
52	TA10237_29730 Expressed protein [Arabidopsis thaliana (Mouse-ear cress)]	4	TTTA	20	5	Plus	Gossypium_raidmondii

Supplementary Table 4. Contd.

	TA22189_3635 Expressed protein [Arabidopsis thaliana (Mouse-ear cress)]	4	TTTA	24	6	Plus	Gossypium_hirsutum
	TA22190_3635 Expressed protein [Arabidopsis thaliana (Mouse-ear cress)]	4	TTTA	24	6	Plus	Gossypium_hirsutum
	DT569576 Expressed protein [Arabidopsis thaliana (Mouse-ear cress)]	4	TTTA	24	6	Plus	Gossypium_hirsutum
53	TA10238_29730 Hypothetical protein [Medicago truncatula (Barrel medic)]	4	TTTA	20	5	Plus	Gossypium_raimondii
	TA22190_3635 Expressed protein [Arabidopsis thaliana (Mouse-ear cress)]	4	TTTA	24	6	Plus	Gossypium_hirsutum
	DT569576 Expressed protein [Arabidopsis thaliana (Mouse-ear cress)]	4	TTTA	24	6	Plus	Gossypium_hirsutum
	TA22189_3635 Expressed protein [Arabidopsis thaliana (Mouse-ear cress)]	4	TTTA	24	6	Plus	Gossypium_hirsutum
54	TA14521_29730 Protein At2g38820 [Arabidopsis thaliana (Mouse-ear cress)]	6	CCTTCA	24	4	Plus	Gossypium_raimondii
	TA39319_3635 Protein At2g38820 [Arabidopsis thaliana (Mouse-ear cress)]	6	CCTTCA	30	5	Plus	Gossypium_hirsutum
55	CO116889 Fas-associated factor 1-like protein [Capsicum annuum (Bell pepper)]	6	GCCTCC	30	5	Plus	Gossypium_raimondii
	TA24449_3635 Fas-associated factor 1-like protein [Capsicum annuum (Bell pepper)]	6	GCCTCC	36	6	Plus	Gossypium_hirsutum
56	TA9155_29730 Splicing factor SR1D [Arabidopsis thaliana (Mouse-ear cress)]	6	GGAGCA	24	4	Plus	Gossypium_raimondii
	TA22897_3635 Splicing factor SR1D [Arabidopsis thaliana (Mouse-ear cress)]	6	GGAGCA	30	5	Plus	Gossypium_hirsutum
57	TA17292_29730 Hypothetical protein OJ1150_A11.18 [Oryza sativa (japonica cultivar-group)]	6	TCACCA	24	4	Plus	Gossypium_raimondii
	TA32583_3635 Hypothetical protein OJ1150_A11.18 [Oryza sativa (japonica cultivar-group)]	6	TCACCA	30	5	Plus	Gossypium_hirsutum
58	CO123990	6	TGCTCC	24	4	Plus	Gossypium_raimondii
	TA22898_3635	6	GGAGCA	36	6	Minus	Gossypium_hirsutum
59	TA9156_29730	6	TGCTCC	24	4	Plus	Gossypium_raimondii
	TA22898_3635	6	GGAGCA	36	6	Minus	Gossypium_hirsutum
60	CO110189	6	TGCTCC	24	4	Plus	Gossypium_raimondii
	TA22898_3635	6	GGAGCA	36	6	Minus	Gossypium_hirsutum
61	CO086499	6	TGCTCC	24	4	Plus	Gossypium_raimondii
	TA22898_3635	6	GGAGCA	36	6	Minus	Gossypium_hirsutum

Supplementary Table 5.

Group I							
HG	Sequence ID	Period Size	Period	Rep. Length	Copy Num.	Blast Strand	Species
1	BQ405858	2	GA	18	9	Plus	Gossypium_arboreum
	CO103483 F26K24.14 protein [Arabidopsis thaliana (Mouse-ear cress)]	2	GA	18	9	Plus	Gossypium_aimondii
2	BQ402652 Eukaryotic translation initiation factor 2 subunit beta [Triticum aestivum (Wheat)]	3	AAG	18	6	Plus	Gossypium_arboreum
	CO088220 Eukaryotic translation initiation factor 2 subunit beta [Triticum aestivum (Wheat)]	3	AAG	18	6	Plus	Gossypium_aimondii
	TA14327_29730 Eukaryotic translation initiation factor 2 beta subunit-like [Solanum tuberosum (Potato)]	3	AAG	18	6	Plus	Gossypium_aimondii
3	BE052321 Putative ubiquinol-cytochrome-c reductase cytochrome c1 [Oryza sativa (japonica cultivar-group)]	3	ACC	18	6	Plus	Gossypium_arboreum
	TA9532_29730 Putative ubiquinol-cytochrome-c reductase cytochrome c1 [Oryza sativa (japonica cultivar-group)]	3	ACC	18	6	Plus	Gossypium_aimondii
4	BG440558 Putative ubiquinol-cytochrome-c reductase cytochrome c1 [Oryza sativa (japonica cultivar-group)]	3	ACC	18	6	Plus	Gossypium_arboreum
	TA9532_29730 Putative ubiquinol-cytochrome-c reductase cytochrome c1 [Oryza sativa (japonica cultivar-group)]	3	ACC	18	6	Plus	Gossypium_aimondii
5	BG443450	3	ACC	18	6	Plus	Gossypium_arboreum
	TA9532_29730 Putative ubiquinol-cytochrome-c reductase cytochrome c1 [Oryza sativa (japonica cultivar-group)]	3	ACC	18	6	Plus	Gossypium_aimondii
6	TA5263_29729 Cytochrome c1, heme protein, mitochondrial precursor [Solanum tuberosum (Potato)]	3	ACC	18	6	Plus	Gossypium_arboreum
	TA9532_29730 Putative ubiquinol-cytochrome-c reductase cytochrome c1 [Oryza sativa (japonica cultivar-group)]	3	ACC	18	6	Plus	Gossypium_aimondii
7	BM360664 Cytochrome c1 [Arabidopsis thaliana (Mouse-ear cress)]	3	ACC	18	6	Plus	Gossypium_arboreum
	TA9532_29730 Putative ubiquinol-cytochrome-c reductase cytochrome c1 [Oryza sativa (japonica cultivar-group)]	3	ACC	18	6	Plus	Gossypium_aimondii
8	BQ411088 4-alpha-glucanotransferase [Solanum tuberosum (Potato)]	3	ATT	51	17	Plus	Gossypium_arboreum
	CO075512	3	AAT	51	17	Minus	Gossypium_aimondii
	TA9504_29730 Putative 4-alpha-glucanotransferase [Oryza sativa (japonica cultivar-group)]	3	ATT	51	17	Plus	Gossypium_aimondii
9	BG443488 Putative Rar1 protein [Solanum demissum (Wild potato)]	3	CCA	21	7	Plus	Gossypium_arboreum
	CO092245 RAR1 [Arabidopsis thaliana (Mouse-ear cress)]	3	CCA	21	7	Plus	Gossypium_aimondii
10	BF276058 Putative Rar1 protein [Solanum demissum (Wild potato)]	3	CCA	21	7	Plus	Gossypium_arboreum
	CO092245 RAR1 [Arabidopsis thaliana (Mouse-ear cress)]	3	CCA	21	7	Plus	Gossypium_aimondii
11	BQ403789 RAR1 [Arabidopsis thaliana (Mouse-ear cress)]	3	CCA	21	7	Plus	Gossypium_arboreum
	CO092245 RAR1 [Arabidopsis thaliana (Mouse-ear cress)]	3	CCA	21	7	Plus	Gossypium_aimondii

Supplementary Table 5. Contd.

