Full Length Research Paper

# Novel expressed sequence tag- simple sequence repeats (EST-SSR) markers characterized by new bioinformatic criteria reveal high genetic similarity in sugarcane (*Saccharum* spp.) breeding lines

Kittipat Ukoskit<sup>1</sup>\*, Penjun Thipmongkolcharoen<sup>1</sup> and Prasert Chatwachirawong<sup>2</sup>

<sup>1</sup>Department of Biotechnology, Faculty of Science and Technology, Thammasat University (Rangsit Campus) Klong Luang, Pathumtani 12121, Thailand.

<sup>2</sup>Department of Agronomy, Faculty of Agriculture, Kasetsart University, Kamphaengsean Campus, Kamphaengsean, Nakhon Pathom 73140, Thailand.

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Using different bioinformatic criteria, the SUCEST database was used to mine for simple sequence repeat (SSR) markers. Among 42,189 clusters, 1,425 expressed sequence tag- simple sequence repeats (EST-SSRs) were identified *in silico*. Trinucleotide repeats were the most abundant SSRs detected. Of 212 primer pairs selected, based on repeat patterns of n≥8 for di-, tri-, tetra- and penta-nucleotide repeat motifs verified using 15 sugarcane (*Saccharum* spp.) genotypes and marker segregation using F1 progenies of a cultivated sugarcane and *Saccharum spontaneum*, 191 loci were identified. All new EST-SSR loci detected a total of 1,529 markers ranging from 2 to 21 markers per locus, with an average of eight markers per locus. Observed polymorphism ranged from 0.12 to 0.93 with a mean of 0.74. A total of 426 and 333 markers were putatively identified as simplex in the cultivated sugarcane and *S. spontaneum*, respectively and corresponding to 2.23 and 1.74 markers per primer, respectively while 167 markers were identified as double-simplex markers, with 0.87 markers per primer. Cluster analysis revealed a high genetic similarity among the sugarcane (*Saccharum* spp.) breeding lines which could reduce the genetic gain in sugarcane breeding.

Key words: sugarcane, expressed sequence tag- simple sequence repeats (EST-SSRs) markers, genetic similarity.

#### INTRODUCTION

In current years, with the rapid increase of expressed sequence tag (EST) sequence in public data base, the development of EST containing simple sequence repeats (SSRs) becomes an attractive choice for the development of SSR markers. With evolving bioinformatic tools, it is easy to download the ESTs from public databases, scan for EST containing SSRs and develop EST–SSR markers at a large scale with a time saving and cost

effective way (Kantety et al., 2002; Yan et al., 2008). EST-SSRs have some advantages over genomic SSRs since these markers are derived from expressed genes, they are more conserved and have a better potential for their applications across the species than anonymous DNA markers like amplified fragment length polymorphisms (AFLPs), random amplified polymorphic DNA (RAPD) and genomic SSR markers (Feng et al., 2009). Consequently, they are useful as anchor markers for identifying conserved genomic regions among species and genera, comparative genomics, and evolutionary studies (Cordeiro et al., 2001; Kantety et al., 2002; Thiel et al., 2003). Moreover, EST-SSRs may be directly

<sup>\*</sup>Corresponding author. E-mail: ku@tu.ac.th.Tel: 662- 5644500. Fax: 662-5644500.

related with a coding gene, used as functional SSR markers, and are better resources for their use in breeding since they may be directly associated with the genes affecting a particular trait (Andersen and Lubberstedt, 2003).

The sugarcane EST project (SUCEST) generated 291,689 ESTs (Vettore et al., 2001). Trimming and clustering ESTs were performed to obtain 43,141 clusters (Telles and Silva, 2001). These large datasets of non-redundant (NR) EST sequences are publicly released on the public domain sugarcane EST (http://sucest. lbi.ic.unicamp.br/public/) and available for developing EST–SSR markers at a large scale. Although, the sugarcane EST database had been surveyed for ESTs containing SSRs (Oliveira et al., 2007; Oliveira et al., 2009; Pinto et al., 2004; Silva, 2001), a large number of EST–SSR markers are still available for marker development.

The current study was designed (1) to develop and characterize a novel set of EST-SSR markers from the sugarcane EST using different search EST-SSR criteria from previous reports (2) to evaluate the ability to detect polymorphism and to determine simplex alleles segregating in mapping population derived from an interspecific hybridization between a cultivated sugarcane and *Saccharum spontaneum* (3) to assess their potential for diversity and pedigree relationship studies. The new EST-SSR markers developed from this study provide a robust set of polymerase chain reaction (PCR) primers that are a useful addition for functional sugarcane genome mapping facilitating introgression of favorable wild alleles in sugarcane breeding programs and for sugarcane genotyping.

#### MATERIALS AND METHODS

#### Plant materials

Thirteen sugarcane breeding lines and 2 cultivars, Phil66-107 and KU60, (Table 1) were used for evaluation of selected EST-SSR markers. Ten random  $F_1$  progenies obtained from the interspecific cross between the cultivated sugarcane 'Phil6607' and *S. spontaneum* 'S6' were used for simplex marker segregation analysis. Leaf material was collected and DNA was extracted following the cetyltrimethylammonium bromide (CTAB) method described by (Gawel and Jarret, 1991). DNA quantity and quality were determined using agarose gel electrophoresis and spectrophotometric measurements, and then the samples were diluted appropriately for marker analyses.

#### Data mining for EST-SSR markers and primer design

We collected 42,189 clusters from 37 libraries publicly provided from the SUCEST database and surveyed electronically using the PERL program, Simple Sequence Repeat Identification Tool(SSRIT), downloaded from the Cornell University web site http://www.gramene.org/gramene/searches/ssrtool. The parameters

in SSRIT program were set for detection of di-, tri-, tetra-, and penta nucleotide motifs with a minimum of 5 repeats. The identified ESTs containing repeat motifs were subjected to masking of other repeat sequences from the Gramineae family as well as low-complexity sequences, including the SSRs and interspersed repeats, with the RepeatMasker Program (A.F.A. Smit, R. Hubley & P. Green RepeatMasker at http://repeatmasker.org). The Primer3 software (freely available at http://www.genome.wi.mit.edu/genome software/ other/ primer3.html) was used to design the primers (Rozen and Skaletsky, 2000) to amplify the selected EST-SSRs based on the following parameters: primer length from 18 to 24 with 20 as the optimum, PCR product size from 150 to 350, optimum annealing temperature of 60°C, and GC contents from 40 to 70%, with 50% as optimum. PCR reactions were carried out in 20 µl reaction volumes containing 1× Buffer, 1.5 mM of MgCl<sub>2</sub>, 20 µM of each dNTPs, 0.25 µM of each primer, 0.5 U of Taq DNA polymerase and 20 ng of DNA template and were performed on MJ Thermal Cycler at 94 ℃ for 5 min, 40 cycles of 30 s at 94 ℃, 60 s at appropriate annealing temperature of each primer and 1 min at 72°C, with a final extension of 7 min at 72°C. PCR products were run on 6% denaturing polyacrylamide gels and silver-stained as described by (Benbouza et al., 2006).

#### Gene identity of characterized EST-SSRs

To obtain sequence homology and putative function of genes represented by the EST-SSRs characterized from the Repeat Masker program, the EST-SSRs were BLAST searched against NCBI non-redundant (nr) database using Blast2GO freely available through Java Web Start at http://www.blast2go.de; (Conesa et al., 2005). BLASTX results were loaded into the program and the default settings were used to assign GO terms to all EST-SSRs.

# Evaluation of EST-SSR polymorphisms and determining simplex alleles

Primarily, the selected EST-SSRs were screened for polymorphism between the two parents, Phil6607 and S6 used to generate a mapping population for constructing linkage maps. Secondly, the resulting polymorphic EST-SSRs evaluated between the two parents were determined for putative simplex markers (markers present in one parent but absent in another and segregate 1:1) and double simplex markers (marker present in both parents and segregate 3:1; (Grattapaglia and Sederoff, 1994; Ritter et al., 1990) using 10 random progenies of  $F_1$  mapping population. Thirdly, based on high polymorphism between the two parents and homology to genes of interest, a subset of 212 primer pairs were selected to determine the polymorphism information content (PIC; Botstein et al., 1980) in 15 sugarcane genotypes, using the equation.

$$PIC = 1 - \sum_{i=1}^{k} p_i^2 - \sum_{i=1}^{k-1} \sum_{j=i+1}^{k} 2p_i^2 p_j^2$$

where *p* is the frequency of the  $j^{th}$  allele pattern of EST-SSR locus  $t^{th}$  and *k* is the number of allele pattern of EST-SSR locus. The selected highly polymorphic 212 EST–SSRs were tested to ascertain the genetic relationships by cluster analysis among 15 sugarcane genotypes including *S. spontaneum* used as an out group. The binary data were used to calculate Jaccard similarity coefficients (Jaccard, 1908) as indicators of genetic similarity

Olama	0		Pedig	ree	
Cione	Source	Female	Breeding*	Male	Breeding
TBy20-0556	Breeding line	K83-74	OCSB	K84-200	OCSB
TBy20-0732	Breeding line	K83-74	OCSB	K84-200	OCSB
TBy20-0734	Breeding line	K83-74	OCSB	K84-200	OCSB
TBy20-0794	Breeding line	K84-200	OCSB	K92-166	OCSB
TBy20-1300	Breeding line	K83-74	OCSB	K84-200	OCSB
TBy20-1455	Breeding line	Co775	Thai Major parent	K84-200	OCSB
TBy20-2248	Breeding line	K83-74	OCSB	K84-200	OCSB
NRCT01-0398	Breeding line	K83-74	OCSB	UT1	DA
NRCT01-0663	Breeding line	KU50	KU	B4362	Thai Major parent
NRCT01-0877	Breeding line	UT1	DA	K83-74	OCSB
NRCT01-1192	Breeding line	UT1	DA	K83-74	OCSB
NRCT01-1202	Breeding line	UT1	DA	KU50	KU
NRCT01-1256	Breeding line	Co775	Thai Major parent	K82-32	OCSB
KU60-1	Cultivar	Co775	Thai Major parent	K84-200	OCSB
Phil6607	Cutivar	Phil5460	Unknown	Co440	Thai Major parent
S6	S. spontaneum				

 Table 1. Sources and parents of sugarcane clones used for evaluation of developed EST-SSR markers.

\*OCSB = Office of the Cane and Sugar Board; KU= Kasetsart University; DA = Department of Agriculture.



Figure 1. Frequency of repeat motif classes.

among pairs of genotypes as follows: GSij = a/(a+b+c) where GSij is the genetic similarity measurement between individuals i and j, a is the number of polymorphic bands that are shared by *i* and *j*, *b* and *c* are the number of bands present in individual *i* and *j*, respectively. The resulting similarity matrices were used to construct dendrograms by the unweighted pair-group method with arithmetic means (UPGMA) using software packages NTSYSpc ver 2.02 (Rohlf, 1998).

#### RESULTS

#### Type and frequency of EST-SSRs

A search of the EST from the SUCEST database

usingthe PERL program, SSRIT found 4,401 ESTs containing repeat motifs according to the search criteria. Since the SSRIT program identifies ESTs solely based on the fact that they contain a certain repeat motif, all these ESTs containing repeat motifs were subjected to masking of other repeat sequences from the Gramineae family as well as low-complexity sequences, including the SSRs and interspersed repeats, with the Repeat Masker pro-gram. A total of 1,425 EST-SSRs were identified, accounting for approximately 3.4% of the total cluster searched. Of the total EST-SSRs identified (Figure 1), 1,141 (80.1%) were perfect repeats representing the majority of the SSR structure types, 31

Demost motif					N	umbe	r of repeat	t			Tatal	<b>F</b> actor <b>1 (0</b> ( <b>)</b>
Repeat motif	5	6	7	8	9	10	11–15	16–25	26–40	41–60	lotal	Frequency (%)
AG/CT	55	34	24	65	42	21	57	40	4	0	342	19.1
AC/GT	33	15	4	22	16	8	11	12	3	1	125	7
AT/AT	30	11	6	14	6	8	26	15	16	3	135	7.6
CG/CG	51	10	1	5	1	0	0	0	0	0	68	3.8
ACG/CGT	28	18	7	8	2	1	0	0	0	0	64	3.6
ACT/AGT	3	0	1	1	0	0	0	0	0	0	5	0.3
ATT/AAT	1	1	1	1	2	0	4	1	0	0	11	0.6
AAC/GTT	4	4	7	6	5	0	2	0	0	0	28	1.6
CAT/ATG	10	6	5	1	2	3	1	1	0	0	29	1.6
CTT/AAG	12	3	7	4	3	0	1	2	0	0	32	1.8
GGT/ACC	23	15	10	5	7	1	2	0	0	0	63	3.5
CCT/AGG	50	35	27	11	6	2	2	0	0	0	133	7.4
AGC/GCT	60	42	20	14	6	1	4	0	0	0	147	8.2
CGG/CCG	200	132	88	42	22	2	6	0	0	0	492	27.5
AAAG/CTTT	4	2	1	2	1	1	2	0	0	0	13	0.7
AAAT/ATTT	2	0	1	0	0	0	0	0	0	0	3	0.2
ACAT/ATGT	4	1	0	2	0	0	0	1	0	0	8	0.4
AGCT/AGCT	2	1	0	0	0	0	0	0	0	0	3	0.2
AGGA/TCCT	1	1	1	1	1	0	0	0	0	0	5	0.3
AGGC/GCCT	5	0	0	0	0	0	0	0	0	0	5	0.3
ATGG/CCAT	5	0	0	0	0	0	0	0	0	0	5	0.3
CAAT/ATTG	2	0	0	0	0	0	0	0	0	0	2	0.1
CCCG/CGGG	4	0	0	0	0	0	0	0	0	0	4	0.2
CCTC/GAGG	7	2	0	0	0	0	0	0	0	0	9	0.5
CGCT/AGCG	2	0	0	0	0	0	0	0	0	0	2	0.1
TCTA/TAGA	1	1	0	0	0	0	0	0	0	0	2	0.1
Other tetra-repeats	9	1	0	0	0	0	1	0	0	0	11	0.6
ATGTA/TACAT	2	0	0	0	0	0	1	0	0	0	3	0.2
ATCCA/TGGAT	2	0	0	0	0	0	0	0	0	0	2	0.1
CCTTT/AAAGG	2	0	0	0	0	0	0	0	0	0	2	0.1
TCTCT/AGAGA	0	1	0	1	0	0	0	0	0	0	2	0.1
TCTCC/GGAGA	2	1	0	0	0	0	0	0	0	0	3	0.2
CTTTT/AAAAG	3	0	0	0	0	0	0	1	0	0	4	0.2
TCCCT/AGGGA	3	1	0	0	0	0	0	0	0	0	4	0.2
Other penta-repeats	16	2	0	1	1	0	2	0	0	0	22	1.2
Total	638	340	211	206	123	48	122	73	23	4	1,788	100

Table 2. Number and frequency of different SSR-repeat motifs identified in the analyzed 42,189 clusters from the SUCEST database.

(2.1%) were imperfect repeats with one or more interruptions in the run of repeats and 253 (17.6%) were compound repeats with adjacent tandem simple repeats of a different sequence, resulting in the total number of SSRs of 1,788 obtained.Analysis of SSR motifs in this study (Figure 1 and Table 2) revealed that the trinucleotide motifs were the most abundant type of SSRs found in the database searched (56.2%), followed by di(38.3%), tetra- (4%), and penta-nucleotide repeats (2.3%). The dominance of trinucleotide motifs in this study may be explained by the suppression of non-trinucleotide motifs in coding regions because of the risk of frame shift mutations that can occur when there is length variation in these motifs (Thiel et al., 2003; Varshney et al., 2005). Among the dinucleotide motif sequences, AG/CT motif was the most common (19.1%)

followed by AT/AT (7.6%) and AC/GT (7.0%) motifs, whereas CG/CG motif was the least common (3.8%).

Among the trinucleotide motifs sequences, the motif CGG/CCG was the most common (27.5%) followed by the motifs AGC/GCT (8.2%) and CCT/AGG (7.4%) while the motif ACT/AGT was the least common (0.3%). However, the most common tetra- and pentanucleotide motif sequences were found in insig-nificant numbers (0.7 and 0.2%, respectively) due to the high cut-off used for mining of tetra- and pentanucleotide motifs.

# Gene annotation and function of characterized EST-SSRs

Of 1,425 EST-SSRs, the BLAST2GO searches showed that 856 (60%) matched to genes of known functions at e values <10<sup>-6</sup>, while 222 (16%) and 342 (24%) had matched to hypothetical proteins and had no significant matches, respectively. To provide a general representation of the annotation, the Slim GO Classification was obtained for the whole set of EST-SSRs. Of the biological processes, 260, 172, 99, 99, 53, 45 and 29 EST-SSRs were related with cellular process, metabolic process, localization, establishment of localization, biological regulation, response to stimuli and developmental process, respectively. In the category cellular component, two main types were associated with cellular and organelle, 461 and 293, respectively. Under the category of molecular function, the vast majority of EST-SSRs were involved in catalytic activity and in binding activities, 132 and 130 respectively. Among the known function EST-SSRs, numerous EST sequences related to a wide range of proteins of interest (Supplementary Table 1) including enzymes involved in sugar metabolism, disease resistance related proteins, abiotic related proteins and growth regulatory proteins.

#### EST-SSR polymorphism and segregation analysis

Of the total 1,425 EST-SSRs identified, the selected 424 and 36 primer pairs were designed based on SSRs containing repeat patterns with  $n \ge 8$  and on homology to genes of interest, respectively and then assayed to detect polymorphisms between the two parents, Phill6607 and S6. Four hundred and thirty-four (434) primer pairs (94.4%) successfully amplified either Phill6607 or S6 while 26 primer pairs completely failed to yield PCR products from both parents at various annealing temperatures. Of the total 460 primer pairs, 74 (16.1%) and 26 (5.7%) primers pairs failed to amplify S6 and Phill6607, respectively. Among the 434 working primer pairs, 424 produced PCR products at the expected sizes, while 20 primer pairs yielded larger PCR product size than expected from the EST sequence, likely due to the presence of small introns. The EST-SSR markers developed in this study were highly polymorphic between the parents and among 14 sugarcane genotypes (Fig 2a). The polymorphism assay revealed that 407 primer pairs (93.7%) were polymorphic between the two parents reflecting the fact that the alleles between the cultivated sugarcane 'Phil6607' and *S. spontaneum* are distinct. The dominant scoring of the SSR bands yielded 1, 256 and 1,115 total polymorphic bands corresponding to an average of 3.1 and 2.7 polymorphic bands per primer pair in Phill6607 and S6, respectively.

All 407 polymorphic primers were tested for the simplex marker segregation in the 10 randomly selected F<sub>1</sub> progenies generated from the interspecific hybridization between the two parents. The simplex mrkers and double simplex markers in pseudo testcross configuration were expected to flow 1:1 (fig 2b) and 3:1 segragation patterns in the f<sub>1</sub> progeny, respectively. All polymorphic primers generated 2,371 polymorphic markers (bands). Of the total polymorphic markers, 828 and 165 markers were putatively identified as simplex and double simplex corresponding to 2 and 0.4 markers per primer, respectively. Based on high polymorphism between the two parents and on homology to genes of interest, a subset of 212 primer pairs were selected from 407 polymorphic primers to determine informativeness of EST-SSR markers in 15 sugarcane. Characteristics, putative function and segregation pattern of the 212 EST-SSR markers are shown in Supplementary Table 1.

Comparing redundancy to other EST-SSR data mining works in sugarcane (Oliveira et al., 2007, 2009; Pinto et al., 2006; Silva, 2001) illustrates that of 212 primer pairs, 191 primer pairs are new EST-SSR markers developed from this study (Supplementary Table 2). The new EST-SSR primer pairs detected a total of 1,529 markers ranging from 2 to 21 with the average of 8 markers per locus. The mean of PIC determined from 191 primer pairs were similar to those obtained from a previous study (Pinto et al., 2006). The PIC values ranged from 0.12 to 0.93 (except five monomorphic loci) with a mean of 0.74. 426 and 333 markers were putatively identified as simplex in Phill6607 and S6, corresponding to 2.23 and 1.74 markers per primer, respectively, while 167 markers were identified as double simplex corresponding 0.87 markers per primer.

# Genetic similarity

The similarity coefficient based on 1,743 polymorphic markers (alleles) scored from 212 primer pairs ranged from 0.56 to 0.80 with a mean of 0.72. Based on the marker data, the dendrogram generated with the UPGMA clustering method illustrates that the tested germplam were clearly resolved in two distinct clusters and one separated commercial cultivar on the level of similarity



Figure 2. The UPGMA dendrogram of the 13 sugarcane breeding lines and 2 cultivars based on 212 EST-SSR primer pairs. *S. spontaneum* (S6) was included as an out species.

coefficient 0.68 as expected of their pedigree (Figure 2). *S spontanuem* were included in the analysis as an out group and clearly differentiated from the sugarcane breeding lines and two commercial cultivars. TBY family and KU60-1 cultivar was grouped on the level of similarity coefficient of 0.72, while NRCT family was grouped in the same cluster on the level of similarity coefficient of 0.71. The dendrogram further validated the placement of the old commercial cultivar, Phil6607, as the most distant to the new breeding lines and the new commercial cultivar, KU60-1.

#### DISCUSSION

On the basic of the average length of 790 bp per EST sequence (data from Blast2Go), at least one SSR motif was found per 18.6 kb in the approximately 33.3 Mb ESTs that were searched. Data mining of EST-SSRs in cotton and wheat showed close values with one SSR for every 20.0 (Cardle et al., 2000) and 15.6 kb (Kantety et al., 2002), respectively. This value was lower than that of barley (1/6.3 kb; Thiel et al., 2003), soybean (1/7.4 kb; Cardle et al., 2000) coffee (1/1.56 kb; Aggarwal et al., 2007) tomato (1/11.1 kb; Gupta et al., 2003) Medicago truncatula (1/12 kb; Mun et al., 2006). However, the density of EST-SSRs in wheat (1/9.2 kb; Cardle et al., 2000) and M. truncatula (1/1.7kb; Gupta and Prasad, 2009) was varied in other studies. In sugarcane, a density of one SSR every 16.9 kb was estimated from a previous study (Pinto et al., 2004). The abundance level of EST-SSR may vary because of SSR search criteria. SSR mining tools and the size of the database searched (Varshney et al., 2005). In the present study, the parameters set for detection of di-, tri-, tetra-, and penta nucleotide motifs in SSRIT program were a minimum of 5 repeats, subsequently, the identified EST-SSRs were subjected to masking for interspersed repeats and low complexity DNA sequences using the Repeat Masker program whereas surveying EST containing SSRs in sugarcane from the previous study (Cordeiro et al., 2001; Pinto et al., 2004) used the BLASTn software to search for dinucleotide, trinucleotide, and tetranucleotide repeat patterns with  $n \ge 7$ , 5 and 3, respectively.

Di- and tri-nucleotide repeat motifs were mostly reported in plants, but the frequency of repeat motifs were different. Di-nucleotide repeat motifs were dominant in coffee (Aggarwal et al., 2007) apricot, peach (Jung et al., 2005) and Kiwi (Fraser et al., 2004). The analysis of our results revealed that the trinucleotide motifs were the leading repeat motif type of SSRs found in the database searched. This result is cosistent with previous research in sugarcane (Duarte Filho et al., 2010), and close evolutionary species such as in maize, rice, sorghum, wheat (Kantety et al., 2002), barley (Thiel et al., 2003), and oat (Becher, 2007). Based on the previous study (Pinto et al., 2004), tetra-nucleotide repeat motifs were reported to be the most abundant in sugarcane. This also verified a previous point of view that EST-SSR frequency was related to the search criteria (Aggarwal et al., 2007; Kantety et al., 2002; Pinto et al., 2004; Thiel et al., 2003).

Duarte Filho et al. (2010, Sugar Tech Volume 12, Number 2, 145-149). The result is very similar, were di-, tri- and tetracleotide is very similar with the presents here.

Earlier reports on the abundance of different SSR motifs in plant databases showed that AT motif was the most common repeat motif type (Lagercrantz et al.,

1993). Among the dinucleotide motif sequences in our sugarcane EST-SSRs, AG/CT motif was the most common (19.1%). This contrasts to the report of Pinto et al. (2004) in which, AT/AT motif was observed preferentially among dinucleotide motif sequences. The AG/CT motif was also the most frequently observed EST-SSRs in plants (Scott et al., 2000; Kantety et al., 2002; Gao et al., 2004; Thiel et al., 2003; Saha et al., 2004; Feng et al., 2009). Expressed sequences had shown a higher frequency of AG repeats than AT repeats (Morgante et al., 2002; Mun et al., 2006). A wide variety of tri-nucleotide repeat motifs were represented at high percentages. However, the repeat motif CCG/CGG was highly represented in monocots (Cho et al., 2000; Kantety et al., 2002; Thiel et al., 2003). This result is in agreement with our results and the result from the previous surveyed in SUCEST data base (Pinto et al., 2004). Rich GC content in rice was reported in the coding regions (Cho et al., 2000). The GC content was significantly higher in monocot species than in dicot species. Codon bias had been reported to correlate with GC content at the third codon position (Kawabe and Miyashita, 2003). This could be one of the reasons why CCG/CGG motifs are present at such high frequencies in EST collections of monocot species. This result (motifs rich in GC - CCG/GGC or GCG/CGC) is similar to Duarte Filho et al. (2010), where trinucleotidie rich in CG is most frequent in SUCEST, different to Pinto et al. (2004). You can improve your discussion, including this information about EST-SSR in SUCEST.

The result of transferability of EST-SSR markers developed from the present study indicated that the rate of amplification in the commercial cultivar (94.3%) was higher than that of its wild relative, S. spontaneum (83.9%), for the primer pairs which were designed from ESTs generated from commercial cultivars (Vettore et al., 2001) have a high homology sequence for annealing to the DNA template of the commercial cultivar. The failure of PCR amplification in both Saccharum species may be explained by the fact that primers extend across a splice site or that there are large introns in the genomic sequence. In the present study, the total of 460 and the subset new 191 EST-SSR primer pairs revealed that EST-SSRs were highly polymorphic between the two parents, the cultivated sugarcane and S. spontaneum and showed a high PIC (0.74) among sugarcane breeding lines determined in this study. The high PIC and the average number of alleles (8.8) showed close values to previous reports in analysis of EST-SSR informativeness (Oliveira et al., 2009; Pinto et al., 2006, 2004). The high percentage of polymorphism between the two parents is due to a different genome composition and a complex polyploid with different chromosome numbers between the cultivated sugarcane, Phil6607, (2n = 10 0-130 chromosomes) and S. spontaneum (2n = 40-128)chromosomes), S6, (Price, 1963). Owing to the high

ploidy number of sugarcane, most EST-SSRs yielded more than two PCR products which were assumed to be alleles. The multiple allele characteristic of SSR combined with the polyploidy nature of sugarcane, which resulted in the high PIC providing the capability of EST-SSR to create unique sugarcane fingerprints.

The new 191 EST-SSR primers generated the larger numbers of putative simplex markers (759 markers) both in Phill6607 and S6 as well as double simplex markers (167). As reflected by the much higher percentage (80%) of putative simplex markers, these types of markers represented alleles differed by the interspecific hybridization. In the case of crossing between two parents sharing alleles of heterozygous markers, the larger proportion of double simplex markers would be expected (Garcia et al., 2006). Although, double simplex markers are less informative than simplex markers (Maliepaard et al., 1998; Wu et al., 2000) double simplex markers can provide a locus connection between the mapping parents (Grattapaglia and Sederoff, 1994). Regarding both types of markers, these EST-SSR markers will be very useful for its potential to incorporate both improved and wild alleles in sugarcane linkage maps by using the simplex polymorphism approach (Wu et al., 1992) facilitating introgression favorable wild alleles with known function in sugarcane breeding programs.

The achievement of the sugarcane breeding program lies in the proper choice of parents based on genetic diversity. A cluster analysis of genetic relationships performed in sugarcane breeding lines and commercial cultivars using EST-SSR markers developed from the present study revealed two major groups of sugarcane breeding lines. This clustering result corresponded well to their known pedigree relationships and source of the breeding program. There are three main organizations in Thailand conducting research in sugarcane breeding, the Office of the Cane and Sugar Board (OCSB), the Department of Agriculture (DA), and Kasetsart University (KU), which have conducted breeding programs during the past 40 years in Thailand. Within the TBy breeding lines (including cv. KU60-1), all of them were derived from a cross between two parents from OCSB except TBy20-1455 and KU60-1 which one parent was the Thai major parent used in most breeding programs in Thailand. Therefore the clustering of TBv breeding lines and KU60-1 was due to the fact that their parental breeding lines are the same or are very close to each other in a breeding program. Although, the NRCT breeding lines involved germplasm from all three programs (Table 1), they were still grouped in the same cluster but separated from TBy breeding lines. The clustering of NRCT breeding lines was contributed by using common parents within them. Clearly, separation of the old cultivar, Phill6607, from the new breeding lines was due to dissimilarity of the parents used for breeding the cultivar, as compared to those used for generating

the new breeding lines. It should be noted that the genetic resources have been used repeatedly among the three breeding programs. Consequently, the sugarcane breeder should, in the future, carefully choose more distantly related clones for crossing in order to broaden genetic variation. The consequence of large genetic variation existing over the whole national crop would also reduce the genetic vulnerability to pests and disease of sugarcane cultivars used in commercial production. The main reason for the failure of base broadening programs is the inability to trace or follow the incorporated germplasm into the germplasm of the advanced breeding population through visual selection. EST-SSR markers developed from this study will help breeders to investigate germplasm for the selection of genetically distant parents used in future breeding, and for the selection of particular sugarcane genotypes based on higher variability among the progenies in order to broaden the gene pool in the breeding programs.

Our study also revealed a high similarity coefficient (0.70) among the two breeding line families, including Phill6607 and suggested that the Saccharum germplasm collection in the breeding programs presented a genetically narrow base. This result supports sveral reports of narrow genetic varition in sugarcane. Refferences to the narrow genetic base of sugarcane varieties are available from several regions, including commercial sugarcane clones from Brazil(Duarte Filho et al., 2010; Oliviera et al. 2009; Pinto et al. 2006)USA (Alwala et al. 2006; Pan 2006; Glynn et al. 2009) Mexico(Rodriguez et al. 2005) tropical and subtropical regions (Selvi al. 2003). An early report on the coefficient of parentage (Chang et al., 1991) of major sugarcane clones in Thailand revealed that the major ancestral S. officinarum clone in the pedigrees of the OCSB, DA, and KU cultivars was cv. Black Cheribon (Chatwachirawong and Srinives, 1999). For the Saccharum barberi, cv. Kansoer was the predominant genetic resource of OCSB and DA, whereas cv. Kansoer cv. Chunee predominated at KU (http:// and cropthai.ku.ac.th/coefparent/fracoef.htm). Consequently, the narrow genetic base of Thai sugarcane germplasm is descended primarily from the ancestral cultivar Black Cheribon contributing most germplasm to the improved cultivars developed by all three programs. Previous studies have also indicated that the genetic basis of modern hybrid sugarcane cultivars are essentially derivatives of no more than 15-20 nobilized cultivars (Berding and Roach, 1987; D'Hont et al., 1995; Ming et al., 2010). Since early interspecific hybridization between Saccharum officinarum and other species, mostly S. spontaneum, followed by a back-crossing process referred to as nobilization, was so successful in producing superior hybrid cultivars, they were selected and became the ancestry of most, if not all, modern cultivars grown in most countries today (Jackson, 2005). Consequently, a genetic bottleneck has occurred in

development of sugarcane. Utilization of wild species with known functional markers developed from this study to tag desirable and undesirable genes in *S. spontaneum* would be an effective way to change this situation to perform more effective introgression breeding for a shortand long-term breeding program.

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Supplemental Table 1. Functional annotation of 212 EST-SSR sequences.

