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(54) **GENES ASSOCIATED TO SUCROSE CONTENT**

(75) Inventors: **GlauCIA Mendes Souza**, Sao Paulo (BR); **Flavia Stal Papini-Terzi**, Sao Paulo (BR); **Flavia Riso Rocha**, Sao Paulo (BR); **Alessandro Jaquiel Wacławovsky**, Sao Paulo (BR); **Ricardo Zorzetto Nicollielo Vencio**, Sao Paulo (BR); **Josélia Oliveira Marques**, Sao Paulo (BR); **Juliana de Maria Felix**, Campinas (BR); **Marcelo Menossi Teixeira**, Campinas (BR); **Marcos Buckeridge**, Rua do Matao (BR); **Amanda Pereira de Souza**, Rua do Matao (BR); **Eugênio César Ulian**, Piracicaba (BR)

(73) Assignees: **Universidade de Sao Paulo - USP**, Sao Paulo (BR); **Universidade Estadual de Campinas - Unicamp.**, Sao Paulo (BR); **Fundacao de Amparo a Pesquisa do Estado de Sao Paulo - Fapesp.**, Sao Paulo (BR); **Centro de Tecnologia Canavieira**, Sao Paulo (BR); **Central de Alcool Lucelia Ltda.**, Sao Paulo (BR)

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(60) Provisional application No. 60/780,693, filed on Mar. 8, 2006, provisional application No. 60/861,496, filed on Nov. 27, 2006.

(51) **Int. Cl.**  
**A01H 5/00** (2006.01)  
**A01H 5/04** (2006.01)  
**A01H 5/10** (2006.01)  
**C12N 15/82** (2006.01)  
**C12N 15/00** (2006.01)

(52) **U.S. Cl.** ..... **800/285; 800/278; 800/295; 800/298; 435/320.1; 536/23.1**

(58) **Field of Classification Search** ..... None  
See application file for complete search history.

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*Primary Examiner*—Anne Marie Grunberg  
*Assistant Examiner*—Brent Page  