12	BG446135	3	CTT	18	6	Plus	Gossypium_arboreum
	TA14664_29730 Zinc finger, RING-type; RINGv [Medicago truncatula (Barrel medic)]	3	CTT	18	6	Plus	Gossypium_aimondii
13	BE052283 Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:K14A3 [Arabidopsis thaliana (Mouse-ear cress)]	3	CTT	18	6	Plus	Gossypium_arboreum
	CO080640 Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:K14A3 [Arabidopsis thaliana (Mouse-ear cress)]	3	CTT	18	6	Plus	Gossypium_aimondii
14	BQ405354 Ultraviolet-B-repressible protein [Gossypium hirsutum (Upland cotton)]	3	CTT	21	7	Plus	Gossypium_arboreum
	TA14710_29730 Ultraviolet-B-repressible protein [Gossypium hirsutum (Upland cotton)]	3	CTT	21	7	Plus	Gossypium_aimondii
15	BG445086	3	GAT	18	6	Plus	Gossypium_arboreum
	TA15485_29730 Hypothetical protein At3g20260 [Arabidopsis thaliana (Mouse-ear cress)]	3	GAT	18	6	Plus	Gossypium_aimondii
16	BG442229 Von Willebrand factor, type A; Ubiquitin interacting motif [Medicago truncatula (Barrel medic)]	3	TGC	18	6	Plus	Gossypium_arboreum
	CO088783 Von Willebrand factor, type A; Ubiquitin interacting motif [Medicago truncatula (Barrel medic)]	3	TGC	18	6	Plus	Gossypium_aimondii
	CO105343 Von Willebrand factor, type A; Ubiquitin interacting motif [Medicago truncatula (Barrel medic)]	3	TGC	18	6	Plus	Gossypium_aimondii
17	BQ404857 Hypothetical protein [Medicago truncatula (Barrel medic)]	3	TTC	21	7	Plus	Gossypium_arboreum
	CO099414 Hypothetical protein OJ1734_E02.2 [Oryza sativa (japonica cultivar-group)]	3	TTC	21	7	Plus	Gossypium_aimondii
	TA13626_29730 Hypothetical protein [Medicago truncatula (Barrel medic)]	3	TTC	21	7	Plus	Gossypium_aimondii
18	TA7048_29729 Hypothetical protein [Medicago truncatula (Barrel medic)]	3	TTC	21	7	Plus	Gossypium_arboreum
	CO099414 Hypothetical protein OJ1734_E02.2 [Oryza sativa (japonica cultivar-group)]	3	TTC	21	7	Plus	Gossypium_aimondii
	TA13626_29730 Hypothetical protein [Medicago truncatula (Barrel medic)]	3	TTC	21	7	Plus	Gossypium_aimondii
19	BM357948 Mitogen-activated protein kinase [Euphorbia esula (Leafy spurge)]	4	TATG	20	5	Plus	Gossypium_arboreum
	TA14305_29730 Mitogen-activated protein kinase 1 [Lycopersicon esculentum (Tomato)]	4	TATG	20	5	Plus	Gossypium_aimondii
	TA16726_29730 Mitogen-activated protein kinase 2 [Lycopersicon esculentum (Tomato)]	4	TATG	20	5	Plus	Gossypium_aimondii
20	TA7673_29729 Transthyretin-like protein [Arabidopsis thaliana (Mouse-ear cress)]	5	AGAAG	25	5	Plus	Gossypium_arboreum
	CO107385 Transthyretin-like protein [Arabidopsis thaliana (Mouse-ear cress)]	5	AGAAG	25	5	Plus	Gossypium_aimondii
	TA10548_29730 Transthyretin-like protein [Arabidopsis thaliana (Mouse-ear cress)]	5	AGAAG	25	5	Plus	Gossypium_aimondii
	CO106914 Transthyretin-like protein [Arabidopsis thaliana (Mouse-ear cress)]	5	AGAAG	25	5	Plus	Gossypium_aimondii
	CO071413 Transthyretin-like protein [Arabidopsis thaliana (Mouse-ear cress)]	5	AGAAG	25	5	Plus	Gossypium_aimondii
21	BG444055 DNA-binding protein-related-like [Oryza sativa (japonica cultivar-group)]	5	AGAGA	30	6	Plus	Gossypium_arboreum

Supplementary Table 5. Contd.

	TA13177_29730 DNA-binding protein-related-like [Oryza sativa (japonica cultivar-group)]	5	AGAGA	30	6	Plus	Gossypium_aimondii
22	BQ412345	5	CAAAC	25	5	Plus	Gossypium_arboreum
	CO107215	5	CAAAC	25	5	Plus	Gossypium_aimondii
Group II							
HG	Sequence ID	Period Size	Period	Rep. Length	Copy Num.	Blast Strand	Species
1	BF269259	3	CAG	21	7	Plus	Gossypium_arboreum
	CO086279	3	CTG	18	6	Minus	Gossypium_aimondii
2	BQ413494	3	CAT	24	8	Plus	Gossypium_arboreum
	CO119751	3	CAT	21	7	Plus	Gossypium_aimondii
3	BQ415217 CBS1 [Hyacinthus orientalis (Common hyacinth)]	3	GAT	24	8	Plus	Gossypium_arboreum
	TA14678_29730 CBS1 [Hyacinthus orientalis (Common hyacinth)]	3	GAT	21	7	Plus	Gossypium_aimondii
4	TA7800_29729 CBS1 [Hyacinthus orientalis (Common hyacinth)]	3	GAT	24	8	Plus	Gossypium_arboreum
	TA14678_29730 CBS1 [Hyacinthus orientalis (Common hyacinth)]	3	GAT	21	7	Plus	Gossypium_aimondii
5	BQ405592 unknown protein [Arabidopsis thaliana]	3	GTG	21	7	Plus	Gossypium_arboreum
	TA10731_29730 unknown protein [Arabidopsis thaliana]	3	GTG	18	6	Plus	Gossypium_aimondii
6	BG444426	3	TCT	24	8	Plus	Gossypium_arboreum
	CO128567 Putative arabinogalactan-protein [Oryza sativa (japonica cultivar-group)]	3	TCT	21	7	Plus	Gossypium_aimondii
7	CK640498 Late embryogenesis-like protein [Prunus armeniaca (Apricot)]	3	TGA	24	8	Plus	Gossypium_arboreum
	CO076869 Late embryogenesis-like protein [Prunus armeniaca (Apricot)]	3	GAT	18	6	Plus	Gossypium_aimondii
	CO125503 Late embryogenesis-like protein [Prunus armeniaca (Apricot)]	3	TGA	18	6	Plus	Gossypium_aimondii
	CO123383 Salt tolerance protein [Sesuvium portulacastrum (Shoreline sea purslane)]	3	TGA	21	7	Plus	Gossypium_aimondii
	TA9193_29730 Salt tolerance protein [Sesuvium portulacastrum (Shoreline sea purslane)]	3	TGA	21	7	Plus	Gossypium_aimondii
8	BQ410226	3	TGA	24	8	Plus	Gossypium_arboreum
	CO121651	3	TGA	21	7	Plus	Gossypium_aimondii
9	BF277771 Alanine aminotransferase [Capsicum annuum (Bell pepper)]	3	TTC	21	7	Plus	Gossypium_arboreum
	TA10152_29730 Alanine aminotransferase [Arabidopsis thaliana (Mouse-ear cress)]	3	CTT	18	6	Plus	Gossypium_aimondii

Supplementary Table 5. Contd.