S/N	Marker	Cluster	Motif	Forward primer	Reverse primer	Time (℃)	Expected
1	SEM1	SCEPB71008B02 g	(anc)10			56	215
2	SEM2	SCACAD1035E09 g	$(agc) = 10^{-10}$	ACACCGAGCTGTCCCCAT	GCATCTGATGAGCCTGTGAA	56	164
2	SEM7	SCAGI B2047G03 g	(tttc)15	GGAAGGTATGGGTGCTATGC		58	167
1	SEM11	SCAGBT20/1411 a	(ta)16			58	190
т 5	SEM13	SCREAM2022D09 a	(19)10 (naaa)11		CGCAGATCCTCTTGAACCTC	62	161
6	SEM14	SCBGAM1091405 g	(gaaa) 11 (ta)10(caa)5	GAGCAACGAGCTGAAAAGTG	TGTCCTGACCTAGGATGTGC	59	245
7	SEM15	SCBGL B1119D12 a	(ta) 10(cag) 3 (ta) 26(at) 5	TGTCCACAATTTTGGCTGAT	GTTGCTTGCCTGATCATTGT	56	240
, 8	SEM16	SCCCAD1003H03 g	(la)20(al)3	COTTOCTTOGCOTOTTOTOT	TECTEGTCECAGTACTTEAT	58	248
a	SEM10	SCCCCI /002408 g	(aag) 10	CAGCCCATTAACCAAGCAAT	GAAGCAGCTGTTGCTCACTG	58	18/
10	SEM20	SCCCCI 4004D08 g	(gea)5(caa)10 (ataga)12	CCGGCTGTGAAAATTAGGTT	TCGAATTGGTCAAGACTCTCC	58	219
11	SEM24	SCCCCI 4015G07 g	$(a(aga))^2$ (ct)10(ac)5	CAATTOGTOGCTTGTGTTTG		58	197
12	SEM27	SCCCCI 6001E08 a	(ag)16	AGGTCTCGGCACTTGGAGTA	GATCGATCCTCCTCTTTCC	62	172
13	SEM29	SCCCCI 6005E10 g	(ct)21(cca)7	GATCGATCCTCCCTCTTTCC	AGGTCTCGGCACTTGGAGTA	62	187
14	SEM36	SCCCI B1078G05.g	(ta)12	CCATGTGCAGCATTTAACAA	TGGACATGCTAATGACTACTGC	56	152
15	SEM37	SCCCI B1079D03 g	(a) 15	CTTCCTGCTTCGAACATTTG	ACGAGGTAGATCCCGAAGG	56	214
16	SEM38	SCCCLR1080G12.g	(ga)10	TGAATTGCACAAAACACCAA	GACGGTGTAAACAAGCTGTGA	55	249
17	SEM41	SCCCRT2001B06.g	(ag)24	CCCCCTTGACACCTCTGTAT	TAGAACGAACCAGACGACCA	59	248
18	SEM42	SCCCRZ2004G11.g	(aag)7(ta)15	GACTTCGGGAAGAAGGAGGT	ACCAAGCACATCCAGCAGTA	59	285
19	SEM46	SCCCST1002H09.a	(act)11	GCGGTCTTGTAGTGGTAGAGC	TGATCCTCCTGTTCCTCACA	59	232
20	SEM53	SCEPAM1020C01.g	(ct)20(ct)20	CCGCCTTCTCCTTAGTGACA	CCACAAGCCTAATACAGCTCAA	62	192
21	SEM55	SCEPAM2057B09.g	(ct)15(ct)5	ACGGCATCAGATTCAGATCA	ATGGCTTTCCATCTCGTGAC	56	277
22	SEM57	SCEPRT2048F09.g	(cag)11	TCCAGAAGTACGTGGAGACG	ACGACAGCAGGTCGAACAT	56	222
23	SEM58	SCEPSB1130G10.g	(cacta)15	CCAACCAACCTCGACATTCT	CCATGTGATCTGACCTGGTG	60	209
24	SEM60	SCEQAM1041B03.g	(ag)12	TGCTAACACATTTCAAGAAAGAGA	GATCCAATCCGAGGAAAAGT	58	155
25	SEM61	SCEQAM1041H02.g	(ct)12	GTTCAGAACACGTGCAGCAT	CACGCTTGACATGAGAGGAA	59	165
26	SEM63	SCEQHR1078A09.g	(ag)25	GGTCGGTGCTCTGTTCTTT	CCTGCAGCAGAGACGAGAT	59	197
27	SEM68	SCEQRT1032H07.g	(ta)6(ac)11(tc)6	CCCTGAGGTCTCTCTCCACT	TGCCATAGGACAAGAGTTTAACA	64	239
28	SEM72	SCEQSD2075F10.g	(ag)14	GAACCTTATCGGTAGCCTCCT	GAGCGCCATAGGAGAAGTG	58	158
29	SEM76	SCEZHR1048C09.g	(gata)14	ATATGCCATGCACGTGTGAC	CAATGTAACCATCGCAGCAT	58	190
30	SEM78	SCEZRT2023F09.g	(ggt)5(atag)14	GTGGTCGCAGACGAGGTC	CTCCGCATTAGCCATTTCC	58	222
31	SEM79	SCEZRT2024C04.g	(ac)13	GATGGAACAGATGCGACAAG	GTTCATCGTAACCTGCTGGA	58	207
32	SEM80	SCEZRZ3015G05.g	(ta)27	GCAGATGAGAGGGCAAAAGT	CGCCTGCAGATGAATCATAG	59	244
33	SEM82	SCEZRZ3017G04.g	(ga)12	AGTACAAGGCACAGCCAGAG	GGACATGAGGTACACCCAGA	62	197

34	SEM83	SCEZRZ3096G10.g	(atg)10	TCCTCCTCTTGTTGCAGTTG	GTCGTCGTCACGATCATCTC	58	184
35	SEM84	SCEZSB1094A08.g	(tc)10	TGTAGCAATTCCTTGCGTTG	CAACAAATACAATGCCAATCG	58	229
36	SEM85	SCJFAD1011F07.b	(ga)10(agag)5	CACCTAGTGAAAGGGGCAAA	CCTGAAGCCTTGGTAGCATC	59	242
37	SEM86	SCJFLR1035E04.g	(ga)10	CGAGAACTAGCATAGCACAAGA	AACAACTGGTGCAAGTCCAT	58	172
38	SEM90	SCJFRZ2010C01.g	(ag)17	CGTGGGCTAATACAGCTCAA	CCCACTGGCACAATCTTCTT	60	190
39	SEM92	SCJFSB1010B12.g	(tc)10	TGTGCCGTTGCCTAATAACA	GGCAAGCTTCCTCAGTTTCTT	56	209
40	SEM94	SCJFST1014E07.g	(tc)10	TTATCTCTTCCCTGCGGTCT	CTGGCTGGGGAGCAACTT	56	196
41	SEM97	SCJLLR1033A04.g	(cgt)10	TTTGGGGGTTCTTAGTCCAG	GAAGACAGTGGACGAGGTCA	59	233
42	SEM98	SCJLRT1019D02.g	(tg)15	GCCAGCAGAATGCTTAACAA	TCTTACTCTGTCCCCCAACC	58	233
43	SEM99	SCJLRT3076A02.g	(ta)12	TTACCTCCGGCAACGTTAAA	TGCAGGCATATGGTAGTCCA	56	175
44	SEM105	SCMCAM1100G01.g	(ctttt)18	AGGGGCCTCAAGTTGTTCTT	CGGTCTCATGGTCACCTTTT	58	220
45	SEM106	SCMCCL6027C07.g	(tc)24	AGGTTGCTGATGGTCCTCAC	CAAGAAGGGAAGCAGGGACT	62	197
46	SEM108	SCMCFL5008F03.g	(ag)10	CGACTTGTGTGGAGGTGAAA	TGGATCAATGTGAACAAAATCG	58	164
47	SEM110	SCMCRT2103A12.g	(at)12(tg)25(ccg)5	GTCTCCTCCTCAACCACTGC	GTGGGGTATGTAACCCATGC	62	202
48	SEM112	SCMCST1057D03.g	(tc)14	CCTTCTGCAGACGAGTTGAA	ACCTGACCAGCAAATCAACA	58	159
49	SEM113	SCPIRT3024F01.g	(ga)17(gga)5	TTCCGGTTTACCCTGCATAG	TTCCTCAGGGCCCTTTTATT	58	232
50	SEM117	SCQGLV1018G08.g	(at)41	GCGTGGCACTGACTACAAGT	CAATGTTCTGTGGTCTGCACT	56	246
51	SEM119	SCQSHR1020F04.g	(ct)16	CCGCGTGCTCTCTCTCTCT	ATTGCCATCACCTCATGCTT	56	206
52	SEM120	SCQSRT2032H08.g	(ccg)10	TAGCAGCTCGATTCACGATT	ATCCTAGTGTGGTGGGTGCT	58	176
53	SEM124	SCRFLB1055F01.g	(tcc)11	CCTTGATGTGCTTGACGAG	CCAACGAGCAAAAGTAAACG	56	270
54	SEM125	SCRFRT3058D07.g	(ct)16	TATTCTCTCCGGATCCCCTA	ATTCAAAGCGCAACACAGTC	58	160
55	SEM127	SCRLAD1139G03.g	(ag)23	GCAGGATAAGCTTGGCAGTT	CTCAAGGCAAGGAACGAATC	58	286
56	SEM131	SCRUFL4024B04.g	(ac)18(cgc)6	AAAGGAAAGCAAACCCAAGG	GCAGTCGTTGTCGTAGCAGA	58	245
57	SEM132	SCRURT2010E12.g	(ct)18	CCCTCCACCTCTTTGCTC	TAGAAAGACCTGCCCTCCTG	58	202
58	SEM136	SCSBAM1085C09.g	(cgg)12	CTCTGACCCGAGCAAAGG	GCCAATAAACAGCAGGGGTA	56	238
59	SEM140	SCSFAD1114H02.g	(at)23	GTGTTTTGGAGACCGTGTCA	CGATTGTTGCGCTGTACATC	58	127
60	SEM141	SCSFFL4083B01.g	(ac)16(ag)13(gt)5	ATCATCCACAGCTAGCAGCA	GGTTTTGCCTTGGTTTTTGA	56	174
61	SEM143	SCSFHR1045G08.g	(ct)9(ct)12	CCCCTCTCCCTCAGTCTTCT	CCATGCTGTCAGGATCCAC	60	279
62	SEM147	SCSGHR1070F11.g	(tcc)10	GCCTCTTCCTCCTCCACTC	GACGACCGTCCTTGTTGAG	58	250
63	SEM148	SCSGLR1025D03.g	(tca)12	GCTACCGGATGGATAAAAGC	CTGACCGAAATGATCAAGGA	56	245
64	SEM154	SCUTCL6035D02.g	(ct)14	ACCGAGGTAGGAGGGAGTGT	GCTCGCCATGAATAGAAAGG	58	219
65	SEM158	SCVPCL6044A06.g	(ag)12	GGATGGTTAAAGCGGAAACA	GGAAACAGTGTACGCCCAGT	56	151
66	SEM159	SCVPHR1089A09.g	(ag)13	CTGGTGGAATAACTCGCTGA	CTCAAGGCAAGAACGAATCC	60	279
67	SEM161	SCVPHR1094C01.g	(agg)10	GAACTGCTCACTGGCTCCTC	GTAGAAGTCCGTCGCCGTAA	58	186
68	SEM164	SCVPLR2019H04.g	(ag)18	GAGGTTATGGGGAAACCAGA	GATTGCAGCCGTAAACTTGA	56	211
69	SEM166	SCVPRT2080G09.g	(gt)22	AGCGCATCTTGCTTATTTGA	ATGCATGATCATCGAGGAAG	56	171

70	SEM167	SCVPRT2083D03.g	(gt)30	CGGATCTTGGCTCCTTCTCT	AGCCTTGATTGGCAATGGTA	58	223
71	SEM168	SCVPRZ2037E02.g	(ct)11	AACGTCAGCCGCTACAACTT	CTTCCCTTTTGCGAAGAAAA	56	143
72	SEM174	SCQGFL3059G12.g	(ta)11	CTCACCGCAGCTCTTTTCT	CACAAGCTATGCGGTCAAAA	58	249
73	SEM176	SCRFFL1029H06.g	(cctc)5(ct)10	CGCCATAACCATAACCACAG	CCTCCCTCCGCTACTTCCTA	58	188
74	SEM179	SCSBFL1101G01.g	(aaag)10	TATTCCACCGGGAACAAGAA	GGGATTGTAGCGACGAGTTG	58	210
75	SEM180	SCSBFL1104E01.b	(ct)12(tgc)6	TTCCACATCAAGCAAGCAAG	ATGACATCAGGAGGGAGACC	58	206
76	SEM184	SCVPFL1073A11.g	(ga)10(ggc)7	ACCAACGCGACGAGAGAG	GCCTGAACTGGTCGTAGGTC	58	206
77	SEM189	SCJFAD1013E12.g	(agg)6(ggaa)8	GAACTGCTCACTGGCTCCTC	GTAGAAGTCCGTCGCCGTAA	59	209
78	SEM190	SCRLAD1098A04.g	(ct)9	CTAGCACGGCAATACAGGC	AGATCTGTTGGGTGCTCGTC	59	189
79	SEM191	SCRLAD1138A05.g	(gcc)8(cca)5	CCAGTCGCGATTCTTCCAC	AAGGGACGGGGAGAAAAATA	55	176
80	SEM195	SCSGAD1008F08.g	(ggc)9(gag)5	CTTCCCGTCGCTCTTACCT	CTCCTCCTCCTCCTCCAC	60	183
81	SEM199	SCEPAM1021B02.g	(tg)9	CTCTCGAGGAGGTGGATGAG	CTGCAAGTTTGTTGGCTGAA	56	237
82	SEM200	SCEPAM1050A03.g	(tc)9	CTGCAGGATCACCTGGAAC	TAAACCCACGCTGACAGACA	56	238
83	SEM203	SCEQAM1036D03.g	(cgc)6(cgc)8	GCGGCCTCATACGTGTAGAT	TCTCTTCCCCTCACCAGAAA	56	237
84	SEM206	SCVPAM1056A04.g	(tctt)9	CATGGTAGCTCCGCTTCTTC	GCGAGAAGCTAGGAAGCACA	59	197
85	SEM207	SCACAM2043G03.g	(gct)8	GGCACACCTCGAGAGACC	ACTCCTCCTCCTCGCTTAGG	60	151
86	SEM208	SCACAM2044B11.g	(ca)8(ac)5	TGAAGACGATGATGGGATGA	TCTGTTTTGCTCCTCCGTCT	56	302
87	SEM211	SCCCAM2001E04.g	(cgc)8	CGGTCGTCTCTTCCTCCTC	CTACTACCACCCGGACCAGA	59	212
88	SEM213	SCCCAM2C08B11.g	(tc)5(tc)5(ct)5(ct)6	CTCTCCGACTCGTCTTCCAC	GCGGACTGCAAAAGAGAGAT	56	241
89	SEM214	SCEQAM2037C11.g	(cag)8(cg)5	ATCGGCTCCAGTCAGAGAGA	CCTGGTGAAGGCTCATGATT	59	323
90	SEM215	SCEZAM2033H10.g	(tc)8	GCCGAAGAGGAATCTACGAG	GTTTGTCTTCCTCCCTGTGC	56	193
91	SEM217	SCEZAM2096F07.g	(ga)9	CACGGGGAGACGAGAGAC	CCAACAACAACCAGAATATCG	54	174
92	SEM219	SCMCAM2084A04.g	(cag)6(cag)5(gca)5(cag)5	AAGTACGGAGCGCAGTGTAG	ACCGCCTTGTACTCCAAATC	56	228
93	SEM220	SCMCAM2084F10.b	(at)8	AAGCTCCTTGCCTGCTACTC	CAAAGGGCATCCTTTCTGAT	55	218
94	SEM221	SCQGAM2028B01.g	(ccg)8	GCCTCTCTCTGCTCAGCCTA	CTCCTCATCTCTCGCCAAA	56	170
95	SEM223	SCSGAM2076E10.g	(tc)8	CACAGCACTTGCCAAGCTAA	AGTTTCACAAAGGGCGACTG	56	216
96	SEM227	SCCCCL3005D03.b	(ct)8	GCTACAGTGCCTCTCCCTCT	CTAGAAGCAGAAGTGGAGTGCT	59	287
97	SEM229	SCCCCL4007E05.g	(cga)9	AGAACCACAACCACCAGGAG	ACAGTTGAATAGGCCGGATG	58	343
98	SEM231	SCCCCL4013B10.g	(cgt)5(gcg)9(cg)5	CCGTTCTACACCTCCAACAT	GACCGTGACCATCTGCTG	57	426
99	SEM232	SCCCCL4014F09.g	(ga)8	CAACTCCAGCTCCAGTCTCC	CTTTTCGCGAAGTGAACACA	58	311
100	SEM233	SCCCCL4015B01.g	(tgt)8	TTGCTTGGGACAAAAGGCTA	ATCTTGCAAAGGAAGGAGCA	55	336
101	SEM234	SCACCL6009D08.g	(acc)8	GGACATGCTGCTCCCTACAT	AGGAGGACTGGTGGTTGAGG	60	211
102	SEM235	SCACCL6010C05.g	(tc)9	CATCGGCTCATCATAACGAA	AGCTACTTCAGCCCCAAGTG	55	250
103	SEM236	SCCCCL6003H04.g	(ct)9	CCCTTTGCTTCCCCTTTACT	GAGGCGCCTTACTGTTCTTG	56	193
104	SEM237	SCEPCL6023G01.g	(gca)8	AGGGAAAGAGACGAGGGAGA	CGTATCTCCGACCACTCCAC	59	167
105	SEM238	SCEPCL6029D06.g	(gcg)8	CTCTCCCCCAACTCTCTCTG	TCCGACGTCAACGTCTCAG	59	176

Supplemental Table 1. Continue.

	106	SEM239	SCRLCL6030D09.g	(ct)9	CGAGAAACCGTGTCCCCTA	CCCTCTCCCTCTTCCTCCT	59	155
	107	SEM246	SCJLFL4097F08.b	(cg)5(gaaa)8	AATCGATCTTAGGGCCGGTA	ACGCCGACGAGTGAGGAC	58	276
	108	SEM250	SCRLFL4109G12.g	(ga)8	ACGACTGTTTGTTCGTGCTC	TTCAAAGGGGCTATCTTGCT	55	233
	109	SEM254	SCBGFL5080G03.g	(cgg)8	ACCTTACAGAGCCCACTGCT	TCGCGATAATGAGATTGAGC	59	152
	110	SEM255	SCCCFL5062D10.g	(ag)8	CGGCGTCCACTGAAAGAG	CAGCCTCGAGTTGGGATG	56	178
	111	SEM257	SCEZFL5084A01.g	(tg)8	TGCTGGAGACGGAGTAGCTT	ATCAGGCAAGCACACAATCA	57	159
	112	SEM258	SCEZFL5091D04.g	(cac)9	GGAAGAGGAGGCTTCGAGAT	CTGGATAATCACGCCCAAAT	55	343
	113	SEM261	SCAGFL8042E05.g	(cgg)8	CCATCCATCCTCTCATCTCC	AAGAGTGCTTGAGCGGATCT	56	187
	114	SEM263	SCRLFL8053B05.g	(gga)5(gca)8	AGCCTCTGACGCTAAGATCC	CACACGCTGCAGATGTTGTT	56	208
	115	SEM265	SCAGHR1018C11.g	(cca)8	ACACTAGCTAGCCAGCCACA	GAAGCGAGGCTATGGCTATG	57	163
	116	SEM271	SCJFHR1034E09.g	(ccg)9	AGCAGATTCACTTCGCCACT	CGATGAGCTTGGAGAGGAG	55	157
	117	SEM273	SCQSHR1022B03.g	(cat)9	TTTCTTTTCGTCACACCCAAT	ACTCCCGTCACTCACCTGAC	55	180
	118	SEM275	SCRUHR1074E09.g	(gag)9	TCTCATCGGATTCACACACA	GGGCAGCTTCGTAATGGT	55	242
	119	SEM276	SCSFHR1043F12.g	(tg)5(tg)8(ag)5	AACCCGTTCTTCTTCCCCTA	CAGAGGGAGATTTGCCATGT	55	241
	120	SEM279	SCVPHR1092G06.g	(gt)8	AACCTAAACGACGACGATGG	AGCGAGGAAACGTCGTACAT	58	343
	121	SEM280	SCCCLB1002D05.g	(ac)5(tac)8(ct)7(act)5	ATGGAGCTCCGTCTTCTTGT	AGTACCGTAGTTGGGGGTTG	54	222
	122	SEM282	SCQGLB1038F11.g	(gcc)9	GAACCTCGCAGTCTTCACAA	CACTACCTGCCTTTCTCTCG	56	191
	123	SEM285	SCVPLB1020B05.g	(gcc)9	TCCTTGAACCTCGCAGTCTT	CTACCTGCCTCTCTCGTTCC	54	192
	124	SEM287	SCRULB2062C01.b	(ac)5(ac)9	CCAATTCAACAAGCATCGAG	GGGAGGACATGAAGTCTGGT	59	187
	125	SEM288	SCACLR1057E07.g	(ga)8(gct)5(ctg)7	TCCGATCACAATCACAGACC	GCTGCAGCAGATGACAAACT	58	227
	126	SEM290	SCBGLR1002F11.g	(cgc)9	AAACGCAAACCCTTATCTCG	GCTTGGAGGTCACCTTCTTC	55	250
	127	SEM294	SCCCLR1066D07.g	(cca)5(ccg)8	CCATACCCTGTACCGTACCC	GATGCTTGCATTCATCCTTG	55	184
	128	SEM295	SCCCLR1066F12.g	(tc)8	CACCTCCCAGACTCTTCTCC	GTGACACCATGGTCCTGAAG	56	176
	129	SEM297	SCCCLR1075D10.g	(cgc)8(cac)6	CACCAAACAGACTCGCATTT	CGGATCGAACTCTGTGACAT	54	214
	130	SEM298	SCCCLR1076A04.g	(ca)8	ACGCGAGAGGGGAGAGAGATA	GTCAGCAGCACGAACAGC	59	163
	131	SEM302	SCEPLR1008H10.g	(ggc)5(cgg)8	GCGGTTTCTTGTTTTCCTTC	ACCACGACCTCGATCTCAAC	56	282
	132	SEM303	SCEPLR1030D11.g	(agg)8	CGAAAACCCTCAAACCCTAA	CTCCTCTAGCTTCCGCTTGT	55	193
	133	SEM306	SCJFLR1013A08.g	(cag)8(cag)9	ACCACCAATACCACCACCAC	TCGACGTTGGACTTGAGAAG	56	247
	134	SEM307	SCJFLR1074A10.g	(ac)5(ca)9(ag)7	CAAACTTTTGCCCGATAGGT	CGGAGCATACCAAGTGAAGA	54	244
	135	SEM308	SCJLLR1101F02.g	(gt)8	TCTCGACTCCCCTAATCACC	CGGACAGAAAGATCGCAGTA	55	242
	136	SEM310	SCQGLR1019C10.g	(ga)8	AAGAAACCAACCCTCAAAGC	GTAGGGTAGCGCTGGGTAAT	55	230
	137	SEM313	SCSGLR1084A02.g	(gcg)9	GAGGGAACACATCCCTTCTC	GCCGTAGATGAAGACCTCCT	56	211
	138	SEM314	SCVPLR1049G12.g	(ct)8(ct)5(cgc)7	GAATATAACCGCCACCTTGC	TGGCTTTCCATCTCGTGACT	58	250
	139	SEM315	SCACLR2007A01.g	(ca)5(ag)9	GAGGTCCTGGGAGAGACAGA	GTCTGGCCCGTAAGCTGT	60	152
	140	SEM319	SCAGLR2026C05.g	(cgc)8	ATCGTCATCGCAAAATGC	CAACCGGAGGCACTGAGTA	56	150
_	141	SEM320	SCCCLR2002F05.g	(ag)9(ag)7	GAGGCAGCTCGACGACAC	GTCAGCTCCGCTCCTGCT	62	111

	142	SEM321	SCQGLR2032D06.g	(ga)8(gc)5	GTCCGTCTCCACTCGAAAAC	GCGGTTGAGGTCGAGGTAG	59	222
	143	SEM327	SCCCRT1001G10.g	(cct)8	CTCCCCTCTCGCTCATCA	AGGTTGACGATGGTGGTGAC	59	196
	144	SEM328	SCCCRT1003H03.g	(ct)16	TCTTGCCTGTTCGTCTTCCT	ATTCCGATTCCGATTCCAAC	55	239
	145	SEM329	SCEQRT1025C10.g	(cgg)8	CACCCAGCTCAAGTACAGCA	GCCTGTAAAAGCCTCCTGTG	59	222
	146	SEM332	SCJFRT1009B09.g	(ggc)8	CCGCAAGGAAGAACACCTT	GCAGTGGAAGTCGACGTAGG	56	232
	147	SEM336	SCJLRT1006C08.g	(at)5(aag)8	GCCAGGGTTCTTCAAGTGAT	TTCGTCATAGCCATCGTCAT	55	155
	148	SEM337	SCJLRT1013F12.g	(ga)8	AGCAATGGTACGCACAAGAG	TTGCTAGTCGTCGTTCTTGG	55	202
	149	SEM338	SCJLRT1018G02.g	(ga)8	GATCGGATCGAGAGGAGTTTT	ATACGACGAGGACGAAGTGG	56	216
	150	SEM339	SCJLRT1019C06.g	(ag)8	AAGCGAGCGTACACCAAATC	ACGGCTCAGATGGTTGAGAG	58	163
	151	SEM341	SCAGRT2041D09.g	(cgg)8	GTGGTTTGAGTACGCTCGTG	AGAGGGATGGCAGTATCCAG	56	249
	152	SEM344	SCEPRT2047A05.g	(ct)15	CGTGCGCTCTCTCTCTCTCT	ATTTTGAGATGGCTGCATCA	57	171
	153	SEM349	SCEQRT2099E08.g	(gca)8	CGAGAGGCCTTCTCTCTCTG	CGCTGACGTAGTCCTGGTAG	59	180
	154	SEM350	SCJFRT2057F04.g	(gca)9	CCAATGGAGACGACACTCCT	GCGGACGTAGATGGAGAAGA	59	228
	155	SEM351	SCMCRT2085E08.g	(tg)8	CGACTGTGGGAGGAGTTTGT	TTGCAGCAGTTGCTAGCTGT	57	119
	156	SEM353	SCQSRT2033C08.g	(ttg)9	TTGCTTCTGTTGGGTTTCAA	TGGTTAAGGTTTGTCGGTGA	54	191
	157	SEM355	SCSFRT2067E08.g	(ag)8	ACCAAATCCAAACACAGCAG	CGATGGTTGAGAGCTTGTGT	57	144
	158	SEM358	SCAGRT3048C12.g	(gaa)9	CTGGCCTCAAGAGGAAACTG	ACCAACCTCTTGACCAGCAC	59	124
	159	SEM361	SCCCRT3001D09.g	(ct)9	GTAGCCGTGGAGCATGAAGT	CTGCTGCCATTAGGAGCAAT	59	173
	160	SEM366	SCBFRZ2045C02.g	(ca)9	CCACCTCTTCTGCCAAGAAC	CATCTTAAACTCCGGTCCACA	55	167
	161	SEM367	SCCCRZ2001C02.g	(ag)8	AGTCAGCATCCATCCAGTCC	ATTTCTCCTGCCCTCCTCTC	59	196
	162	SEM368	SCCCRZ2004C05.g	(gcg)9	AAACCCTCGCCTCCGATT	CCCAATGGTACCAGCAGAGT	59	241
	163	SEM369	SCJFRZ2015A10.g	(ga)8	CGCTTCCATATCTTCTTCTTGG	TGACTCTCCGGTCCCTACAC	55	123
	164	SEM371	SCJFRZ2034B06.g	(tg)9	GGAGAAGCATTTCAGCAACC	CCCGCTTTTCCTCTTTCTTT	54	238
	165	SEM372	SCVPRZ2036E01.g	(at)8	GCCAAGCTAAATAGCTGCTG	ACCACCGTTTCTTTCCTGAC	57	205
	166	SEM373	SCVPRZ2038E05.g	(ccg)8	GCGACCAAATCTGCCGTAT	CATGTAGTCGAGCGCAGAGA	58	189
	167	SEM374	SCCCRZ3003B01.g	(ag)9	GCCTCCTCCCTCCTCTTCTA	GACTGGCTCGGAAACCCTA	59	141
	168	SEM375	SCEPRZ3128D05.g	(ct)6(tc)9	ATGGAGGCTCGTTGTCTTTG	CCGTAATCGCCTCCACTAAA	55	174
	169	SEM377	SCEQRZ3020E12.g	(gcg)8	GGAGAGGACGAAACCCTAGC	CGCATTGAACGCAGTTTCTA	55	233
	170	SEM379	SCJFRZ3C03A08.b	(ctgtg)9	ACGAGGCCACCATAGAACAT	GCACAAGGTGATTGTGCTGT	56	221
	171	SEM384	SCUTRZ3103F01.g	(cgg)9	TAGTAGCAAGCGAGGCGATA	GTCTGTTGCCTTTGATCGTG	55	228
	172	SEM390	SCSGSB1005B12.g	(ag)9	GGGGAAGTAAGTCTCAGGTCA	GCCACCACCTCCATTATCTT	57	116
	173	SEM391	SCUTSB1033C02.g	(ag)8	GTTCAGACTCGCGTGTTTTT	GCTGAGAACCCTTCAGCTCT	55	104
	174	SEM392	SCUTSB1075H09.g	(ta)8	TCATGCTCACCAGCAAAGAC	TCCCGATCAGTGTGTAGACG	55	234
	175	SEM398	SCEPSD1006D03.g	(ta)9	CGTGCAAGCTCCAATATGAT	TGCCACTGTATAGCAGCGTA	54	184
	176	SEM400	SCEZSD1081A02.g	(ccg)8	CAGCTCATCCTCGTCAACCT	CTCCTCTGCTCCTTGTTGCT	59	225
-	177	SEM401	SCMCSD1059G09.g	(ct)9	GCTCCATTCATTTCCTCCTC	TTCGATCGATTGATGGTTGA	53	111