(74) *Attorney, Agent, or Firm*—Morrison & Foerster LLP

(57) **ABSTRACT**

Modern sugarcane cultivars are complex hybrids resulting from crosses among several species of the *Saccharum* genus. Traditional breeding methods have been extensively employed in different countries along the past decades to develop varieties with increased sucrose yield, and resistant to plagues and diseases. Conventional varietal improvement is, however, limited by the narrow pool of suitable markers. In this sense, molecular genetics is seen as a promising tool to assist in the process of molecular marker identification. The present invention concerns the identification of 348 genes associated with sucrose content in sugarcane plants. The genes were found to be differentially expressed when high sucrose and low sucrose plants and populations of plants were compared and/or when high and low sucrose internodes were compared. The expression data was obtained using cDNA microarray and quantitative PCR technologies. The genes identified can be used to identify, distinguish, characterize and/or develop plants with increased sucrose content. More preferably SEQ ID Nos: 1 to 203 should be useful as molecular markers. SEQ ID Nos: 204 to 228 are given as controls or examples of genes never associated with sucrose content. SEQ ID Nos. 1-203 and SEQ ID Nos. 229 to 373 can be targeted in the development of transgenic or non-transgenic varieties with increased sucrose content.

**2 Claims, 9 Drawing Sheets**

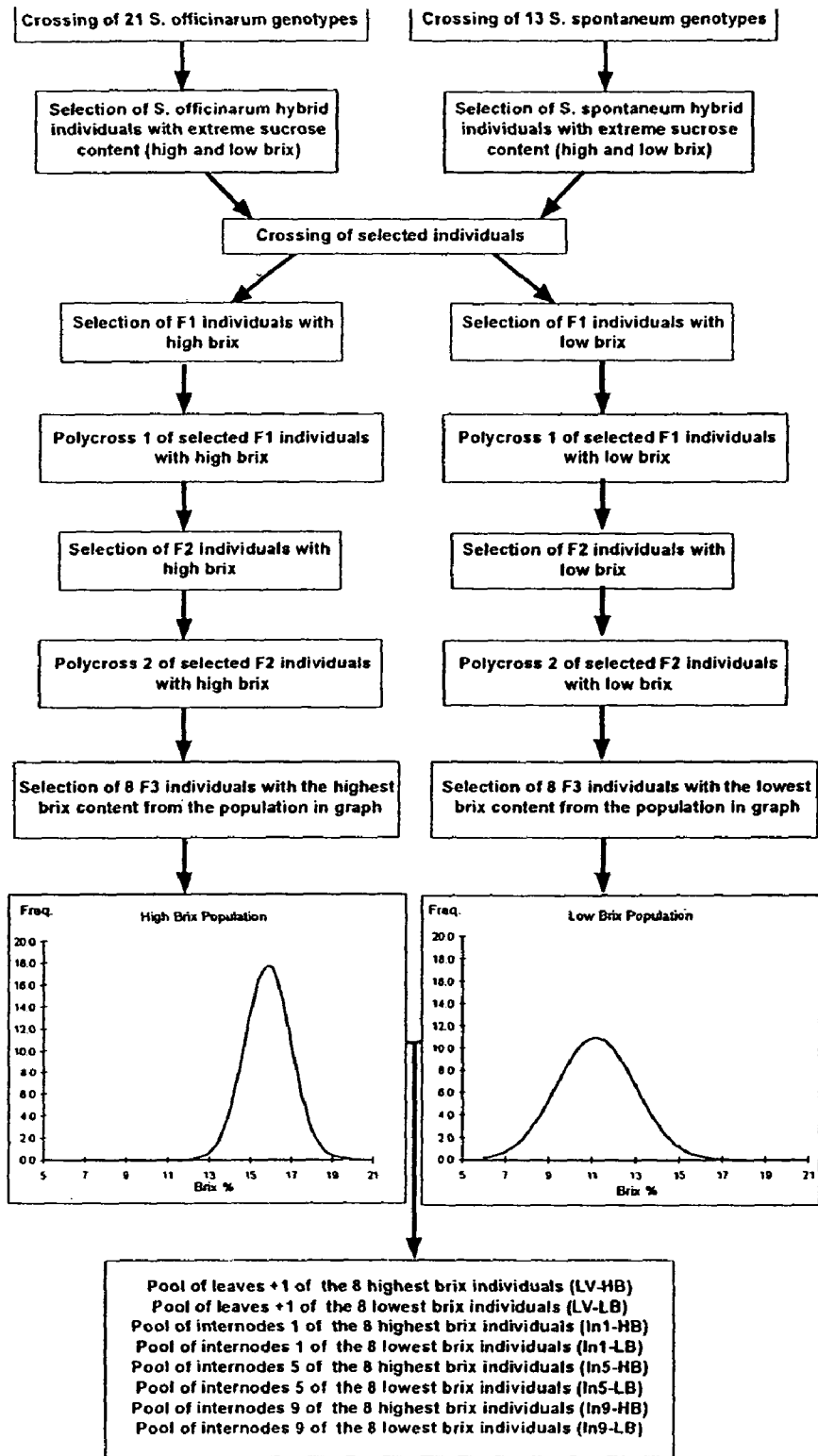
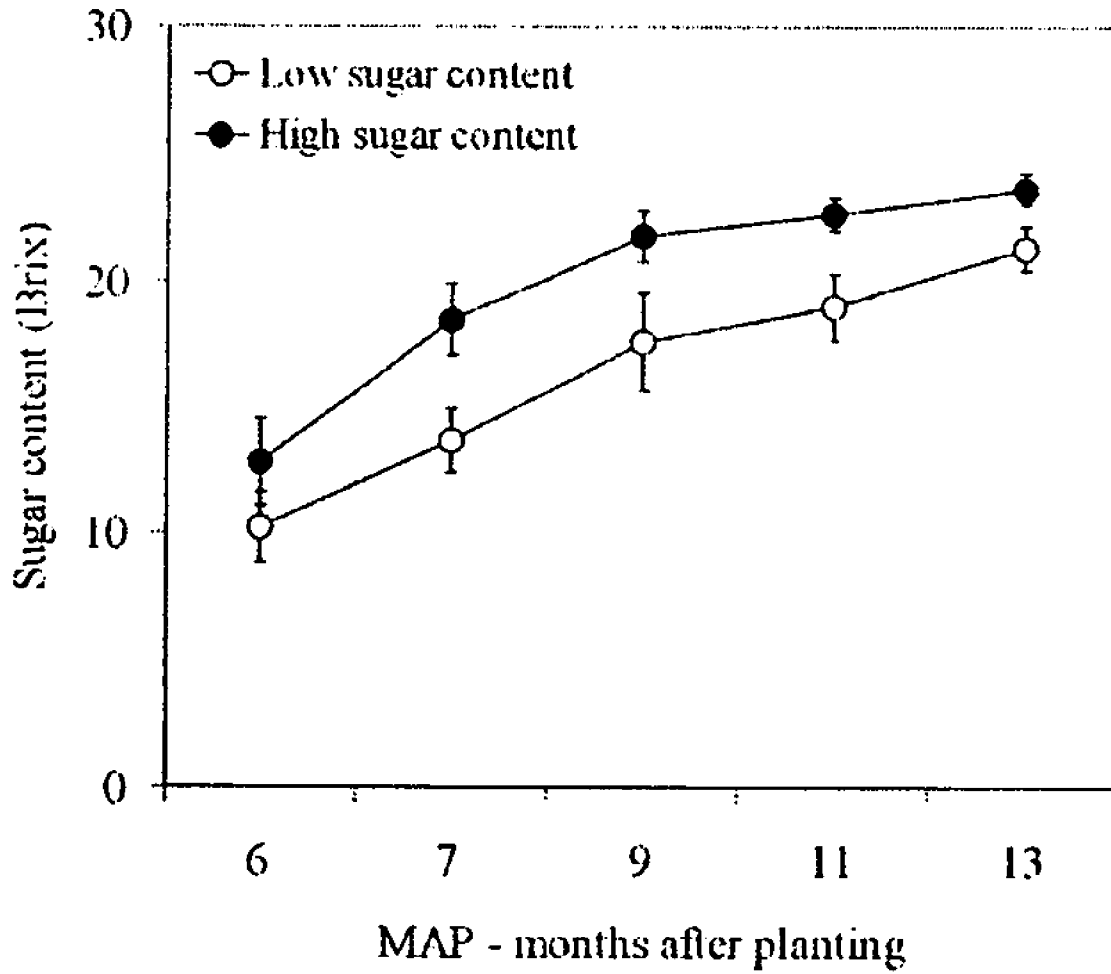