Group III		Period Size	Period	Rep. Length	Copy Num.	Blast Strand	Species
HG	Sequence ID						
1	BF268601	2	TA	24	12	Plus	Gossypium_arboreum
	CO102551	2	AT	28	14	Minus	Gossypium_raidmondii
2	BF270284 Pentaxin [Medicago truncatula (Barrel medic)]	2	TC	18	9	Plus	Gossypium_arboreum
	CO108840 F6I1.14 protein [Arabidopsis thaliana (Mouse-ear cress)]	2	TC	20	10	Plus	Gossypium_raidmondii
3	BG444624	3	AGA	18	6	Plus	Gossypium_arboreum
	CO116035 Adenylate translocator (Brittle-1)-like protein [Arabidopsis thaliana (Mouse-ear cress)]	3	AGA	21	7	Plus	Gossypium_raidmondii
	CO129567 Adenylate translocator (Brittle-1)-like protein [Arabidopsis thaliana (Mouse-ear cress)]	3	AGA	21	7	Plus	Gossypium_raidmondii
4	BE055500 MYC2 [Catharanthus roseus (Rosy periwinkle) (Madagascar periwinkle)]	3	CTC	18	6	Plus	Gossypium_arboreum
	TA17138_29730 MYC2 [Catharanthus roseus (Rosy periwinkle) (Madagascar periwinkle)]	3	CTC	21	7	Plus	Gossypium_raidmondii
5	BE054572 Calnexin [Glycine max (Soybean)]	3	GAA	21	7	Plus	Gossypium_arboreum
	TA9085_29730	3	TCT	27	9	Minus	Gossypium_raidmondii
	TA9084_29730 Calnexin [Glycine max (Soybean)]	3	GAA	27	9	Plus	Gossypium_raidmondii
6	BM359886 Cleft lip and palate associated transmembrane protein-like [Arabidopsis thaliana (Mouse-ear cress)]	3	GGA	21	7	Plus	Gossypium_arboreum
	CO085114 Cleft lip and palate associated transmembrane protein-like [Arabidopsis thaliana (Mouse-ear cress)]	3	GGA	24	8	Plus	Gossypium_raidmondii
7	BQ402342	3	TCT	21	7	Plus	Gossypium_arboreum
	TA9085_29730	3	TCT	27	9	Plus	Gossypium_raidmondii
8	TA5514_29729 Salt tolerance protein [Sesuvium portulacastrum (Shoreline sea purslane)]	3	TGA	18	6	Plus	Gossypium_arboreum
	CO076869 Late embryogenesis-like protein [Prunus armeniaca (Apricot)]	3	GAT	18	6	Plus	Gossypium_raidmondii
	CO125503 Late embryogenesis-like protein [Prunus armeniaca (Apricot)]	3	TGA	18	6	Plus	Gossypium_raidmondii
	CO123383 Salt tolerance protein [Sesuvium portulacastrum (Shoreline sea purslane)]	3	TGA	21	7	Plus	Gossypium_raidmondii
	TA9193_29730 Salt tolerance protein [Sesuvium portulacastrum (Shoreline sea purslane)]	3	TGA	21	7	Plus	Gossypium_raidmondii
9	TA5985_29729 Protein At3g63460 [Arabidopsis thaliana (Mouse-ear cress)]	3	TTA	18	6	Plus	Gossypium_arboreum
	TA17231_29730 Protein At3g63460 [Arabidopsis thaliana (Mouse-ear cress)]	3	TTA	21	7	Plus	Gossypium_raidmondii
10	BQ405038 Hypothetical protein T5J17.10 [Arabidopsis thaliana (Mouse-ear cress)]	4	AATT	20	5	Plus	Gossypium_arboreum

Supplementary Table 5. Contd.

	CO102888 Hypothetical protein T5J17.10 [Arabidopsis thaliana (Mouse-ear cress)]	4	AATT	24	6	Plus	Gossypium_raidmondii
	CO078485 Hypothetical protein [Medicago truncatula (Barrel medic)]	4	AATT	24	6	Plus	Gossypium_raidmondii
11	BG445815 T5A14.7 protein [Arabidopsis thaliana (Mouse-ear cress)]	6	GATAGG	24	4	Plus	Gossypium_arboreum
	TA11166_29730 Zinc finger, RING-type; RINGv [Medicago truncatula (Barrel medic)]	6	GATAGG	30	5	Plus	Gossypium_raidmondii
12	BG445177	6	GATAGG	24	4	Plus	Gossypium_arboreum
	TA11166_29730 Zinc finger, RING-type; RINGv [Medicago truncatula (Barrel medic)]	6	GATAGG	30	5	Plus	Gossypium_raidmondii

Supplementary Table 6.

HG with identical repeat number		Period Size	Period	Rep. Length	Copy Num.	Blast Strand	Species
HG	Sequence ID						
1	BQ402652 Eukaryotic translation initiation factor 2 subunit beta [Triticum aestivum (Wheat)]	3	AAG	18	6	Plus	Gossypium_arboreum
	CO088220 Eukaryotic translation initiation factor 2 subunit beta [Triticum aestivum (Wheat)]	3	AAG	18	6	Plus	Gossypium_raidmondii
	TA14327_29730 Eukaryotic translation initiation factor 2 beta subunit-like [Solanum tuberosum (Potato)]	3	AAG	18	6	Plus	Gossypium_raidmondii
	TA28888_3635 Eukaryotic translation initiation factor 2 beta subunit-like [Solanum tuberosum (Potato)]	3	AAG	18	6	Plus	Gossypium_hirsutum
2	BQ403789 RAR1 [Arabidopsis thaliana (Mouse-ear cress)]	3	CCA	21	7	Plus	Gossypium_arboreum
	DN800615 RAR1 [Arabidopsis thaliana (Mouse-ear cress)]	3	CCA	21	7	Plus	Gossypium_hirsutum
	CO092245 RAR1 [Arabidopsis thaliana (Mouse-ear cress)]	3	CCA	21	7	Plus	Gossypium_raidmondii
	TA23709_3635 Putative Rar1 protein [Solanum demissum (Wild potato)]	3	CCA	21	7	Plus	Gossypium_hirsutum
3	BF276058 Putative Rar1 protein [Solanum demissum (Wild potato)]	3	CCA	21	7	Plus	Gossypium_arboreum
	DN800615 RAR1 [Arabidopsis thaliana (Mouse-ear cress)]	3	CCA	21	7	Plus	Gossypium_hirsutum
	CO092245 RAR1 [Arabidopsis thaliana (Mouse-ear cress)]	3	CCA	21	7	Plus	Gossypium_raidmondii
	TA23709_3635 Putative Rar1 protein [Solanum demissum (Wild potato)]	3	CCA	21	7	Plus	Gossypium_hirsutum
4	BG443488 Putative Rar1 protein [Solanum demissum (Wild potato)]	3	CCA	21	7	Plus	Gossypium_arboreum
	DN800615 RAR1 [Arabidopsis thaliana (Mouse-ear cress)]	3	CCA	21	7	Plus	Gossypium_hirsutum
	CO092245 RAR1 [Arabidopsis thaliana (Mouse-ear cress)]	3	CCA	21	7	Plus	Gossypium_raidmondii

Supplementary Table 6. Contd.