	178	SEM403	SCEQSD2077B12.g	(cga)8	CCTGCATCAACCTCTCCAC	GAAGGCGAGAGAGAAGATCG	55	242
	179	SEM407	SCCCST1006B01.g	(cga)8	GCGAAACTAGCGCTGCTAAA	GGAGGTTCGGGTACGAGTC	58	295
	180	SEM408	SCJFST1048G04.g	(ga)9	CAGAGCCAGCCAGGTAAAAG	TCATCGTGTGCTGCTGGT	58	228
	181	SEM412	SCJLST1022C09.g	(ct)8(ga)7	CAAGGCTGCTTCTGGTGTC	CCTCTTTGGGTTCTCTGCTC	58	246
	182	SEM415	SCMCST1050H06.g	(tc)8	CAGCAGACGAGACGAGAGAG	AGGGTGATGAAGGGAATGAG	56	163
	183	SEM417	SCQGST1032E05.g	(agga)9	GTCTCCTCCCCCTCCTCTC	AGAAGGAGTCGCTCATCTCG	60	167
	184	SEM418	SCQGST1032G11.g	(gt)8	CGGACGTCTCATGTTCTTTG	CAGTGTCCAGTGCAAGTTCC	55	244
	185	SEM419	SCSFST1066E06.g	(gcc)8	TGCGTGGTTGATTGAAGAAG	AGAAGCCTCTTCTGCTGCTG	60	199
	186	SEM421	SCSGST1069F04.g	(gga)5(ctc)8	CACCCTGCTGGTCTCCTC	TCGACGTCGTGTAGTGAACC	59	170
	187	SEM422	SCSGST1072B03.g	(ag)8	GAAGAGTGGGGACGTCTCAG	GCCAGAGGATGTGGTAGAGG	59	199
	188	SEM425	SCSFAD1070E12.g	(gcc)5	GTGCCACCAGCAGCAAT	TCTCGTAGCTGCTCGACTTC	56	244
	189	SEM426	SCVPAM1059C01.g	(at)5	TCGAGAGCGGTTTCATCTTT	CTTTCCTGTCAGCCAAGTGA	56	471
	190	SEM427	SCSBFL1105H11.b	(ca)6	AAGTAGCGGAAGCATTAGTTCA	CCAAGTTCCTCCTCACCAGTA	57	277
	191	SEM428	SCSGLV1008C05.g	(cg)7	CAGGAAGAAACAGTAGGAAGCA	AGGTACTTGGCGGTCTTGAT	57	178
	192	SEM430	SCRUSB1064F09.g	(cgg)5	TCCGACTACCTCAAGTGCAAG	GACGGCATCTTCTTCTTCTCC	55	224
	193	SEM432	SCJLST1019B07.g	(gc)6	CGCGTCCGTAGATTAGTAGCTC	AGCGAGTAGATGTTGATGACCC	56	195
	194	SEM433	SCSBST3094H07.g	(cga)6	GACACGCCCAAAGGAAAAG	GAGATCCGGACACACATGG	54	245
	195	SEM434	SCEZLB1007E12.g	(ta)7	TTCTTGCTTCTTTCTTTCCGTC	TCAAATCGTGCTTGCTTGAG	52	236
	196	SEM435	SCQGLR1041A05.g	(ga)5	AGGCTGAGAGAGCAAAGAAAGA	CCTAGGATCCTTCGGGTTTC	55	164
	197	SEM436	SCJLRT1021D04.g	(tcc)5	GGTCCCATACATAACACAAGCA	TGCATGAAGAAGCTCAGGTG	57	248
	198	SEM437	SCQSRT2031C10.g	(tc)5	CCTGGTTCCTGCACTTGTCT	CATCACTTGCCATCTGCATT	57	217
	199	SEM439	SCACSB1117C07.g	(cgg)6	CGTCAAGCTGTAGTCCGAGAG	CTCGTCCCAGACCAGGAG	59	197
	200	SEM440	SCACSD1018E05.g	(gac)5	AGCAACCTAATCACAGCAACAA	CCATCATCCGATCATCCTTC	56	229
	201	SEM442	SCMCST1057C10.g	(gct)5	CATTTATTTGCCACCTAGAAGGG	AAACAGAAACCGGACAGCAC	56	195
	202	SEM443	SCRLAD1043B06.g	(ggt)7	GGAATGGGAACAGCCACTAAC	AAGAAGGCTATCGAGGTGGG	55	323
	203	SEM444	SCBGAD1027C03.g	(ggc)7	CACGGTTCTCCTGCTGAAAG	GACGGGGTTGTTGAAGGTG	55	313
	204	SEM446	SCCCCL3001D10.b	(ccg)5	GAGCAGTCCCTTGCCATGT	GCCGTCGAGTACACCGTC	59	389
	205	SEM447	SCEZFL5083C02.g	(gc)5	TGAGTTCAGTTCCTTCCCC	AGAACTCCAAGGAGCAGCAG	56	300
	206	SEM449	SCEZLB1006B07.g	(gcc)5	TGGTGTGAGTTAGTGCCTGAGT	TAGAAGGTGTTGATGATGAGCG	55	265
	207	SEM450	SCEZLB1007E12.g	(ta)7	TTCTTGCTTCTTTCTTTCCGTC	AGATGAACACATAGTTGCACCG	56	189
	208	SEM453	SCBFRZ2045E11.g	(ggc)5	AGCGACATGAGCTACCGTCT	TAGTACCGCGACAGACCTTTCT	58	287
	209	SEM454	SCSBRZ3122D09.g	(gga)6	GTAACTAGCAGCAACCCTAGCC	ATCCTCTTTTGCCTCCCCT	55	387
	210	SEM456	AY302083	(tgc)6	TCGTCCTACAACCACGACTACA	GAGAGGCAAGCAAGGAAAGAT	56	164
	211	SEST3	SCSFSB1097B02.g	(ta)8	CCCCGAAGATCAAGGATAGG	CGCATCTCAAATGGGAAAAT	56	413
_	212	SEST4	SCRLAD1040D08.g	(at)5	CAGGCACTGATGTCATGGAT	GAACTACACTCGCCGCTCAC	56	313

#### Supplimentary Table 1. Contd.

C/N	Morkor		E voluo		Allele	Mark	er number	Segre	gation ratio
3/IN	ivial kei	BLASI	E-value	FIC	number	S6	Phil6607	1:1	3:1
1	SEM1	hypothetical protein	3.0E-34	0.64	9	1	6	6	1
2	SEM2	glycosyl hydrolase family protein 17	6.0E-19	0.9	7	1	3	3	1
3	SEM7	Hit not found		0.61	8	1	5	5	0
4	SEM11	hypothetical protein OsJ_018777	1.0E-11	0.93	11	2	7	6	1
5	SEM13	lysine decarboxylase-like protein	3.0E-50	0.68	7	2	2	4	0
6	SEM14	Hit not found		0.83	10	4	3	5	1
7	SEM15	Hit not found		0.45	5	1	1	2	0
8	SEM16	harpin-induced protein 1 family (HIN1)-like	5.0E-14	0.91	3	1	0	0	0
9	SEM19	ARFE_ORYSJAuxin response factor 5	1.0E-177	0.86	13	2	7	7	1
10	SEM20	NADH-plastoquinone oxidoreductase subunit K	1.0E-100	0	6	2	3	4	0
11	SEM24	Hit not found		0	9	1	5	5	0
12	SEM27	mediator complex subunit SOH1	3.0E-54	0.9	14	3	7	8	0
13	SEM29	Probable mediator complex subunit SOH1	0.42	0.92	12	3	6	8	1
14	SEM36	Hit not found		0.69	5	1	4	3	0
15	SEM37	unknown protein	1.0E-30	0.88	7	2	4	5	1
16	SEM38	WD-repeat containing protein	0	0.9	4	1	4	1	1
17	SEM41	Hit not found		0.85	13	8	4	5	1
18	SEM42	hypothetical protein	2.0E-18	0.88	6	1	3	2	0
19	SEM46	pi starvation-induced protein	588	0.87	7	1	3	1	0
20	SEM53	hypothetical protein OsJ_026388	2.0E-18	0.77	10	1	7	6	0
21	SEM55	zinc transporter	1.0E-49	0.73	6	2	1	1	0
22	SEM57	Hit not found		0.91	11	2	8	6	0
23	SEM58	sugar-starvation induced protein	0.001	0.84	9	5	5	5	0
24	SEM60	unfertilized embryo sac 16	1.0E-53	0.86	8	2	4	3	2
25	SEM61	zinc-finger protein	1.0E-11	0.72	12	6	2	7	1
26	SEM63	Hit not found		0.12	9	3	1	1	1
27	SEM68	Hit not found		0.7	5	6	2	4	1
28	SEM72	30S ribosomal protein S17, chloroplast precursor	0.081	0.31	4	2	1	3	1
29	SEM76	cysteine proteinase	3.0E-53	0.92	15	4	9	0	0
30	SEM78	ubiquitin-protein ligase-like	4.0E-15	0	13	2	5	3	3
31	SEM79	Nitrilase-associated protein	1.0E-11	0.91	7	3	2	1	1
32	SEM80	heavy meromyosin-like	8.0E-19	0.92	5	1	1	1	0
33	SEM82	cbs domain-containing	6.0E-74	0.82	4	3	1	3	0
34	SEM83	Dof zinc finger protein MNB1A	5.0E-12	0.88	17	8	4	7	2

35	SEM84	Hit not found		0.91	10	2	2	4	0
36	SEM85	pectin-glucuronyltransferase	1.0E-37	0.91	4	1	2	0	1
37	SEM86	chitin-inducible gibberellin-responsive protein	1.0E-81	0.64	8	4	4	4	0
38	SEM90	hypothetical protein	9.0E-18	0.71	8	2	4	3	0
39	SEM92	bZIP transcription factor	7.0E-24	0.58	8	2	1	0	0
40	SEM94	Hit not found		0.82	6	0	3	2	1
41	SEM97	ankyrin-like protein	3.0E-17	0.83	17	0	2	0	1
42	SEM98	Hit not found		0.79	8	2	3	5	1
43	SEM99	Hit not found		0.9	11	1	3	2	0
44	SEM105	exocyst subunit EXO70 family protein	6.0E-46	0.92	10	2	2	3	0
45	SEM106	hypothetical protein	2.0E-10	0.91	5	2	2	3	0
46	SEM108	VP15	4.0E-30	0.66	7	3	5	2	1
47	SEM110	Cortical cell delineating protein precursor	3.0E-24	0.9	14	5	3	2	0
48	SEM112	S-adenosylmethionine decarboxylase	7.0E-31	0.92	8	3	3	6	0
49	SEM113	hypothetical protein	8.0E-39	0.92	11	6	3	5	2
50	SEM117	nuclease I	1.0E-71	0.76	6	2	1	2	0
51	SEM119	hypothetical protein Osl_018669	1.0E-35	0.41	7	3	1	3	1
52	SEM120	protein	1.0E-29	0.84	5	1	0	0	0
53	SEM124	bet v i allergen-like	4.0E-70	0.23	7	2	3	0	1
54	SEM125	hypothetical protein	1.0E-17	0.59	7	3	4	1	0
55	SEM127	Hit not found		0.92	7	2	1	3	0
56	SEM131	lipid transfer protein precursor	1.0E-28	0.85	4	4	4	3	0
57	SEM132	RRM-containing protein	1.0E-16	0.93	11	3	4	5	2
58	SEM136	Hit not found		0.93	6	2	2	3	1
59	SEM140	Hit not found		0.89	5	0	1	1	1
60	SEM141	GRC14_ORYSJPutative glutaredoxin-C14 precursor	1.0E-43	0.81	21	4	7	2	0
61	SEM143	Hit not found		0.74	3	5	4	7	0
62	SEM147	hypothetical protein OsJ_003463	1.0E-18	0.78	8	7	2	0	0
63	SEM148	Hit not found		0.91	4	3	1	2	0
64	SEM154	ribosomal protein L4/L1 family protein	8.0E-133	0.85	9	3	4	5	1
65	SEM158	Hit not found		0.72	10	2	5	5	1
66	SEM159	exhydrolase II	1.0E-18	0.91	10	4	2	4	0
67	SEM161	auxin efflux carrier	1.0E-37	0.68	6	6	2	6	0
68	SEM164	Hit not found		0.86	11	4	4	5	1
69	SEM166	Hit not found		0.62	12	5	3	4	0
70	SEM167	Hit not found		0.92	15	7	5	11	2

71	SEM168	glucanase	1.0E-42	0.5	7	3	3	4	0
72	SEM174	hypothetical protein	3.0E-05	0.2	4	6	3	2	0
73	SEM176	(DSRNA-BINDING PROTEIN 3); double-stranded RNA binding	1.0E-55	0.88	5	2	1	1	1
74	SEM179	receptor protein kinase PERK1	1.0E-50	0.89	6	4	1	2	0
75	SEM180	hypothetical protein Osl_012598	1.0E-12	0.58	8	2	3	4	1
76	SEM184	positive transcription elongation factor/ zinc ion binding	2.0E-46	0.92	6	1	4	3	0
77	SEM189	auxin efflux carrier	3.0E-62	0.91	15	0	3	2	2
78	SEM190	Hit not found		0.74	9	4	5	3	0
79	SEM191	Hit not found		0.61	4	1	2	1	0
80	SEM195	Hit not found		0.44	3	1	2	1	0
81	SEM199	hypothetical protein OsJ_007772	1.0E-29	0.66	11	3	7	3	0
82	SEM200	cytochrome p450	5.0E-66	0.9	8	2	4	0	2
83	SEM203	wd40 repeat protein	1.0E-171	0.79	5	0	5	0	0
84	SEM206	lysine decarboxylase-like protein	3.0E-86	0.86	12	3	2	5	1
85	SEM207	disease resistance protein	3.0E-104	0.72	5	0	4	0	1
86	SEM208	phytoene synthase	1.0E-76	0.83	9	1	7	7	1
87	SEM211	hypothetical protein Osl_020099	7.0E-38	0.5	5	2	4	1	0
88	SEM213	Hit not found		0.68	7	1	3	4	0
89	SEM214	Hit not found		0.87	4	2	2	1	0
90	SEM215	Hit not found		0.5	5	2	0	2	0
91	SEM217	hypothetical protein	3.0E-16	0.91	6	1	4	0	1
92	SEM219	zinc finger	1.0E-32	0.37	14	3	3	4	2
93	SEM220	Chitin-inducible gibberellin-responsive protein 1	2.0E-56	0.82	6	5	4	2	0
94	SEM221	calcium-responsive transcription coactivator	1.0E-54	0.92	17	4	1	5	1
95	SEM223	DNA-dependent RNA polymerase II	8.0E-24	0.81	14	8	9	4	0
96	SEM227	GT-2 factor	0.001	0.83	7	1	2	2	1
97	SEM229	diphosphate-fructose-6-phosphate 1-phosphotransferase	0	0.65	5	3	3	4	1
98	SEM231	lateral root primordia	3.0E-40	0.86	6	5	5	2	0
99	SEM232	ubiquitin C-terminal hydrolase	1.0E-101	0.9	9	0	3	2	1
100	SEM233	gene X-like protein	4.0E-49	0.77	6	0	6	1	0
101	SEM234	family transcription factor containing protein	6.0E-11	0.79	5	0	4	0	0
102	SEM235	Auxin-responsive GH3-like protein 1	5.0E-34	0.93	11	1	4	2	1
103	SEM236	S-receptor kinase homolog precursor-like	4.0E-04	0.87	5	2	3	2	0
104	SEM237	hypothetical protein	0.011	0.12	3	3	2	5	3
105	SEM238	protein kinase domain containing	5.0E-15	0.79	13	11	4	5	0
106	SEM239	CAD1 (constitutively activated cell death 1);oxidoreductase	3.0E-21	0.83	6	1	3	4	1

107       SEM246       hypothetical protein       5.5       0.64       8       3       4       2       0         108       SEM250       flavonol 4'-sulfotransferase       5.0E-13       0.62       4       4       0       2       0         109       SEM255       hypothetical protein Osl_008638       1.0E-16       0.64       9       5       4       0       0         111       SEM257       Hit not found       0.88       9       6       5       7       1       0       0       4       4       0       0         112       SEM256       hypothetical protein Osl_008782       1.0E-12       0.93       12       2       7       7       0 <td< th=""><th></th><th></th><th></th><th></th><th></th><th></th><th></th><th></th><th></th><th></th></td<>										
108       SEM250       flavonol 4'-sulfotransferase       5.0E-13       0.62       4       4       0       2       0         109       SEM254       uv-damaged dna-binding       3.0E-92       0.88       9       6       5       7       1         110       SEM255       hypothetical protein Osl_00838       1.0E-16       0.64       9       5       4       0       0         111       SEM255       Hit not found       0.89       4       0       4       2       1       0         112       SEM261       hypothetical protein       1.0E-16       0.61       7       1       5       3       0         114       SEM263       hypothetical protein       0.08782       1.0E-12       0.93       12       2       7       7       0         115       SEM265       liverleat whitefly-induced protein       9.0E-77       0.56       5       1       2       2       2       1       0         118       SEM275       iron deficiency protein lds3       3.0E-12       0.93       7       1       3       0       3       1         120       SEM279       phospholipid transfer protein       1.0E-19       0.81	107	SEM246	hypothetical protein	5.5	0.64	8	3	4	2	0
109       SEM254       uv-damaged dna-binding       3.0E-92       0.88       9       6       5       7       1         110       SEM255       hypothetical protein Osl_008838       1.0E-16       0.64       9       5       4       0       0         111       SEM257       Hit not found       0.89       4       0       4       2       1       0         112       SEM258       TPA_exp: GRP21       7.7       0.92       10       4       2       1       0         113       SEM261       hypothetical protein osl_008782       1.0E-12       0.93       12       2       7       7       0         116       SEM271       silverleaf whitefly-induced protein 1       9.0E-77       0.56       5       1       2       2       2       2       1       0       3	108	SEM250	flavonol 4'-sulfotransferase	5.0E-13	0.62	4	4	0	2	0
110       SEM255       hypothetical protein Osl_00838       1.0E-16       0.64       9       5       4       0         111       SEM257       Hit not found       0.89       4       0       4       0         112       SEM258       TPA_exp: GRP21       7.7       0.92       10       4       2       1       0         113       SEM261       hypothetical protein Osl_008782       1.0E-12       0.93       12       2       7       7       0         115       SEM263       Hit not found       0.85       6       0       2       0       0         116       SEM273       silverleaf whitefly-induced protein 1       9.0E-77       0.56       5       1       2       2       2       1       0         118       SEM275       iron deficiency protein lds3       3.0E-12       0.93       7       1       3       0       3       1         120       SEM279       phospholipid transfer protein       1.0E-19       0.81       10       3       2       0       0         121       SEM280       retrotransposon protein, putative, Ty1-copia subclass       1.0E-75       0.83       9       1       3       3       <	109	SEM254	uv-damaged dna-binding	3.0E-92	0.88	9	6	5	7	1
111       SEM258       Hit not found       0.89       4       0       4       4       0         112       SEM258       TPA_exp: GRP21       7.7       0.92       10       4       2       1       0         113       SEM261       hypothetical protein       1.0E-12       0.93       12       2       7       7       0         114       SEM265       Hit not found       0.85       6       0       2       0       0         115       SEM265       Hit not found       0.85       6       0       2       2       2       0         116       SEM275       indeferminate spikelet protein 1       9.0E-77       0.56       5       1       2       2       1       0       3         119       SEM276       indeferminate spikelet 1       3.0E-96       0.76       6       1       4       4       1         120       SEM279       phospholipid transfer protein       1.0E-19       0.81       10       3       3       1         122       SEM282       retrotransposon protein, putative, Ty1-copia subclass       1.0E-75       0.83       9       1       3       3       1       1       0	110	SEM255	hypothetical protein OsI_008838	1.0E-16	0.64	9	5	4	0	0
112       SEM258       TPA_exp: GRP21       7.7       0.92       10       4       2       1       0         113       SEM261       hypothetical protein       1.0E-08       0.61       7       1       5       3       0         114       SEM265       Hit not found       0.85       6       0       2       0       0         115       SEM265       Hit not found       0.85       6       0       2       2       2         117       SEM273       cdc2 protein kinases-like       1.0E-126       0.68       5       2       2       1       0       3         118       SEM276       indeterminate spikelet 1       3.0E-12       0.93       7       1       3       0       3       1         120       SEM276       indeterminate spikelet 1       3.0E-12       0.83       9       2       1       3       1         121       SEM280       peroxidase atp8a       6.0E-147       0.89       9       2       1       3       1         122       SEM285       renotransposon protein, putative, Ty1-copia subclass       1.0E-140       0.79       12       2       5       4       0	111	SEM257	Hit not found		0.89	4	0	4	4	0
113       SEM261       hypothetical protein       1.0E-08       0.61       7       1       5       3       0         114       SEM263       hypothetical protein Osl_008782       1.0E-12       0.93       12       2       7       7       0         115       SEM265       Hit not found       0.85       6       0       2       0       0         116       SEM271       silverleaf whitefly-induced protein 1       9.0E-77       0.56       5       1       2       2       2       1       0         118       SEM273       cdc2 protein kinases-like       1.0E-126       0.68       5       2       2       1       0         119       SEM275       indeferminate spikelet 1       3.0E-96       0.76       6       1       4       4       1         120       SEM279       phospholipid transfer protein       1.0E-19       0.81       10       3       2       0       0         121       SEM280       peroxidase atp8a       6.0E-147       0.89       9       2       1       3       1       1       0       0       0       0       0       0       0       0       0       0       0 <td>112</td> <td>SEM258</td> <td>TPA_exp: GRP21</td> <td>7.7</td> <td>0.92</td> <td>10</td> <td>4</td> <td>2</td> <td>1</td> <td>0</td>	112	SEM258	TPA_exp: GRP21	7.7	0.92	10	4	2	1	0
114       SEM263       hypothetical protein OsJ_008782       1.0E-12       0.93       12       2       7       7       0         115       SEM265       Hit not found       0.85       6       0       2       0       0         116       SEM271       silverleaf whitefly-induced protein 1       9.0E-77       0.56       5       1       2       2       1       0         118       SEM275       iron deficiency protein lds3       3.0E-12       0.93       7       1       3       0       3         119       SEM276       indeterminate spikelet 1       3.0E-96       0.76       6       1       4       4       1         120       SEM279       phospholipid transfer protein       1.0E-19       0.81       10       3       2       0       0         121       SEM280       peroxidase atp8a       6.0E-147       0.89       9       2       1       3       1       1       0       0         123       SEM285       retrotransposon protein, putative, Ty1-copia subclass       2.0E-75       0.91       5       1       1       0       0         124       SEM285       ring-P12 finger proteinexpressed       1.0E-126	113	SEM261	hypothetical protein	1.0E-08	0.61	7	1	5	3	0
115       SEM265       Hit not found       0.85       6       0       2       0       0         116       SEM271       silverleat whitefly-induced protein 1       9.0E-77       0.56       5       1       2       2       2         117       SEM273       cdc2 protein kinases-like       1.0E-77       0.56       5       1       2       2       1       0         118       SEM275       iron deficiency protein lds3       3.0E-12       0.93       7       1       3       0       3         119       SEM276       indeterminate spikelet 1       3.0E-96       0.76       6       1       4       4       1         120       SEM279       phospholipid transfer protein       1.0E-19       0.81       10       3       2       0       0         121       SEM280       retrotransposon protein, putative, Ty1-copia subclass       2.0E-75       0.83       9       1       3       3       1       1       0       0         123       SEM287       tranched-chain amino acid aminotransferase       9.0E-38       0.74       11       6       1       5       0         126       SEM290       Proteasome subunit alpha type 4-1	114	SEM263	hypothetical protein OsJ_008782	1.0E-12	0.93	12	2	7	7	0
116       SEM271       silverleaf whitefly-induced protein 1       9.0E-77       0.56       5       1       2       2       1         117       SEM273       cdc2 protein kinases-like       1.0E-126       0.88       5       2       2       1       0         118       SEM275       iron deficiency protein lds3       3.0E-12       0.93       7       1       3       0       3         119       SEM276       indeterminate spikelet 1       3.0E-96       0.76       6       1       4       4       1         120       SEM280       peroxidase atp8a       6.0E-147       0.89       9       2       1       3       1         122       SEM280       peroxidase atp8a       6.0E-147       0.89       9       2       1       3       1         123       SEM285       retrotransposon protein, putative, Ty1-copia subclass       2.0E-75       0.83       9       1       3       3       1       1       0       0         124       SEM285       retrotransposon protein, putative, Ty1-copia subclass       1.0E-140       0.79       12       2       5       4       0         124       SEM287       branched-chain amino acid aminotra	115	SEM265	Hit not found		0.85	6	0	2	0	0
117       SEM273       cdc2 protein kinases-like       1.0E-126       0.68       5       2       2       1       0         118       SEM275       iron deficiency protein lds3       3.0E-12       0.93       7       1       3       0       3         119       SEM276       indeterminate spikelet 1       3.0E-96       0.76       6       1       4       4       1         120       SEM279       phospholipid transfer protein       1.0E-19       0.81       10       3       2       0       0         121       SEM280       peroxidase atp8a       6.0E-147       0.89       9       2       1       3       1         122       SEM285       retrotransposon protein, putative, Ty1-copia subclass       2.0E-75       0.83       9       1       3       3       1         123       SEM287       branched-chain amino acid aminotransferase       9.0E-38       0.74       11       6       1       5       0         124       SEM280       Proteasome subunit alpha type 4-1       5.0E-80       0.89       13       3       1       1       1       1       0       0       2       1       0       0       2       1	116	SEM271	silverleaf whitefly-induced protein 1	9.0E-77	0.56	5	1	2	2	2
118       SEM275       iron deficiency protein Ids3       3.0E-12       0.93       7       1       3       0       3         119       SEM276       indeterminate spikelet 1       3.0E-96       0.76       6       1       4       4       1         120       SEM279       phospholipid transfer protein       1.0E-19       0.81       10       3       2       0       0         121       SEM280       peroxidase atp8a       6.0E-147       0.89       9       2       1       3       1         122       SEM285       retrotransposon protein, putative, Ty1-copia subclass       2.0E-75       0.83       9       1       3       3       1         123       SEM285       retrotransposon protein, putative, Ty1-copia subclass       1.0E-75       0.91       5       1       1       0       0         124       SEM287       branched-chain amino acid aminotransferase       9.0E-38       0.74       11       6       1       5       0         125       SEM288       ring-A2 finger proteinexpressed       1.0E-12       0.61       5       3       2       1       0         126       SEM290       Proteasome subunit alpha type 4-1       5.0E-80	117	SEM273	cdc2 protein kinases-like	1.0E-126	0.68	5	2	2	1	0
119       SEM276       indeterminate spikelet 1       3.0E-96       0.76       6       1       4       4       1         120       SEM279       phospholipid transfer protein       1.0E-19       0.81       10       3       2       0       0         121       SEM280       peroxidase atp8a       6.0E-147       0.89       9       2       1       3       1         122       SEM282       retrotransposon protein, putative, Ty1-copia subclass       2.0E-75       0.83       9       1       3       3       1         123       SEM285       retrotransposon protein, putative, Ty1-copia subclass       1.0E-75       0.91       5       1       1       0       0         124       SEM287       branched-chain amino acid aminotransferase       9.0E-38       0.74       11       6       1       5       0         125       SEM288       ring-h2 finger proteinexpressed       1.0E-140       0.79       12       2       5       4       0         126       SEM290       Proteasome subunit alpha type 4-1       5.0E-80       0.89       13       3       1       1       1         127       SEM294       Hypothetical protein OsJ_014087       1.0E-12<	118	SEM275	iron deficiency protein Ids3	3.0E-12	0.93	7	1	3	0	3
120       SEM279       phospholipid transfer protein       1.0E-19       0.81       10       3       2       0       0         121       SEM280       peroxidase atp8a       6.0E-147       0.89       9       2       1       3       1         122       SEM282       retrotransposon protein, putative, Ty1-copia subclass       2.0E-75       0.83       9       1       3       3       1         123       SEM285       retrotransposon protein, putative, Ty1-copia subclass       1.0E-75       0.91       5       1       1       0       0         124       SEM287       branched-chain amino acid aminotransferase       9.0E-38       0.74       11       6       1       5       0         125       SEM288       ring-h2 finger proteinexpressed       1.0E-140       0.79       12       2       5       4       0         126       SEM290       Proteasome subunit alpha type 4-1       5.0E-80       0.89       13       3       1       1       1         127       SEM294       hypothetical protein OSJ_014087       1.0E-12       0.61       5       3       2       1       0         128       SEM295       Hit not found       0.83 <td< td=""><td>119</td><td>SEM276</td><td>indeterminate spikelet 1</td><td>3.0E-96</td><td>0.76</td><td>6</td><td>1</td><td>4</td><td>4</td><td>1</td></td<>	119	SEM276	indeterminate spikelet 1	3.0E-96	0.76	6	1	4	4	1
121       SEM280       peroxidase atp8a       6.0E-147       0.89       9       2       1       3       1         122       SEM282       retrotransposon protein, putative, Ty1-copia subclass       2.0E-75       0.83       9       1       3       3       1         123       SEM285       retrotransposon protein, putative, Ty1-copia subclass       1.0E-75       0.91       5       1       1       0       0         124       SEM287       branched-chain amino acid aminotransferase       9.0E-38       0.74       11       6       1       5       0         125       SEM288       ring-h2 finger proteinexpressed       1.0E-140       0.79       12       2       5       4       0         126       SEM290       Proteasome subunit alpha type 4-1       5.0E-80       0.89       13       3       1       1       1         127       SEM297       g-patch domain containing       3.0E-104       0.87       11       0       6       3       2       1       0         128       SEM297       g-patch domain containing       3.0E-104       0.87       11       0       6       3       2       1       1         130       SEM302 <td>120</td> <td>SEM279</td> <td>phospholipid transfer protein</td> <td>1.0E-19</td> <td>0.81</td> <td>10</td> <td>3</td> <td>2</td> <td>0</td> <td>0</td>	120	SEM279	phospholipid transfer protein	1.0E-19	0.81	10	3	2	0	0
122       SEM282       retrotransposon protein, putative, Ty1-copia subclass       2.0E-75       0.83       9       1       3       3       1         123       SEM285       retrotransposon protein, putative, Ty1-copia subclass       1.0E-75       0.91       5       1       1       0       0         124       SEM287       branched-chain amino acid aminotransferase       9.0E-38       0.74       11       6       1       5       0         125       SEM288       ring-h2 finger proteinexpressed       1.0E-140       0.79       12       2       5       4       0         126       SEM290       Proteasome subunit alpha type 4-1       5.0E-80       0.89       13       3       1       1       1       1         127       SEM294       hypothetical protein OS_014087       1.0E-12       0.61       5       3       2       1       0         128       SEM295       Hit not found       0.88       7       1       3       0       0         129       SEM292       Hit not found       0.83       8       1       2       3       0         130       SEM303       hypothetical protein       8.0E-23       0.9       5       2 <td>121</td> <td>SEM280</td> <td>peroxidase atp8a</td> <td>6.0E-147</td> <td>0.89</td> <td>9</td> <td>2</td> <td>1</td> <td>3</td> <td>1</td>	121	SEM280	peroxidase atp8a	6.0E-147	0.89	9	2	1	3	1
123       SEM285       retrotransposon protein, putative, Ty1-copia subclass       1.0E-75       0.91       5       1       1       0       0         124       SEM287       branched-chain amino acid aminotransferase       9.0E-38       0.74       11       6       1       5       0         125       SEM288       ring-h2 finger proteinexpressed       1.0E-140       0.79       12       2       5       4       0         126       SEM290       Proteasome subunit alpha type 4-1       5.0E-80       0.89       13       3       1       1       1         127       SEM294       hypothetical protein OsJ_014087       1.0E-12       0.61       5       3       2       1       0         128       SEM297       g-patch domain containing       3.0E-104       0.87       11       0       6       3       2         130       SEM298       Hit not found       0.72       8       4       3       3       0         131       SEM302       hit not found       0.72       8       4       3       2       1       1       0         132       SEM303       hypothetical protein       8.0E-23       0.9       5       2	122	SEM282	retrotransposon protein, putative, Ty1-copia subclass	2.0E-75	0.83	9	1	3	3	1
124       SEM287       branched-chain amino acid aminotransferase       9.0E-38       0.74       11       6       1       5       0         125       SEM288       ring-h2 finger proteinexpressed       1.0E-140       0.79       12       2       5       4       0         126       SEM290       Proteasome subunit alpha type 4-1       5.0E-80       0.89       13       3       1       1       1         127       SEM294       hypothetical protein OsJ_014087       1.0E-12       0.61       5       3       2       1       0         128       SEM295       Hit not found       0.88       7       1       3       0       0         129       SEM297       g-patch domain containing       3.0E-104       0.87       11       0       6       3       2         130       SEM298       Hit not found       0.83       8       1       2       3       0         131       SEM302       Hit not found       0.72       8       4       3       3       0         133       SEM308       hypothetical protein       8.0E-23       0.9       5       2       1       1       0         133       SEM	123	SEM285	retrotransposon protein, putative, Ty1-copia subclass	1.0E-75	0.91	5	1	1	0	0
125       SEM288       ring-h2 finger proteinexpressed       1.0E-140       0.79       12       2       5       4       0         126       SEM290       Proteasome subunit alpha type 4-1       5.0E-80       0.89       13       3       1       1       1         127       SEM294       hypothetical protein OsJ_014087       1.0E-12       0.61       5       3       2       1       0         128       SEM295       Hit not found       0.88       7       1       3       0       0         129       SEM297       g-patch domain containing       3.0E-104       0.87       11       0       6       3       2       0         130       SEM298       Hit not found       0.83       8       1       2       3       0         131       SEM302       Hit not found       0.72       8       4       3       3       0         133       SEM303       hypothetical protein       8.0E-23       0.9       5       2       1       1       0         133       SEM306       ccr4-not transcription complex subunit 7       2.0E-14       0       6       3       2       1       1         134	124	SEM287	branched-chain amino acid aminotransferase	9.0E-38	0.74	11	6	1	5	0
126       SEM290       Proteasome subunit alpha type 4-1       5.0E-80       0.89       13       3       1       1       1         127       SEM294       hypothetical protein OsJ_014087       1.0E-12       0.61       5       3       2       1       0         128       SEM295       Hit not found       0.88       7       1       3       0       0         129       SEM297       g-patch domain containing       3.0E-104       0.87       11       0       6       3       2         130       SEM298       Hit not found       0.83       8       1       2       3       0         131       SEM302       Hit not found       0.72       8       4       3       3       0         132       SEM303       hypothetical protein       8.0E-23       0.9       5       2       1       1       0         133       SEM306       ccr4-not transcription complex subunit 7       2.0E-14       0       6       3       2       1       1         134       SEM307       Hit not found       0.77       7       0       4       2       1         135       SEM308       Hit not found       0	125	SEM288	ring-h2 finger proteinexpressed	1.0E-140	0.79	12	2	5	4	0
127       SEM294       hypothetical protein OsJ_014087       1.0E-12       0.61       5       3       2       1       0         128       SEM295       Hit not found       0.88       7       1       3       0       0         129       SEM297       g-patch domain containing       3.0E-104       0.87       11       0       6       3       2         130       SEM298       Hit not found       0.83       8       1       2       3       0         131       SEM302       Hit not found       0.72       8       4       3       3       0         132       SEM303       hypothetical protein       8.0E-23       0.9       5       2       1       1       0         133       SEM306       ccr4-not transcription complex subunit 7       2.0E-14       0       6       3       2       1       1         134       SEM307       Hit not found       0.77       7       0       4       2       1         135       SEM308       Hit not found       0.77       7       0       4       2       1         136       SEM310       Hit not found       0.89       10       6	126	SEM290	Proteasome subunit alpha type 4-1	5.0E-80	0.89	13	3	1	1	1
128       SEM295       Hit not found       0.88       7       1       3       0       0         129       SEM297       g-patch domain containing       3.0E-104       0.87       11       0       6       3       2         130       SEM298       Hit not found       0.83       8       1       2       3       0         131       SEM302       Hit not found       0.72       8       4       3       3       0         132       SEM303       hypothetical protein       8.0E-23       0.9       5       2       1       1       0         133       SEM306       ccr4-not transcription complex subunit 7       2.0E-14       0       6       3       2       1       1       0         133       SEM307       Hit not found       0.7       7       0       4       2       1         134       SEM308       Hit not found       0.93       5       2       5       7       2         136       SEM310       Hit not found       0.89       10       6       3       4       0         137       SEM313       bicoid-interacting 3       6.0E-52       0.9       6       3 </td <td>127</td> <td>SEM294</td> <td>hypothetical protein OsJ_014087</td> <td>1.0E-12</td> <td>0.61</td> <td>5</td> <td>3</td> <td>2</td> <td>1</td> <td>0</td>	127	SEM294	hypothetical protein OsJ_014087	1.0E-12	0.61	5	3	2	1	0
129       SEM297       g-patch domain containing       3.0E-104       0.87       11       0       6       3       2         130       SEM298       Hit not found       0.83       8       1       2       3       0         131       SEM302       Hit not found       0.72       8       4       3       3       0         132       SEM303       hypothetical protein       8.0E-23       0.9       5       2       1       1       0         133       SEM306       ccr4-not transcription complex subunit 7       2.0E-14       0       6       3       2       1       1       0         134       SEM307       Hit not found       0.77       7       0       4       2       1         135       SEM308       Hit not found       0.93       5       2       5       7       2         136       SEM310       Hit not found       0.89       10       6       3       4       0         137       SEM313       bicoid-interacting 3       6.0E-52       0.9       6       3       3       0       0         138       SEM314       zinc transporter       9.0E-56       0.83	128	SEM295	Hit not found		0.88	7	1	3	0	0
130       SEM298       Hit not found       0.83       8       1       2       3       0         131       SEM302       Hit not found       0.72       8       4       3       3       0         132       SEM303       hypothetical protein       8.0E-23       0.9       5       2       1       1       0         133       SEM306       ccr4-not transcription complex subunit 7       2.0E-14       0       6       3       2       1       1       0         134       SEM307       Hit not found       0.7       7       0       4       2       1         135       SEM308       Hit not found       0.93       5       2       5       7       2         136       SEM310       Hit not found       0.89       10       6       3       4       0         137       SEM313       bicoid-interacting 3       6.0E-52       0.9       6       3       3       0       0         138       SEM314       zinc transporter       9.0E-56       0.83       8       1       5       0       0         139       SEM315       membrane protein-like       1.0E-41       0.91	129	SEM297	g-patch domain containing	3.0E-104	0.87	11	0	6	3	2
131       SEM302       Hit not found       0.72       8       4       3       3       0         132       SEM303       hypothetical protein       8.0E-23       0.9       5       2       1       1       0         133       SEM306       ccr4-not transcription complex subunit 7       2.0E-14       0       6       3       2       1       1       0         134       SEM307       Hit not found       0.7       7       0       4       2       1         135       SEM308       Hit not found       0.93       5       2       5       7       2         136       SEM310       Hit not found       0.89       10       6       3       4       0         137       SEM313       bicoid-interacting 3       6.0E-52       0.9       6       3       3       0       0         138       SEM314       zinc transporter       9.0E-56       0.83       8       1       5       0       0         139       SEM315       membrane protein-like       1.0E-41       0.91       8       5       0       2       2	130	SEM298	Hit not found		0.83	8	1	2	3	0
132       SEM303       hypothetical protein       8.0E-23       0.9       5       2       1       1       0         133       SEM306       ccr4-not transcription complex subunit 7       2.0E-14       0       6       3       2       1       1         134       SEM307       Hit not found       0.7       7       0       4       2       1         135       SEM308       Hit not found       0.93       5       2       5       7       2         136       SEM310       Hit not found       0.89       10       6       3       4       0         137       SEM313       bicoid-interacting 3       6.0E-52       0.9       6       3       3       0       0         138       SEM314       zinc transporter       9.0E-56       0.83       8       1       5       0       0         139       SEM315       membrane protein-like       1.0E-41       0.91       8       5       0       2       2	131	SEM302	Hit not found		0.72	8	4	3	3	0
133       SEM306       ccr4-not transcription complex subunit 7       2.0E-14       0       6       3       2       1       1         134       SEM307       Hit not found       0.7       7       0       4       2       1         135       SEM308       Hit not found       0.93       5       2       5       7       2         136       SEM310       Hit not found       0.89       10       6       3       4       0         137       SEM313       bicoid-interacting 3       6.0E-52       0.9       6       3       3       0       0         138       SEM314       zinc transporter       9.0E-56       0.83       8       1       5       0       0         139       SEM315       membrane protein-like       1.0E-41       0.91       8       5       0       2       2	132	SEM303	hypothetical protein	8.0E-23	0.9	5	2	1	1	0
134       SEM307       Hit not found       0.7       7       0       4       2       1         135       SEM308       Hit not found       0.93       5       2       5       7       2         136       SEM310       Hit not found       0.89       10       6       3       4       0         137       SEM313       bicoid-interacting 3       6.0E-52       0.9       6       3       3       0       0         138       SEM314       zinc transporter       9.0E-56       0.83       8       1       5       0       0         139       SEM315       membrane protein-like       1.0E-41       0.91       8       5       0       2       2	133	SEM306	ccr4-not transcription complex subunit 7	2.0E-14	0	6	3	2	1	1
135       SEM308       Hit not found       0.93       5       2       5       7       2         136       SEM310       Hit not found       0.89       10       6       3       4       0         137       SEM313       bicoid-interacting 3       6.0E-52       0.9       6       3       3       0       0         138       SEM314       zinc transporter       9.0E-56       0.83       8       1       5       0       0         139       SEM315       membrane protein-like       1.0E-41       0.91       8       5       0       2       2	134	SEM307	Hit not found		0.7	7	0	4	2	1
136SEM310Hit not found0.89106340137SEM313bicoid-interacting 36.0E-520.963300138SEM314zinc transporter9.0E-560.8381500139SEM315membrane protein-like1.0E-410.9185022	135	SEM308	Hit not found		0.93	5	2	5	7	2
137       SEM313       bicoid-interacting 3       6.0E-52       0.9       6       3       3       0       0         138       SEM314       zinc transporter       9.0E-56       0.83       8       1       5       0       0         139       SEM315       membrane protein-like       1.0E-41       0.91       8       5       0       2       2	136	SEM310	Hit not found		0.89	10	6	3	4	0
138       SEM314       zinc transporter       9.0E-56       0.83       8       1       5       0       0         139       SEM315       membrane protein-like       1.0E-41       0.91       8       5       0       2       2	137	SEM313	bicoid-interacting 3	6.0E-52	0.9	6	3	3	0	0
139 SEM315 membrane protein-like 1.0E-41 0.91 8 5 0 2 2	138	SEM314	zinc transporter	9.0E-56	0.83	8	1	5	0	0
	139	SEM315	membrane protein-like	1.0E-41	0.91	8	5	0	2	2
140 SEM319 Hit not found 0.67 5 1 2 1 1	140	SEM319	Hit not found		0.67	5	1	2	1	1
141 SEM320 Hit not found 0.5 6 2 3 2 1	141	SEM320	Hit not found		0.5	6	2	3	2	1
142         SEM321         6b-interacting protein 1         3.0E-40         0.5         10         1         2         2         0	142	SEM321	6b-interacting protein 1	3.0E-40	0.5	10	1	2	2	0