FIGURE 1



**FIGURE 2**

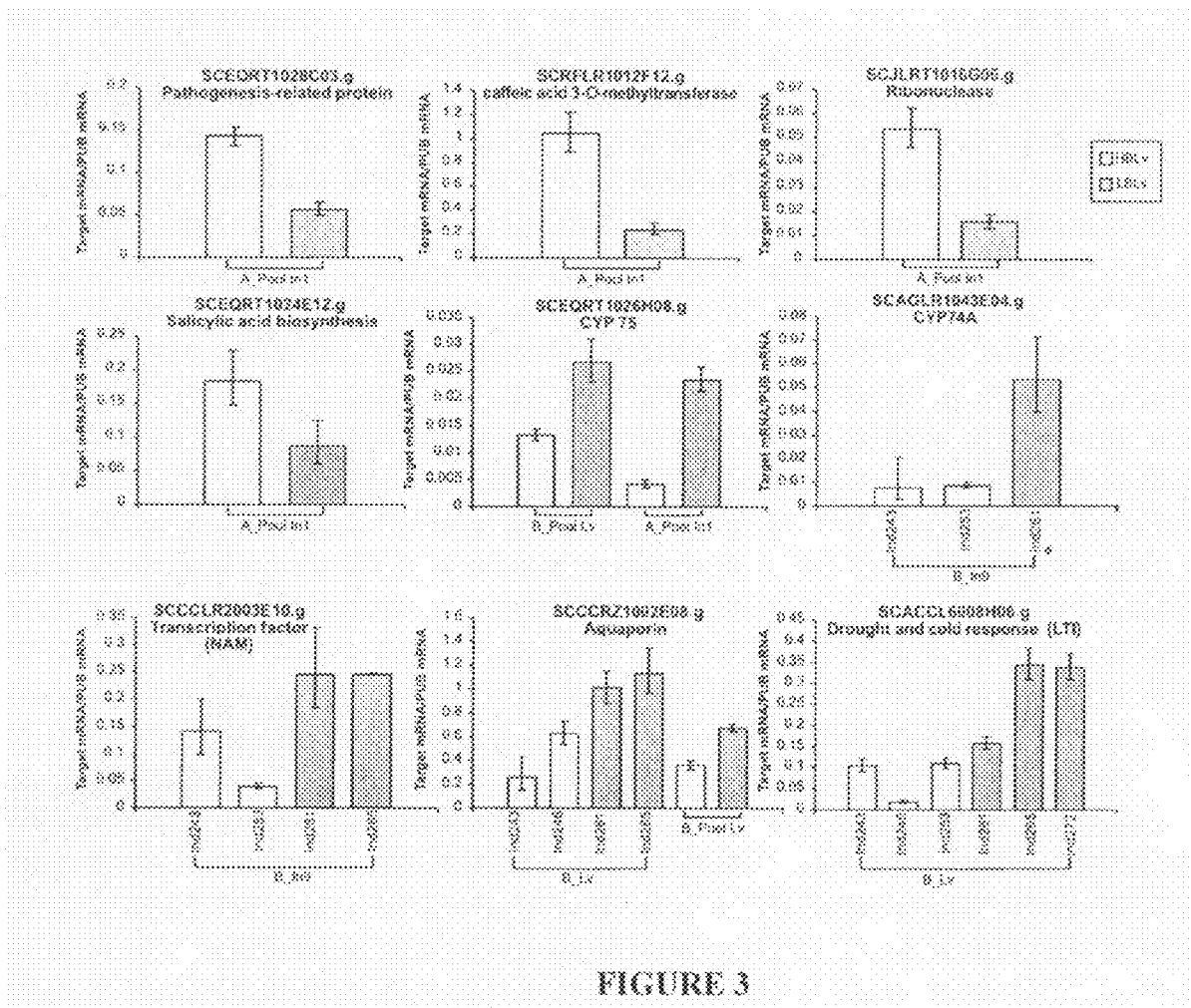


FIGURE 3

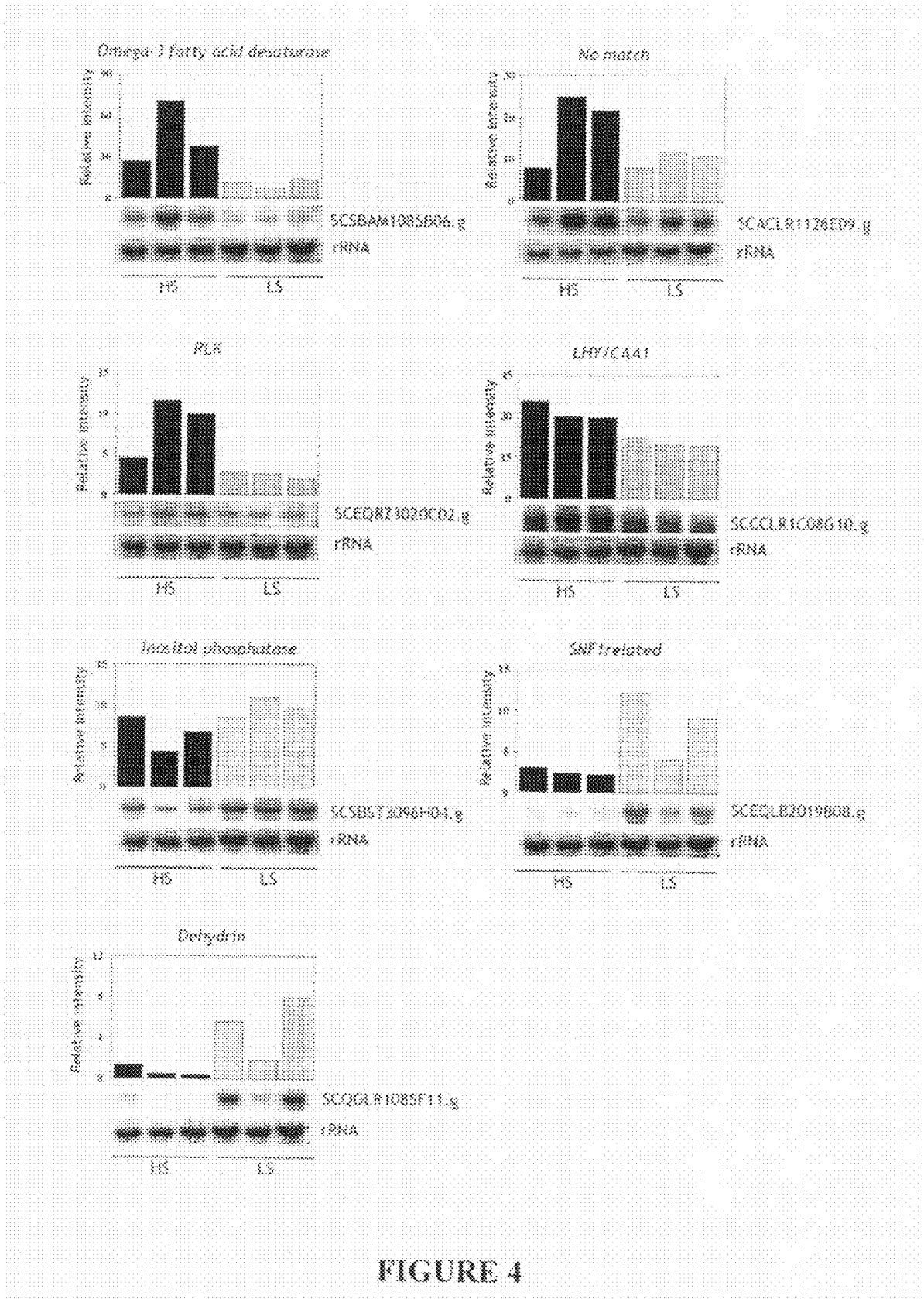


FIGURE 4

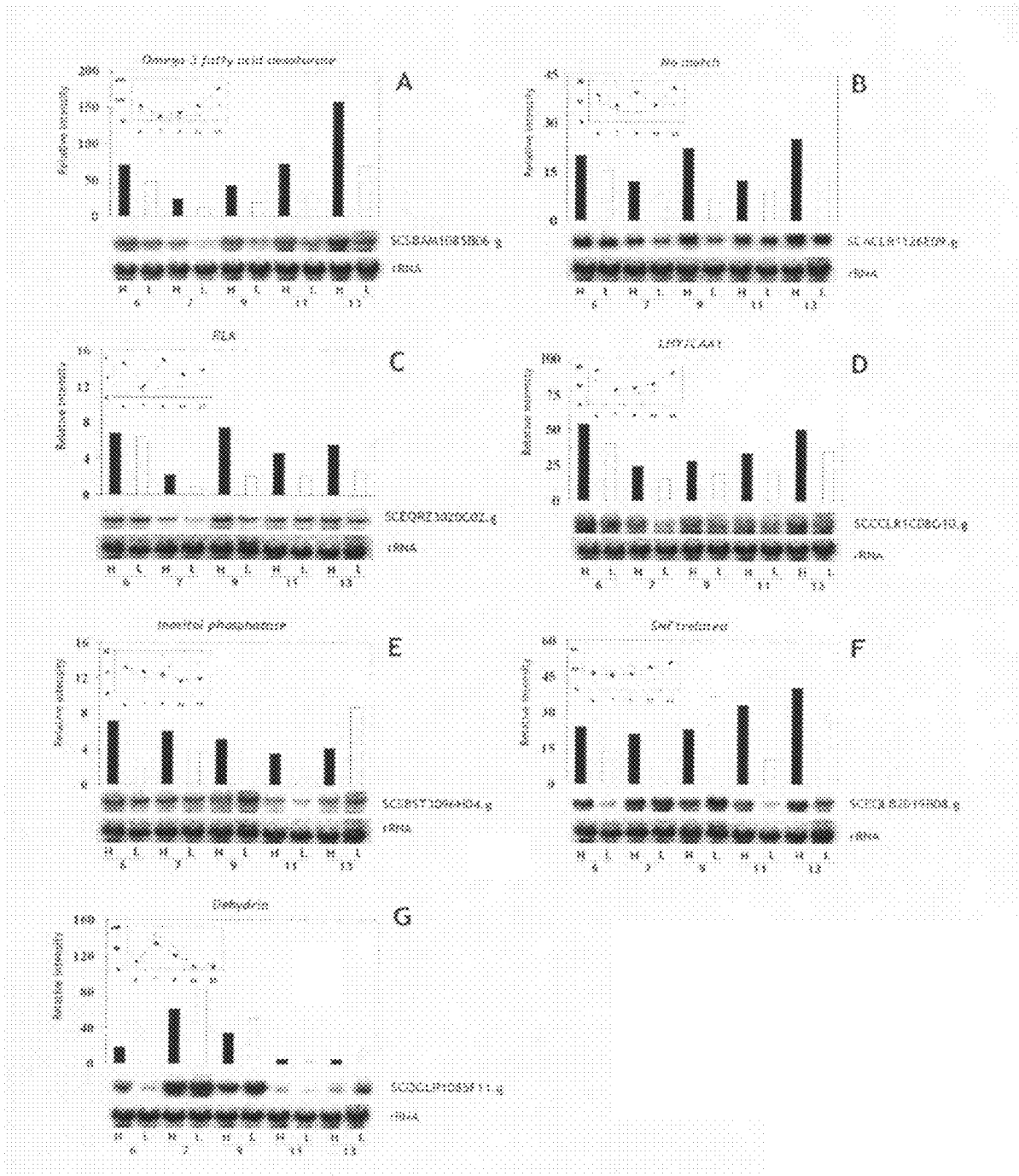


FIGURE 5

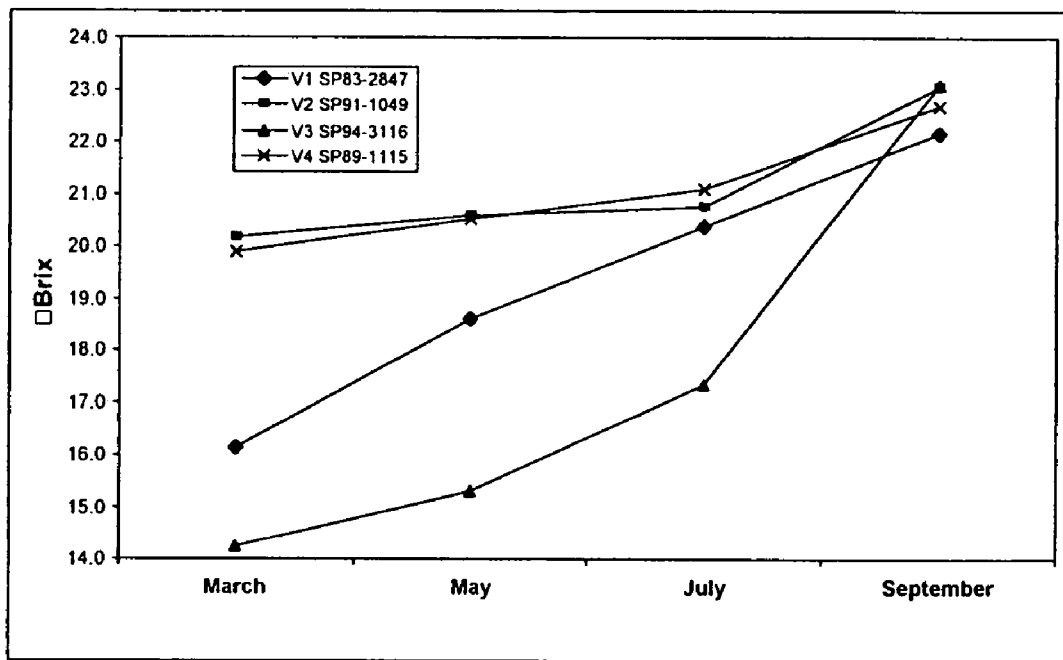


FIGURE 6

Sequence Alignment of SEQ ID No. 411: CIPK-8 (SCEQLB2019B08.g); SEQ ID No. 412: CIPK-29 (SCSGHR1070F12.g); and SEQ ID No. 413: CIPK-1 (SCCCCL5001D11.g) using CLUSTALW

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SCEQLB2019B08.g -----TTTCCAAGGACAGTGAACCACAGGACCGGAGGAGACTCCTGACATTCATTCCATTCGGTTCCAAAGGGGTGAG
SCSGHR1070F12.g -----TTCCAGTGCCTGACAGTGAACACAGGACCGGAGGAGACTCCTGACATTCATTCCATTCGGTTCCAAAGGGGTGAG
SCCCCL5001D11.g -----GGGAGCAGATTCAGCTTCTGACAGTGAACCATTGCTTCTCTAGATCTCCTGACCGCTTCT-----AAATGCAGTAAGGCA

SCEQLB2019B08.g GGAATGAGTACAACCAAGGTGAAGAGACGCTGTGGCAAGTATGAGCTCGGGCCGACCATAGGGGAGGGCACATTGGCAAAGGTCAGSTTC