	TA23709_3635 Putative Rar1 protein [Solanum demissum (Wild potato)]	3	CCA	21	7	Plus	Gossypium_hirsutum
5	BE052283 Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:K14A3 [Arabidopsis thaliana (Mouse-ear cress)]	3	CTT	18	6	Plus	Gossypium_arboreum
	DW496704 Hypothetical protein [Brassica oleracea (Wild cabbage)]	3	CTT	18	6	Plus	Gossypium_hirsutum
	CO080640 Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:K14A3 [Arabidopsis thaliana (Mouse-ear cress)]	3	CTT	18	6	Plus	Gossypium_raimondii
6	BM357948 Mitogen-activated protein kinase [Euphorbia esula (Leafy spurge)]	4	TATG	20	5	Plus	Gossypium_arboreum
	TA14305_29730 Mitogen-activated protein kinase 1 [Lycopersicon esculentum (Tomato)]	4	TATG	20	5	Plus	Gossypium_raimondii
	TA23495_3635 Mitogen-activated protein kinase 1 [Lycopersicon esculentum (Tomato)]	4	TATG	20	5	Plus	Gossypium_hirsutum
	TA16726_29730 Mitogen-activated protein kinase 2 [Lycopersicon esculentum (Tomato)]	4	TATG	20	5	Plus	Gossypium_raimondii
HG with different repeat number							
HG	Sequence ID	Period Size	Period	Rep. Length	Copy Num.	Blast Strand	Species
1	BF268204	2	TC	28	14	Plus	Gossypium_arboreum
	TA13307_29730 Hypothetical protein [Medicago truncatula (Barrel medic)]	2	CT	26	13	Plus	Gossypium_raimondii
	DN802296	2	CT	20	10	Plus	Gossypium_hirsutum
	TA35543_3635 Hypothetical protein [Medicago truncatula (Barrel medic)]	2	TC	22	11	Plus	Gossypium_hirsutum
2	TA5890_29729 LIM-domain SF3 protein [Nicotiana tabacum (Common tobacco)]	2	CT	30	15	Plus	Gossypium_arboreum
	CO094613 LIM-domain SF3 protein [Nicotiana tabacum (Common tobacco)]	2	CT	20	10	Plus	Gossypium_raimondii
	DR458537 Putative LIM domain protein PLIM-2 [Oryza sativa (japonica cultivar-group)]	2	CT	22	11	Plus	Gossypium_hirsutum
	AI054962 Putative LIM domain protein PLIM-2 [Oryza sativa (japonica cultivar-group)]	2	CT	22	11	Plus	Gossypium_hirsutum
3	TA7156_29729 Hypothetical protein [Medicago truncatula (Barrel medic)]	2	TC	28	14	Plus	Gossypium_arboreum
	TA13307_29730 Hypothetical protein [Medicago truncatula (Barrel medic)]	2	CT	26	13	Plus	Gossypium_raimondii
	DN802296	2	CT	20	10	Plus	Gossypium_hirsutum
	TA35543_3635 Hypothetical protein [Medicago truncatula (Barrel medic)]	2	TC	22	11	Plus	Gossypium_hirsutum
4	BF272268 OSJNBb0039L24.7 protein [Oryza sativa (japonica cultivar-group)]	2	CT	30	15	Plus	Gossypium_arboreum
	CO094613 LIM-domain SF3 protein [Nicotiana tabacum (Common tobacco)]	2	CT	20	10	Plus	Gossypium_raimondii
	DR458537 Putative LIM domain protein PLIM-2 [Oryza sativa (japonica cultivar-group)]	2	CT	22	11	Plus	Gossypium_hirsutum
	AI054962 Putative LIM domain protein PLIM-2 [Oryza sativa (japonica cultivar-group)]	2	CT	22	11	Plus	Gossypium_hirsutum

Supplementary Table 6. Contd.

5	BE052113	2	CT	26	13	Plus	Gossypium_arboreum
	TA12822_29730	2	CT	22	11	Plus	Gossypium_raidmondii
	TA30762_3635 Targeting protein for Xklp2 containing protein, expressed [Oryza sativa (japonica cultivar-group)]	2	TC	22	11	Plus	Gossypium_hirsutum
6	BF270284 Pentaxin [Medicago truncatula (Barrel medic)]	2	TC	18	9	Plus	Gossypium_arboreum
	CO108840 F6I1.14 protein [Arabidopsis thaliana (Mouse-ear cress)]	2	TC	20	10	Plus	Gossypium_raidmondii
	TA44152_3635 F6I1.14 protein [Arabidopsis thaliana (Mouse-ear cress)]	2	TC	22	11	Plus	Gossypium_hirsutum
7	BF276199 Putative early nodule-specific-like protein ENOD8 [Oryza sativa (japonica cultivar-group)]	3	AAG	21	7	Plus	Gossypium_arboreum
	CO086777 Putative early nodule-specific-like protein ENOD8 [Oryza sativa (japonica cultivar-group)]	3	AAG	18	6	Plus	Gossypium_raidmondii
	TA35757_3635 Putative early nodule-specific-like protein ENOD8 [Oryza sativa (japonica cultivar-group)]	3	AAG	24	8	Plus	Gossypium_hirsutum
8	TA5263_29729 Cytochrome c1, heme protein, mitochondrial precursor [Solanum tuberosum (Potato)]	3	ACC	18	6	Plus	Gossypium_arboreum
	TA9532_29730 Putative ubiquinol-cytochrome-c reductase cytochrome c1 [Oryza sativa (japonica cultivar-group)]	3	ACC	18	6	Plus	Gossypium_raidmondii
	TA24730_3635 Putative ubiquinol-cytochrome-c reductase cytochrome c1 [Oryza sativa (japonica cultivar-group)]	3	ACC	24	8	Plus	Gossypium_hirsutum
9	BG444624	3	AGA	18	6	Plus	Gossypium_arboreum
	CO116035 Adenylate translocator (Brittle-1)-like protein [Arabidopsis thaliana (Mouse-ear cress)]	3	AGA	21	7	Plus	Gossypium_raidmondii
	CO129567 Adenylate translocator (Brittle-1)-like protein [Arabidopsis thaliana (Mouse-ear cress)]	3	AGA	21	7	Plus	Gossypium_raidmondii
	TA23448_3635 Adenylate translocator (Brittle-1)-like protein [Arabidopsis thaliana (Mouse-ear cress)]	3	AGA	18	6	Plus	Gossypium_hirsutum
10	BQ411088 4-alpha-glucanotransferase [Solanum tuberosum (Potato)]	3	ATT	51	17	Plus	Gossypium_arboreum
	CO075512	3	AAT	51	17	Minus	Gossypium_raidmondii
	TA9504_29730 Putative 4-alpha-glucanotransferase [Oryza sativa (japonica cultivar-group)]	3	ATT	51	17	Plus	Gossypium_raidmondii
	TA38929_3635 4-alpha-glucanotransferase [Solanum tuberosum (Potato)]	3	ATT	33	11	Plus	Gossypium_hirsutum
11	TA6708_29729	3	CAG	33	11	Plus	Gossypium_arboreum
	TA16599_29730	3	CAG	24	8	Plus	Gossypium_raidmondii
	TA22510_3635	3	CAG	27	9	Plus	Gossypium_hirsutum
12	BF269259	3	CAG	21	7	Plus	Gossypium_arboreum
	CO086279	3	CTG	18	6	Minus	Gossypium_raidmondii
	TA37795_3635	3	TGC	18	6	Minus	Gossypium_hirsutum

Supplementary Table 6. Contd.