143	SEM327	peroxisomal Ca-dependent solute carrier	1.0E-84	0.93	9	3	5	1	0
144	SEM328	Transcriptional corepressor LEUNIG	3.0E-28	0.93	7	0	4	3	0
145	SEM329	beta-1,3-glucanase precursor	3.0E-36	0.91	5	1	1	2	0
146	SEM332	rna recognition motif-containing	2.0E-89	0.72	7	3	3	3	1
147	SEM336	ubiquitin-conjugating enzyme -like	8.0E-45	0.81	5	2	2	3	0
148	SEM337	Hit not found		0.66	9	4	7	4	0
149	SEM338	nodulin21 family	5.0E-73	0.7	20	1	13	12	2
150	SEM339	Hypoxia induced protein conserved region containing protein,	6.0E-18	0.91	15	5	0	4	0
151	SEM341	Glucan 1,3-beta-glucosidase precursor	3.0E-46	0.75	15	4	3	3	1
152	SEM344	enhancer of rudimentary	6.0E-53	0.5	2	1	5	6	1
153	SEM349	symbiosis-related protein-like protein	6.0E-62	0.93	6	2	3	0	1
154	SEM350	ring-h2 zinc finger protein	5.0E-51	0.87	6	0	5	0	0
155	SEM351	Hit not found		0.92	5	2	3	0	0
156	SEM353	reverse transcriptase family member	1.0E-120	0.71	4	1	2	3	1
157	SEM355	Hypoxia induced protein conserved region containing protein	8.0E-23	0.64	6	4	1	2	0
158	SEM358	Hit not found		0.92	8	2	5	3	0
159	SEM361	Hit not found		0.93	11	4	3	6	0
160	SEM366	Hit not found		0.9	6	4	1	0	0
161	SEM367	Hit not found		0.88	6	4	0	4	0
162	SEM368	protein tyrosine phosphatase	2.0E-84	0.77	10	2	3	2	0
163	SEM369	ethylene-responsive transcriptional coactivator	2.0E-71	0.93	7	0	2	1	4
164	SEM371	phosphatidate cytidylyltransferase family	5.0E-53	0.64	8	4	4	2	0
165	SEM372	hypothetical protein	3.0E-14	0.8	13	6	7	2	0
166	SEM373	hypothetical protein Osl_028313	1.0E-50	0.88	4	1	3	1	0
167	SEM374	mitochondrial carrier protein	8.0E-50	0.65	7	3	3	1	0
168	SEM375	ETCHED1 protein	4.0E-20	0.9	11	4	6	8	2
169	SEM377	wound-responsive protein-related	3.0E-11	0.75	5	2	3	3	1
170	SEM379	hypothetical protein	8.0E-26	0.93	8	1	7	1	0
171	SEM384	Hit not found		0.86	4	0	3	2	1
172	SEM390	cytochrome p450	1.0E-57	0.92	13	7	5	3	0
173	SEM391	Hit not found		0.92	6	2	2	0	1
174	SEM392	hypothetical protein OsJ_000721	1.0E-59	0.76	3	0	1	0	0
175	SEM398	Hit not found		0.91	4	2	1	3	0
176	SEM400	Hit not found		0.93	8	0	3	3	0
177	SEM401	Alcohol dehydrogenase 2	3.0E-100	0.41	10	10	8	2	0
178	SEM403	hypothetical protein	3.0E-13	0.69	6	1	2	0	2

179       SEM407       diphosphate-fructose-6-phosphate 1- phosphotransferase       4.0E-69       0.83       4       1       5       1       0         180       SEM408       growth-regulating factor 6       5.0E-72       0.83       14       4       8       4       2         181       SEM417       Hit not found       0.33       14       4       8       4       2         182       SEM417       Int not found       0.83       28       1       3       0       0         184       SEM418       Hit not found       0.83       9       1       2       0       0         185       SEM417       Inportein factor iib       7.0E-114       0.83       9       1       2       0       0         186       SEM421       hypothetical protein Oci 10647       1.0E-16       0.91       6       3       3       0       0         187       SEM422       Sugar transporter family protein       1.0E-14       0.81       13       2       2       0       0       2       0       0       2       0       0       2       0       0       2       0       0       2       0       0       2										
180       SEM402       growth-regulating factor 6       5.0E-72       0       6       1       3       3       2         181       SEM412       Hit not found       0.93       14       4       8       4       2         181       SEM417       Hit not found       0.93       14       4       8       4       2         183       SEM417       transcription factor ib       7.0E-114       0.93       28       1       3       0       0         184       SEM418       Hit not found       0.8       9       1       2       0       0         185       SEM42       hypothetical protein OS1_010647       1.0E-16       0.91       11       2       3       2       2         186       SEM426       Suctores -16-bisphosphatase, chloroplast precursor (FBPase)       2.0E-60       0.8       10       3       4       2       0         187       SEM426       Suctores synthase       3.0E-70       0.91       7       6       4       5       0         188       SEM425       fructores-16-bisphosphatase       3.0E-70       0.92       11       0       3       2       0       2       2       0	179	SEM407	diphosphate-fructose-6-phosphate 1- phosphotransferase	4.0E-69	0.83	4	1	5	1	0
181       SEM412       Hit not found       0.33       14       4       8       4       2         182       SEM415       Rop ramily GTPase ROP5       8.0E-65       0.9       4       1       2       1       0         184       SEM415       Hit not found       0.8       9       1       2       0       0         184       SEM412       hypothetical protein cols_010647       0.0E-16       0.91       6       3       3       0       0         185       SEM422       cytochrome p450       8.0E-32       0.89       8       6       4       4       0         186       SEM422       cytochrome p450       8.0E-32       0.89       8       6       4       4       0         189       SEM425       rutose-16-bisphosphatase, chloroplast precursor (FBPase)       2.0E-26       0.58       10       3       4       2       0       0       2       2       2       2       2       2       2       0       0       2       2       0       0       2       2       0       0       2       2       0       0       2       2       0       0       2       2       0	180	SEM408	growth-regulating factor 6	5.0E-72	0	6	1	3	3	2
182       SEM415       Rop family GTPase ROP5       8.0.6       0.9       4       1       2       1       0         183       SEM417       transcription factor iib       7.0E-114       0.93       28       1       3       0       0         184       SEM418       Hit not found       0.8       9       1       2       3       1       1         185       SEM412       hypothetical protein Col_010647       1.0E-16       0.91       6       3       3       0       0         186       SEM425       ructose-1,6-bisphosphatase, chloroplast precursor (FBPase)       2.0E-26       0.58       10       3       4       2       0         189       SEM426       Sugar transporter family protein       1.0E-16       0.91       7       6       4       5       0         191       SEM428       sucrose synthase       1.0E-50       0.91       7       6       4       1       0         192       SEM433       sucrose synthase       1.0E-160       0.91       7       2       0       0       2       0       1       1       0       1       1       0       1       1       0       1       0	181	SEM412	Hit not found		0.93	14	4	8	4	2
183       SEM417       transcription factor iib       7.0E-114       0.93       28       1       3       0       0         184       SEM418       Hit not found       0.8       9       1       2       0       0         184       SEM419       serine threonine protein kinase       0.60E-16       0.91       11       2       3       1       1         185       SEM421       hypothetical protein Osl_010647       1.0E-16       0.91       6       3       3       0       0         187       SEM425       cytochrome p450       8.0E-32       0.58       10       3       4       2       0         188       SEM425       Fructose-16-bisphosphatae, chloroplast precursor (FBPase)       2.0E-26       0.58       10       3       4       2       0         189       SEM425       ducrose 4-5-deptydratase       1.0E-50       0.91       7       6       4       5       0       1       1         191       SEM433       diposphate fuctose-6-phosphate 1-phosphotransferase       3.0E-47       0.92       11       1       4       1       0       1       0       1       0       1       0       1       0       1 </td <td>182</td> <td>SEM415</td> <td>Rop family GTPase ROP5</td> <td>8.0E-65</td> <td>0.9</td> <td>4</td> <td>1</td> <td>2</td> <td>1</td> <td>0</td>	182	SEM415	Rop family GTPase ROP5	8.0E-65	0.9	4	1	2	1	0
184       SEM418       Hit not found       0.8       9       1       2       0       0         185       SEM419       serine threonine protein kinase       6.0E-16       0.91       16       3       0       0         185       SEM421       hypothetical protein Col_010647       1.0E-16       0.91       6       3       3       0       0         188       SEM425       Fructose-1,6-bisphosphatase, chloroplast precursor (FBPase)       2.0E       0.58       10       3       4       2       0         188       SEM426       Sugar transporter family protein       1.0E-14       0.8       13       2       3       2       2         191       SEM427       TDD-glucose 4-6-dehydratase       1.0E-50       0.91       7       6       4       5       0         191       SEM430       sucrose synthase       3.0E-70       0.92       11       1       4       1       0         192       SEM430       disease resistance protein family protein       3.0E-70       0.27       11       1       4       1       0         193       SEM431       disease resistance protein homologue       2.0E-40       0.76       9       2       2 </td <td>183</td> <td>SEM417</td> <td>transcription factor iib</td> <td>7.0E-114</td> <td>0.93</td> <td>28</td> <td>1</td> <td>3</td> <td>0</td> <td>0</td>	183	SEM417	transcription factor iib	7.0E-114	0.93	28	1	3	0	0
186       SEM419       serine threonine protein kinase       6.0E-16       0.91       11       2       3       1       1         186       SEM421       hypothetical protein Osl_010647       1.0E-16       0.91       6       3       3       0       0         188       SEM422       cytochrome p450       8.0E-32       0.89       8       6       4       4       0         188       SEM425       Fructose-1,6-bisphosphatase, chloroplast precursor (FBPase)       2.0E-26       0.58       10       3       4       2       0         189       SEM426       fructose-1,6-bisphosphatase, chloroplast precursor (FBPase)       2.0E-26       0.58       10       3       1       1         191       SEM423       stogar transporter family protein       1.0E-50       0.91       7       6       4       2       0         192       SEM433       diptosphate-functose-6-phosphate 1-phosphotransferase       3.0E-07       0.76       9       2       3       2       0       1       0       1       0       1       0       1       0       1       0       1       0       1       0       1       0       1       0       1       0 <td< td=""><td>184</td><td>SEM418</td><td>Hit not found</td><td></td><td>0.8</td><td>9</td><td>1</td><td>2</td><td>0</td><td>0</td></td<>	184	SEM418	Hit not found		0.8	9	1	2	0	0
186       SEM421       hypothetical protein OsI_010647       1.0E-16       0.91       6       3       3       0       0         187       SEM422       cytochrome p450       8.0E-32       0.89       8       6       4       4       0         188       SEM425       Fructose 1.6-bisphosphatase, chloroplast precursor (FBPase)       2.0E-26       0.58       10       3       4       2       0         188       SEM427       dTDP-glucose 4-6-dehydratase       1.0E-50       0.91       7       6       4       5       0         191       SEM428       fructose-bisphosphate adolase       3.0E-70       0.92       11       0       3       1       1         192       SEM433       diptosphate-fructose-chopsphate 1-phosphotransferase       3.0E-70       0.76       9       2       3       2       0         195       SEM434       disease resistance protein f11       1.0E-31       0.88       9       1       2       2       0         195       SEM435       disease resistance erotein homologue       2.0E-16       0.83       14       3       2       1       0       1       0         196       SEM437       NBS-LRR disease resistanc	185	SEM419	serine threonine protein kinase	6.0E-16	0.91	11	2	3	1	1
187       SEM422       cytochrome p450       8.0E-32       0.89       8       6       4       4       0         188       SEM425       Fructose-1,6-bisphosphatase, chloroplast precursor (FBPase)       2.0E-26       0.58       10       3       4       2       0         188       SEM425       Gructose-1,6-bisphosphatase, chloroplast precursor (FBPase)       2.0E-26       0.58       10       3       4       2       0         191       SEM425       Gructose-1,6-bisphosphate family protein       1.0E-50       0.91       7       6       4       5       0         191       SEM430       sucrose synthase       7.0E-40       0.12       7       2       0       0       2         193       SEM433       diphosphate-fructose-6-phosphate 1-phosphotransferase       3.0E-70       0.27       11       1       4       1       0         195       SEM433       disease resistance protein (TIR-NBS-LRR class)       8.0E-67       0.76       9       2       3       2       0         195       SEM435       stress-induced protein sti1       1.0E-31       0.89       9       1       2       2       0       2       2       0       2       0 <td< td=""><td>186</td><td>SEM421</td><td>hypothetical protein OsI_010647</td><td>1.0E-16</td><td>0.91</td><td>6</td><td>3</td><td>3</td><td>0</td><td>0</td></td<>	186	SEM421	hypothetical protein OsI_010647	1.0E-16	0.91	6	3	3	0	0
188       SEM425       Fructose-1,6-bisphosphatase, chloroplast precursor (FBPase)       2,0E-26       0,58       10       3       4       2       0         189       SEM426       Sugar transporter family protein       1,0E-14       0.8       13       2       3       2       2         191       SEM427       dTDP-glucose 4-6-dehydratase       1,0E-14       0.8       13       2       0       0       2         191       SEM438       fructose-bisphosphate aldolase       3,0E-70       0.92       11       0       3       1       1         192       SEM433       diptosphate-fructose-6-phosphate 1-phosphotransferase       3,0E-70       0,7C       9       2       3       2       0         195       SEM434       disease resistance protein (TIR-NBS-LRR class)       8,0E-07       0,76       9       2       3       2       0         196       SEM435       disease resistance response protein homologue       2,0E-16       0,83       14       3       2       1       0         197       SEM430       disease resistance responsive family protein       2,0E-16       0,83       14       3       2       1       0         198       SEM437       N	187	SEM422	cytochrome p450	8.0E-32	0.89	8	6	4	4	0
189       SEM426       Sugar transporter family protein       1.0E-14       0.8       13       2       3       2       2         190       SEM427       dTDP-glucose 4-6-dehydratase       1.0E-50       0.91       7       6       4       5       0         191       SEM428       fructose-bisphosphate aldolase       3.0E-70       0.27       11       1       4       1       0         192       SEM432       Sugar transporter family protein       3.0E-70       0.27       11       1       4       1       0         194       SEM432       disease resistance protein (TIR-NBS-LRR class)       8.0E-07       0.76       9       2       3       2       0         195       SEM434       disease resistance protein related/dirigent protein-related       6.0E-45       0.7       8       1       0       1       0         196       SEM435       stress-induced protein BR-1       2.0E-16       0.83       14       3       2       0       0         197       SEM436       disease resistance protein nomologue       2.0E-19       0.2       5       2       0       2       0       0         198       SEM439       Pathogenesis-related protein PR-1<	188	SEM425	Fructose-1,6-bisphosphatase, chloroplast precursor (FBPase)	2.0E-26	0.58	10	3	4	2	0
190       SEM427       dTDP-glucose 4-6-dehydratase       1.0E-50       0.91       7       6       4       5       0         191       SEM428       fructose-bisphosphate aldolase       3.0E-07       0.92       11       0       3       1       1         192       SEM430       sucrose synthase       7.0E-40       0.12       7       2       0       0       2         193       SEM432       diphosphate-fructose-6-phosphate 1-phosphotransferase       3.0E-70       0.76       9       2       3       2       0         194       SEM434       disease resistance protein (TIR-NBS-LRR class)       8.0E-07       0.76       9       2       3       2       0         195       SEM434       disease resistance protein sti1       1.0E-31       0.89       9       1       2       2       0         198       SEM437       NBS-LRR disease resistance protein-related/dirigent protein-related       6.0E-45       0.7       8       1       0       1       0       1       0         198       SEM437       NBS-LRR disease resistance protein PR-1       2.0E-19       0.2       5       2       0       2       0         190       SEM442 <td< td=""><td>189</td><td>SEM426</td><td>Sugar transporter family protein</td><td>1.0E-14</td><td>0.8</td><td>13</td><td>2</td><td>3</td><td>2</td><td>2</td></td<>	189	SEM426	Sugar transporter family protein	1.0E-14	0.8	13	2	3	2	2
191       SEM428       fructose-bisphosphate aldolase       3.0E-07       0.92       11       0       3       1       1         192       SEM430       sucrose synthase       7.0E-40       0.12       7       2       0       0       2         193       SEM433       diphosphate-fructose-6-phosphate 1-phosphotransferase       3.0E-70       0.76       9       2       3       2       0         195       SEM434       disease resistance protein (TIR-NBS-LRR class)       8.0E-07       0.76       9       2       3       2       0         196       SEM436       disease resistance protein sti1       1.0E-31       0.89       9       1       2       2       0         197       SEM437       NBS-LRR disease resistance protein homologue       2.0E-16       0.83       14       3       2       1       0         198       SEM439       Pathogenesis-related protein PR-1       2.0E-16       0.83       14       3       2       0       2       0       2       0       2       0       2       0       2       0       2       0       2       0       2       0       2       0       2       0       2       1	190	SEM427	dTDP-glucose 4-6-dehydratase	1.0E-50	0.91	7	6	4	5	0
192       SEM430       sucrose synthase       7.0E-40       0.12       7       2       0       0       2         193       SEM432       Sugar transporter family protein       3.0E-70       0.27       11       1       4       1       0         194       SEM433       diphosphate-fructose-6-phosphate 1-phosphotransferase       3.0E-42       0.85       5       2       3       2       0         194       SEM434       disease resistance protein (TIR-NBS-LRR class)       8.0E-07       0.76       9       2       2       0         196       SEM435       stress-induced protein sti1       1.0E-31       0.89       9       1       2       2       0         197       SEM436       disease resistance protein homologue       2.0E-16       0.83       14       3       2       1       0         198       SEM437       NBS-LRR disease resistance protein PR-1       2.0E-16       0.83       14       3       2       0       2       0       2       0       2       0       2       0       2       0       2       0       2       0       2       0       2       0       2       0       2       0       2       <	191	SEM428	fructose-bisphosphate aldolase	3.0E-07	0.92	11	0	3	1	1
193       SEM432       Sugar transporter family protein       3.0E-70       0.27       11       1       4       1       0         194       SEM433       diphosphate-fructose-6-phosphate 1-phosphotransferase       3.0E-42       0.85       5       2       3       2       0         195       SEM434       disease resistance protein (TIR-NBS-LRR class)       8.0E-07       0.76       9       2       3       2       0         196       SEM436       disease resistance protein (TIR-NBS-LRR class)       8.0E-07       8.0E-07       8       1       0       1       0         197       SEM436       disease resistance protein related/dirigent protein-related       6.0E-45       0.7       8       1       0       1       0         198       SEM437       NBS-LRR disease resistance protein homologue       2.0E-16       0.83       14       3       2       0       2       0         200       SEM440       disease resistance-responsive family protein       2.0E-18       0.4E       10       3       1       0       1       0         201       SEM440       disease resistance-responsive family protein       2.0E-13       0.31       12       2       1       1       0	192	SEM430	sucrose synthase	7.0E-40	0.12	7	2	0	0	2
194       SEM433       diphosphate-fructose-6-phosphate 1-phosphotransferase       3.0E-42       0.85       5       2       3       2       0         195       SEM434       disease resistance protein (TIR-NBS-LRR class)       8.0E-07       0.76       9       2       3       2       0         196       SEM435       stress-induced protein stil       1.0E-31       0.89       9       1       2       2       0         197       SEM436       disease resistance response protein-related/dirigent protein-related       6.0E-45       0.7       8       1       0       1       0         198       SEM437       NBS-LRR disease resistance protein homologue       2.0E-16       0.83       14       3       2       0       2       0         199       SEM439       Pathogenesis-related protein PR-1       2.0E-19       0.2       5       2       0       2       0         201       SEM444       disease resistance protein homologue       2.0E-24       0.46       12       0       2       2       0         202       SEM444       dehydration responsive element-binding protein 2D (DREB2D protein)       9.0E-15       0.82       13       1       5       3       0       1	193	SEM432	Sugar transporter family protein	3.0E-70	0.27	11	1	4	1	0
195       SEM434       disease resistance protein (TIR-NBS-LRR class)       8.0E-07       0.76       9       2       3       2       0         196       SEM435       stress-induced protein sti1       1.0E-31       0.89       9       1       2       2       0         197       SEM436       disease resistance response protein-related/dirigent protein-related       6.0E-45       0.7       8       1       0       1       0         198       SEM437       NBS-LRR disease resistance protein honologue       2.0E-16       0.83       14       3       2       0       2       0         199       SEM430       disease resistance protein PR-1       2.0E-16       0.83       14       3       2       0       2       0         200       SEM440       disease resistance protein       2.0E-24       0.46       12       0       2       2       0         201       SEM441       dehydration responsive element binding protein       9.0E-13       0.31       12       2       1       1       0         202       SEM444       Dehydration-responsive element-binding protein 2D (DREB2D protein)       9.0E-15       0.82       13       1       5       3       0	194	SEM433	diphosphate-fructose-6-phosphate 1-phosphotransferase	3.0E-42	0.85	5	2	3	2	0
196       SEM435       stress-induced protein sti1       1.0E-31       0.89       9       1       2       2       0         197       SEM436       disease resistance response protein-related/dirigent protein-related       6.0E-45       0.7       8       1       0       1       0         198       SEM437       NBS-LRR disease resistance protein homologue       2.0E-16       0.83       14       3       2       1       0         199       SEM430       Pathogenesis-related protein PR-1       2.0E-19       0.2       5       2       0       2       0         200       SEM440       disease resistance protein       2.0E-49       0.46       12       0       2       2       0         201       SEM442       disease resistance protein       4.0E-49       0.85       10       3       3       1       0         202       SEM443       dehydration responsive element-binding protein 2D (DREB2D protein)       9.0E-15       0.82       13       1       5       3       0         203       SEM444       Dehydration-responsive protein-like       4.0E-12       0.37       3       0       1       1       1       1       1       0         204 </td <td>195</td> <td>SEM434</td> <td>disease resistance protein (TIR-NBS-LRR class)</td> <td>8.0E-07</td> <td>0.76</td> <td>9</td> <td>2</td> <td>3</td> <td>2</td> <td>0</td>	195	SEM434	disease resistance protein (TIR-NBS-LRR class)	8.0E-07	0.76	9	2	3	2	0
197SEM436disease resistance response protein-related/dirigent protein-related6.0E-450.781010198SEM437NBS-LRR disease resistance protein homologue2.0E-160.83143210199SEM439Pathogenesis-related protein PR-12.0E-190.252020200SEM440disease resistance-responsive family protein2.0E-240.46120220201SEM442disease resistance protein4.0E-490.85103310202SEM443dehydration responsive element binding protein 2D (DREB2D protein)9.0E-150.82131530203SEM444Dehydration-responsive element-binding protein 2D (DREB2D protein)9.0E-150.82131530204SEM445cold shock protein-11.0E-290.9211111111205SEM447low temperature and salt responsive protein-like4.0E-120.3730110206SEM449Heat shock protein 81-12.0E-460.3642110207SEM450light-dependent short hypocotyl 12.0E-460.3642110208SEM453cold induced protein-like4.0E-260.9352310208SEM454 <td>196</td> <td>SEM435</td> <td>stress-induced protein sti1</td> <td>1.0E-31</td> <td>0.89</td> <td>9</td> <td>1</td> <td>2</td> <td>2</td> <td>0</td>	196	SEM435	stress-induced protein sti1	1.0E-31	0.89	9	1	2	2	0
198       SEM437       NBS-LRR disease resistance protein homologue       2.0E-16       0.83       14       3       2       1       0         199       SEM439       Pathogenesis-related protein PR-1       2.0E-19       0.2       5       2       0       2       0         200       SEM440       disease resistance-responsive family protein       2.0E-24       0.46       12       0       2       2       0         201       SEM42       disease resistance protein       4.0E-49       0.85       10       3       3       1       0         202       SEM443       dehydration responsive element binding protein       9.0E-13       0.31       12       2       1       1       0         203       SEM444       Dehydration-responsive element-binding protein 2D (DREB2D protein)       9.0E-15       0.82       13       1       5       3       0         204       SEM446       cold shock protein-1       1.0E-29       0.92       11       1       1       1       1       1       0         205       SEM445       logt-dependent shork protein 81-1       5.0E-99       0.89       17       2       2       2       0         206       SEM450	197	SEM436	disease resistance response protein-related/dirigent protein-related	6.0E-45	0.7	8	1	0	1	0
199SEM439Pathogenesis-related protein PR-12.0E-190.252020200SEM440disease resistance-responsive family protein2.0E-240.46120220201SEM442disease resistance protein4.0E-490.85103310202SEM43dehydration responsive element binding protein9.0E-130.31122110203SEM444Dehydration-responsive element-binding protein 2D (DREB2D protein)9.0E-150.82131530204SEM446cold shock protein-11.0E-290.921111111205SEM447low temperature and salt responsive protein-like4.0E-120.3730110206SEM449Heat shock protein 81-15.0E-990.89172220207SEM450light-dependent short hypocotyl 12.0E-460.3642110208SEM454water-stress protein-like protein4.0E-160.842110208SEM454water-stress protein-like protein4.0E-160.842110208SEM454water-stress protein-like protein4.0E-160.842110208SEM454water-stress protein-like protein4.0E-160.84211<	198	SEM437	NBS-LRR disease resistance protein homologue	2.0E-16	0.83	14	3	2	1	0
200       SEM440       disease resistance-responsive family protein       2.0E-24       0.46       12       0       2       2       0         201       SEM442       disease resistance protein       4.0E-49       0.85       10       3       3       1       0         202       SEM443       dehydration responsive element binding protein       9.0E-13       0.31       12       2       1       1       0         203       SEM444       Dehydration-responsive element-binding protein 2D (DREB2D protein)       9.0E-15       0.82       13       1       5       3       0         204       SEM446       cold shock protein-1       1.0E-29       0.92       11       1       1       1       1         205       SEM447       low temperature and salt responsive protein-like       4.0E-12       0.37       3       0       1       1       0         206       SEM449       Heat shock protein 81-1       2.0E-46       0.36       4       2       1       1       0         207       SEM450       light-dependent short hypocotyl 1       2.0E-46       0.36       4       2       1       1       0         208       SEM453       cold induced protein-like prote	199	SEM439	Pathogenesis-related protein PR-1	2.0E-19	0.2	5	2	0	2	0
201       SEM442       disease resistance protein       4.0E-49       0.85       10       3       3       1       0         202       SEM443       dehydration responsive element binding protein       9.0E-13       0.31       12       2       1       1       0         203       SEM444       Dehydration-responsive element-binding protein 2D (DREB2D protein)       9.0E-15       0.82       13       1       5       3       0         204       SEM446       cold shock protein-1       1.0E-29       0.92       11       0       2       2       2       0       0       1       1       0       2       1       1       0       2       1       1       0       2       0       0       1       1       0       2       1       1       0<	200	SEM440	disease resistance-responsive family protein	2.0E-24	0.46	12	0	2	2	0
202SEM443dehydration responsive element binding protein9.0E-130.31122110203SEM444Dehydration-responsive element-binding protein 2D (DREB2D protein)9.0E-150.82131530204SEM446cold shock protein-11.0E-290.921111111205SEM447low temperature and salt responsive protein-like4.0E-120.3730110206SEM449Heat shock protein 81-15.0E-990.89172220207SEM450light-dependent short hypocotyl 12.0E-460.3642110208SEM453cold induced protein-like protein4.0E-160.842110208SEM454water-stress protein-like protein4.0E-160.842110209SEM454water-stress protein-like protein4.0E-160.842110210SEM456Saccharum hybrid cultivar soluble acid invertase (ShinvA) mRNASaccharum0.4152001211SEST4early-responsive to dehydration protein6.0E-590.65191110212SEST4early-responsive to dehydration protein6.0E-590.65191110	201	SEM442	disease resistance protein	4.0E-49	0.85	10	3	3	1	0
203SEM444Dehydration-responsive element-binding protein 2D (DREB2D protein)9.0E-150.82131530204SEM446cold shock protein-11.0E-290.921111111205SEM447low temperature and salt responsive protein-like4.0E-120.3730110206SEM449Heat shock protein 81-15.0E-990.89172220207SEM450light-dependent short hypocotyl 12.0E-460.3642110208SEM453cold induced protein-like4.0E-260.9352310209SEM454water-stress protein-like protein4.0E-160.8421110210SEM456Saccharum hybrid cultivar soluble acid invertase (ShinvA) mRNASaccharum0.4152001211SEST3disease resistance protein I22.0E-140.5452520212SEST4early-responsive to dehydration protein6.0E-590.65191110Note: Markers highlighted with blue have been reported from other studies.	202	SEM443	dehydration responsive element binding protein	9.0E-13	0.31	12	2	1	1	0
204SEM446cold shock protein-11.0E-290.9211111111205SEM447low temperature and salt responsive protein-like4.0E-120.3730110206SEM449Heat shock protein 81-15.0E-990.89172220207SEM450light-dependent short hypocotyl 12.0E-460.3642110208SEM453cold induced protein-like4.0E-260.9352310209SEM454water-stress protein-like protein4.0E-160.8421110210SEM456Saccharum hybrid cultivar soluble acid invertase (ShinvA) mRNASaccharum0.4152001211SEST3disease resistance protein I22.0E-140.5452520212SEST4early-responsive to dehydration protein6.0E-590.65191110Note: Markers highlighted with blue have been reported from other studies.5.0E-990.65191110	203	SEM444	Dehydration-responsive element-binding protein 2D (DREB2D protein)	9.0E-15	0.82	13	1	5	3	0
205SEM447low temperature and salt responsive protein-like4.0E-120.3730110206SEM449Heat shock protein 81-15.0E-990.89172220207SEM450light-dependent short hypocotyl 12.0E-460.3642110208SEM453cold induced protein-like4.0E-260.9352310209SEM454water-stress protein-like protein4.0E-160.8421110210SEM456Saccharum hybrid cultivar soluble acid invertase (ShinvA) mRNASaccharum0.4152001211SEST3disease resistance protein l22.0E-140.5452520212SEST4early-responsive to dehydration protein6.0E-590.65191110Note: Markers highlighted with blue have been reported from other studies.	204	SEM446	cold shock protein-1	1.0E-29	0.92	11	1	1	1	1
206SEM449Heat shock protein 81-15.0E-990.89172220207SEM450light-dependent short hypocotyl 12.0E-460.3642110208SEM453cold induced protein-like4.0E-260.9352310209SEM454water-stress protein-like protein4.0E-160.8421110210SEM456Saccharum hybrid cultivar soluble acid invertase (ShinvA) mRNASaccharum0.4152001211SEST3disease resistance protein I22.0E-140.5452520212SEST4early-responsive to dehydration protein6.0E-590.65191110Note: Markers highlighted with blue have been reported from other studies.5191110	205	SEM447	low temperature and salt responsive protein-like	4.0E-12	0.37	3	0	1	1	0
207SEM450light-dependent short hypocotyl 12.0E-460.3642110208SEM453cold induced protein-like4.0E-260.9352310209SEM454water-stress protein-like protein4.0E-160.8421110210SEM456Saccharum hybrid cultivar soluble acid invertase (ShinvA) mRNASaccharum0.4152001211SEST3disease resistance protein I22.0E-140.5452520212SEST4early-responsive to dehydration protein6.0E-590.65191110Note: Markers highlighted with blue have been reported from other studies.	206	SEM449	Heat shock protein 81-1	5.0E-99	0.89	17	2	2	2	0
208SEM453cold induced protein-like4.0E-260.9352310209SEM454water-stress protein-like protein4.0E-160.8421110210SEM456Saccharum hybrid cultivar soluble acid invertase (ShinvA) mRNASaccharum0.4152001211SEST3disease resistance protein I22.0E-140.5452520212SEST4early-responsive to dehydration protein6.0E-590.6519110Note: Markers highlighted with blue have been reported from other studies.	207	SEM450	light-dependent short hypocotyl 1	2.0E-46	0.36	4	2	1	1	0
209SEM454water-stress protein-like protein4.0E-160.842110210SEM456Saccharum hybrid cultivar soluble acid invertase (ShinvA) mRNASaccharum0.4152001211SEST3disease resistance protein I22.0E-140.5452520212SEST4early-responsive to dehydration protein6.0E-590.6519110Note: Markers highlighted with blue have been reported from other studies.	208	SEM453	cold induced protein-like	4.0E-26	0.93	5	2	3	1	0
210SEM456Saccharum hybrid cultivar soluble acid invertase (ShinvA) mRNASaccharum0.4152001211SEST3disease resistance protein I22.0E-140.5452520212SEST4early-responsive to dehydration protein6.0E-590.6519110Note: Markers highlighted with blue have been reported from other studies.	209	SEM454	water-stress protein-like protein	4.0E-16	0.84	2	1	1	1	0
211SEST3disease resistance protein I22.0E-140.5452520212SEST4early-responsive to dehydration protein6.0E-590.6519110Note: Markers highlighted with blue have been reported from other studies.	210	SEM456	Saccharum hybrid cultivar soluble acid invertase (ShinvA) mRNA	Saccharum	0.41	5	2	0	0	1
212       SEST4 early-responsive to dehydration protein       6.0E-59       0.65       19       1       1       0         Note: Markers highlighted with blue have been reported from other studies.	211	SEST3	disease resistance protein I2	2.0E-14	0.54	5	2	5	2	0
Note: Markers highlighted with blue have been reported from other studies.	212	SEST4	early-responsive to dehydration protein	6.0E-59	0.65	19	1	1	1	0
		Note: Mar	kers highlighted with blue have been reported from other studies.							