SCSGHR1070F12.g GGAATGAGTACAACCAAGGTGAAGAGACGCTGTGGCAAGTATGAGCTCGGGCCGACCATAGGGGAGGGCACATTGGCAAAGGTCAGSTTC
SCCCCL5001D11.g GGAATGAGTACAACCAAGGTGAAGAGACGCTGTGGCAAGTATGAGCTCGGGGATAGCCATAGGCCAGGCACATTGGCAAAGGTCAGSTTC

SCEQLB2019B08.g CGGTGACCAGCGAGCCGTAGCCATCAAGATCCTAGATAAGGAGAAGTACTCAAGCACAGATGGTTGAGCAGATTAAGCGGGAAATGCT
SCSGHR1070F12.g CGGTGACCAGCGAGCCGTAGCCATCAAGATCCTAGATAAGGAGAAGTACTCAAGCACAGATGGTTGAGCAGATTAAGCGGGAAATGCT
SCCCCL5001D11.g CGGTGACCAGCGAGCCGTAGCCATCAAGATCCTAGATAAGGAGAAGTACTCAAGCACAGATGGTTGAGCAGATTAAGCGGGAAATGCT

SCEQLB2019B08.g GTTGAATGAGCACCCTAATGTTGTCGGCATATGAGGTGATGGCAAGTAAACAAAATACATTGTTGCTGCTTACTGGTGGCGAGCTTT
SCSGHR1070F12.g GTTGAATGAGCACCCTAATGTTGTCGGCATATGAGGTGATGGCAAGTAAACAAAATACATTGTTGCTGCTTACTGGTGGCGAGCTTT
SCCCCL5001D11.g GTTGAATGAGCACCCTAATGTTGTCGGCATATGAGGTGATGGCAAGTAAACAAAATACATTGTTGCTGCTTACTGGTGGCGAGCTTT
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FIGURE 7