13	BE055500 MYC2 [Catharanthus roseus (Rosy periwinkle) (Madagascar periwinkle)]	3	CTC	18	6	Plus	Gossypium_arboreum
	TA17138_29730 MYC2 [Catharanthus roseus (Rosy periwinkle) (Madagascar periwinkle)]	3	CTC	21	7	Plus	Gossypium_raidmondii
	TA21503_3635	3	CTC	21	7	Plus	Gossypium_hirsutum
14	BQ405354 Ultraviolet-B-repressible protein [Gossypium hirsutum (Upland cotton)]	3	CTT	21	7	Plus	Gossypium_arboreum
	TA14710_29730 Ultraviolet-B-repressible protein [Gossypium hirsutum (Upland cotton)]	3	CTT	21	7	Plus	Gossypium_raidmondii
	TA39593_3635 Ultraviolet-B-repressible protein [Gossypium hirsutum (Upland cotton)]	3	CTT	24	8	Plus	Gossypium_hirsutum
15	BE054572 Calnexin [Glycine max (Soybean)]	3	GAA	21	7	Plus	Gossypium_arboreum
	TA9085_29730	3	TCT	27	9	Minus	Gossypium_raidmondii
	TA9084_29730 Calnexin [Glycine max (Soybean)]	3	GAA	27	9	Plus	Gossypium_raidmondii
	TA22700_3635 Calnexin [Glycine max (Soybean)]	3	GAA	21	7	Plus	Gossypium_hirsutum
16	BM359886 Cleft lip and palate associated transmembrane protein-like [Arabidopsis thaliana (Mouse-ear cress)]	3	GGA	21	7	Plus	Gossypium_arboreum
	CO085114 Cleft lip and palate associated transmembrane protein-like [Arabidopsis thaliana (Mouse-ear cress)]	3	GGA	24	8	Plus	Gossypium_raidmondii
	TA28051_3635 Cleft lip and palate associated transmembrane protein-like [Arabidopsis thaliana (Mouse-ear cress)]	3	GGA	24	8	Plus	Gossypium_hirsutum
	DT559190 Cleft lip and palate associated transmembrane protein-like [Arabidopsis thaliana (Mouse-ear cress)]	3	GGA	27	9	Plus	Gossypium_hirsutum
17	BQ405592 unknown protein [Arabidopsis thaliana]	3	GTG	21	7	Plus	Gossypium_arboreum
	TA10731_29730 unknown protein [Arabidopsis thaliana]	3	GTG	18	6	Plus	Gossypium_raidmondii
	TA38018_3635 unknown protein [Arabidopsis thaliana]	3	GTG	18	6	Plus	Gossypium_hirsutum
18	TA5514_29729 Salt tolerance protein [Sesuvium portulacastrum (Shoreline sea purslane)]	3	TGA	18	6	Plus	Gossypium_arboreum
	CO125503 Late embryogenesis-like protein [Prunus armeniaca (Apricot)]	3	TGA	18	6	Plus	Gossypium_raidmondii
	CO123383 Salt tolerance protein [Sesuvium portulacastrum (Shoreline sea purslane)]	3	TGA	21	7	Plus	Gossypium_raidmondii
	TA9193_29730 Salt tolerance protein [Sesuvium portulacastrum (Shoreline sea purslane)]	3	TGA	21	7	Plus	Gossypium_raidmondii
	AJ513319 Late embryogenesis-like protein [Prunus armeniaca (Apricot)]	3	TGA	21	7	Plus	Gossypium_hirsutum
	DT047070	3	TCA	21	7	Minus	Gossypium_hirsutum
	DW225975 Late embryogenesis-like protein [Prunus armeniaca (Apricot)]	3	GAT	21	7	Plus	Gossypium_hirsutum
	DW499141 Late embryogenesis-like protein [Prunus armeniaca (Apricot)]	3	TGA	21	7	Plus	Gossypium_hirsutum
	TA20630_3635 Late embryogenesis-like protein [Prunus armeniaca (Apricot)]	3	TGA	21	7	Plus	Gossypium_hirsutum
	CO493420 Late embryogenesis-like protein [Prunus armeniaca (Apricot)]	3	TGA	24	8	Plus	Gossypium_hirsutum
19	CK640498 Late embryogenesis-like protein [Prunus armeniaca (Apricot)]	3	TGA	24	8	Plus	Gossypium_arboreum

Supplementary Table 6. Contd.