Supplemental Table 2. Details of the new 191 EST–SSR markers developed from the SUCEST database.

					Timo	Expected			Simplex		Double
MarkerClusterSEM1SCEPRZSEM2SCACADSEM7SCAGLB2SEM11SCAGRTSEM13SCBFAMSEM14SCBGAMSEM15SCBGLRSEM16SCCCADSEM17SCCCLASEM20SCCCCLASEM24SCCCCLASEM36SCCCLRSEM37SCCCLRSEM38SCCCLRSEM39SCCCCRSEM41SCCCCRSEM53SCEPAMSEM55SCEPAMSEM56SCEPAMSEM61SCEQAWSEM63SCEQAWSEM63SCEQARSEM63SCEQRTSEM63SCEQRTSEM78SCEZRTSEM80SCEZRTSEM80SCEZRTSEM80SCEZRTSEM81SCEZRTSEM82SCEZRTSEM83SCEZRTSEM84SCEZSBSEM85SCJFADSEM86SCUFAD	Cluster	Motif	Forward primer	Reverse primer	(°C)	size (bp)	PIC	number	Phil6 607	S6	simplex
SEM1	SCEPRZ1008B02.g	(agc)10	ACCATCGCAATCGATGTTTA	AACTGGATGGCGTACAATCA	56	215	0.6	9	5	1	1
SEM2	SCACAD1035F09.g	(cg)7(ct)14	ACACCGAGCTGTCCCAAT	GCATCTGATGAGCCTGTGAA	56	164	0.9	7	2	1	1
SEM7	SCAGLB2047G03.g	(tttc)15	GGAAGGTATGGGTGCTATGC	ACAGGGCAATAACAGGGGTA	58	167	0.6	8	4	1	0
SEM11	SCAGRT2041A11.g	(tg)16	AGGGCTTGGAAGAAAGGAAT	TGGCAAGCAACAGCTAAAAC	58	190	0.9	11	4	2	1
SEM13	SCBFAM2022D09.g	(gaaa)11	GCGAGAGAAGCTAGGAAGCA	CGCAGATCCTCTTGAACCTC	62	161	0.7	7	2	2	0
SEM14	SCBGAM1091A05.g	(ta)10(cag)5	GAGCAACGAGCTGAAAAGTG	TGTCCTGACCTAGGATGTGC	59	245	0.8	10	2	4	1
SEM15	SCBGLR1119D12.g	(ta)26(at)5	TGTCCACAATTTTGGCTGAT	GTTGCTTGCCTGATCATTGT	56	200	0.5	5	0	2	0
SEM16	SCCCAD1003H03.g	(aag)15	CCTTCCTTGGCCTCTTCTCT	TGCTGGTCGCAGTACTTGAT	58	248	0.9	3	0	0	0
SEM19	SCCCCL4002A08.g	(gca)5(caa)13	CAGCCCATTAACCAAGCAAT	GAAGCAGCTGTTGCTCACTG	58	184	0.9	13	5	2	1
SEM20	SCCCCL4004D08.g	(ataga)12	CCGGCTGTGAAAATTAGGTT	TCGAATTGGTCAAGACTCTCC	58	219	0	6	2	2	0
SEM24	SCCCCL4015G07.g	(ct)10(ac)5	CAATTCGTGGCTTGTGTTTG	AGCAGAATCGGCAAGGTAAA	58	197	0	9	4	1	0
SEM36	SCCCLR1078G05.g	(ta)12	CCATGTGCAGCATTTAACAA	TGGACATGCTAATGACTACTGC	56	152	0.7	5	3	0	0
SEM37	SCCCLR1079D03.g	(ga)15	CTTCCTGCTTCGAACATTTG	ACGAGGTAGATCCCGAAGG	56	214	0.9	7	3	2	1
SEM38	SCCCLR1080G12.g	(ca)10	TGAATTGCACAAAACACCAA	GACGGTGTAAACAAGCTGTGA	55	249	0.9	4	1	3	0
SEM41	SCCCRT2001B06.g	(ag)24	CCCCCTTGACACCTCTGTAT	TAGAACGAACCAGACGACCA	59	248	0.9	13	4	8	1
SEM42	SCCCRZ2004G11.g	(aag)7(ta)15	GACTTCGGGAAGAAGGAGGT	ACCAAGCACATCCAGCAGTA	59	285	0.9	6	2	0	0
SEM53	SCEPAM1020C01.g	(ct)20(ct)20	CCGCCTTCTCCTTAGTGACA	CCACAAGCCTAATACAGCTCAA	62	192	0.8	10	6	0	0
SEM55	SCEPAM2057B09.g	(ct)15(ct)5	ACGGCATCAGATTCAGATCA	ATGGCTTTCCATCTCGTGAC	56	277	0.7	6	1	2	1
SEM57	SCEPRT2048F09.g	(cag)11	TCCAGAAGTACGTGGAGACG	ACGACAGCAGGTCGAACAT	56	222	0.9	11	4	2	0
SEM58	SCEPSB1130G10.g	(cacta)15	CCAACCAACCTCGACATTCT	CCATGTGATCTGACCTGGTG	60	209	0.8	9	4	2	1
SEM60	SCEQAM1041B03.g	(ag)12	TGCTAACACATTTCAAGAAAGAGA	GATCCAATCCGAGGAAAAGT	58	155	0.9	8	4	0	3
SEM61	SCEQAM1041H02.g	(ct)12	GTTCAGAACACGTGCAGCAT	CACGCTTGACATGAGAGGAA	59	165	0.7	12	3	5	2
SEM63	SCEQHR1078A09.g	(ag)25	GGTCGGTGCTCTGTTCTTTT	CCTGCAGCAGAGACGAGAT	59	197	0.1	9	1	0	2
SEM68	SCEQRT1032H07.g	(ta)6(ac)11(tc)6	CCCTGAGGTCTCTCTCCACT	TGCCATAGGACAAGAGTTTAACA	64	239	0.7	5	1	3	1
SEM72	SCEQSD2075F10.g	(ag)14	GAACCTTATCGGTAGCCTCCT	GAGCGCCATAGGAGAAGTG	58	158	0.3	4	1	2	1
SEM78	SCEZRT2023F09.g	(ggt)5(atag)14	GTGGTCGCAGACGAGGTC	CTCCGCATTAGCCATTTCC	58	222	0	13	3	0	3
SEM79	SCEZRT2024C04.g	(ac)13	GATGGAACAGATGCGACAAG	GTTCATCGTAACCTGCTGGA	58	207	0.9	7	1	2	1
SEM80	SCEZRZ3015G05.g	(ta)27	GCAGATGAGAGGGCAAAAGT	CGCCTGCAGATGAATCATAG	59	244	0.9	5	0	1	0
SEM82	SCEZRZ3017G04.g	(ga)12	AGTACAAGGCACAGCCAGAG	GGACATGAGGTACACCCAGA	62	197	0.8	4	1	3	0
SEM83	SCEZRZ3096G10.g	(atg)10	TCCTCCTCTTGTTGCAGTTG	GTCGTCGTCACGATCATCTC	58	184	0.9	17	1	6	2
SEM84	SCEZSB1094A08.g	(tc)10	TGTAGCAATTCCTTGCGTTG	CAACAAATACAATGCCAATCG	58	229	0.9	10	3	4	3
SEM85	SCJFAD1011F07.b	(ga)10(agag)5	CACCTAGTGAAAGGGGCAAA	CCTGAAGCCTTGGTAGCATC	59	242	0.9	4	2	0	0
SEM86	SCJFLR1035E04.g	(ga)10	CGAGAACTAGCATAGCACAAGA	AACAACTGGTGCAAGTCCAT	58	172	0.6	8	1	2	1

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SEM90	SCJFRZ2010C01.g	(ag)17			60 50	190	0.7	8	0	3	0
SEM92	SCJFSB1010B12.g	(tc)10	TGTGCCGTTGCCTAATAACA	GGCAAGCTTCCTCAGTTTCTT	56	209	0.6	8	0	2	2
SEM94	SCJFST1014E07.g	(tc)10		CIGGCIGGGGGGGGGGCACII	56	196	0.8	6	2	0	1
SEM98	SCJLRT1019D02.g	(tg)15	GCCAGCAGAATGCTTAACAA		58	233	0.8	8	3	2	1
SEM99	SCJLRT3076A02.g	(ta)12	TTACCTCCGGCAACGTTAAA	TGCAGGCATATGGTAGTCCA	56	175	0.9	11	5	0	0
SEM105	SCMCAM1100G01.g	(ctttt)18	AGGGGCCTCAAGTTGTTCTT	CGGTCTCATGGTCACCTTTT	58	220	0.9	10	1	5	2
SEM106	SCMCCL6027C07.g	(tc)24	AGGTTGCTGATGGTCCTCAC	CAAGAAGGGAAGCAGGGACT	62	197	0.9	5	1	2	0
SEM108	SCMCFL5008F03.g	(ag)10	CGACTTGTGTGGAGGTGAAA	TGGATCAATGTGAACAAAATCG	58	164	0.7	7	2	2	0
SEM112	SCMCST1057D03.g	(tc)14	CCTTCTGCAGACGAGTTGAA	ACCTGACCAGCAAATCAACA	58	159	0.9	8	3	3	0
SEM113	SCPIRT3024F01.g	(ga)17(gga)5	TTCCGGTTTACCCTGCATAG	TTCCTCAGGGCCCTTTTATT	58	232	0.9	11	2	3	2
SEM117	SCQGLV1018G08.g	(at)41	GCGTGGCACTGACTACAAGT	CAATGTTCTGTGGTCTGCACT	56	246	0.8	6	3	1	1
SEM119	SCQSHR1020F04.g	(ct)16	CCGCGTGCTCTCTCTCTCT	ATTGCCATCACCTCATGCTT	56	206	0.4	7	1	2	1
SEM124	SCRFLB1055F01.g	(tcc)11	CCTTGATGTGCTTGACGAG	CCAACGAGCAAAAGTAAACG	56	270	0.2	7	3	0	2
SEM125	SCRFRT3058D07.g	(ct)16	TATTCTCTCCGGATCCCCTA	ATTCAAAGCGCAACACAGTC	58	160	0.6	7	2	3	0
SEM131	SCRUFL4024B04.g	(ac)18(cgc)6	AAAGGAAAGCAAACCCAAGG	GCAGTCGTTGTCGTAGCAGA	58	245	0.9	4	0	1	2
SEM132	SCRURT2010E12.g	(ct)18	CCCTCCACCTCTTTGCTC	TAGAAAGACCTGCCCTCCTG	58	202	0.9	11	3	2	1
SEM136	SCSBAM1085C09.g	(cgg)12	CTCTGACCCGAGCAAAGG	GCCAATAAACAGCAGGGGTA	56	238	0.9	6	1	2	1
SEM140	SCSFAD1114H02.g	(at)23	GTGTTTTGGAGACCGTGTCA	CGATTGTTGCGCTGTACATC	58	127	0.9	5	1	0	1
SEM141	SCSFFL4083B01.g	(ac)16(ag)13(gt)5	ATCATCCACAGCTAGCAGCA	GGTTTTGCCTTGGTTTTTGA	56	174	0.8	21	6	6	2
SEM143	SCSFHR1045G08.g	(ct)9(ct)12	CCCCTCTCCCTCAGTCTTCT	CCATGCTGTCAGGATCCAC	60	279	0.7	3	1	1	1
SEM147	SCSGHR1070F11.g	(tcc)10	GCCTCTTCCTCCTCCACTC	GACGACCGTCCTTGTTGAG	58	250	0.8	8	1	2	0
SEM148	SCSGLR1025D03.g	(tca)12	GCTACCGGATGGATAAAAGC	CTGACCGAAATGATCAAGGA	56	245	0.9	4	1	3	0
SEM154	SCUTCL6035D02.q	(ct)14	ACCGAGGTAGGAGGGAGTGT	GCTCGCCATGAATAGAAAGG	58	219	0.9	9	4	1	1
SEM158	SCVPCL6044A06.g	(ag)12	GGATGGTTAAAGCGGAAACA	GGAAACAGTGTACGCCCAGT	56	151	0.7	10	4	1	1
SEM159	SCVPHR1089A09.g	(ag)13	CTGGTGGAATAACTCGCTGA	CTCAAGGCAAGAACGAATCC	60	279	0.9	10	4	3	1
SEM161	SCVPHR1094C01.g	(agg)10	GAACTGCTCACTGGCTCCTC	GTAGAAGTCCGTCGCCGTAA	58	186	0.7	6	1	1	1
SEM164	SCVPLR2019H04.a	(ag)18	GAGGTTATGGGGAAACCAGA	GATTGCAGCCGTAAACTTGA	56	211	0.9	11	1	4	1
SEM166	SCVPRT2080G09.g	(at)22	AGCGCATCTTGCTTATTTGA	ATGCATGATCATCGAGGAAG	56	171	0.6	12	4	1	1
SEM167	SCVPRT2083D03.g	(at)30	CGGATCTTGGCTCCTTCTCT	AGCCTTGATTGGCAATGGTA	58	223	0.9	15	4	7	2
SEM168	SCVPRZ2037E02.g	(ct)11	AACGTCAGCCGCTACAACTT	CTTCCCTTTTGCGAAGAAAA	56	143	0.5	7	2	2	0
SEM174	SCQGFL3059G12.g	(ta)11	CTCACCGCAGCTCTTTTTCT	CACAAGCTATGCGGTCAAAA	58	249	0.2	4	0	1	0
SEM176	SCRFFL1029H06.a	(cctc)5(ct)10	CGCCATAACCATAACCACAG	CCTCCCTCCGCTACTTCCTA	58	188	0.9	5	1	2	0
SEM179	SCSBFI 1101G01.g	(aaag)10	TATTCCACCGGGAACAAGAA	GGGATTGTAGCGACGAGTTG	58	210	0.9	6	0	2	0
SEM180	SCSBFI 1104F01.b	(ct)12(tac)6	TTCCACATCAAGCAAGCAAG	ATGACATCAGGAGGGAGACC	58	206	0.6	8	2	2	1
SEM184	SCVPEL 1073A11 g	(aa)10(aac)7	ACCAACGCGACGAGAGAG	GCCTGAACTGGTCGTAGGTC	58	206	0.9	6	-	0	0
SEM189	SCJFAD1013F12.g	(agg)6(ggaa)8	GAACTGCTCACTGGCTCCTC	GTAGAAGTCCGTCGCCGTAA	59	209	0.9	15	4	3	2
SEM100	SCRI AD1098A04 g	(ct)9		AGATCTGTTGGGTGCTCGTC	59	189	0.7	9	2	3	0
00000	5 51 (L) (B 1000) (07.9	(01)0	0110010000111101000		55	100	0.1	5	2	5	v

SEM191	SCRLAD1138A05.g	(gcc)8(cca)5	CCAGTCGCGATTCTTCCAC	AAGGGACGGGGAGAAAAATA	55	176	0.6	4	2	0	1
SEM195	SCSGAD1008F08.g	(ggc)9(gag)5	CTTCCCGTCGCTCTTACCT	CTCCTCCTCCTCCTCCAC	60	183	0.4	3	0	1	0
SEM199	SCEPAM1021B02.g	(tg)9	CTCTCGAGGAGGTGGATGAG	CTGCAAGTTTGTTGGCTGAA	56	237	0.7	11	6	3	1
SEM200	SCEPAM1050A03.g	(tc)9	CTGCAGGATCACCTGGAAC	TAAACCCACGCTGACAGACA	56	238	0.9	8	2	1	4
SEM203	SCEQAM1036D03.g	(cgc)6(cgc)8	GCGGCCTCATACGTGTAGAT	TCTCTTCCCCTCACCAGAAA	56	237	0.8	5	3	0	0
SEM206	SCVPAM1056A04.g	(tctt)9	CATGGTAGCTCCGCTTCTTC	GCGAGAAGCTAGGAAGCACA	59	197	0.9	12	2	3	1
SEM207	SCACAM2043G03.g	(gct)8	GGCACACCTCGAGAGACC	ACTCCTCCTCCTCGCTTAGG	60	151	0.7	5	3	0	1
SEM211	SCCCAM2001E04.g	(cgc)8	CGGTCGTCTCTTCCTCCTC	CTACTACCACCCGGACCAGA	59	212	0.5	5	1	1	1
SEM213	SCCCAM2C08B11.g	(tc)5(tc)5(ct)5(ct)6	CTCTCCGACTCGTCTTCCAC	GCGGACTGCAAAAGAGAGAT	56	241	0.7	7	3	1	0
SEM214	SCEQAM2037C11.g	(cag)8(cg)5	ATCGGCTCCAGTCAGAGAGA	CCTGGTGAAGGCTCATGATT	59	323	0.9	4	1	2	1
SEM215	SCEZAM2033H10.g	(tc)8	GCCGAAGAGGAATCTACGAG	GTTTGTCTTCCTCCTGTGC	56	193	0.5	5	0	3	0
SEM217	SCEZAM2096F07.g	(ga)9	CACGGGGAGACGAGAGAC	CCAACAACAACCAGAATATCG	54	174	0.9	6	3	0	1
SEM219	SCMCAM2084A04.g	(cag)6(cag)5(gca)5(c ag)5	AAGTACGGAGCGCAGTGTAG	ACCGCCTTGTACTCCAAATC	56	228	0.4	14	3	1	2
SEM220	SCMCAM2084F10.b	(at)8	AAGCTCCTTGCCTGCTACTC	CAAAGGGCATCCTTTCTGAT	55	218	0.8	6	1	2	1
SEM221	SCQGAM2028B01.g	(ccg)8	GCCTCTCTCTGCTCAGCCTA	CTCCTCATCTCTCGCCAAA	56	170	0.9	17	5	1	2
SEM223	SCSGAM2076E10.g	(tc)8	CACAGCACTTGCCAAGCTAA	AGTTTCACAAAGGGCGACTG	56	216	0.8	14	7	4	0
SEM227	SCCCCL3005D03.b	(ct)8	GCTACAGTGCCTCTCCCTCT	CTAGAAGCAGAAGTGGAGTGCT	59	287	0.8	7	2	1	0
SEM231	SCCCCL4013B10.g	(cgt)5(gcg)9(cg)5	CCGTTCTACACCTCCAACAT	GACCGTGACCATCTGCTG	57	426	0.9	6	1	2	0
SEM232	SCCCCL4014F09.g	(ga)8	CAACTCCAGCTCCAGTCTCC	CTTTTCGCGAAGTGAACACA	58	311	0.9	9	4	1	0
SEM233	SCCCCL4015B01.g	(tgt)8	TTGCTTGGGACAAAAGGCTA	ATCTTGCAAAGGAAGGAGCA	55	336	0.8	6	3	0	0
SEM234	SCACCL6009D08.g	(acc)8	GGACATGCTGCTCCCTACAT	AGGAGGACTGGTGGTTGAGG	60	211	0.8	5	3	0	0
SEM235	SCACCL6010C05.g	(tc)9	CATCGGCTCATCATAACGAA	AGCTACTTCAGCCCCAAGTG	55	250	0.9	11	5	0	1
SEM236	SCCCCL6003H04.g	(ct)9	CCCTTTGCTTCCCCTTTACT	GAGGCGCCTTACTGTTCTTG	56	193	0.9	5	2	1	0
SEM237	SCEPCL6023G01.g	(gca)8	AGGGAAAGAGACGAGGGAGA	CGTATCTCCGACCACTCCAC	59	167	0.1	3	1	1	0
SEM238	SCEPCL6029D06.g	(gcg)8	CTCTCCCCCAACTCTCTCTG	TCCGACGTCAACGTCTCAG	59	176	0.8	13	3	7	2
SEM239	SCRLCL6030D09.g	(ct)9	CGAGAAACCGTGTCCCCTA	CCCTCTCCCTCTTCCTCCT	59	155	0.8	6	1	1	0
SEM246	SCJLFL4097F08.b	(cg)5(gaaa)8	AATCGATCTTAGGGCCGGTA	ACGCCGACGAGTGAGGAC	58	276	0.6	8	2	3	1
SEM254	SCBGFL5080G03.g	(cgg)8	ACCTTACAGAGCCCACTGCT	TCGCGATAATGAGATTGAGC	59	152	0.9	9	4	4	1
SEM255	SCCCFL5062D10.g	(ag)8	CGGCGTCCACTGAAAGAG	CAGCCTCGAGTTGGGATG	56	178	0.6	9	1	0	0
SEM257	SCEZFL5084A01.g	(tg)8	TGCTGGAGACGGAGTAGCTT	ATCAGGCAAGCACACAATCA	57	159	0.9	4	1	1	1
SEM258	SCEZFL5091D04.g	(cac)9	GGAAGAGGAGGCTTCGAGAT	CTGGATAATCACGCCCAAAT	55	343	0.9	10	1	4	1
SEM261	SCAGFL8042E05.g	(cgg)8	CCATCCATCCTCTCATCTCC	AAGAGTGCTTGAGCGGATCT	56	187	0.6	7	4	1	1
SEM263	SCRLFL8053B05.g	(gga)5(gca)8	AGCCTCTGACGCTAAGATCC	CACACGCTGCAGATGTTGTT	56	208	0.9	12	7	0	0
SEM265	SCAGHR1018C11.g	(cca)8	ACACTAGCTAGCCAGCCACA	GAAGCGAGGCTATGGCTATG	57	163	0.9	6	0	0	0
SEM271	SCJFHR1034E09.g	(ccg)9	AGCAGATTCACTTCGCCACT	CGATGAGCTTGGAGAGGAG	55	157	0.6	5	2	0	2