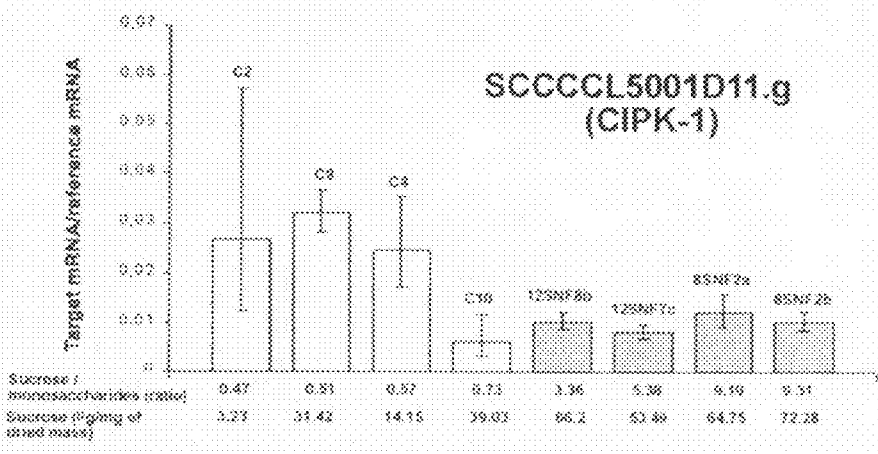
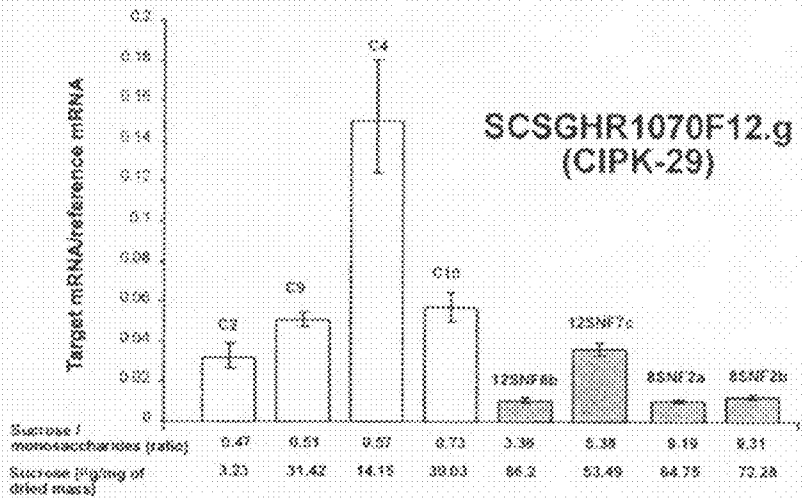
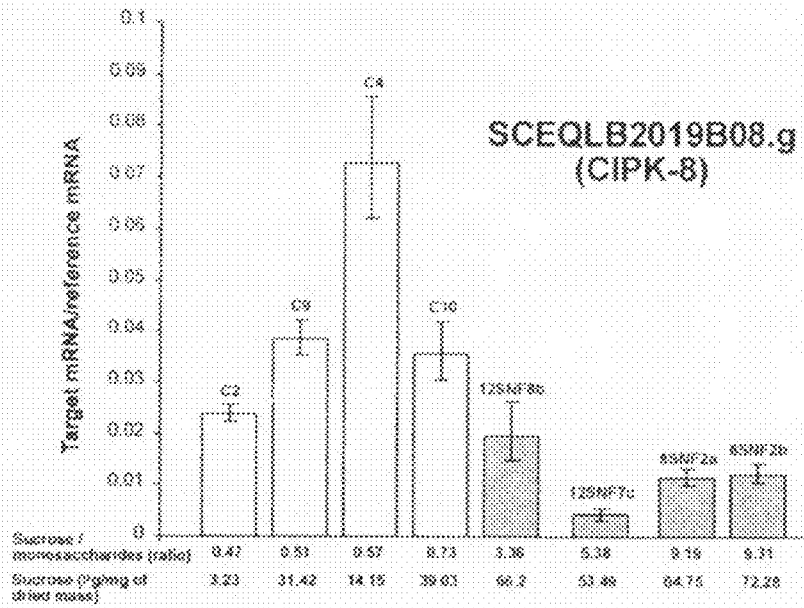


FIGURE 8

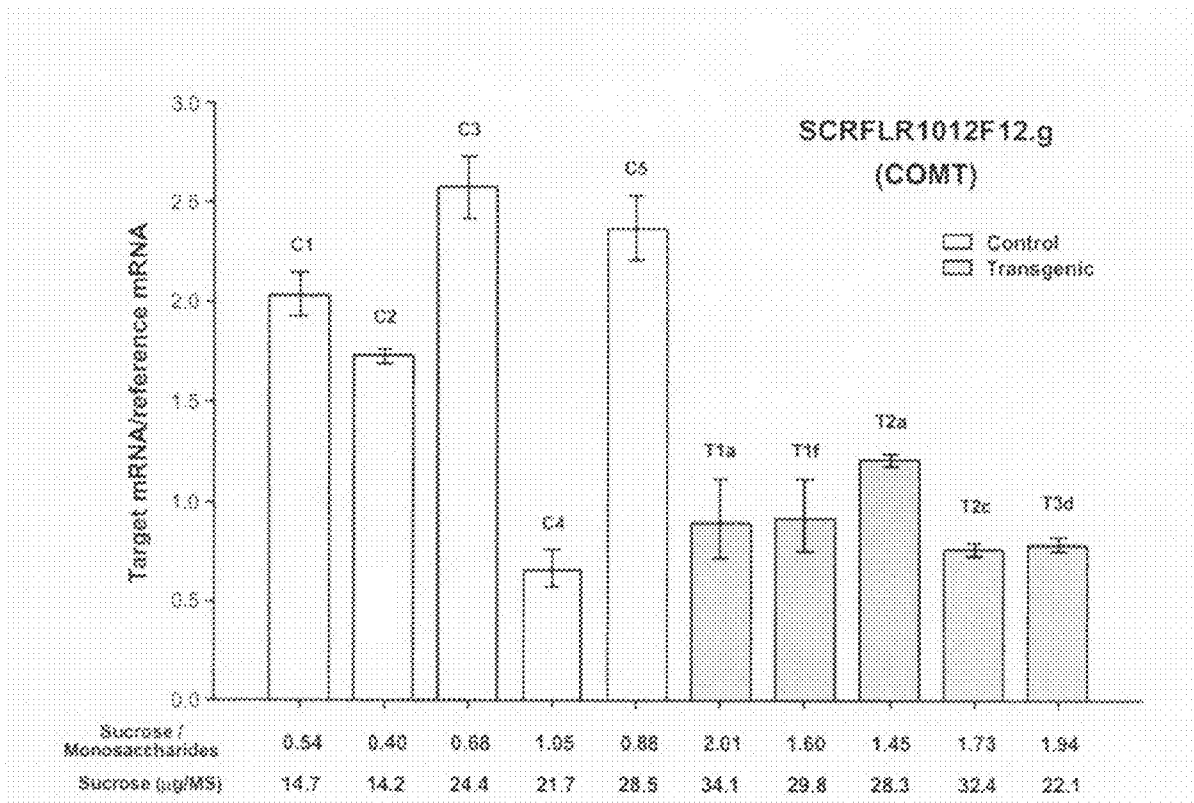


FIGURE 9

## GENES ASSOCIATED TO SUCROSE CONTENT

### RELATED APPLICATIONS

This application claims the benefit of U.S. Provisional Application No. 60/780,693, titled SUGAR CANE WITH INCREASED SUGAR LEVELS, filed Mar. 8, 2006, and U.S. Provisional Application No. 60/861,496, titled GENES ASSOCIATED TO SUCROSE CONTENT, filed Nov. 27, 2006, both of which are hereby incorporated by reference in their entirety.

### FIELD OF THE INVENTION

The present invention refers to a method for discriminating plants with different abilities to accumulate sugars as well as methods to produce plants with increased sucrose content.