	CO125503 Late embryogenesis-like protein [Prunus armeniaca (Apricot)]	3	TGA	18	6	Plus	Gossypium_raidmondii
	CO076869 Late embryogenesis-like protein [Prunus armeniaca (Apricot)]	3	GAT	18	6	Plus	Gossypium_raidmondii
	CO123383 Salt tolerance protein [Sesuvium portulacastrum (Shoreline sea purslane)]	3	TGA	21	7	Plus	Gossypium_raidmondii
	TA9193_29730 Salt tolerance protein [Sesuvium portulacastrum (Shoreline sea purslane)]	3	TGA	21	7	Plus	Gossypium_raidmondii
	DT047070	3	TCA	21	7	Minus	Gossypium_hirsutum
	AJ513319 Late embryogenesis-like protein [Prunus armeniaca (Apricot)]	3	TGA	21	7	Plus	Gossypium_hirsutum
	DW499141 Late embryogenesis-like protein [Prunus armeniaca (Apricot)]	3	TGA	21	7	Plus	Gossypium_hirsutum
	DW225975 Late embryogenesis-like protein [Prunus armeniaca (Apricot)]	3	GAT	21	7	Plus	Gossypium_hirsutum
	TA20630_3635 Late embryogenesis-like protein [Prunus armeniaca (Apricot)]	3	TGA	21	7	Plus	Gossypium_hirsutum
	CO493420 Late embryogenesis-like protein [Prunus armeniaca (Apricot)]	3	TGA	24	8	Plus	Gossypium_hirsutum
20	TA5985_29729 Protein At3g63460 [Arabidopsis thaliana (Mouse-ear cress)]	3	TTA	18	6	Plus	Gossypium_arboreum
	TA17231_29730 Protein At3g63460 [Arabidopsis thaliana (Mouse-ear cress)]	3	TTA	21	7	Plus	Gossypium_raidmondii
	TA26634_3635	3	TAA	18	6	Minus	Gossypium_hirsutum
	TA26636_3635	3	ATA	21	7	Minus	Gossypium_hirsutum
	TA26635_3635 Protein At3g63460 [Arabidopsis thaliana (Mouse-ear cress)]	3	TTA	21	7	Plus	Gossypium_hirsutum
21	BQ404857 Hypothetical protein [Medicago truncatula (Barrel medic)]	3	TTC	21	7	Plus	Gossypium_arboreum
	TA13626_29730 Hypothetical protein [Medicago truncatula (Barrel medic)]	3	TTC	21	7	Plus	Gossypium_raidmondii
	CO099414 Hypothetical protein OJ1734_E02.2 [Oryza sativa (japonica cultivar-group)]	3	TTC	21	7	Plus	Gossypium_raidmondii
	TA26423_3635 Hypothetical protein [Medicago truncatula (Barrel medic)]	3	TTC	27	9	Plus	Gossypium_hirsutum
	DR459816 Hypothetical protein [Medicago truncatula (Barrel medic)]	3	TTC	27	9	Plus	Gossypium_hirsutum
22	TA7048_29729 Hypothetical protein [Medicago truncatula (Barrel medic)]	3	TTC	21	7	Plus	Gossypium_arboreum
	TA13626_29730 Hypothetical protein [Medicago truncatula (Barrel medic)]	3	TTC	21	7	Plus	Gossypium_raidmondii
	CO099414 Hypothetical protein OJ1734_E02.2 [Oryza sativa (japonica cultivar-group)]	3	TTC	21	7	Plus	Gossypium_raidmondii
	TA26423_3635 Hypothetical protein [Medicago truncatula (Barrel medic)]	3	TTC	27	9	Plus	Gossypium_hirsutum
	DR459816 Hypothetical protein [Medicago truncatula (Barrel medic)]	3	TTC	27	9	Plus	Gossypium_hirsutum
23	BQ405038 Hypothetical protein T5J17.10 [Arabidopsis thaliana (Mouse-ear cress)]	4	AATT	20	5	Plus	Gossypium_arboreum
	CO078485 Hypothetical protein [Medicago truncatula (Barrel medic)]	4	AATT	24	6	Plus	Gossypium_raidmondii
	CO102888 Hypothetical protein T5J17.10 [Arabidopsis thaliana (Mouse-ear cress)]	4	AATT	24	6	Plus	Gossypium_raidmondii
	DV850022 Hypothetical protein [Medicago truncatula (Barrel medic)]	4	AATT	20	5	Plus	Gossypium_hirsutum
	DW235242	4	AATT	20	5	Plus	Gossypium_hirsutum

Supplementary Table 6. Contd.

24	BG445815 T5A14.7 protein [Arabidopsis thaliana (Mouse-ear cress)]	6	GATAGG	24	4	Plus	Gossypium_arboreum
	TA11166_29730 Zinc finger, RING-type; RINGv [Medicago truncatula (Barrel medic)]	6	GATAGG	30	5	Plus	Gossypium_raidmondii
	TA37112_3635 Zinc finger, RING-type; RINGv [Medicago truncatula (Barrel medic)]	6	GATAGG	24	4	Plus	Gossypium_hirsutum
25	BG445177	6	GATAGG	24	4	Plus	Gossypium_arboreum
	TA11166_29730 Zinc finger, RING-type; RINGv [Medicago truncatula (Barrel medic)]	6	GATAGG	30	5	Plus	Gossypium_raidmondii
	TA37112_3635 Zinc finger, RING-type; RINGv [Medicago truncatula (Barrel medic)]	6	GATAGG	24	4	Plus	Gossypium_hirsutum

Supplementary Table 7.

GO Term		All SSR-ESTs	Dinucleotides	Trinucleotides	AC motif	AG motif	AT motif	AAC motif	AAG motif	AAT motif	ACC motif
Ga	Gh	Gr	Ga	Gh	Gr	Ga	Gh	Gr	Ga	Gh	Gr
585	1680	937	175	267	289	283	993	476	10	37	20
Biological process	Biological regulation	27(4.62)	113(6.73)	98(10.46)	9(5.14)	25(9.36)	31(10.73)	11(3.89)	68(6.85)	43(9.03)	2(20.00)
	Cellular component organization	49(8.38)	60(3.57)	38(4.06)	9(5.14)	13(4.87)	7(2.42)	35(12.37)	30(3.02)	23(4.83)	1(10.00)
	Cellular process	219(37.44)	591(35.18)	429(45.78)	72(41.14)	107(40.07)	141(48.79)	109(38.52)	346(34.84)	212(44.54)	8(80.00)
	Death	6(1.03)	12(0.71)	8(0.85)	1(0.57)	0(0.00)	2(0.69)	3(1.06)	9(0.91)	2(0.42)	0(0.00)
	Developmental process	45(7.69)	119(7.08)	80(8.54)	22(12.57)	22(8.24)	25(8.65)	17(6.01)	67(6.75)	41(8.61)	0(0.00)
	Growth	9(1.54)	24(1.43)	16(1.71)	6(3.43)	8(3.00)	2(0.69)	1(0.35)	15(1.51)	9(1.89)	0(0.00)
	Localization	36(6.15)	112(6.67)	73(7.79)	12(6.86)	21(7.87)	26(9.00)	14(4.95)	57(5.74)	31(6.51)	0(0.00)
	Metabolic process	189(32.31)	545(32.44)	394(42.05)	65(37.14)	107(40.07)	138(47.75)	95(33.57)	311(31.32)	190(39.92)	6(60.00)
	Multicellular organismal process	39(6.67)	115(6.85)	81(8.64)	18(10.29)	21(7.87)	25(8.65)	16(5.65)	63(6.34)	42(8.82)	0(0.00)
	Multi-organism process	1(0.17)	11(0.65)	5(0.53)	0(0.00)	3(1.12)	1(0.35)	0(0.00)	6(0.60)	3(0.63)	0(0.00)
	Reproduction	27(4.62)	69(4.11)	43(4.59)	15(8.57)	13(4.87)	15(5.19)	9(3.18)	35(3.52)	18(3.78)	0(0.00)
	Response to stimulus	77(13.16)	241(14.35)	161(17.18)	31(17.71)	35(13.11)	55(19.03)	38(13.43)	153(15.41)	69(14.50)	2(20.00)
	Signaling	23(3.93)	75(4.46)	84(8.96)	7(4.00)	18(6.74)	27(9.34)	10(3.53)	40(4.03)	35(7.35)	0(0.00)
Cellular component	Cell	298(50.94)	747(44.46)	517(55.18)	88(50.29)	124(46.44)	145(50.17)	140(49.47)	429(43.20)	279(58.61)	7(70.00)
	Extracellular region	43(7.35)	26(1.55)	8(0.85)	10(5.71)	3(1.12)	4(1.38)	11(3.89)	8(0.81)	2(0.42)	0(0.00)
	Macromolecular complex	17(2.91)	26(1.55)	16(1.71)	5(2.86)	4(1.50)	5(1.73)	0(0.00)	11(1.11)	8(1.68)	2(20.00)
	Membrane-enclosed lumen	42(7.18)	36(2.14)	64(6.83)	12(6.86)	4(1.50)	19(6.57)	23(8.13)	23(2.32)	39(8.19)	1(10.00)
	Organelle	193(32.99)	509(30.30)	353(37.67)	53(30.29)	86(32.21)	98(33.91)	116(40.99)	298(30.01)	197(41.39)	4(40.00)
Binding	218(37.26)	655(38.99)	438(46.74)	67(38.29)	109(40.82)	132(45.67)	110(38.87)	397(39.98)	227(47.69)	5(50.00)	

Supplementary Table 7. Contd.