SEM27         SOCSHRID2803.g         (etil)         TITCITTOGTCADACCCAAT         ACTCCCGTCACCCTORAC         55         180         0.7         5         1         2         0           SEM275         SOCSHRID2803.g         (gap)9         TICGTATGGATTCACAACA         GGGACGTTGGTAATGGT         55         241         0.8         6         1         1         1           SEM285         SOCGLB1036F11.g         (gcc)9         GAACCTGGAGTTCTACAA         CACTACCTGCCTTCTTCTCG         56         191         0.8         9         4         1         2           SEM285         SOCALR106FDF.g         (gsc)8         CCCTACCCCGACCTCTCCCC         GCTGCAGCACAAACAACAC         58         227         0.8         1.2         1         4           SEM285         SOCCLR106FDF.g         (gsc)8(cac)6         CACCTACCAACACACACCCCCC         GCTGCTCGCTGAACA         56         176         0.9         7         2         1         3         3         2         0           SEM285         SOCCLR1075010.g         (gsc)8(cac)6         CACCACAAACACACACCCCCTGAACC         59         180         0.8         8         3         2         0           SEM285         SOCCLR107504.g         (gsc)8(gsg)8         CACGCAAAAGAAGACACACCCTCTAACACCTGAACCACACACCCCTGAAC												
SEMUP:         SCRUMERUPATION         GGGCACCTTCGTANTGGT         55         242         0.9         7         1         0         1           SEMUPS         SCRUMERUSFIG         (gsc)glengis         AACCTGCATTCTTCTCCCA         CACAGAGGAATTTCCCATG         55         241         0.8         9         4         1         2           SEM28         SCVPLB1020B05.9         (gsc)glengisficity         TCCTGAACCTCGCAGTCTT         CACACTCGCACATGACACATCACAGACACGATGACACAT         58         191         0.8         1         1         2           SEM28         SCACLINGFED7         (gsl)gglschichty         TCCTGAACCACATGACACATGACACATGATCTTGC         54         182         0.6         5         2         3         0           SEM28         SCACLINGFED7.9         (gsl)gglschichty         TCCGAACCTGTGTGACAT         54         214         0.9         11         5         1         1           SEM29         SCACLINGFEM29         (gsl)gglschichty         CACCAAACGAGGAACACACACCTGTGACTGTACAT         54         242         0.9         1         1         2         0           SEM29         SCACLINGFEM29         (gsl)gglschichty         CACCAAACGAGGAACACACACGCTGTACACAGCAGCACACACGCGTGTGT         55         130         0.8         2         0         2	SEM273	SCQSHR1022B03.g	(cat)9	TTTCTTTTCGTCACACCCAAT	ACTCCCGTCACTCACCTGAC	55	180	0.7	5	1	2	0
SEM27         SCSEHRIGHAFL2g         (highlighed)         AACCGATCTTCTCCCTA         CAGAGGAGATTCTCCCGATGT         55         241         0.8         6         1         1           SEM282         SCOLEN108F11g         (goc)8         TCCTTGAACCTGCGAGTCTC         CTACCTGCCTTCTCGTTCC         54         192         0.9         5         1         1         2           SEM285         SCACLRIGHTOR         (gabliget)5(rd)7         TCCGTGAACCATCGCGAGTCTC         CTACCTGCCACCACATCTTCTC         55         184         0.6         5         2         3         0           SEM295         SCCCLRIGHTOR         (cap)8         CACCTCCCCAACACTTTCCG         GTACACCATGCACACACTCTGCTGAACA         54         142         1         1         3           SEM295         SCCCLRIVTSDIQ         (cap)8(req)6         CACCACACACACCACCACACACACACC         55         183         0.8         8         3         2         0           SEM305         SCCLRIVTGAALQ         (cap)8(req)6         CACACACACACCACACACACCACCACACACACACCC         55         193         0.9         5         0         3         4         1           SEM305         SCLRIVTAALQ         (gap)8(req)6(req)7         CAAAACCCTAACACACACCACACACACACACACACACAC	SEM275	SCRUHR1074E09.g	(gag)9	TCTCATCGGATTCACACACA	GGGCAGCTTCGTAATGGT	55	242	0.9	7	1	0	1
SEM28         SCOLB 8103FH 1.g.         (gor)9         CAACCTCGCATCTTCACAA         CACTACCTGCCTTTCTTCTCC         65         191         0.8         9         4         1         2           SEM285         SCVLRIBGTED7         (gor)8(gor)8(ct)8(7)         TCCGATCACATCACAGACC         GGTCGAGCAGAAACT         58         227         0.8         12         1         1         4           SEM285         SCCCLRIBGFED7         (gor)8(gor)8(ct)8(ct)87         TCCGATCACATCACGGACCTCCC         GGTCGAGCACATCACTCTTC         GGTCGAGCACATCACTCTTC         56         144         0.6         5         2         3         0           SEM295         SCCCLRIBGFED7         (gor)8(gor)8         CACCAAACGACTCGCATTTC         CGGACCACCGACACGACACG         59         163         0.8         8         3         2         0           SEM295         SCCCLRIBGFED7         (gor)8(gor)8         CGAAACCCTCAAACCCTCACACCCCCACACGCACCACCCCCCCACACGACCACCC         59         163         0.8         8         3         2         0           SEM305         SCCLRIBTGAAD         (gor)8(gor)8         CGAAACCCTCCAATCACCCCCCACACGCCCCCAACGACACACC         59         193         0.9         5         0         3         0           SEM305         SCCLRIBTGAADD         (gor)8(gor)8 <t< td=""><td>SEM276</td><td>SCSFHR1043F12.g</td><td>(tg)5(tg)8(ag)5</td><td>AACCCGTTCTTCTTCCCCTA</td><td>CAGAGGGAGATTTGCCATGT</td><td>55</td><td>241</td><td>0.8</td><td>6</td><td>1</td><td>1</td><td>1</td></t<>	SEM276	SCSFHR1043F12.g	(tg)5(tg)8(ag)5	AACCCGTTCTTCTTCCCCTA	CAGAGGGAGATTTGCCATGT	55	241	0.8	6	1	1	1
SEM28         SCVPLB1020805.g         (pc)B         TCCTTCAACCTOGCAGTCT         CTACCTGOCACAAACAACA         54         12         1         1         2           SEM284         SACALRISFED7.g         (ps)8(grijk)gr         CCCATACACATACAACAACAACACACACC         GATGCTGCACAAAAACAACT         58         227         0.8         12         1         1         4           SEM294         SACCLRIGED07.g         (ps)8(grijk)         CCCATACACATACACACACACCTCGCACAAACAACT         58         148         0.6         5         2         3         0           SEM295         SCCCLRIGED10         (ps)8(grijk)         CACAAACAACTCGTGACACAACACCTCAAACAACACTCGCACACACC         59         163         0.8         8         3         2         0           SEM303         SCEPLRI00810.g         (ps)8(grijk)         CCGAAACACCTCAAACCACA         CTCCCTAACACAACACACCTCAAACCACCACAACCACCAC	SEM282	SCQGLB1038F11.g	(gcc)9	GAACCTCGCAGTCTTCACAA	CACTACCTGCCTTTCTCTCG	56	191	0.8	9	4	1	2
SEM28         SCACR1057E07.g         (gs)Rgs/gs/seldy17         TCCGATCACATTCACAGACC         GCTGCGACGATACACAACT         58         27         0.8         12         1         4           SEM294         SCCCLR1066D7.g         (gca)R/gca)         CCATACCCTGTACCGTACCC         GCTGCAGCAGACACATCGTGAGG         55         184         0.6         5         2         3         0           SEM295         SCCCLR1066F12g         (tb)         CACCTOCCAACTCTTCTCC         GTGACACATCGTGACACC         56         176         0.9         7         2         1         3           SEM295         SCCCLR1076AUA         (ga)R         CACCTCCAACCCTTAACCCTGAACCCTGACTCGACTCGA	SEM285	SCVPLB1020B05.g	(gcc)9	TCCTTGAACCTCGCAGTCTT	CTACCTGCCTCTCTCGTTCC	54	192	0.9	5	1	1	2
SEM24         SCCCLR1066D7.g         (cca)(sccg)(8         CCATACCCTGTACCGTACCC         GATCGTTCGTGACGTACTCCTG         55         184         0.6         5         2         3         0           SEM295         SCCCLR106F12.g         (ca)8         CACCTACCAGACTTTCTCC         GTGACACCATGGTCCTGAAG         56         176         0.9         7         2         1         3           SEM297         SCCCLR1075D10.g         (cg)8(ca)6         CACCAAACGAGACTGCATTA         GTGAGACACGACGACACAC         59         163         0.8         8         3         2         0           SEM303         SCEPLR1080H10.g         (cg)8(ca)6         CGAAAACCCTCAAACCCTAA         CTCCTCTAGCTTCAACAG         56         227         0         6         1         2         0         5         0         3         0           SEM303         SCLIR1017A10         (ca)8(ca)9         ACCACCAATACCAACGTCAAACATCCACGACAC         CGGAGCATACCAAGGTAACAT         55         242         0.9         5         1         1         2         1         1         2         1         1         2         1         1         2         1         1         2         1         0         1         2         2         1         1         2	SEM288	SCACLR1057E07.g	(ga)8(gct)5(ctg)7	TCCGATCACAATCACAGACC	GCTGCAGCAGATGACAAACT	58	227	0.8	12	1	1	4
SEK263       SCCCLR1075010.g       (top8)       CACCTCOCAGACTCTTCCC       GGACACAGACGCAGGTCGAAGAT       54       116       0.9       7       2       1       3         SEM297       SCCCLR1075010.g       (top8)(cac)6       CACCAAACAGACTCGCATT       CGGACAGACGACACAGC       59       163       0.8       8       3       2       0         SEM308       SCCCLR107504.0.g       (top8)(cop3)8       GCGGTTTCTTCTTTTCTTC       ACCACACACACACCCACAAC       56       222       0.7       8       3       4       1         SEM305       SCJFLR1013A40.g       (top3)(cop3)8       CGGAATACCACACACCC       TCGCACTGCAAGAGGAA       55       242       0.7       7       4       0       1       2       0         SEM305       SCJFLR1013A40.g       (top3)(cop3)8       ACCACCATATCCACAGCACACACACGCAGAAGA       55       242       0.9       5       1       1       2       1       1       2       1       1       2       1       1       2       1       1       2       1       1       2       0       1       2       0       1       2       0       1       2       0       1       2       0       1       2       1       1       1	SEM294	SCCCLR1066D07.g	(cca)5(ccg)8	CCATACCCTGTACCGTACCC	GATGCTTGCATTCATCCTTG	55	184	0.6	5	2	3	0
SEN297         SCCCLR1075D10.g         (goc)8(cac)6         CACCAAACGACTCGCATTT         CCGATCGAACTCGTGACACT         54         214         0.9         11         5         1         1           SEM302         SCCCLR1075A04.g         (ca)8         ACGCGAGAGGAGAGATA         GTCAGCAGCACACACG         59         163         0.8         8         3         2         0           SEM302         SCEPLR1003D011.g         (gog)8(cag)8         CGGATTCTTGTTTTCCTTC         ACCACGAACACCCGATCACCCTA         55         193         0.9         5         0         3         0           SEM303         SCJELR1017AH.0.g         (ca)8(cag)8(cag)8         ACGACCAACACCACCCAC         CTCGACGTGAGATGGAAGGAAGA         54         244         0.7         7         4         0         1         2           SEM303         SCJLR1107AH.0.g         (ca)8(cag)8(cag)9         ACACCAACACCCCTCAACCC         CGGACAACACACCCCTGAAGC         55         242         0.9         5         1         1         2           SEM313         SCGLR108402.g         (gog)9         GAGGGAACACATCCCTCTACC         CGGAGGACCGAT         55         20         0.8         2         2         2           SEM313         SCGLR109601.g         (a)864CTCGCAGGAGACACA         GTCTGCCCGTAGATGAAGC	SEM295	SCCCLR1066F12.g	(tc)8	CACCTCCCAGACTCTTCTCC	GTGACACCATGGTCCTGAAG	56	176	0.9	7	2	1	3
SEM28         SCCCLR1076A04.g         (ca)8         ACGCGACAGCAGGAGAGATA         GCCCACACACCACACC         59         163         0.8         8         3         2         0           SEM302         SCEPLR1030H10.g         (gg0)6(cg0)8         GCGATTCTTGTTTCTTCT         ACCACGACCTCAATCCAAC         56         282         0.7         8         3         4         1           SEM303         SCEPLR1030H10.g         (gg0)8         CGAAAACCTCACACCCAC         CTCCTCAGCTTCGAGAG         56         247         0         6         1         2         0           SEM305         SCJLR10174A10.g         (ac)5(ca)8(ag)7         CAAACTTTCCCCTAATCACC         CGGACACAAACGTCGAGGA         55         242         0.9         5         1         1         2           SEM305         SCOLR101010.0         (gg)8         AAGGAACCACCCTCCATACA         CGGACACAAGACCTCT         56         241         0.9         6         3         3         0           SEM315         SCOLR1084A02.g         (gr0)9         GAGGAACCATCCCTTCTC         CGCGACAGAAGACTCTCT         56         211         0.9         6         3         3         0           SEM315         SCOLR1084A02.g         (gr0)8         AAGGGAACCATCCCTTCTCTC         CGCGAGAGACATGCTCT <td< td=""><td>SEM297</td><td>SCCCLR1075D10.g</td><td>(cgc)8(cac)6</td><td>CACCAAACAGACTCGCATTT</td><td>CGGATCGAACTCTGTGACAT</td><td>54</td><td>214</td><td>0.9</td><td>11</td><td>5</td><td>1</td><td>1</td></td<>	SEM297	SCCCLR1075D10.g	(cgc)8(cac)6	CACCAAACAGACTCGCATTT	CGGATCGAACTCTGTGACAT	54	214	0.9	11	5	1	1
SEH302         SCEPLR:1008H10.g         (ggc)6(cg)8         GCGGTTCTTGTTTCCTTC         ACACGACACCTCAAACCCT         ACACGACAACCTCAAACCCT         ACACGACAACCTCAAACCCT         ACACGACAACACCACCAC         TCGAAGTTGACATGACAG         56         222         0.7         8         3         4         1           SEM303         SCEPLR:1031A08.g         (cag)8(cag)9         ACACCACATACCACCACCAC         TCGAAGTTGACAGAG         56         247         0         6         1         2         0           SEM304         SCJLLR:101404.0.g         (ac)5(ca)8(ag)7         CAAACTTTGCCCCATATCACC         CGGAACAACACCCCAAAGGA         55         242         0.9         5         1         1         2           SEM303         SCGLR:1016(10.g         (ga)8         ACGAACCACACCCCTAAGC         GTGAGGCAGCGCGGGTAAT         55         240         0.9         10         2         4         1           SEM313         SCGLR:1016404.0.g         (ga)8         ACGAACCACACCCCTTACC         GCGCTGAGGCACTGAAT         56         211         0.9         6         3         3         0           SEM315         SCACLR:2007A01.g         (ca)8(ag)9         GAGGCACCTCGAACACC         GTCGGCCCGTAGGTAT         56         150         0.7         5         2         1         0	SEM298	SCCCLR1076A04.g	(ca)8	ACGCGAGAGGGGAGAGAGATA	GTCAGCAGCACGAACAGC	59	163	0.8	8	3	2	0
SEM303       SCEPLER1030D11.g       (agg)8       CGAAAACCCTCAAACCCTAA       CTCCTCTAGCTCGCGTTGT       55       193       0.9       5       0       3       0         SEM306       SCLFLR1013A08.g       (cag)8(cag)8       ACCACCACACCACCACC       CTCCGACGTGGACATACCAAGTGAAG       54       244       0.7       7       4       0       1       2         SEM307       SCLLR1014101F02.g       (gt)8       TCTCGACTCCCCTAATCACC       CGGAACGAAAGACTCGCGTTG       55       242       0.9       5       1       1       2         SEM307       SCGLR108140.g       (gt)8       ACAGAACCATCCCTTCT       CGGAGCACACACTCCTTCT       56       211       0.9       6       3       3       0         SEM313       SCGLR108140.g       (gt)99       GAGGACACACACTCCTTCT       CGCCTTAGATCACTCGT       58       250       0.8       8       2       1       1         SEM315       SCACLR2007A01.g       (ca)(s(cg)7)       GAATATAACCGCCACCTTGC       TGGCTTCGCCTACTACT       58       100       7       5       2       1       0       5       2       1       0       5       2       1       1       1       5       5       2       1       1       1       1       1	SEM302	SCEPLR1008H10.g	(ggc)5(cgg)8	GCGGTTTCTTGTTTTCCTTC	ACCACGACCTCGATCTCAAC	56	282	0.7	8	3	4	1
SEM306       SCJFLR1013A08.g       (cag)8(cag)9       ACCACCATACCACCACCA       TCGACGTTGACATGG       56       247       0       6       1       2       0         SEM307       SCJFLR10174A10.g       (ac)5(ca)8(ag)17       CAAACTTTGCCCGATAGCT       CGGACCAAACGCACACA       55       242       0.9       5       1       1       2         SEM308       SCGLILR1101FC10.g       (ga)8       AAGAAACCAACCCTCCAAAGC       CGGACGAAAGATCGCACGATA       55       230       0.9       10       2       4       1         SEM318       SCGUR1019C10.g       (ga)8       AAGAAACCAACCTCTCTC       CGGATCGAAGAAGACCTC       56       211       0.9       6       3       3       0         SEM315       SCACLR207A01.g       (ac)5(ag)9       GAAGTCACGCACCTTGC       TGGCTTCCACTGCGACGACCACTGCT       60       152       0.9       8       2       1       0         SEM319       SCACLR2027A01.g       (ag)8(ag)16       GTCGTCACTCGGACGACAC       GTCGGTCCAGTGGTGAGTA       56       150       0.7       5       2       1       0         SEM319       SCACLR2020205.g       (ag)8(ag)16       GTCCGTCTCCACTGCAGAACAC       GCGGTGAGGTGGAGGTG       59       222       0.5       10       4       1       1 <td>SEM303</td> <td>SCEPLR1030D11.g</td> <td>(agg)8</td> <td>CGAAAACCCTCAAACCCTAA</td> <td>CTCCTCTAGCTTCCGCTTGT</td> <td>55</td> <td>193</td> <td>0.9</td> <td>5</td> <td>0</td> <td>3</td> <td>0</td>	SEM303	SCEPLR1030D11.g	(agg)8	CGAAAACCCTCAAACCCTAA	CTCCTCTAGCTTCCGCTTGT	55	193	0.9	5	0	3	0
SEM307       SCJFLR1074A10.g       (ac)5(ca)9(ag)7       CAAACTTTTGCCCGATAGGT       CGGAGCATACCAAGTGAAGA       54       244       0.7       7       4       0       1         SEM308       SCJLLR1101F02.g       (gt)8       TCTGGACTCCCTAATCACC       CGGACAGAAAGATCCCAGTAG       55       242       0.9       5       1       1       2         SEM310       SCOGLR1019C10.g       (ga)8       AAGAAACCAACCCTCAAAGC       GTAGGTAGCGCTGGGTAGT       55       230       0.9       10       2       4       1         SEM313       SCSGLR104AA02.g       (gcg)9       GAGGGAACACATCCCTTCC       GCCGTAGTAGCAACCTCCT       58       250       0.8       8       2       1       1         SEM314       SCVPLR1049G12.g       (cl)8(cl)5(cgc)7       GAATTAACCCCACCCTTCC       TGGCTTTCACTGCGCAGAGTG       68       150       0.7       5       2       1       0       5         SEM319       SCACLR2007A01.g       (ca)9(ag)17       GAGGCAGCTCGACAACC       GTCGCCCGAGGAGCACGAGTGG       69       10       0.7       5       2       1       0       5       5       10       4       1       1       5         SEM320       SCCCLR2002P05.g       (ag)9(ag)17       GAGGCAGCTCGACGACAC       GCCGTC	SEM306	SCJFLR1013A08.g	(cag)8(cag)9	ACCACCAATACCACCACCAC	TCGACGTTGGACTTGAGAAG	56	247	0	6	1	2	0
SEM308       SCJLLR1101F02.g       (g)8       TCTCGACTCCCCTAATCACC       CGGACAGAAAGATCGCAGTA       55       242       0.9       5       1       1       2         SEM310       SCQGLR1019C10.g       (g)8       AAGAAACCAACCCTCAAAGC       GTAGGGTAGCGCTGGGTAAT       55       230       0.9       10       2       4       1         SEM313       SCSGLR104A02.g       (g)8       AAGAAACCATCCCTTCTC       GCGGTAGTGAAGACCTCTCT       56       211       0.9       8       2       1       1         SEM314       SCVPLR1049G12.g       (g)8(q)7       GAATATAACCGCCACCTTGC       TGGCTTTCCATCTCGTGACT       56       150       0.7       5       2       1       1         SEM315       SCACLR2007A01 g       (q)8(q)7       GAAGCACTCGCAGAAATGC       CACCGGGAGCACTGAGTA       56       150       0.7       5       2       1       0         SEM320       SCCCLR2002F05.g       (q)8(q)7       GAAGCACTCGACCAACC       GTCAGCTCGACGAGGAGTAG       55       239       0.9       1       3       1       1       2       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1	SEM307	SCJFLR1074A10.g	(ac)5(ca)9(ag)7	CAAACTTTTGCCCGATAGGT	CGGAGCATACCAAGTGAAGA	54	244	0.7	7	4	0	1
SEM310       SCQGLR1019C10.g       (ga)8       AAGAAACCAACCCTCAAAGC       GTAGGGTAGCGCTGGGTAAT       55       230       0.9       10       2       4       1         SEM313       SCSGLR1084A02.g       (gcq)9       GAGGGAACACATCCTTCTC       GCCGTAGAGAAGACCCTC       56       211       0.9       6       3       3       0         SEM315       SCSGLR1084A02.g       (ct)8(ct)5(cgc)7       GAATATAACCGCCACCTTGC       TGGCTTCCATCGTGAACTGT       60       152       0.9       8       2       2       2       2       2       2       2       2       2       2       1       0       5       56       10       0.7       5       2       1       0       5       56       2       9       3       3       0       3       3       0       3       3       0       3       3       0       3       3       0       3       3       0       3       3       0       3       3       0       3       3       0       3       3       0       3       3       0       3       3       0       3       3       0       3       3       0       3       3       0       3       3	SEM308	SCJLLR1101F02.g	(gt)8	TCTCGACTCCCCTAATCACC	CGGACAGAAAGATCGCAGTA	55	242	0.9	5	1	1	2
SEM313       SCSGLR1084A02.g       (gcg)9       GAGGGAACACATCCCTTCTC       GCCGTAGATGAAGACCTCCT       56       211       0.9       6       3       3       0         SEM314       SCVPLR1049G12.g       (ct)8(ct)5(cgc)7       GAATATAACCGCCACCTTGC       TGCTTTCACTCTCGTGACT       58       250       0.8       8       2       1       1         SEM315       SCACLR2007A01.g       (ca)5(ag)9       GAGGCACGACAGAG       GTCTGGCCGTAAGCTGT       60       152       0.9       8       2       2       2         SEM319       SCAGLR2022600.5       (cap)8       ATCGTCATCGCAAAATGC       CAACCGGAGACGAGTGAG       59       222       0.5       10       4       1       1         SEM320       SCCCLR2002F05.g       (ag)8(ag)7       GAGGCAGCTCGACGACAC       GCGGTGAGGTGGAGGTGG       59       222       0.5       10       4       1       1         SEM321       SCCCRT100160.g       (ct)18       CTCCCCTCTGCTCATCA       AGGTGACGAGTGGAGGTGG       59       222       0.9       7       4       0	SEM310	SCQGLR1019C10.g	(ga)8	AAGAAACCAACCCTCAAAGC	GTAGGGTAGCGCTGGGTAAT	55	230	0.9	10	2	4	1
SEM314       SCVPLR1049G12.g       (ct)8(ct)5(cgc)7       GAATATAACCGCCACCTTGC       TGGCTTTCCATCTCGTGACT       58       250       0.8       8       2       1       1         SEM315       SCACLR2007A01.g       (ca)5(cg)9       GAGGTCCTGGGAGAGACAGA       GTCTGGCCCGTAAGCTGT       60       152       0.9       8       2       2       2         SEM319       SCAGLR2026D5.g       (cg)8       ATCGTCATCGCAAAATGC       CAACCGGAGGCACTGAGTA       56       150       0.7       5       2       1       0         SEM320       SCCCR2002F05.g       (ag)9(ag)7       GAGGCACTCGACACCAC       GTCAGCTCACCGCACTGGT       62       11       0.5       6       2       2       1       1         SEM321       SCQGLR2032D06.g       (ga)8(gc)5       GTCCGTCTCCACTCGAAAAC       GCGGTTGAGGTGGGGAG       59       196       0.9       9       1       3       1         SEM321       SCCCRT1001G10.g       (cct)8       CTCCCCTCTGCTCATCA       AGGTGACTCGAGGTGGGGG       59       222       0.9       5       1       1       0       0         SEM322       SCCRT1001G10.g       (ct)8       CTCCCCACGACGAAAGCACTT       GCCGTAAAGCAGGAGGGGGGGG       5       22       0.9       5       1       1 </td <td>SEM313</td> <td>SCSGLR1084A02.g</td> <td>(gcg)9</td> <td>GAGGGAACACATCCCTTCTC</td> <td>GCCGTAGATGAAGACCTCCT</td> <td>56</td> <td>211</td> <td>0.9</td> <td>6</td> <td>3</td> <td>3</td> <td>0</td>	SEM313	SCSGLR1084A02.g	(gcg)9	GAGGGAACACATCCCTTCTC	GCCGTAGATGAAGACCTCCT	56	211	0.9	6	3	3	0
SEM315       SCACLR2007A01.g       (ca)5(ag)9       GAGGTCCTGGGAGAGACAGA       GTCTGGCCCGTAAGCTGT       60       152       0.9       8       2       2       2         SEM319       SCACLR2026005.g       (cg)8       ATCGTCATCGCAAAATGC       CAACCGGAGGCACTGAGTA       56       150       0.7       5       2       1       0         SEM320       SCCCLR2002F05.g       (ag)9(ag)7       GAGGCAGTCGACGACAC       GTCAGCTCCGCTCGTCT       62       111       0.5       6       2       2       1         SEM321       SCCQGLR2032D06.g       (ga)8(ap)5       GTCCCCTCTCGCTCATCA       AGGTTGACGATGGTGGTGAG       59       222       0.5       10       4       1         SEM327       SCCCRT1001610.g       (ct)18       CTCCCCTCTGCTCATCA       AGGTTGCAGGTGTGCAGG       59       122       0.9       7       4       0       0         SEM328       SCCCRT1003H03.g       (ct)16       TCTGCCGTTCCATCACT       GCCGTGAAAGCCTCCGTGTG       59       222       0.9       5       1       1       0         SEM328       SCLRT1009B09.g       (gg)8       CACCCAGGACAACACTT       GCAGTGGAAGCACACTGTGTG       55       202       0.7       7       1       2       0       0         <	SEM314	SCVPLR1049G12.g	(ct)8(ct)5(cgc)7	GAATATAACCGCCACCTTGC	TGGCTTTCCATCTCGTGACT	58	250	0.8	8	2	1	1
SEM319       SCAGLR2026C05.g       (cgc)8       ATCGTCATCGCAAAATGC       CAACCGGAGGCACTGAGTA       56       150       0.7       5       2       1       0         SEM320       SCCCLR2002F05.g       (ag)9(ag)7       GAGGCAGCTCGACCACC       GTCAGCTCCGCTCCTCCT       62       111       0.5       6       2       2       1         SEM321       SCCGLR2032D06.g       (a)8(gc)5       GTCCGTCTCCACTCGAAAAC       GCGGTTGAGGTGGGGGAGC       59       222       0.5       10       4       1         SEM321       SCCCRT1001610.g       (cc)8       CTCCCCCTCTGCTCTACT       AGGTTGAGGTGGTGAC       59       196       0.9       9       1       3       1         SEM328       SCCCRT1003H03.g       (ct)16       CTCCCCCTCTGCTCTCT       ATTCGATTCCAATCCAAC       55       239       0.9       7       4       0       0         SEM328       SCCRT1003H03.g       (ct)16       CTCCCCATCCAAGTAAGCA       GCCTGTAAAAGCCTCCGTGTG       59       222       0.9       5       1       1       0         SEM336       SCJLRT1009B0.g       (gg)8       CACCCAGGTCAAGTAGAT       TTCGTATAGCCATCGTCAT       55       155       0.8       5       2       1       0         SEM336 <td< td=""><td>SEM315</td><td>SCACLR2007A01.g</td><td>(ca)5(ag)9</td><td>GAGGTCCTGGGAGAGACAGA</td><td>GTCTGGCCCGTAAGCTGT</td><td>60</td><td>152</td><td>0.9</td><td>8</td><td>2</td><td>2</td><td>2</td></td<>	SEM315	SCACLR2007A01.g	(ca)5(ag)9	GAGGTCCTGGGAGAGACAGA	GTCTGGCCCGTAAGCTGT	60	152	0.9	8	2	2	2
SEM320       SCCCLR2002F05.g       (ag)9(ag)7       GAGGCAGCTCGACGACAC       GTCAGCTCCGCTCTGCT       62       111       0.5       6       2       2       1         SEM321       SCQGLR2032D06.g       (ga)8(gc)5       GTCCGTCTCCACTCGAAAAC       GCGGTTGAGGTGGGGAC       59       222       0.5       10       4       1       1         SEM327       SCCCRT1001G10.g       (cct)8       CTCCCCTCTCGCTCATCA       AGGTTGACGATGGTGGTGAC       59       196       0.9       9       1       3       1         SEM328       SCCCRT1003H03.g       (c1)16       TCTTGCTGTTCGTTCT       ATTCCGATTCCAAC       55       239       0.9       7       4       0       0         SEM329       SCEQRT1025C10.g       (cgg)8       CACCCAGGCAAGAAGAACACCTT       GCAGTGAAAAGCCATCGTGGTGAC       59       222       0.9       5       1       0         SEM336       SCJLRT100809.g       (ggc)8       CACCCAGGCAAAGAGA       TTCGTATAGCCATCGTCAT       55       50.8       5       2       1       0         SEM337       SCJLRT1013F12.g       (ga)8       AGCAATGGTACGCACAAGAG       TTGCTAGTCGTGTGAGG       56       216       0.7       20       11       1       1         SEM338       SCJLRT1018	SEM319	SCAGLR2026C05.g	(cgc)8	ATCGTCATCGCAAAATGC	CAACCGGAGGCACTGAGTA	56	150	0.7	5	2	1	0
SEM321       SCQGLR2032D06.g       (ga)8(gc)5       GTCCGTCTCCACTCGAAAAC       GCGGTTGAGGTCGAGGTAG       59       222       0.5       10       4       1       1         SEM327       SCCCRT1001G10.g       (cct)8       CTCCCCTCTGCGTCATCA       AGGTTGACGATGGTGGTGAC       59       196       0.9       9       1       3       1         SEM328       SCCCRT1003H03.g       (ct)16       TCTTGCCTGTCGCTCTCCT       ATTCCGATTCCGATCCAAC       55       239       0.9       7       4       0       0         SEM329       SCCCRT1003H03.g       (ct)16       TCTTGCCGTGTCAAGGA       GCCTGTAAAAGCCTCTGGG       59       222       0.9       5       1       1       0         SEM332       SCJLRT109609.g       (gg)28       CCGCAAGGAAGAACACCTT       GCAGTGGGAGGTAGG       56       232       0.7       7       1       2       0         SEM336       SCJLRT1013F12.g       (ga)8       ACCAATGGTACGACAAGAG       TTGCTATGCGTGTTCTGG       55       202       0.7       9       1 </td <td>SEM320</td> <td>SCCCLR2002F05.g</td> <td>(ag)9(ag)7</td> <td>GAGGCAGCTCGACGACAC</td> <td>GTCAGCTCCGCTCCTGCT</td> <td>62</td> <td>111</td> <td>0.5</td> <td>6</td> <td>2</td> <td>2</td> <td>1</td>	SEM320	SCCCLR2002F05.g	(ag)9(ag)7	GAGGCAGCTCGACGACAC	GTCAGCTCCGCTCCTGCT	62	111	0.5	6	2	2	1
SEM327       SCCCRT1001G10.g       (cct)8       CTCCCCTCTGGCTCATCA       AGGTTGACGATGGTGGTGAC       59       196       0.9       9       1       3       1         SEM328       SCCCRT1003H03.g       (ct)16       TCTTGCCTGTTCGTCTCCT       ATTCCGATTCCAAC       55       239       0.9       7       4       0       0         SEM329       SCEQRT1025C10.g       (cgg)8       CACCCAGCTCAAGTACAGCA       GCCTGTAAAAGCCTCCTGTG       59       222       0.9       5       1       1       0         SEM329       SCJFRT1009B09.g       (ggc)8       CCGCAAGGAAGAACACCTT       GCAGTGGAAGTGACGCACTGGTG       56       232       0.7       7       1       2       0         SEM336       SCJLRT1016C08.g       (at)5(aag)8       GCCAGGGTCTCAAGTGAT       TTCGTCATAGCCATCGTCTTGG       55       202       0.7       9       1       1       1         SEM337       SCJLRT1013F12.g       (ga)8       AGCAATGGATCGACGAAGAGGTTT       ATACGACGAGGAGAGGGG       56       216       0.7       20       11       1       1       1         SEM338       SCJLRT1018C02.g       (ga)8       AGCGAGCGTACACCAAAATC       ACGGCTCCAGATGAGGGGG       58       163       0.9       15       2       2       0 <td>SEM321</td> <td>SCQGLR2032D06.g</td> <td>(ga)8(gc)5</td> <td>GTCCGTCTCCACTCGAAAAC</td> <td>GCGGTTGAGGTCGAGGTAG</td> <td>59</td> <td>222</td> <td>0.5</td> <td>10</td> <td>4</td> <td>1</td> <td>1</td>	SEM321	SCQGLR2032D06.g	(ga)8(gc)5	GTCCGTCTCCACTCGAAAAC	GCGGTTGAGGTCGAGGTAG	59	222	0.5	10	4	1	1
SEM328       SCCCRT1003H03.g       (ct)16       TCTTGCCTGTTCGTCTTCCT       ATTCCGATTCCGAC       55       239       0.9       7       4       0       0         SEM329       SCEQRT1025C10.g       (cgg)8       CACCCAGCTCAAGTACAGCA       GCCTGTAAAAGCCTCGTGG       59       222       0.9       5       1       1       0         SEM329       SCJFRT1009B09.g       (ggc)8       CCGCAAGGAAGACACCTT       GCAGTGGAAGTCGACGTAGG       56       232       0.7       7       1       2       0         SEM336       SCJLRT1006C08.g       (at)5(aag)8       GCCAGGGTTCTTCAAGTGAT       TTCGTCATAGCCATCGTCTTGG       55       202       0.7       9       1       1       1         SEM337       SCJLRT1013F12.g       (ga)8       AGCAATGGTACGCACAAGAG       TTGCTATGCGGTCGTTCTTGG       55       202       0.7       9       1       1       1         SEM338       SCJLRT1018602.g       (ga)8       AGCGAGCGTACACCAAATC       ACGGCTCAGAGGAGGAGGAGG       56       216       0.7       20       11       1       1       1       1         SEM339       SCJLRT1019C06.g       (ag)8       AAGCGAGCGTACACCAAATC       ACGGCTCAGATGGCAGTATCCAG       56       249       0.8       15       5       3<	SEM327	SCCCRT1001G10.g	(cct)8	CTCCCCTCTCGCTCATCA	AGGTTGACGATGGTGGTGAC	59	196	0.9	9	1	3	1
SEM329       SCEQRT1025C10.g       (cgg)8       CACCCAGCTCAAGTACAGCA       GCCTGTAAAAGCCTCCTGTG       59       222       0.9       5       1       1       0         SEM322       SCJFRT1009B09.g       (ggc)8       CCGCAAGGAAGAACACCTT       GCAGTGGAAGTCGACGTAGG       56       232       0.7       7       1       2       0         SEM336       SCJLRT1006C08.g       (at)5(aag)8       GCCAGGGTTCTTCAAGTGAT       TTCGTCATAGCCATCGTCAT       55       10.8       5       2       1       0         SEM337       SCJLRT1013F12.g       (ga)8       AGCAATGGTACGCACAAGAG       TTGCTATGCGTCGTTCTTGG       55       202       0.7       9       1       1       1         SEM338       SCJLRT1013F12.g       (ga)8       AGCCAATGGTACGCACAAGAG       TTGCTAGTCGTCGTTCTTGG       55       202       0.7       9       1       1       1         SEM339       SCJLRT1018G02.g       (ga)8       AGCGAGCGTACACCAAATC       ACGGCTCAGATGGTGAGAG       58       163       0.9       15       2       2       0         SEM341       SCAGRT2041D09.g       (cgg)8       GTGGTTTGAGTACGCTCTCTCTCTCTCT       ATTTGAGAGGAGGAGTAGCACACAC       57       171       0.5       2       0       1       1	SEM328	SCCCRT1003H03.g	(ct)16	TCTTGCCTGTTCGTCTTCCT	ATTCCGATTCCGATTCCAAC	55	239	0.9	7	4	0	0
SEM332       SCJFRT1009B09.g       (ggc)8       CCGCAAGGAAGAACACCTT       GCAGTGGAAGTCGACGTAGG       56       232       0.7       7       1       2       0         SEM336       SCJLRT1006C08.g       (at)5(aag)8       GCCAGGGTTCTTCAAGTGAT       TTCGTCATAGCCATCGTCAT       55       155       0.8       5       2       1       0         SEM337       SCJLRT1013F12.g       (ga)8       AGCAATGGTACGCACAAGAG       TTGCTAGTCGTCGTTCTTGG       55       202       0.7       9       1       1         SEM338       SCJLRT1018G02.g       (ga)8       AGCCAGTGGAGGAGGAGTTT       ATACGACGAGGAGGAGGTGG       56       216       0.7       20       11       1         SEM339       SCJLRT1019C06.g       (ga)8       AAGCGAGCGTACACCAAATC       ACGGCTCAGATGGTGGAGGAG       58       163       0.9       15       2       2       0         SEM341       SCAGRT2041D09.g       (cgg)8       GTGGTTGGCGCTCTCTCTCTCT       ATTTGAGATGGCTGCATCA       57       171       0.5       2       0       1       1         SEM344       SCEPRT2047A05.g       (ct)15       CGAGAGGCCTTCTCTCTCTCT       ATTTGAGATGGCTGGAGGAGAGA       59       180       0.9       6       3       2       0         SEM349 <td>SEM329</td> <td>SCEQRT1025C10.g</td> <td>(cgg)8</td> <td>CACCCAGCTCAAGTACAGCA</td> <td>GCCTGTAAAAGCCTCCTGTG</td> <td>59</td> <td>222</td> <td>0.9</td> <td>5</td> <td>1</td> <td>1</td> <td>0</td>	SEM329	SCEQRT1025C10.g	(cgg)8	CACCCAGCTCAAGTACAGCA	GCCTGTAAAAGCCTCCTGTG	59	222	0.9	5	1	1	0
SEM336       SCJLRT1006C08.g       (at)5(aag)8       GCCAGGGTTCTTCAAGTGAT       TTCGTCATAGCCATCGTCAT       55       155       0.8       5       2       1       0         SEM337       SCJLRT1013F12.g       (ga)8       AGCAATGGTACGCACAAGAG       TTGCTAGTCGTCGTTCTTGG       55       202       0.7       9       1       1       1         SEM338       SCJLRT1018G02.g       (ga)8       GATCGGATCGAGAGGAGGTTTT       ATACGACGAGGGACGAAGTGG       56       216       0.7       20       11       1       1         SEM339       SCJLRT1019C06.g       (ag)8       AAGCGAGCGTACACCAAATC       ACGGCTCAGATGGTTGAGAG       58       163       0.9       15       2       2       0         SEM341       SCAGRT2041D09.g       (cgg)8       GTGGTTTGAGTACGCTCGTG       AGAGGGATGGCAGTATCCAG       56       249       0.8       15       5       3       1         SEM344       SCEPRT2047A05.g       (ct)15       CGTGCGCTCTCTCTCTCTC       ATTTTGAGATGGCTGGATAGCTGGTAG       57       171       0.5       2       0       1       1         SEM349       SCEQRT2099E08.g       (gca)8       CGAAGGGAGCACACTCCT       GCGGACGTAGATGGAGAGAGA       59       180       0.9       6       3       2       0	SEM332	SCJFRT1009B09.g	(ggc)8	CCGCAAGGAAGAACACCTT	GCAGTGGAAGTCGACGTAGG	56	232	0.7	7	1	2	0
SEM337       SCJLRT1013F12.g       (ga)8       AGCAATGGTACGCACAAGAG       TTGCTAGTCGTCGTTCTTGG       55       202       0.7       9       1       1         SEM338       SCJLRT1013G02.g       (ga)8       GATCGGATCGAGAGGAGTTTT       ATACGACGAGGAGGAGTGG       56       216       0.7       20       11       1         SEM339       SCJLRT1019C06.g       (ag)8       AAGCGAGCGTACACCAAATC       ACGGCTCAGATGGTTGAGAG       58       163       0.9       15       2       2       0         SEM339       SCJLRT1019C06.g       (ag)8       AAGCGAGCGTACACCAAATC       ACGGCTCAGATGGTTGAGAG       58       163       0.9       15       2       2       0         SEM341       SCAGRT2041D09.g       (cgg)8       GTGGTTTGAGTACGCTCGTG       AGAGGGATGGCAGTATCCAG       56       249       0.8       15       5       3       1         SEM344       SCEPRT2047A05.g       (ct)15       CGTGGCTCTCTCTCTCTCT       ATTTGGACGCTGCATCA       57       171       0.5       2       0       1       1         SEM349       SCEQRT2099E08.g       (gca)8       CGAGAGGACGACACTCCT       GCGGACGTAGATGGAGAGAA       59       228       0.9       6       5       0       0         SEM350       SC	SEM336	SCJLRT1006C08.g	(at)5(aag)8	GCCAGGGTTCTTCAAGTGAT	TTCGTCATAGCCATCGTCAT	55	155	0.8	5	2	1	0
SEM338       SCJLRT1018G02.g       (ga)8       GATCGGATCGAGAGGAGGAGTTTT       ATACGACGAGGACGAAGTGG       56       216       0.7       20       11       1       1         SEM339       SCJLRT1019C06.g       (ag)8       AAGCGAGCGTACACCAAATC       ACGGCTCAGATGGTTGAGAG       58       163       0.9       15       2       2       0         SEM339       SCJLRT1019C06.g       (ag)8       AAGCGAGCGTACACCAAATC       ACGGCTCAGATGGTTGAGAG       58       163       0.9       15       2       2       0         SEM341       SCAGRT2041D09.g       (cgg)8       GTGGTTTGAGTACGCTCGTG       AGAGGGATGGCAGTATCCAG       56       249       0.8       15       5       3       1         SEM344       SCEPRT2047A05.g       (ct)15       CGTGCGCTCTCTCTCTCTCT       ATTTTGAGATGGCTGCATCA       57       171       0.5       2       0       1       1         SEM349       SCEQRT2099E08.g       (gca)8       CGACAGGGAGCACTCCT       GCGGGACGTAGATGGAGAGAG       59       180       0.9       6       3       2       0         SEM350       SCJFRT2057F04.g       (gca)9       CCAATGGAGAGACACTCCT       GCGGGACGAGTGCTAGCTGGTGCAGCT       57       119       0.9       5       2       1       1	SEM337	SCJLRT1013F12.g	(ga)8	AGCAATGGTACGCACAAGAG	TTGCTAGTCGTCGTTCTTGG	55	202	0.7	9	1	1	1
SEM339       SCJLRT1019C06.g       (ag)8       AAGCGAGCGTACACCAAATC       ACGGCTCAGATGGTTGAGAG       58       163       0.9       15       2       2       0         SEM341       SCAGRT2041D09.g       (cgg)8       GTGGTTTGAGTACGCTCGTG       AGAGGGATGGCAGTATCCAG       56       249       0.8       15       5       3       1         SEM341       SCEPRT2047A05.g       (ct)15       CGTGCGCTCTCTCTCTCTCT       ATTTTGAGATGGCTGCATCA       57       171       0.5       2       0       1       1         SEM349       SCEQRT2099E08.g       (gca)8       CGAGAGGCCTTCTCTCTCTGT       CGCTGACGTAGTCCTGGTAG       59       180       0.9       6       3       2       0         SEM350       SCJFRT2057F04.g       (gca)9       CCAATGGAGAGACACTCCT       GCGGACGTAGATGGAGAGAGA       59       228       0.9       6       5       0       0         SEM351       SCMCRT2085E08.g       (tg)8       CGACTGTGGGAGGAGTTTGT       TTGCAGCAGTTGCTAGCTGT       57       119       0.9       5       2       1       1         SEM358       SCAGRT3048C12.g       (gaa)9       CTGGCCTCAAGAGGAAACTG       ACCAACCTCTTGACCAGCAC       59       124       0.9       8       5       2       1    <	SEM338	SCJLRT1018G02.g	(ga)8	GATCGGATCGAGAGGAGTTTT	ATACGACGAGGACGAAGTGG	56	216	0.7	20	11	1	1
SEM341       SCAGRT2041D09.g       (cgg)8       GTGGTTTGAGTACGCTCGTG       AGAGGGATGGCAGTATCCAG       56       249       0.8       15       5       3       1         SEM344       SCEPRT2047A05.g       (ct)15       CGTGCGCTCTCTCTCTCT       ATTTTGAGATGGCTGCATCA       57       171       0.5       2       0       1       1         SEM349       SCEQRT2099E08.g       (gca)8       CGAGAGGCCTTCTCTCTCTGT       CGCTGACGTAGTCCTGGTAG       59       180       0.9       6       3       2       0         SEM350       SCJFRT2057F04.g       (gca)9       CCAATGGAGAGACGACACTCCT       GCGGGACGTAGGTGGCAGGAGAGA       59       228       0.9       6       5       0       0         SEM351       SCMCRT2085E08.g       (tg)8       CGACTGTGGGAGGAGATTGT       TTGCAGCAGTTGCTAGCTGT       57       119       0.9       5       2       1       1         SEM358       SCAGRT3048C12.g       (gaa)9       CTGGCCTCAAGAGGAAACTG       ACCAACCTCTTGACCAGCAC       59       124       0.9       8       5       2       1	SEM339	SCJLRT1019C06.g	(ag)8	AAGCGAGCGTACACCAAATC	ACGGCTCAGATGGTTGAGAG	58	163	0.9	15	2	2	0
SEM344       SCEPRT2047A05.g       (ct)15       CGTGCGCTCTCTCTCTCTCT       ATTTTGAGATGGCTGCATCA       57       171       0.5       2       0       1       1         SEM349       SCEQRT2099E08.g       (gca)8       CGAGAGGCCTTCTCTCTCTG       CGCTGACGTAGTCCTGGTAG       59       180       0.9       6       3       2       0         SEM350       SCJFRT2057F04.g       (gca)9       CCAATGGAGAGACGACACTCCT       GCGGACGTAGATGGAGAAGA       59       228       0.9       6       5       0       0         SEM351       SCMCRT2085E08.g       (tg)8       CGACTGTGGGAGGAGATTGT       TTGCAGCAGTTGCTAGCTGT       57       119       0.9       5       2       1         SEM358       SCAGRT3048C12.g       (gaa)9       CTGGCCTCAAGAGGGAAACTG       ACCAACCTCTTGACCAGCAC       59       124       0.9       8       5       2       1	SEM341	SCAGRT2041D09.g	(cgg)8	GTGGTTTGAGTACGCTCGTG	AGAGGGATGGCAGTATCCAG	56	249	0.8	15	5	3	1
SEM349         SCEQRT2099E08.g         (gca)8         CGAGAGGCCTTCTCTCTCTG         CGCTGACGTAGTCCTGGTAG         59         180         0.9         6         3         2         0           SEM350         SCJFRT2057F04.g         (gca)9         CCAATGGAGACGACACTCCT         GCGGACGTAGATGGAGAAGA         59         228         0.9         6         5         0         0           SEM351         SCMCRT2085E08.g         (tg)8         CGACTGTGGGAGGAGTTTGT         TTGCAGCAGTTGCTAGCTGT         57         119         0.9         5         2         1         1           SEM358         SCAGRT3048C12.g         (gaa)9         CTGGCCTCAAGAGGGAAACTG         ACCAACCTCTTGACCAGCAC         59         124         0.9         8         5         2         1	SEM344	SCEPRT2047A05.g	(ct)15	CGTGCGCTCTCTCTCTCTCT	ATTTTGAGATGGCTGCATCA	57	171	0.5	2	0	1	1
SEM350         SCJFRT2057F04.g         (gca)9         CCAATGGAGACGACACTCCT         GCGGACGTAGATGGAGAAGA         59         228         0.9         6         5         0         0           SEM351         SCMCRT2085E08.g         (tg)8         CGACTGTGGGAGAGAGATTGT         TTGCAGCAGTTGCTAGCTGT         57         119         0.9         5         2         1         1           SEM358         SCAGRT3048C12.g         (gaa)9         CTGGCCTCAAGAGGAAACTG         ACCAACCTCTTGACCAGCAC         59         124         0.9         8         5         2         1	SEM349	SCEQRT2099E08.g	(gca)8	CGAGAGGCCTTCTCTCTCTG	CGCTGACGTAGTCCTGGTAG	59	180	0.9	6	3	2	0
SEM351         SCMCRT2085E08.g         (tg)8         CGACTGTGGGAGGAGTTTGT         TTGCAGCAGTTGCTAGCTGT         57         119         0.9         5         2         1         1           SEM358         SCAGRT3048C12.g         (gaa)9         CTGGCCTCAAGAGGAAACTG         ACCAACCTCTTGACCAGCAC         59         124         0.9         8         5         2         1	SEM350	SCJFRT2057F04.g	(gca)9	CCAATGGAGACGACACTCCT	GCGGACGTAGATGGAGAAGA	59	228	0.9	6	5	0	0
SEM358 SCAGRT3048C12.g (gaa)9 CTGGCCTCAAGAGGAAACTG ACCAACCTCTTGACCAGCAC 59 124 0.9 8 5 2 1	SEM351	SCMCRT2085E08.g	(tg)8	CGACTGTGGGAGGAGTTTGT	TTGCAGCAGTTGCTAGCTGT	57	119	0.9	5	2	1	1
	SEM358	SCAGRT3048C12.g	(gaa)9	CTGGCCTCAAGAGGAAACTG	ACCAACCTCTTGACCAGCAC	59	124	0.9	8	5	2	1