### BACKGROUND OF THE INVENTION

The tropical crop sugarcane is of great economical interest, contributing to about two thirds of the world's raw sugar production (Pessoa Jr. et al., 2005). In some countries, part of the crop is destined to the production of ethanol, an important alternative energy source and a less polluting fuel. Due to its unique capacity of storing sucrose in the stems, sugarcane is an interesting model for studies on sugar synthesis, transport and accumulation. Sugarcane is a C4 grass capable of accumulating sucrose in its stems to levels exceeding 50% of its dry weight. Stem internodes mature progressively towards the base of the culm and there is a corresponding increase in sucrose concentration. Sucrose metabolism components and regulators are likely to be key players in determining sugarcane sucrose yield (Moore, 2005; Lunn and Furbank, 1999). Sugarcane is a complex polyploid grass with commercial varieties derived from conventional breeding. Recent yield data indicates that this technology may be reaching a limit in sugar productivity increases. It could be greatly advantageous to have genes associated with desirable traits targeted for directed improvement of varieties. Traditional breeding methods have been extensively employed in different countries along the past decades to develop varieties with increased sucrose yield, and resistant to plagues and diseases. Conventional varietal improvement is, however, limited by the narrow pool of suitable markers. In this sense, molecular genetics is seen as a promising tool to assist in the process of molecular marker identification. Knowledge on the genes that participate in sucrose content regulation may assist in the development of new varieties with increased productivity. This improvement is not only economically relevant, but has also a strong environmental appeal, considering it can lessen the need to expand cultivation areas and that ethanol is a source for renewable energy. Furthermore, a broader understanding of the highly specialized sugar production and accumulation mechanisms in sugarcane can bring new insights into sugar metabolism in other species.

Sugarcane is the common name given to the several species of the genus *Saccharum*, native to Asia, but cultivated for centuries in all five continents. It is a very efficient photosynthesizer making it one of the world's most important crop grasses. Sugarcane is perennial and has sturdy, jointed fibrous stalks 2-6 m tall, capable of storing large quantities of sucrose. Its cultivation requires warm and humid tropical or subtropical climate. Brazil, India and China are the largest producers. The major commercial cultivars are complex hybrids selected from crosses between *S. officinarum*, *S. bar-*

*beri*, *S. robustum*, *S. spontaneum* and *S. edule*, as well as related genera that cross with *Saccharum*, such as *Erianthus*, *Miscanthus*, *Narenga* and *Sclerostachya*.

*S. spontaneum* genotypes, found from Afghanistan to the South Pacific Islands, have the broadest geographical distribution in the genus *Saccharum*. Together with *S. officinarum*, it is the species most used in breeding programs aiming to improve vigor, fiber content, ratooning ability, environmental stress and disease resistance (Perez et al., 1997). The origin of *S. spontaneum* is not yet clear. It is believed that it might have originated from an introgression of *Miscanthus*, *Erianthus* and *Sclerostachya* (Roach and Daniels, 1987). *S. officinarum* genotypes have originated in New Guinea from *S. robustum* by natural and/or human selection. They produce thick stems and are capable of accumulating high levels of sucrose. They do not flower abundantly and are usually used as females in breeding programs (Perez et al., 1997).

The sequencing of 238 thousand sugarcane ESTs (Expressed Sequence Tags) by the Brazilian consortium SUC-EST (Vettore et al., 2003) was a landmark for the sugarcane biotechnology field and also for the study of basic genetics and physiology of grasses. The ESTs were clustered and a total of 43 thousand SAS (Sugarcane Assembled Sequences) were identified and categorized (Vettore et al., 2003). Functional characterization of the transcripts can be viewed on the World Wide Web at [sucest-fun.org](http://sucest-fun.org).

This work describes the use of cDNA microarrays to identify genes differentially expressed in two sugarcane populations contrasting for sugar content. The methods used to identify differential expression, the construction of cDNA microarrays, hybridization conditions and data analysis have been previously described (Papini-Terzi et al., 2005). A total of 5154 genes had their expression profiled.

The plants analyzed in the present invention are derived from multiple crossings among *S. officinarum* and *S. spontaneum* genotypes and from commercial varieties that have been selected for sugar content for over 12-15 years. A useful strategy for target-gene identification has been denominated "genetical genomics". First introduced by Jansen and Nap (2001), the method aims to apply large-scale analysis of gene expression to a segregating population. The use of cDNA microarrays to evaluate a sugarcane population that segregates for a certain trait may provide more insight into plant signaling and gene function than classical mutagenesis studies (Meyers et al., 2004). Although *S. officinarum* and *S. spontaneum* present a large genetic variability in nature, very few representatives participated in the generation of the modern commercial hybrids. Certainly, there are genes conferring favourable traits to be identified among them that can be explored in breeding programs. Likewise, the comparison of progenies from different commercial varieties carefully selected for sucrose enrichment is a strategy that can point to genes that have been selected for over the years by traditional breeding methods.

### SUMMARY OF THE INVENTION

This invention provides methods for producing transgenic plants, and non-naturally occurring plants with increased sugar levels. The invention further provides methods for determining the ability of a plant to accumulate sugar as well as methods for altering the ability of plants to accumulate sugar. In preferred embodiments, the plants are from the genus *Saccharum*. In particularly preferred embodiments, the plants are sugarcane.

In some embodiments, the invention provides methods for determining the ability of a plant to accumulate sugar by

providing a plant sample and measuring the expression level in the sample of at least one polynucleotide having sequence identity to or comprising SEQ ID NO:s 1 to 203 or SEQ ID NO:s 229 to 373, their complements, and sequences which hybridize to SEQ ID NO:s 1 to 203 or SEQ ID NO:s 229 to 373 under high stringency conditions. High stringency conditions refers to hybridization to filter-bound DNA in 5×SSC, 2% sodium dodecyl sulfate (SDS), 100 ug/ml single stranded DNA at 55-65° C., and washing in 0.1×SSC and 0.1% SDS at 60-65° C. For example, the polynucleotide can have 65% sequence identity, 75% sequence identity, 85% sequence identity, 95% sequence identity, 99% sequence identity, or be identical. In other embodiments, the polynucleotide is a fragment at least 14 nucleotides length of SEQ ID NO:s 1 to 203 or SEQ ID NO:s 229 to 373, their complements, and sequences which hybridize to SEQ ID NO:s 1 to 203 or SEQ ID NO:s 229 to 373 under high stringency conditions.

Polynucleotide expression levels are preferably detected by measurement of RNA levels, which can be detected by any method known to those of skill in the art, preferably PCR or hybridization to oligonucleotides. Samples are preferably taken from the leaf, internode, lateral bud, root, or inflorescence.

In other embodiments, the invention provides methods for determining the ability of a plant to accumulate sugar by providing a plant sample and measuring the expression level in the sample of at least one polypeptide encoded by polynucleotides having sequence identity to or comprising SEQ NO:s 1 to 203 or SEQ ID NO:s 229 to 373, their complements, and sequences which hybridize to SEQ ID NO:s 1 to 203 or SEQ ID NO:s 229 to 373 under high stringency conditions. For example, the polynucleotide can have 65% sequence identity, 75% sequence identity, 85% sequence identity, 95% sequence identity, 99% sequence identity, or be identical.