Ga	Gh	Gh	Gr	Ga	Gh	Gr	Ga	Gh	Gr	Ga	Gh
585	1680	286	149	34	114	83	32	116	41	8	30
Biological process	Biological regulation	2(5.88)	4(4.60)	17(5.94)	7(4.70)	1(2.94)	3(2.63)	3(3.61)	3(9.38)	13(11.21)	4(9.76)
	Cellular component organization	1(2.94)	23(26.44)	7(2.45)	3(2.01)	0(0.00)	4(3.51)	4(4.82)	4(12.50)	3(2.59)	0(0.00)
	Cellular process	15(44.12)	52(59.77)	116(40.56)	71(47.65)	11(32.35)	46(40.35)	31(37.35)	15(46.88)	42(36.21)	19(46.34)
	Death	0(0.00)	3(3.45)	6(2.10)	2(1.34)	0(0.00)	1(0.88)	0(0.00)	0(0.00)	0(0.00)	0(0.00)
	Developmental process	2(5.88)	3(3.45)	18(6.29)	7(4.70)	2(5.88)	7(6.14)	2(2.41)	3(9.38)	3(2.59)	3(7.32)
	Growth	0(0.00)	0(0.00)	3(1.05)	1(0.67)	0(0.00)	0(0.00)	1(1.20)	0(0.00)	1(0.86)	0(0.00)
	Localization	1(2.94)	5(5.75)	17(5.94)	11(7.38)	1(2.94)	10(8.77)	8(9.64)	1(3.13)	7(6.03)	3(7.32)
	Metabolic process	15(44.12)	28(32.18)	98(34.27)	70(46.98)	11(32.35)	43(37.72)	29(34.94)	21(65.63)	38(32.76)	14(34.15)
	Multicellular organismal process	2(5.88)	3(3.45)	17(5.94)	7(4.70)	2(5.88)	7(6.14)	3(3.61)	2(6.25)	3(2.59)	3(7.32)
	Multi-organism process	0(0.00)	0(0.00)	2(0.70)	0(0.00)	0(0.00)	1(0.88)	0(0.00)	0(0.00)	0(0.00)	0(0.00)
	Reproduction	2(5.88)	1(1.15)	9(3.15)	3(2.01)	2(5.88)	4(3.51)	2(2.41)	2(6.25)	0(0.00)	0(0.00)
	Response to stimulus	3(8.82)	12(13.79)	37(12.94)	19(12.75)	1(2.94)	10(8.77)	8(9.64)	8(25.00)	26(22.41)	8(19.51)
	Signaling	1(2.94)	3(3.45)	5(1.75)	6(4.03)	1(2.94)	2(1.75)	3(3.61)	3(9.38)	10(8.62)	4(9.76)
Cellular component	Cell	19(55.88)	53(60.92)	129(45.10)	83(55.70)	11(32.35)	52(45.61)	49(59.04)	22(68.75)	52(44.83)	26(63.41)
	Extracellular region	0(0.00)	0(0.00)	2(0.70)	2(1.34)	0(0.00)	3(2.63)	0(0.00)	0(0.00)	1(0.86)	0(0.00)
	Macromolecular complex	0(0.00)	2(2.30)	0(0.00)	3(2.01)	1(2.94)	1(0.88)	0(0.00)	4(12.50)	4(3.45)	1(2.44)
	Membrane-enclosed lumen	7(20.59)	4(4.60)	0(0.00)	9(6.04)	2(5.88)	2(1.75)	4(4.82)	4(12.50)	3(2.59)	1(2.44)
	Organelle	13(38.24)	46(52.87)	85(29.72)	58(38.93)	6(17.65)	35(30.70)	30(36.14)	17(53.13)	36(31.03)	18(43.90)
Molecular function	Binding	19(55.88)	45(51.72)	115(40.21)	76(51.01)	10(29.41)	40(35.09)	29(34.94)	20(62.50)	50(43.10)	16(39.02)
	Catalytic activity	4(11.76)	40(45.98)	72(25.17)	51(34.23)	11(32.35)	43(37.72)	31(37.35)	14(43.75)	12(10.34)	5(12.20)
	Enzyme regulator activity	0(0.00)	0(0.00)	0(0.00)	1(0.67)	0(0.00)	0(0.00)	2(2.41)	0(0.00)	0(0.00)	0(0.00)
	Molecular transducer activity	1(2.94)	1(1.15)	12(4.20)	3(2.01)	0(0.00)	1(0.88)	1(1.20)	2(6.25)	1(0.86)	0(0.00)
	Structural molecule activity	0(0.00)	22(25.29)	1(0.35)	1(0.67)	1(2.94)	1(0.88)	1(1.20)	4(12.50)	5(4.31)	3(7.32)
	Transcription regulator activity	7(20.59)	5(5.75)	25(8.74)	9(6.04)	2(5.88)	8(7.02)	5(6.02)	4(12.50)	11(9.48)	2(4.88)
	Transporter activity	0(0.00)	3(3.45)	7(2.45)	4(2.68)	1(2.94)	10(8.77)	7(8.43)	0(0.00)	2(1.72)	2(4.88)
GO Term											
Ga	Gh	Gr	Ga	Gh	Gr	Ga	Gh	Gr	Ga	Gh	Gr
585	1680	9	3	12	11	31	100	44	14	43	14
biological process	Biological regulation	0(0.00)	2(6.67)	1(11.11)	0(0.00)	0(0.00)	0(0.00)	1(3.23)	7(7.00)	6(13.64)	1(7.14)
	Cellular component organization	0(0.00)	0(0.00)	0(0.00)	1(33.33)	3(25.00)	1(9.09)	2(6.45)	3(3.00)	2(4.55)	1(7.14)
	Cellular process	0(0.00)	3(10.00)	6(66.67)	1(33.33)	6(50.00)	6(54.55)	7(22.58)	31(31.00)	20(45.45)	4(28.57)
	Death	0(0.00)	0(0.00)	0(0.00)	0(0.00)	0(0.00)	0(0.00)	0(0.00)	0(0.00)	0(0.00)	0(0.00)
	Developmental process	0(0.00)	2(6.67)	1(11.11)	0(0.00)	3(25.00)	2(18.18)	3(9.68)	14(14.00)	9(20.45)	1(7.14)
	Growth	0(0.00)	0(0.00)	0(0.00)	0(0.00)	0(0.00)	0(0.00)	0(0.00)	1(3.23)	3(3.00)	3(6.82)

Supplementary Table 7. Contd.