SEXM6         SUBCH 300100B/g         (cm)9         CTAGLOB IGLAGUATION CONTROL INCOMENDATION CONTROL IN	0 = 1 10 0 1	000007000/000	( ))		07007000177100100117		4=0				•	
SEMM6         SCERZ200102/g         (rs)9         CCACCTENTCTECCAAGAAC         CATCTTAAACCTOSECTACA         65         167         0.9         6         1         0           SEMM67         SCCCR2200102/g         (rs)8         AGTCAGCATCCATCCATCTTCTTGTG         CCCATGGTCACCACGAGT         59         241         0.8         10         3         1           SEMM68         SCCCR2200102/g         (rs)8         CGCTTCCATCATTCTTTCTTGTG         TGCTCCGCCTCCACCA         55         123         0.9         7         1         0         0           SEMM67         SCCR2200102/g         (rs)8         GCGATCCATTCCTCTCTCTCTCGCGTCTCGCCTTTCTTT         54         238         0.6         8         1         2         1           SEMM7         SCVFR22036E01/g         (rs)8         GCCACCAAATTGCCCGTAT         CACCAGCTTTTCTTTT         54         23         0.8         5         3         0         1           SEMM7         SCCR23003081/g         (rs)9         GCGGACACAACCAATGCCCCATACACCCCACCACGACGAACCTTA         55         23         0.8         5         1         0         0           SEMM7         SCLFR23003A81b         (rs)919         ACGAGCACCAATGCGCCTTTTTCT         55         23         0.8         5         1         0	SEM361	SCCCRT3001D09.g	(ct)9	GTAGCCGTGGAGCATGAAGT	CTGCTGCCATTAGGAGCAAT	59	173	0.9	11	3	3	2
SEMAGE         SCCCR22010C02         (ap)B         AATCACCATCCATCCATC         ATTICTCCTCCCCTCCTCCTC         59         196         0.9         6         1         0           SEMAGE         SCCCR22010C02         (ap)B         CACCTCCCTCCTCTCTT         CATGGTACCACCACGAGET         59         241         0.8         10         3         1           SEMAGE         SCLFR2015A100         (ap)B         CACCTCCCTCCTCTCTTTTTTTTTTCTT         54         238         0.6         8         1         2         1           SEMAT         SCVPR22036E01.g         (ap)B         CACCACCTATATCACCTCCTCTTTTTTTTTTTTTTTTT	SEM366	SCBFRZ2045C02.g	(ca)9	CCACCTCTTCTGCCAAGAAC	CATCTTAAACTCCGGTCCACA	55	167	0.9	6	0	2	0
SEM88         SCCCR22040Cb5.g         (gcg)B         AAACCCTCCCCTCCGATT         CCCAATGGTACAGCAGAGAT         59         241         0.8         10         3         1           SEM888         SCLFRZ2015A10g         (g)B         CGGTCCCATACTTCTTTTGTG         TGACTCCCGCGTCCCAACC         55         123         0.9         7         1         0         0           SEM871         SCLFRZ2034B06.g         (tg)B         GCGAGACATTTCACCACC         CCCCCTTTTCTTT         54         238         0.6         8         1         2         1           SEM371         SCLFRZ2034B06.g         (cc)B         GCCAACTTCTCCCTCTTTCTA         ACCACCGTTTTCTTCTGTGGTGAGACCCAAGAS         58         184         0.9         4         2         1         0           SEM371         SCLFRZ3020812.g         (cc)B         ACGAGGCCCCTATGAACCT         CCCTATACGACCTAAGACCT         55         233         0.8         5         3         0         1           SEM371         SCLFRZ3020412.g         (cc)B         ACGAGGCCCATAGAACCT         CCCAACGTCGATAGACCT         55         233         0.8         5         1         0           SEM371         SCLFRZ3020412.g         (cc)B         ACGAGGCCCATAGAACCT         CCCACACCTCATAGACCT         55         234	SEM367	SCCCRZ2001C02.g	(ag)8	AGTCAGCATCCATCCAGTCC	ATTTCTCCTGCCCTCCTCTC	59	196	0.9	6	1	0	0
SEM39         SCIFR23018A010         (99)8         CECTTCCATACTTCTTCTTGE         TEAACTCTCC205GTCCTACAC         55         123         0.9         7         1         0         0           SEM37         SCIFR22038B061g         (61)8         GCCAAGCATAATAGCTGCTG         ACCACCGTTTCTTTCTTGAC         57         205         0.8         13         4         4         0           SEM37         SCVPR22038E05g         (cog)8         GCGACCAATCTGCCGTGT         CATGTAGTCAGCCGAGAGA         58         189         0.9         4         2         1         0           SEM37         SCCPR22038E05g         (cog)8         GCGAAGCATACCACCACCCCCCCCCTCCACTAA         55         141         0.9         4         2         1         0           SEM37         SCCPR2302612g         (cog)8         GGAAGCACAACCACCACCACCACCACCACCACACA         55         123         0.8         5         3         0         1           SEM37         SCCPR2302612g         (cog)8         GGAAGCACACCACCACCACCACCACCTCCATACA         56         221         0.9         8         5         1         0           SEM39         SCSERS100812g         (cog)8         CCTRACACCACCACCCCCCACTACACCT         CCCCACACCCTCCATACACCT         55         244         0.8	SEM368	SCCCRZ2004C05.g	(gcg)9	AAACCCTCGCCTCCGATT	CCCAATGGTACCAGCAGAGT	59	241	0.8	10	3	1	1
SEIM37       SCJFR22034806.g       (tij)9       GGAGAAGCATTCAGCAACC       CCCCGCTTTCTTCTCTAC       54       28       0.6       8       1       2       1         SEM37       SCVPR22038E0.g       (coj)8       GCGACCAATTCGCGTAT       CATGTAGTCGAGCGCAGGA       58       189       0.9       4       2       1       0         SEM373       SCVPR22038E0.g       (coj)8       GCGCCCTCCTCCTCTCTTCTA       GACTGGCTGGGAACCCTAA       59       141       0.7       7       0       2       1         SEM375       SCCPR22030E12.g       (coj)8       GGGACGAACCCTACC       CGCATTGCCCCCCACTTAA       55       174       0.9       14       4       0         SEM375       SCCFR230030A8.b       (ctgtjg)9       ACGAGGCCACCATAGAACCT       CGCACACGCCGCTTTCTT       55       228       0.9       4       2       0       0       2       3       0       1       0       2       3       0       2       3       0       1       0       2       3       0       2       3       0       2       3       0       2       3       0       2       3       0       2       3       0       2       3       3       1       0       2 <td>SEM369</td> <td>SCJFRZ2015A10.g</td> <td>(ga)8</td> <td>CGCTTCCATATCTTCTTCTTGG</td> <td>TGACTCTCCGGTCCCTACAC</td> <td>55</td> <td>123</td> <td>0.9</td> <td>7</td> <td>1</td> <td>0</td> <td>0</td>	SEM369	SCJFRZ2015A10.g	(ga)8	CGCTTCCATATCTTCTTCTTGG	TGACTCTCCGGTCCCTACAC	55	123	0.9	7	1	0	0
SEM37         SCVPR2208E619         (#b)         GCCAAGCTAATAGCTGCTG         ACCACCCUTTCTTTTCTTTCTTCTGCAC         57         205         0.8         13         4         4         0           SEM373         SCVPR2208E619         (eg)8         GCCAACCAAATCGCCGTAT         CATGTAGTCGAGCGAAGGA         58         189         0.9         4         2         1         0           SEM374         SCCR22005019         (eg)8         GCCACCACTCCTCCTCTCTTTA         GACTGGCTGCCACCAAA         55         174         0.9         11         4         4         0           SEM375         SCEPR23128005.9         (eg)80         GGAGGCACCATAGAACCTAC         GCCATGTAGTGCTTTCA         55         230         0.8         5         3         0         1           SEM375         SCEPR23108109.112         (eg)9         ACGAGGCACCATAGAACCT         GCCAAAGGTATTCTTTTTT         57         116         0.9         13         6         2         3         0         2         3         0         3         6         2         3         0         3         5         1         0         3         6         2         3         0         3         5         1         0         3         1         0         2	SEM371	SCJFRZ2034B06.g	(tg)9	GGAGAAGCATTTCAGCAACC	CCCGCTTTTCCTCTTTCTTT	54	238	0.6	8	1	2	1
SEM373       SCVPR22038E05.g       (ccg)B       GCGACCAAATCTCCCCTTAT       CATGTAGTCGACCCACAGAA       58       189       0.9       4       2       1       0         SEM374       SCCPR23038B01.g       (cl)6(tc)9       ATGGAGGCTCGTTGTCTTG       GCCGACCAAACCTAA       55       174       0.9       11       4       4       0         SEM375       SCEPR23128D05.g       (cl)6(tc)9       ATGGAGGCCCATACGC       CCGTAATCGCCCTCACTTA       55       233       0.8       5       3       0       1         SEM377       SCEDR23028D1.g       (cg)9       AGGAGGCACAAACCTAGC       CCCATAGAACGTGTGTCTTT       55       238       0.8       5       1       0       5       584       0.8       5       1       0       5       55       228       0.9       4       2       0       0       5       55       228       0.9       4       2       0       0       2       3       0       2       3       0       2       3       0       2       3       0       2       3       0       2       3       0       2       3       0       2       3       0       2       3       3       1       0       2 <td< td=""><td>SEM372</td><td>SCVPRZ2036E01.g</td><td>(at)8</td><td>GCCAAGCTAAATAGCTGCTG</td><td>ACCACCGTTTCTTTCCTGAC</td><td>57</td><td>205</td><td>0.8</td><td>13</td><td>4</td><td>4</td><td>0</td></td<>	SEM372	SCVPRZ2036E01.g	(at)8	GCCAAGCTAAATAGCTGCTG	ACCACCGTTTCTTTCCTGAC	57	205	0.8	13	4	4	0
SEM37       SCCCR2300801.g       [ap]9       GCCTCCTCCCTCCTCTTTA       GACTGGCTCGAAACCCTA       59       141       0.7       7       0       2       1         SEM375       SCEPR23128D6.g       (c)6(c)9       ATGGAGGCTCGTTGTTTTG       CCGTAATCGCCACTAAA       55       174       0.9       11       4       4       0         SEM377       SCEPR23020E12.g       (ap)8       GGAAGACCACAACCATAGAACT       CCGCATTGACGCAGGTGTTGTGTG       56       221       0.9       8       5       1       0         SEM39       SCGRS81005B12.g       (ap)9       GGGGAAGTAGTCTCAGGTCA       GCCCACCACATATGTT       55       104       0.9       6       2       3       0         SEM39       SCGS81005B12.g       (ap)9       GGGGAAGTAGTCCAGGTGTTTTT       GCCAGACCCTCACATTACTCT       55       104       0.9       6       2       3       0         SEM398       SCGTS81005B12.g       (ap)8       GTGCAACCCCCAATAGAC       TCCCGATCATTGTCTGT       55       124       0.9       6       2       3       0       2       1       0       2       1       0       2       1       0       2       1       0       2       1       0       2       1       0       2<	SEM373	SCVPRZ2038E05.g	(ccg)8	GCGACCAAATCTGCCGTAT	CATGTAGTCGAGCGCAGAGA	58	189	0.9	4	2	1	0
SEM37       SCEPR23128D05.g       (u)b(tb)9       ATGGAGGCTCGTTGTTTTG       CCGATTGATCGCCTCAAAA       55       174       0.9       11       4       4       0         SEM377       SCEQR23020E12.g       (grg)8       GGAGAGGACGAACCCTAGC       CCGCATTGACGCAGTTTCTT       55       233       0.8       5       3       0       1         SEM378       SCUFR23020410.g       (gg)9       TAGTAGCACCCATAGACCAT       GCACAAGGTGATTGTTGCTT       55       228       0.9       4       2       0       0       0       2       3       0       1       0	SEM374	SCCCRZ3003B01.g	(ag)9	GCCTCCTCCTCCTCTTCTA	GACTGGCTCGGAAACCCTA	59	141	0.7	7	0	2	1
SEM37         SCEORF2020E12.g         (gcg)8         GGAGAGGACGAAACCTAGC         CGATTGAACGAGTTTCTA         55         233         0.8         5         3         0         1           SEM379         SCJFR23C03A08.b         (ctgj)9         ACGAGGCCACATAGAACAT         GCACAAGGTGATTGTGCTGT         56         221         0.9         8         5         1         0           SEM39         SCUTR2103P01.g         (cgg)9         TAGTACAAGCGAGGCGATA         GTCTTTGCCTTTGATCTCT         55         104         0.9         13         6         2         3           SEM391         SCUTSB1033C02.g         (a)9         GGGAAGTAGTCCACGGGATTTTT         GCGACACACCTCACGTGTAGTGTGTAGACG         55         224         0.8         3         1         0         2         3           SEM392         SCUTSB1075H09.g         (a)8         TCATCCTCACCAGCAACTCCATGTTGATAGCAGCGTA         54         184         0.9         4         0         2         1         3           SEM400         SCEPSD1081A02.g         (ccg)8         CCTCCATTCATCTCCCC         TTCCATCGAGTGAGAGAAGAGC         55         242         0.7         6         2         1         3         1         1           SEM400         SCECSD20077b12.g         (cg)8         CC	SEM375	SCEPRZ3128D05.g	(ct)6(tc)9	ATGGAGGCTCGTTGTCTTTG	CCGTAATCGCCTCCACTAAA	55	174	0.9	11	4	4	0
SELM787       SCLFR2303A08.b.       (rdgg)9       ACGAGGCCACCATAGAACAT       GCACAAGGTGATTGTGCTGT       56       221       0.9       4       2       0         SEM384       SCUTRZ3103F01.g.       (rgg)9       TAGTAGCAAGCGAGGCGATA       GTCGTGTGCCTTTGATCGTG       55       228       0.9       4       2       0         SEM390       SCSGSB1005B12.g.       (rgg)9       GGGGAAGTAGTCTCAGGTGCA       GCCCACCCTCCATTATCTT       57       116       0.9       6       2       3       0         SEM391       SCUTSB1033002.g.       (rgg)8       GTTCAGACTCGCAATAGT       GCCCACACCTTCAGCGTGTAGAGG       55       234       0.8       3       1       0       2       1         SEM393       SCUTSB1075H08.g.       (rg)8       CAGCTCATCCTCGTCAATAGT       TGCCACATGTGTGTAGACGG       55       242       0.8       5       1       0       2       1       3         SEM400       SCESD1081A02.g.       (rcg)8       CAGGCAACCACCACCACCACCACCACGTAGTGTAGTGGTGA       53       111       0.4       10       1       2       0       6       2       1       3       3       1       1       3       1       1       3       1       1       2       0       5       14	SEM377	SCEQRZ3020E12.g	(gcg)8	GGAGAGGACGAAACCCTAGC	CGCATTGAACGCAGTTTCTA	55	233	0.8	5	3	0	1
SEM384       SCUTR23103F01.g       (cgg)9       TAGTAGCAAGCGAGGCGATA       GTCGTTGCTTTGATCGTG       55       228       0.9       4       2       0       0         SEM390       SCSGSB1005B12.g       (ag)8       GGGGAAGTAAGTCTCAGGTGA       GCCACCACCCTCATTATCTT       57       116       0.9       13       6       2       3         SEM391       SCUTSB1037C9(2g)       (ag)8       GTTCAGACTCGGGTGTTTTTT       GCTGAGACCCTCAGTAAGGC       55       234       0.8       3       1       0       2       1         SEM393       SCUTSB1075H09.g       (ta)8       TCATGCTACCAGCAAAGAC       TCCCGATCATGTTGTGGCT       55       234       0.8       3       1       0       2       1         SEM400       SCEZSD1081A02.g       (ccg)8       CAGCTCATCATTCCTCCT       TTCGATCGATGATGGTGTG       55       242       0.7       6       2       1       3         SEM403       SCEQSD2077B12.g       (cg)8       CCTGCATCATCCTCCACC       GAAGGCGAGAGAGAGAGAGAGAGAGAGAGGG       5       14       3       1       1       2       1       3       1       1       2       1       3       1       1       2       1       3       1       1       2       1       1	SEM379	SCJFRZ3C03A08.b	(ctgtg)9	ACGAGGCCACCATAGAACAT	GCACAAGGTGATTGTGCTGT	56	221	0.9	8	5	1	0
SEM390       SCSGSB1005B12.g       (ag)9       GGGGAAGTAAGTCTCAGGTCA       GCCACCACCTCATTATCTT       57       116       0.9       13       6       2       3         SEM391       SCUTSB1075H09.g       (a)8       GTCAGACTGCCGTGTTTTT       GCGAGAGACCTCCACTGACGAGC       55       104       0.9       6       2       3       0         SEM391       SCUTSB1075H09.g       (a)8       TCATGCTCACCAGCGAAGAC       TCCCACTACGTGTGTAGACG       55       144       0.9       4       0       2       1         SEM393       SCEPSD1006D03.g       (ta)9       CGTGCAAGCTCCAATATGAT       TGCCACTGCATGAGGGAAGACAGCGCAGCGGAGAGAGAGA	SEM384	SCUTRZ3103F01.g	(cgg)9	TAGTAGCAAGCGAGGCGATA	GTCTGTTGCCTTTGATCGTG	55	228	0.9	4	2	0	0
SEM391       SCUTSB1033C02.9       (ag)8       GTTCAGACTCGCGTGTTTTT       GCTGAGAACCCTTCAGCTT       55       104       0.9       6       2       3       0         SEM392       SCUTSB1075H09.9       (a)8       TCATGCTCACCAGCAAAGAC       TCCCCATCAGTGTGAACG       55       234       0.8       3       1       0       2         SEM398       SCUTSB1006D03.9       (ta)9       CGTGCAACCTCACCACTGATATGAT       TGCCACTGTATAGCAGCGAA       54       184       0.9       4       0       2       1         SEM400       SCEZSD1081402.9       (cog)8       CAGCTCATCCTCTCGCACCT       TCCCTCTGCTGCTGTGTGA       53       111       0.4       10       1       2       0         SEM403       SCEQSD2077B12.9       (cog)8       CAGCGCACGCACGAAAGA       TCCTCTGCTCCTCGTG       58       246       0.9       14       3       1       1         SEM408       SCLST1050H06.9       (ga)9       CAGCGCACGCACGAAGAA       AGGGTGATGAAGGAAAGA       56       163       0.9       4       2       1       0         SEM415       SCMCST1050H06.9       (gb)7       CAAGGCGCCTCTTGGTGTC       CCTCTTTGGGTCTCCTCGTG       58       246       0.9       14       3       1       1 <td< td=""><td>SEM390</td><td>SCSGSB1005B12.g</td><td>(ag)9</td><td>GGGGAAGTAAGTCTCAGGTCA</td><td>GCCACCACCTCCATTATCTT</td><td>57</td><td>116</td><td>0.9</td><td>13</td><td>6</td><td>2</td><td>3</td></td<>	SEM390	SCSGSB1005B12.g	(ag)9	GGGGAAGTAAGTCTCAGGTCA	GCCACCACCTCCATTATCTT	57	116	0.9	13	6	2	3
SEM392       SCUTSB1075H09.g       (ta)8       TCATGCTCACCAGCAAAGAC       TCCCGATCAGTGTGTAGACG       55       234       0.8       3       1       0       2         SEM398       SCEPSD100BD03.g       (ta)9       CAGCTCATCATCACTAGCT       TCCCGATCGTGTAGCGGA       54       184       0.9       4       0       2       1         SEM400       SCEPSD100BD03.g       (ccg)8       CAGCTCATCCTCGTCAACCT       TCCCGTCGTTGTTGCT       59       225       0.9       8       5       1       0       2       0         SEM401       SCMCSD1099609.g       (ct)9       GCTCCATCATCTCTCCTCT       TTCGACGATGATGATGTGTGG       55       242       0.7       6       2       1       3         SEM403       SCEQSD2077B12.g       (cga)8       CCTGCATCAACCTCTCCAC       GAAGGCGAGAGAGAGAGAGG       55       242       0.7       6       2       1       1         SEM403       SCLST1012C09.g       (cd)8(ga)7       CAAGCAGAGAGAGAGAGA       AGGCTGATGATGAGGGAATGAG       56       163       0.9       4       2       1       0         SEM419       SCSST1050H06.g       (cc)8       CACCCTGCTGTGTGTATGAGAGA       AGAGACGTGAGGAGAGACACGAGAGAGAGACC       59       170       0.9       6       1 <td< td=""><td>SEM391</td><td>SCUTSB1033C02.g</td><td>(ag)8</td><td>GTTCAGACTCGCGTGTTTTT</td><td>GCTGAGAACCCTTCAGCTCT</td><td>55</td><td>104</td><td>0.9</td><td>6</td><td>2</td><td>3</td><td>0</td></td<>	SEM391	SCUTSB1033C02.g	(ag)8	GTTCAGACTCGCGTGTTTTT	GCTGAGAACCCTTCAGCTCT	55	104	0.9	6	2	3	0
SEM398       SCEPSD1006D03.g       (ta)9       CGTGCAAGCTCCAATATGAT       TGCCACTGTATAGCAGCGTA       54       184       0.9       4       0       2       1         SEM400       SCEZSD1081A02.g       (ccg)8       CAGCTCATCCTGTCACCT       CTCCTTGCTCTTGTTGCT       59       225       0.9       8       5       1       0         SEM401       SCEZSD1081A02.g       (ccg)8       CCTGCATCACTCTCTCCTC       TTCGATCGATGGTTGA       53       111       0.4       10       1       2       0         SEM403       SCEQSD2077B12.g       (cg)8       CCTGCATCAACCTCACC       GAAGCGAGAGAGAGAGAGAGAGAGTGG       55       242       0.7       6       2       1       1         SEM408       SCJFST1048G04.g       (ga)9       CAGAGCGAGCAGAGAGAGAG       TCATCGTGTGCTGCTGGT       58       228       0       6       2       1       1         SEM419       SCJFST1068E06.g       (gc)8       TCAGCGGGTGCTTGGGTGCTGCTGGT       58       246       0.9       14       3       1       1       5         SEM419       SCSFST1068E06.g       (gc)8       TGCGCGGGTGCTCAG       AGGGTGATGAAGGGAATGGAGGG       59       170       0.9       6       1       3       0       5       5242	SEM392	SCUTSB1075H09.g	(ta)8	TCATGCTCACCAGCAAAGAC	TCCCGATCAGTGTGTAGACG	55	234	0.8	3	1	0	2
SEM400       SCEZSD1081A02.g       (ccg)8       CAGCTCATCCTCGTCAACCT       CTCCTCTGCTCCTTGTTGCT       59       225       0.9       8       5       1       0         SEM401       SCMCSD1059G09.g       (ct)9       GCTCCATTCATTTCCTCCTC       TTCGATCGATGATGGTGAA       53       111       0.4       10       1       2       0         SEM403       SCEQSD2077B12.g       (cga)8       CCTGCATCAACCTCTCCAC       GAAGGCGAGAGAGAGTCG       55       242       0.7       6       2       1       3         SEM402       SCLIST102C09.g       (ck)8(ga)7       CAAGGCTCTTCTGGTGCT       58       286       0.9       14       3       1         SEM412       SCLIST102C09.g       (ck)8(ga)7       CAAGGCTGCTTCTGGTGC       CCTCTTTGGTCTCCTC       58       246       0.9       14       3       1         SEM413       SCIST1050H06.g       (tc)8       CAGCAGACGAGAGAGAGA       AGGGTGATGAGGGAATGAG       56       163       0.9       4       2       1       0         SEM412       SCSIST1050H06.g       (gc)8       TGGCGGGTGTTGATTGAAGAAG       AGAGGTGGTGAGAGGGAATGAGG       59       170       0.9       6       1       3       0         SEM422       SCSGST1072B03.g       (gg)8 </td <td>SEM398</td> <td>SCEPSD1006D03.g</td> <td>(ta)9</td> <td>CGTGCAAGCTCCAATATGAT</td> <td>TGCCACTGTATAGCAGCGTA</td> <td>54</td> <td>184</td> <td>0.9</td> <td>4</td> <td>0</td> <td>2</td> <td>1</td>	SEM398	SCEPSD1006D03.g	(ta)9	CGTGCAAGCTCCAATATGAT	TGCCACTGTATAGCAGCGTA	54	184	0.9	4	0	2	1
SEM401       SCMCSD1059G0.g       (c19)       GCTCCATTCATTTCCTCCTC       TTCGATCGATGATGATGGTTGA       53       111       0.4       10       1       2       0         SEM403       SCEQSD2077B12.g       (cga)8       CCTGCATCAACCTCTCCAC       GAAGGCGAGAGAGAAGATCG       55       242       0.7       6       2       1       3         SEM403       SCLFST1048G04.g       (ga)9       CAGAGCCAGCCAGGTAAAAG       TCATCGTGTGCTGCTGCT       58       228       0       6       2       1       1         SEM403       SCLFST1048G04.g       (ga)9       CAGAGCCAGCAGAGAGAAGA       CACTCTTCGGTGCTC       58       246       0.9       14       3       1         SEM419       SCJLST1050060.g       (tc)8       CAGCAGAGAGAGAGAGA       AGGGTGATGAAGGAATGAGGGA       56       163       0.9       4       2       1       0         SEM419       SCSFST106606.g       (gcc)8       TGCGTGGTTCATTGAGGAGAG       AGGAGCGCGTCTCTGGTGTGCTGC       59       170       0.9       6       1       3       0         SEM421       SCSGST1072B03.g       (ag)8       GAAGAGTGGGGACGTCTCAG       GCCAGAGGAGATGTGGTAGAGG       59       199       0.9       8       3       2       1         SEM422 <td>SEM400</td> <td>SCEZSD1081A02.g</td> <td>(ccg)8</td> <td>CAGCTCATCCTCGTCAACCT</td> <td>CTCCTCTGCTCCTTGTTGCT</td> <td>59</td> <td>225</td> <td>0.9</td> <td>8</td> <td>5</td> <td>1</td> <td>0</td>	SEM400	SCEZSD1081A02.g	(ccg)8	CAGCTCATCCTCGTCAACCT	CTCCTCTGCTCCTTGTTGCT	59	225	0.9	8	5	1	0
SEH403       SCEQSD2077B12.g       (cga)8       CCTGCATCAACCTCTCCAC       GAAGGCGAGAGAGAGATCG       55       242       0.7       6       2       1       3         SEM408       SCJFST1048G04.g       (ga)9       CAGAGCCAGCCAGGCAGGTAAAAG       TCATCGTGTGCTCGCTG       58       228       0       6       2       1       1         SEM412       SCJLST1022C09.g       (ct)8(ga)7       CAGCAGCGAGACGAGAGAG       AGGGTGATGAGAGGGAATGAG       56       163       0.9       4       2       1       0         SEM413       SCMCST1050H06.g       (tp)8       CAGCAGCGAGACGAGAGAGA       AGGGTGATGAGAGAGAG       56       163       0.9       4       2       1       0         SEM413       SCSFST1069F04.g       (gga)5(ctb)8       CACCCTGCTCCTC       TCGACGTCGTGTGGTGAGAGG       59       170       0.9       6       1       3       0         SEM421       SCSGST1069F04.g       (gga)5(ctb)8       CACCCTGCTCATC       TCGACGTGGTGAGAGGGAGAGG       59       170       0.9       6       1       3       0         SEM422       SCSGST1072B03.g       (ag)8       GAAGAGTGGGGACGTCTCAG       GCCAGAGGAGTGTGAGAG       59       170       0.9       8       3       2       1       1	SEM401	SCMCSD1059G09.g	(ct)9	GCTCCATTCATTTCCTCCTC	TTCGATCGATTGATGGTTGA	53	111	0.4	10	1	2	0
SEM408       SCJFST1048G04.g       (ga)9       CAGAGCCAGCCAGGTAAAAG       TCATCGTGTGCTGCTGGT       58       228       0       6       2       1       1         SEM412       SCJLST1022C09.g       (ct)8(ga)7       CAAGGCTGCTTCTGGTGC       CCTCTTTGGGTTCTCGCTC       58       246       0.9       14       3       1       1         SEM415       SCMCST1050H06.g       (tc)8       CAGCAGACGAGAGAGAG       AGGGTGATGAAGGGAATGAG       56       163       0.9       4       2       1       0         SEM419       SCSFST1066E06.g       (gcc)8       TGCGTGGTGCTCCTC       TCGACGTGGTGATGAAGGGAACG       59       170       0.9       6       1       3       0         SEM421       SCSGST1069F04.g       (gga)8       GAAGAGTGGGGACGTCCCAG       GCCAGAGGAGTGTGGTGAAGGG       59       199       0.9       8       3       2       1         SEM422       SCSGST1072B03.g       (ag)8       GAAGAGTGGGGACGTCCCAG       GCCAGAGGAGTGGTGAAGAG       56       441       0.6       10       1       4       0       SEM426       SCVPAN1059C01.g       (at)5       TCCGACACGAGGAATTATTTTCCTGTCAGCCAAGTGA       56       244       0.6       10       1       1       1       1       1       1 <t< td=""><td>SEM403</td><td>SCEQSD2077B12.g</td><td>(cga)8</td><td>CCTGCATCAACCTCTCCAC</td><td>GAAGGCGAGAGAGAAGATCG</td><td>55</td><td>242</td><td>0.7</td><td>6</td><td>2</td><td>1</td><td>3</td></t<>	SEM403	SCEQSD2077B12.g	(cga)8	CCTGCATCAACCTCTCCAC	GAAGGCGAGAGAGAAGATCG	55	242	0.7	6	2	1	3
SEM412       SCJLST1022C09.g       (ct)8(ga)7       CAAGGCTGCTTCTGGTGC       CCTCTTTGGGTTCTCGCTC       58       246       0.9       14       3       1       1         SEM412       SCMCST1050H06.g       (tc)8       CAGCAGACGAGAGAG       AGGGTGATGAAGGGAATGAG       56       163       0.9       4       2       1       0         SEM419       SCSFST1066E06.g       (gc)8       TGCGTGGTTGATTGAAGAAG       AGAAGCCTCTTCTGCTGCTG       60       199       0.9       11       2       3       1         SEM421       SCSGST1069F04.g       (gga)5(ctc)8       CACCCTGCTGGTCTCCC       TCGCACGAGGAGTGGTAGGAGGG       59       170       0.9       6       1       3       0         SEM422       SCSGST1072B03.g       (gg)8       GAAGAGTGGGGACGTCTCAG       GCCAGAGGATGGTAGAGG       59       199       0.9       8       3       2       1         SEM425       SCSFAD1070E12.g       (gcc)5       GTGCACCAGCAGCAGTATCTTTT       CTTCTGTGCTGCAGCTGAG       56       471       0.8       13       2       3       1         SEM425       SCSFAD1070E12.g       (qc)6       AGGAGCGGTTTCATCTTT       CTTTCTGTGCAGCAAGTGG       57       77       0.9       7       1       1       1       1	SEM408	SCJFST1048G04.g	(ga)9	CAGAGCCAGCCAGGTAAAAG	TCATCGTGTGCTGCTGGT	58	228	0	6	2	1	1
SEM415       SCMCST1050H06.g       (tc)8       CAGCAGACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	SEM412	SCJLST1022C09.g	(ct)8(ga)7	CAAGGCTGCTTCTGGTGTC	CCTCTTTGGGTTCTCTGCTC	58	246	0.9	14	3	1	1
SEM419       SCSFST1066E06.g       (gcc)8       TGCGTGGTTGATGAAGAAG       AGAAGCCTCTTCTGCTGCTG       60       199       0.9       11       2       3       1         SEM421       SCSGST1069F04.g       (gga)5(ctc)8       CACCCTGCTGGTCTCCTC       TCGACGTCGTGAGTGAACC       59       170       0.9       6       1       3       0         SEM422       SCSGST1072B03.g       (ag)8       GAAGAGTGGGGACGTCTCAG       GCCAGAGGATGTGGTAGAGG       59       199       0.9       8       3       2       1         SEM425       SCSGST1072B03.g       (ag)8       GAAGAGTGGGGACGTCTCAG       GCCAGAGGATGTGGTAGAGGG       59       199       0.9       8       3       2       1         SEM425       SCSFAD1070E12.g       (gcc)5       GTGCCACCAGCAGCAAT       TCTCGTAGCTGACTGCACAGTGG       56       471       0.8       13       2       3       1         SEM426       SCVPAM1059C01.g       (at)5       TCGAGAGCGGATTAGTTCA       CCAAGTCCTCACCAGCAGCAAG       56       471       0.8       13       2       3       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1	SEM415	SCMCST1050H06.g	(tc)8	CAGCAGACGAGACGAGAGAG	AGGGTGATGAAGGGAATGAG	56	163	0.9	4	2	1	0
SEM421       SCSGST1069F04.g       (gga)5(ctc)8       CACCCTGCTGGTCTCCTC       TCGACGTCGTGTAGTGAACC       59       170       0.9       6       1       3       0         SEM422       SCSGST1072B03.g       (ag)8       GAAGAGTGGGGACGTCTCAG       GCCAGAGGATGTGGTAGAGGG       59       199       0.9       8       3       2       1         SEM425       SCSGAD1070E12.g       (gcc)5       GTGCCACCAGCAGCAAT       TCTCGTAGCTGCTCGACTTC       56       244       0.6       10       1       4       0         SEM426       SCVPAM1059C01.g       (at)5       TCGAGAGCGGTTCATCTTT       CTTTCCTGTCAGCCAAGTGA       56       471       0.8       13       2       3       1         SEM426       SCVPAM1059C01.g       (at)5       TCGAGAGCGGATTAGTTCA       CTTTCCTGTCAGCCAGTAGT       57       277       0.9       7       1       1       1         SEM427       SCSBFL1105H11.b       (cag)6       AAGTAGCGGAAGCATTAGTTCA       CCAAGTTCCTCCTCACCAGTAG       57       277       0.9       7       1<	SEM419	SCSFST1066E06.g	(gcc)8	TGCGTGGTTGATTGAAGAAG	AGAAGCCTCTTCTGCTGCTG	60	199	0.9	11	2	3	1
SEM422       SCSGST1072B03.g       (ag)8       GAAGAGTGGGGGACGTCTCAG       GCCAGAGGATGTGGTAGAGG       59       199       0.9       8       3       2       1         SEM425       SCSFAD1070E12.g       (gcc)5       GTGCCACCAGCAGCAAT       TCTCGTAGCTGCTCGACTTC       56       244       0.6       10       1       4       0         SEM426       SCVPAM1059C01.g       (at)5       TCGAGAGCGGTTCATCTTT       CTTTCCTGTCAGCCAAGTGA       56       471       0.8       13       2       3       1         SEM426       SCVPAM1059C01.g       (at)5       TCGAGAGCGGATTCATCTTT       CTTTCCTGTCAGCCAAGTGA       56       471       0.8       13       2       3       1         SEM427       SCSBFL1105H11.b       (ca)6       AAGTAGCGGAAGCATTAGTTCA       CCAAGTTCCTCACCACAGTA       57       277       0.9       7       1       1       1         SEM430       SCRUSB1064F09.g       (cgg)5       TCCGACTACCTCAAGTGAGGAG       GACGGCATCTTCTTCTTCTCTC       55       224       0.1       7       1       0       1         SEM433       SCSBT3094H07.g       (gc)6       CGCGTCCCTAAGATTAGTAGCTC       AGGAGATCCTGGACACACATGG       54       245       0.9       5       1       1       0	SEM421	SCSGST1069F04.g	(gga)5(ctc)8	CACCCTGCTGGTCTCCTC	TCGACGTCGTGTAGTGAACC	59	170	0.9	6	1	3	0
SEM425SCSFAD1070E12.g(gc)5GTGCCACCAGCAGCAGCAGCAGTTCTCGTAGCTGCTCGACTTC562440.610140SEM426SCVPAM1059C01.g(at)5TCGAGAGCGGTTTCATCTTTCTTTCCTGTCAGCCAAGTGA564710.813231SEM427SCSBFL1105H11.b(ca)6AAGTAGCGGAAGCATTAGTTCACCAAGTTCCTCCTCACCAGTA572770.97111SEM430SCRUSB1064F09.g(cgg)5TCCGACTACCTCAAGTGCAAGGACGGCATCTTCTTCTTCC552240.17101SEM432SCJLST1019B07.g(gc)6CGCGTCCGTAGATTAGTAGCTCAGCGAGAGCAGTAGATGTTGATGACCC561950.311221SEM433SCSBST3094H07.g(cga)6GACACGCCCAAAGGAAAAGGAGATCCGGACACACATGG542450.95110SEM434SCEZLB1007E12.g(ta)7TTCTTGCTTCTTTCTTCCGTCTCAAATCGTGCTTGCTTGAGG522360.89012SEM435SCQGLR1041A05.g(ga)5AGGCTGAGAGAGCAAAGAAAGACCTAGGATCCTTCGGGTTTC551640.99213SEM436SCJLRT1021D04.g(tc)5GGTCCCATACATAACACAAGCATGCATGAAGAAGCTCAGGTG572480.78510SEM437SCOSBT2031C10.q(tc)5GGTCCCATACATAACACACAAGCATGCATGAAGAAGCTCAGGTG572480.78510SEM437SCOSBT2031C10.q(tc)5 <td< td=""><td>SEM422</td><td>SCSGST1072B03.g</td><td>(ag)8</td><td>GAAGAGTGGGGACGTCTCAG</td><td>GCCAGAGGATGTGGTAGAGG</td><td>59</td><td>199</td><td>0.9</td><td>8</td><td>3</td><td>2</td><td>1</td></td<>	SEM422	SCSGST1072B03.g	(ag)8	GAAGAGTGGGGACGTCTCAG	GCCAGAGGATGTGGTAGAGG	59	199	0.9	8	3	2	1
SEM426SCVPAM1059C01.g(at)5TCGAGAGCGGTTTCATCTTTCTTTCCTGTCAGCCAAGTGA564710.813231SEM427SCSBFL1105H11.b(ca)6AAGTAGCGGAAGCATTAGTTCACCAAGTTCCTCCTCACCAGTA572770.97111SEM430SCRUSB1064F09.g(cgg)5TCCGACTACCTCAAGTGCAAGGACGGCATCTTCTTCTTCTCC552240.17101SEM432SCJLST1019B07.g(gc)6CGCGTCCGTAGATTAGTAGCTCAGCGAGTAGATGTTGATGACCC561950.311221SEM433SCSBST3094H07.g(cga)6GACACGCCCAAAGGAAAAGGAGATCCGGACACACATGG542450.95110SEM434SCEZLB1007E12.g(ta)7TTCTTGCTTCTTTCTTTCCGTCTCAAATCGTGCTTGCTTGAG522360.89012SEM435SCQGLR1041A05.g(ga)5AGGCTGAGAGAGAGAAAGAACCTAGGATCCTTCGGGTTTC551640.99213SEM436SCJLRT1021D04.g(tc)5GGTCCCATACATAACACAAGCATGCATGAAGAAGCTCAGGTG572480.78510SEM437SCOSRT2031C10.g(tc)5CCIGGTICCTGCACTIGICTCATCACTIGCCATCIGCATT572170.814701	SEM425	SCSFAD1070E12.g	(gcc)5	GTGCCACCAGCAGCAAT	TCTCGTAGCTGCTCGACTTC	56	244	0.6	10	1	4	0
SEM427SCSBFL1105H11.b(ca)6AAGTAGCGGAAGCATTAGTTCACCAAGTTCCTCCTCACCAGTA572770.97111SEM430SCRUSB1064F09.g(cgg)5TCCGACTACCTCAAGTGCAAGGACGGCATCTTCTTCTTCTCC552240.17101SEM432SCJLST1019B07.g(gc)6CGCGTCCGTAGATTAGTAGTCCAGCGAGTAGATGTTGATGACCC561950.311221SEM433SCSBST3094H07.g(cga)6GACACGCCCAAAGGAAAAGGAGATCCGGACACACATGG542450.95110SEM434SCEZLB1007E12.g(ta)7TTCTTGCTTCTTTCTTTCCGTCTCAAATCGTGCTTGCTTGAG522360.89012SEM435SCQGLR1041A05.g(ga)5AGGCTGAGAGAGGAAAAGAACCTAGGATCCTTCGGGTTTC551640.99213SEM436SCJLRT1021D04.g(tc)5GGTCCCATACATAACACAAGCATGCATGAAGAAGCTCAGGTG572480.78510SEM437SCOSBT2031C10.g(tc)5CCTGGTTCCTGCACTTGTCTCATCACTTGCCATT572170.814701	SEM426	SCVPAM1059C01.g	(at)5	TCGAGAGCGGTTTCATCTTT	CTTTCCTGTCAGCCAAGTGA	56	471	0.8	13	2	3	1
SEM430SCRUSB1064F09.g(cgg)5TCCGACTACCTCAAGTGCAAGGACGGCATCTTCTTCTTCTC552240.17101SEM432SCJLST1019B07.g(gc)6CGCGTCCGTAGATTAGTAGCTCAGCGAGTAGATGTGAGACC561950.311221SEM433SCSBST3094H07.g(cga)6GACACGCCCAAAGGAAAAGGAGATCCGGACACACATGG542450.95110SEM434SCEZLB1007E12.g(ta)7TTCTTGCTTCTTTCTTCCGTCTCAAATCGTGCTTGCTGAG522360.89012SEM435SCQGLR1041A05.g(ga)5AGGCTGAGAGAGAGAAAGAACCTAGGATCCTTCGGGTTTC551640.99213SEM436SCJLRT1021D04.g(tc)5GGTCCCATACATAACACAAGCATGCATGAAGAAGCTCAGGTG572480.78510SEM437SCOSBT2031C10.g(tc)5CCTGGTTCCTGCACTTGTCTCATCACTTGCCATTGCATT572170.814701	SEM427	SCSBFL1105H11.b	(ca)6	AAGTAGCGGAAGCATTAGTTCA	CCAAGTTCCTCCTCACCAGTA	57	277	0.9	7	1	1	1
SEM432SCJLST1019B07.g(gc)6CGCGTCCGTAGATTAGTAGTAGTCCAGCGAGTAGATGTTGATGACCC561950.311221SEM433SCSBST3094H07.g(cga)6GACACGCCCAAAGGAAAAGGAGATCCGGACACACTGG542450.95110SEM434SCEZLB1007E12.g(ta)7TTCTTGCTTCTTTCTTTCCGTCTCAAATCGTGCTTGCTGAGG522360.89012SEM435SCQGLR1041A05.g(ga)5AGGCTGAGAGAGAGAAAGAACCTAGGATCCTTCGGGTTTC551640.99213SEM436SCJLRT1021D04.g(tc)5GGTCCCATACATAACACAAGCATGCATGAAGAAGCTCAGGTG572480.78510SEM437SCOSBT2031C10.g(tc)5CCTGGTTCCTGCACTTGTCTCATCACTTGCCATCTGCATT572170.814701	SEM430	SCRUSB1064F09.g	(cqq)5	TCCGACTACCTCAAGTGCAAG	GACGGCATCTTCTTCTTCTCC	55	224	0.1	7	1	0	1
SEM433SCSBST3094H07.g(cga)6GACACGCCCAAAGGAAAAGGAGATCCGGACACACATGG542450.95110SEM434SCEZLB1007E12.g(ta)7TTCTTGCTTCTTTCCGTCTCAAATCGTGCTTGCTTGAG522360.89012SEM435SCQGLR1041A05.g(ga)5AGGCTGAGAGAGAGAGAGAAAGACCTAGGATCCTTCGGGTTTC551640.99213SEM436SCJLRT1021D04.g(tc)5GGTCCCATACATAACACAAGCATGCATGAAGAAGCTCAGGTG572480.78510SEM437SCOSBT2031C10 g(tc)5CCTGGTTCCTGCACTTGTCTCATCACTTGCCATTGCATT572170.814701	SEM432	SCJLST1019B07.a	(ac)6	CGCGTCCGTAGATTAGTAGCTC	AGCGAGTAGATGTTGATGACCC	56	195	0.3	11	2	2	1
SEM434SCEZLB1007E12.g(ta)7TTCTTGCTTCTTTCCGTCTCAAATCGTGCTTGCTTGAG522360.89012SEM435SCQGLR1041A05.g(ga)5AGGCTGAGAGAGAGAAAGAAAGACCTAGGATCCTTCGGGTTTC551640.99213SEM436SCJLRT1021D04.g(tc)5GGTCCCATACATAACACAAGCATGCATGAAGAAGCTCAGGTG572480.78510SEM437SCOSBT2031C10 q(tc)5CCTGGTTCCTGCACTTGTCTCATCACTTGCCATCTGCATT572170.814701	SEM433	SCSBST3094H07.g	(cqa)6	GACACGCCCAAAGGAAAAG	GAGATCCGGACACACATGG	54	245	0.9	5	1	1	0
SEM435SCQGLR1041A05.g(ga)5AGGCTGAGAGAGAGAGAGAAGAAAGACCTAGGATCCTTCGGGTTTC551640.99213SEM436SCJLRT1021D04.g(tcc)5GGTCCCATACATAACACAAGCATGCATGAAGAAGCTCAGGTG572480.78510SEM437SCOSRT2031C10 g(tc)5CCTGGTTCCTGCACTTGTCTCATCACTTGCCATTGCATT572170.814701	SEM434	SCEZLB1007E12.a	(ta)7	TTCTTGCTTCTTTCTTTCCGTC	TCAAATCGTGCTTGCTTGAG	52	236	0.8	9	0	1	2
SEM436 SCJLRT1021D04.g (tcc)5 GGTCCCATACATAACACAAGCA TGCATGAAGAAGCTCAGGTG 57 248 0.7 8 5 1 0 SEM437 SCOSRT2031C10 g (tc)5 CCTGGTTCCTGCACTTGTCT CATCACTTGCCATCTGCCATT 57 217 0.8 14 7 0 1	SEM435	SCQGLR1041A05.a	(ga)5	AGGCTGAGAGAGCAAAGAAAGA	CCTAGGATCCTTCGGGTTTC	55	164	0.9	9	2	1	3
SEM437 SCOSRT2031C10 g (tc)5 CCTGGTTCCTGCACTTGTCT CATCACTTGCCATCTGCATT 57 217 0.8 14 7 0 1	SEM436	SCJLRT1021D04.a	(tcc)5	GGTCCCATACATAACACAAGCA	TGCATGAAGAAGCTCAGGTG	57	248	0.7	8	5	1	0
	SEM437	SCQSRT2031C10.g	(tc)5	CCTGGTTCCTGCACTTGTCT	CATCACTTGCCATCTGCATT	57	217	0.8	14	7	0	1