In still other embodiments, the invention provides methods for determining the ability of a plant to accumulate sugar by providing a plant sample and measuring the expression level in the sample of at least one polypeptide having similarity or comprising a polypeptide encoded by SEQ ID NO:s 1 to 203 or SEQ ID NO:s 229 to 373. The similarity, for example, can be 65%, 75%, 85%, 95%, 99%, or 100%.

In other embodiments, the invention provides methods for altering the ability of a plant to accumulate sugar by providing a plant sample, modulating the expression level of at least one of SEQ ID NO:s 1 to 203 or SEQ ID NO:s 229 to 373 and detecting the expression level of at least one of SEQ ID NO:s 1 to 203 or SEQ ID NO:s 229 to 373. The modulation can be achieved by mutagenesis, preferably by chemical or physical mutagenesis.

In yet another embodiment, the invention provides methods for altering the ability of a plant to accumulate sugar by providing a plant sample, expressing or interfering with the expression of at least one polynucleotide having sequence identity to or comprising SEQ ID NO:s 1 to 203 or SEQ ID NO:s 229 to 373, their fragments, their complements, and sequences which hybridize to SEQ ID NO:s 1 to 203 or SEQ ID NO:s 229 to 373 under high stringency conditions and detecting the expression level of at least one of SEQ ID NO:s 1 to 203 or SEQ ID NO:s 229 to 373. For example, the polynucleotide can have 65% sequence identity, 75% sequence identity, 85% sequence identity, 95% sequence identity, 99% sequence identity, or be identical to the sequence or a fragment of the sequence. The invention also provides methods for altering ability of a plant to accumulate sugar by expressing or interfering with the expression of polypeptides having similarity to or comprising polypeptides

encoded by SEQ ID NO:s 1 to 203 or SEQS ID NO:s 229 to 373 and detecting the expression level of at least one of the polypeptides encoded by SEQ ID NO:s 1 to 203 or SEQ ID NO:s 229 to 373. The similarity, for example, can be of 65%, 75%, 85%, 95%, 99%, or 100%. Typically, expression levels of polynucleotides and the encoded polypeptides are interfered with or decreased using anti-sense RNA or RNA interference methods.

In other embodiments, the invention provides transgenic plants produced by any method having altered expression of at least one polynucleotide having sequence identity to or comprising SEQ ID NO:s 1 to 203 or SEQ ID NO:s 229 to 373, their fragments, their complements, and sequences which hybridize to SEQ ID NO:s 1 to 203 or SEQ ID NO:s 229 to 373 under high stringency conditions or having altered expression of polypeptides having sequence identity to or comprising a polypeptide encoded by SEQ ID NO:s 1 to 203 and SEQ ID NO:s 229 to 373. In still other embodiments, the invention provides transgenic plants produced by methods described above, using genes that express or interfere with the expression of at least one polynucleotide having sequence identity to or comprising SEQ ID NO:s 1 to 203 or SEQ ID NO:s 229 to 373, their fragments, their complements, and sequences which hybridize to SEQ ID NO:s 1 to 203 or SEQ ID NO:s 229 to 373 under high stringency conditions or expressing polypeptides having similarity to or comprising polypeptides encoded by SEQ ID NO:s 1 to 203 or SEQ ID NO:s 229 to 373. Seeds, seed-canes (or setts) of such plants are also provided.

In yet another embodiment, the invention provides non-naturally occurring plants with altered expression levels generated by methods described above, such as mutagenesis. Seeds, seed-canes (or setts) of such plants are also provided.

The present invention identifies genes differentially expressed in sugarcane progenies and varieties with different sugar content. Comparative measures of mRNA for the genes in isolation or combined are indicative of sucrose content. Methods that measure transcript levels for the genes can be used to determine gene expression levels and can include cDNA microarrays, oligonucleotide arrays, quantitative PCR, northern blot or other hybridization techniques. Likewise, methods that measure the proteins encoded by the genes can also be used to characterize plants and progenies originating from traditional breeding programs or transgenic plants with the goal of identifying or selecting candidates that contain high sucrose content. Additionally, the genes can be directly used to increase plant sucrose content if they are introduced in the plant through the generation of a transgenic plant.

The cDNA microarray technology, quantitative PCR and northern blots were used to identify molecular markers associated to sucrose content. The procedures used were as described in Papini-Terzi et al, 2005 and Nogueira et al., 2003. The cDNA microarrays contain 5154 ESTs related to sugarcane signal transduction, stress responses, transcription, hormone signalling, metabolism and other functional categories. The plants analyzed derive (1) from an F3 progeny from multiple crossings among *S. officinarum* and *S. spontaneum* genotypes, (2) an F1 progeny from a crossing between the commercial varieties SP80-180 and SP80-4966, (3) an F1 progeny from a crossing between the commercial varieties SP80-144 and SP85-7215, (4) two varieties precocious and rich in sucrose production, SP91-1049 and SP94-3166 and (5) two varieties late and poor in sucrose production, SP83-2847 and SP89-1115. Sucrose producing tissues, also known as source tissues (herein leaf) and sucrose accumulating tissues, also known as sink tissues (herein internodes) were

collected from field grown plants. Soluble sugar content (Brix) measures were made. Samples were collected from individual and pools of 7 or 8 plants. In some cases, samples were collected throughout the year. Three designs were used to perform transcriptome comparisons for the identification of genes differentially expressed when (I) High Sugar and Low Sugar plants were directly compared, (II) High Sugar and Low Sugar plants were compared to a common reference, or (III) High Sugar and Low Sugar internodes were compared. Experimental Design I and II yielded 208 differentially expressed genes, while Design III revealed 140 differentially expressed genes, totalling 348 genes differentially expressed in at least one of the samples analysed. Several differentially expressed genes were validated by real-time PCR and northern blots using individual plants as the source for tissues or groups of plants which proves that the differential expression is robust enough to distinguish between high and low sucrose plants in a pool of plants.

The gene profiles of one or a plurality of the 203 genes obtained from the comparisons of Design I may be useful as molecular markers for traditional breeding, aid in the selection of ideal progenies and parents generated in traditional breeding or aid in the selection of transgenic events generated in the process of transgenic plants production. The 348 genes themselves, identified in comparisons I, II and III, may be used in the generation of transgenic plants as they may directly function in sucrose synthesis and/or accumulation, be mutated by classical (non-transgenic) methods leading to varieties with improved sucrose content, or be used as probes in search of polymorphisms.

#### BRIEF DESCRIPTION OF THE FIGURES

FIG. 1: Polycrosses performed among *S. officinarum* and *S. spontaneum* cultivars to obtain the sugarcane hybrid populations with high- and low sugar content. The graphs show the frequency of individuals from the F3 progeny corresponding to each of the Brix classes (Brix %). Brix was measured from juice of 500 individuals. Tissues of the 16 extreme individuals were collected and pooled for the microarray analysis. For real-time PCR quantification the RNA was extracted independently for each individual tissue.

FIG. 2—Sugar content along the growing season in the extreme individuals of a sugarcane segregant population. The Brix (soluble solids) values of the most mature internode of each sugarcane segregant plant were measured along the growing season. Average Brix values and standard deviations of the seven individuals with the highest or lowest sugar contents are shown for the indicated times.