	Localization	2(25.00)	0(0.00)	0(0.00)	0(0.00)	1(8.33)	2(18.18)	1(3.23)	7(7.00)	2(4.55)	1(7.14)
	Metabolic process	0(0.00)	1(3.33)	5(55.56)	1(33.33)	7(58.33)	4(36.36)	6(19.35)	33(33.00)	20(45.45)	4(28.57)
	Multicellular organismal process	0(0.00)	2(6.67)	1(11.11)	0(0.00)	3(25.00)	2(18.18)	3(9.68)	14(14.00)	9(20.45)	1(7.14)
	Multi-organism process	0(0.00)	0(0.00)	0(0.00)	0(0.00)	0(0.00)	0(0.00)	0(0.00)	0(0.00)	0(0.00)	0(0.00)
	Reproduction	0(0.00)	2(6.67)	1(11.11)	0(0.00)	0(0.00)	0(0.00)	1(3.23)	9(9.00)	5(11.36)	0(0.00)
	Response to stimulus	0(0.00)	2(6.67)	0(0.00)	0(0.00)	4(33.33)	2(18.18)	1(3.23)	15(15.00)	9(20.45)	2(14.29)
	Signaling	0(0.00)	2(6.67)	1(11.11)	0(0.00)	0(0.00)	0(0.00)	1(3.23)	4(4.00)	6(13.64)	1(7.14)
Cellular component	Cell	3(37.50)	6(20.00)	6(66.67)	1(33.33)	5(41.67)	5(45.45)	12(38.71)	40(40.00)	27(61.36)	11(78.57)
	Extracellular region	0(0.00)	0(0.00)	0(0.00)	0(0.00)	0(0.00)	0(0.00)	0(0.00)	1(1.00)	0(0.00)	0(0.00)
	Macromolecular complex	0(0.00)	1(3.33)	1(11.11)	1(33.33)	0(0.00)	0(0.00)	1(3.23)	3(3.00)	2(4.55)	0(0.00)
	Membrane-enclosed lumen	0(0.00)	0(0.00)	2(22.22)	0(0.00)	0(0.00)	0(0.00)	5(16.13)	6(6.00)	7(15.91)	2(14.29)
Molecular function	Organelle	3(37.50)	5(16.67)	6(66.67)	1(33.33)	5(41.67)	4(36.36)	11(35.48)	33(33.00)	23(52.27)	9(64.29)
	Binding	0(0.00)	3(10.00)	4(44.44)	1(33.33)	4(33.33)	3(27.27)	7(22.58)	43(43.00)	27(61.36)	4(28.57)
	Catalytic activity	2(25.00)	7(23.33)	0(0.00)	0(0.00)	7(58.33)	5(45.45)	4(12.90)	10(10.00)	4(9.09)	1(7.14)
	Enzyme regulator activity	0(0.00)	2(6.67)	1(11.11)	0(0.00)	0(0.00)	0(0.00)	0(0.00)	0(0.00)	0(0.00)	0(0.00)
	Molecular transducer activity	0(0.00)	0(0.00)	0(0.00)	0(0.00)	0(0.00)	0(0.00)	1(3.23)	3(3.00)	2(4.55)	0(0.00)
	Structural molecule activity	0(0.00)	0(0.00)	1(11.11)	0(0.00)	0(0.00)	0(0.00)	1(3.23)	3(3.00)	0(0.00)	1(7.14)
	Transcription regulator activity	0(0.00)	0(0.00)	2(22.22)	0(0.00)	1(8.33)	1(9.09)	0(0.00)	14(14.00)	7(15.91)	3(21.43)
	Transporter activity	2(25.00)	6(20.00)	0(0.00)	0(0.00)	1(8.33)	2(18.18)	0(0.00)	1(1.00)	2(4.55)	1(7.14)
GO Term											
Ga	Gh	Ga	Gh	Gr	Ga	Gh	Gr				
585	1680	55	191	96	12	52	13				
Biological process	Biological regulation	3(6.98)	1(7.14)	1(1.82)	13(6.81)	18(18.75)	0(0.00)	9(17.31)	2(15.38)		
	Cellular component organization	0(0.00)	0(0.00)	1(1.82)	9(4.71)	12(12.50)	0(0.00)	0(0.00)	0(0.00)		
	Cellular process	11(25.58)	7(50.00)	11(20.00)	54(28.27)	39(40.63)	3(25.00)	17(32.69)	4(30.77)		
	Death	0(0.00)	0(0.00)	1(1.82)	1(0.52)	0(0.00)	0(0.00)	0(0.00)	0(0.00)		
	Developmental process	1(2.33)	0(0.00)	5(9.09)	14(7.33)	15(15.63)	0(0.00)	1(1.92)	0(0.00)		
	Growth	0(0.00)	0(0.00)	0(0.00)	5(2.62)	4(4.17)	0(0.00)	2(3.85)	0(0.00)		
	Localization	2(4.65)	0(0.00)	0(0.00)	5(2.62)	2(2.08)	1(8.33)	7(13.46)	2(15.38)		
	Metabolic process	12(27.91)	7(50.00)	18(32.73)	49(25.65)	30(31.25)	3(25.00)	12(23.08)	2(15.38)		
	Multicellular organismal process	1(2.33)	0(0.00)	5(9.09)	11(5.76)	15(15.63)	0(0.00)	1(1.92)	0(0.00)		
	Multi-organism process	0(0.00)	0(0.00)	0(0.00)	3(1.57)	3(3.13)	0(0.00)	0(0.00)	0(0.00)		
	Reproduction	0(0.00)	0(0.00)	4(7.27)	6(3.14)	5(5.21)	0(0.00)	0(0.00)	0(0.00)		
	Response to stimulus	3(6.98)	1(7.14)	15(27.27)	35(18.32)	19(19.79)	0(0.00)	6(11.54)	1(7.69)		
Signaling	3(6.98)	1(7.14)	1(1.82)	8(4.19)	14(14.58)	0(0.00)	3(5.77)	0(0.00)			
Cell	17(39.53)	10(71.43)	15(27.27)	73(38.22)	52(54.17)	6(50.00)	39(75.00)	9(69.23)			

Supplementary Table 7. Contd.

	Extracellular region	0(0.00)	0(0.00)	0(0.00)	1(0.52)	0(0.00)	0(0.00)	0(0.00)	0(0.00)
	Macromolecular complex	0(0.00)	0(0.00)	0(0.00)	0(0.00)	1(1.04)	1(8.33)	2(3.85)	0(0.00)
	Membrane-enclosed lumen	0(0.00)	3(21.43)	2(3.64)	8(4.19)	7(7.29)	0(0.00)	3(5.77)	1(7.69)
	Organelle	13(30.23)	6(42.86)	14(25.45)	57(29.84)	41(42.71)	4(33.33)	17(32.69)	4(30.77)
Molecular function	Binding	19(44.19)	8(57.14)	12(21.82)	64(33.51)	47(48.96)	4(33.33)	24(46.15)	4(30.77)
	Catalytic activity	11(25.58)	6(42.86)	15(27.27)	32(16.75)	23(23.96)	2(16.67)	11(21.15)	1(7.69)
	Enzyme regulator activity	0(0.00)	2(14.29)	0(0.00)	6(3.14)	1(1.04)	0(0.00)	1(1.92)	0(0.00)
	Molecular transducer activity	0(0.00)	0(0.00)	0(0.00)	4(2.09)	4(4.17)	0(0.00)	3(5.77)	0(0.00)
	Structural molecule activity	0(0.00)	0(0.00)	0(0.00)	0(0.00)	2(2.08)	1(8.33)	2(3.85)	0(0.00)
	Transcription regulator activity	3(6.98)	3(21.43)	2(3.64)	20(10.47)	8(8.33)	0(0.00)	2(3.85)	0(0.00)
	Transporter activity	1(2.33)	0(0.00)	0(0.00)	5(2.62)	2(2.08)	0(0.00)	2(3.85)	0(0.00)