SEM439	SCACSB1117C07.g	(cgg)6	CGTCAAGCTGTAGTCCGAGAG	CTCGTCCCAGACCAGGAG	59	197	0.2	5	0	3	2
SEM440	SCACSD1018E05.g	(gac)5	AGCAACCTAATCACAGCAACAA	CCATCATCCGATCATCCTTC	56	229	0.5	12	0	2	3
SEM442	SCMCST1057C10.g	(gct)5	CATTTATTTGCCACCTAGAAGGG	AAACAGAAACCGGACAGCAC	56	195	0.9	10	2	2	1
SEM443	SCRLAD1043B06.g	(ggt)7	GGAATGGGAACAGCCACTAAC	AAGAAGGCTATCGAGGTGGG	55	323	0.3	12	1	3	3
SEM444	SCBGAD1027C03.g	(ggc)7	CACGGTTCTCCTGCTGAAAG	GACGGGGTTGTTGAAGGTG	55	313	0.8	13	1	3	2
SEM446	SCCCCL3001D10.b	(ccg)5	GAGCAGTCCCTTGCCATGT	GCCGTCGAGTACACCGTC	59	389	0.9	11	0	1	0
SEM447	SCEZFL5083C02.g	(gc)5	TGAGTTCAGTTCCTTCCCC	AGAACTCCAAGGAGCAGCAG	56	300	0.4	3	1	0	1
SEM449	SCEZLB1006B07.g	(gcc)5	TGGTGTGAGTTAGTGCCTGAGT	TAGAAGGTGTTGATGATGAGCG	55	265	0.9	17	2	2	2
SEM450	SCEZLB1007E12.g	(ta)7	TTCTTGCTTCTTTCTTTCCGTC	AGATGAACACATAGTTGCACCG	56	189	0.4	4	0	0	2
SEM453	SCBFRZ2045E11.g	(ggc)5	AGCGACATGAGCTACCGTCT	TAGTACCGCGACAGACCTTTCT	58	287	0.9	5	0	0	1
SEM454	SCSBRZ3122D09.g	(gga)6	GTAACTAGCAGCAACCCTAGCC	ATCCTCTTTTGCCTCCCCT	55	387	0.8	2	0	1	1
SEM456	AY302083	(tgc)6	TCGTCCTACAACCACGACTACA	GAGAGGCAAGCAAGGAAAGAT	56	164	0.4	5	1	1	0
SEST3	SCSFSB1097B02.g	(ta)8	CCCCGAAGATCAAGGATAGG	CGCATCTCAAATGGGAAAAT	56	413	0.5	5	0	3	1
SEST4	SCRLAD1040D08.g	(at)5	CAGGCACTGATGTCATGGAT	GAACTACACTCGCCGCTCAC	56	313	0.7	19	0	6	3