FIG. 3: Validation of gene expression data by real-time PCR. mRNA levels were determined for the indicated SAS. Reactions were done in triplicates. A polyubiquitin (PUB) gene was used as reference. The bars show target mRNA levels relative to the polyubiquitin mRNA. Error bars were calculated as described by Livak and Schmittgen (2001). RNA samples from a pool of individuals were used to generate the templates for real-time PCR reactions. Additionally, three high brix (HB) individuals, Ind243, Ind246 and Ind253, and three low brix (LB) individuals, Ind261, Ind265 and Ind272, were analysed in the case of the cross between the commercial varieties (SP80-180 and SP80-4966). A: samples derived from a cross between two commercial varieties (SP80-180 and SP80-4966), B: samples derived from multiple crossings among *S. officinarum* and *S. spontaneum* genotypes. Lv=leaf; In1=internode 1; In9=internode 9.

FIG. 4: Expression levels of differentially expressed genes in sugarcane individuals. RNA blots were prepared using 10

µg of total RNA isolated from mature leaves of three individual clones of each segregant population (HS—high and LS—low sugar content). The time point evaluated in the blots corresponds to the same one used in the cDNA microarray experiments (9 months after planting). Blots were hybridized with the gene-specific radioactive probes indicated. An rDNA fragment was used as a control.

FIG. 5: Expression profiles of differentially expressed genes along the growing season. RNA-blots were prepared from total leaf-RNA from a pool of 7 individuals with high (HS) and low (LS) sugar content collected along the growing season (6, 7, 9, 11 and 13 months after planting). The inset graphs show the expression levels observed for the high (black circles) and low (white circles) sugar content plants. An rDNA fragment was used as a control.

FIG. 6—Sugar content along the growing season in two sugarcane cultivars poor and late in sucrose accumulation (SP83-2847 and SP94-3116) and two sugarcane cultivars rich and precocious in sucrose accumulation (SP91-1049 and SP89-1115). The Brix (soluble solids) values of the most mature internode of each sugarcane segregant plant were measured during the growing season. Average Brix values and standard deviations are shown for the indicated times.

FIG. 7—Alignment of nucleotide sequences for SEQ ID No. 411: CIPK-8 (SCEQLB2019B08.g); SEQ ID No. 412: CIPK-29 (SCSGHR10070F12.g); and SEQ ID No. 413: CIPK-1 (SCCCCL5001D11.g) using CLUSTALW (Thompson et al., 1994). The line above the sequences indicates the sequence fragment of 331 bp amplified and cloned in the plasmid in order to silence the CIPK-8 gene by RNA interference in the transgenic plants.

FIG. 8—Expression analysis of CIPK-8, CIPK-29 and CIPK-1 mRNA levels in control (blank) and transgenic plants (grey) of two-month old plants using quantitative PCR analysis. The bars show mRNA levels of CIPK8 (SCEQLB2019B08.g), CIPK29 (SCSGHR1070F12.g) and CIPK-1 (SCCCCL5001D11.g) relative to mRNA levels of the reference gene (SCQGAM2027G09.g). All reactions were carried out in parallel and each reaction was performed in triplicate. Error bars were calculated as described by Livak and Schmittgen (2001). The graph also shows sucrose levels and the ratio of sucrose to monosaccharides in these plants.

FIG. 9—Expression analysis of COMT mRNA levels in control (blank) and transgenic plants (grey) of two-month old plants using quantitative PCR analysis. The bars show mRNA levels of COMT (SCRFLR1012F12.g) relative to mRNA levels of the reference gene (SCQGAM2027G09.g). All reactions were carried out in parallel and each reaction was performed in triplicate. Error bars were calculated as described by Livak and Schmittgen (2001). The graph also shows sucrose levels and the ratio of sucrose to monosaccharides in these plants.

#### DEFINITIONS

The term “plants” include any plant amenable to transformation techniques, including angiosperms (monocotyledonous and dicotyledonous plants), gymnosperms, ferns, and multicellular algae. It includes plants of a variety of ploidy levels, including aneuploid, polyploid, diploid, haploid and hemizygous. The term “plant” includes whole plants, shoot vegetative organs/structures (e.g. leaves, stems and tubers), roots, flowers and floral organs/structures, seed (including embryo, endosperm, and seed coat) and fruit (the mature ovary), plant tissue (e.g. vascular tissue, ground tissue, and the like) and cells (e.g. guard cells, egg cells, trichomes and the like), and progeny of same. Examples of suitable plant

targets would include but are not limited to Acadia, alfalfa, apple, apricot, *Arabidopsis*, artichoke, arugula, asparagus, avocado, banana, barley, beans, beet, blackberry, blueberry, broccoli, brussels sprouts, cabbage, canola, cantaloupe, carrot, cassaya, castorbean, cauliflower, celery, cherry, chicory, cilantro, citrus, clementines, clover, coconut, coffee, corn, cotton, cucumber, Douglas fir, eggplant, endive, escarole, eucalyptus, fennel, figs, garlic, gourd, grape, grapefruit, honey dew, jicama, kiwifruit, lettuce, Iceks, lemon, lime, Loblolly pine, linseed, mango, melon, mushroom, nectarine, nut, oat, oil palm, oil seed rape, okra, olive, onion, orange, an ornamental plant, palm, papaya, parsley, parsnip, pea, peach, peanut, pear, pepper, persimmon, pine, pineapple, plantain, plum, pomegranate, poplar, potato, pumpkin, quince, radiata pine, radischio, radish, rapeseed, raspberry, rice, rye, sorghum, Southern pine, soybean, spinach, squash, strawberry, sugarbeet, sugarcane, sunflower, sweet potato, sweetgum, tangerine, tea, tobacco, tomato, triticale, turf, turnip, a vine, watermelon, wheat, yams, and zucchini. Particularly preferred plant targets would include sugarcane and sugarbeet. More preferably the plant is a crop plant used to produce sucrose or that can be transformed into a sucrose producing plant. Further preferably, the plant is sugarcane.

The term "sugarcane plants" can be/or be derived from:

any *Saccharum* wild-type genotype (for example, *Saccharum officinarum*, *Saccharum spontaneum*, *Saccharum robustum*)

any genus that crosses with *Saccharum* (for example, *Miscanthus*, *Erianthus*, *Narenga*, *Sclerestachya*)

any sugarcane hybrid generated spontaneously

any sugarcane hybrid generated by traditional breeding techniques

any sugarcane progenies generated from crosses of wild-type or commercial varieties

any sugarcane plant generated by the introduction of a transgene (transgenic plants)

The term "promoter" refers to regions or sequence located upstream and/or downstream from the start of transcription and which are involved in recognition and binding of RNA polymerase and other proteins to initiate transcription. A "plant promoter" is a promoter capable of initiating transcription in plant cells.

The term "seed-cane" (or setts) refers to stem cuttings or pieces of sugarcane stalk used to vegetatively propagate sugarcane cultures.

#### DETAILED DESCRIPTION OF INVENTION

Very little is known on the molecular mechanisms governing sucrose synthesis and accumulation in sugarcane. Although varieties exist capable of accumulating different amounts of sucrose, studies designed to compare these cultivars at the molecular level are scarce. The identification of genes conferring favourable traits to commercial hybrids is highly desirable for the sugarcane industry, since they could be used as markers for assisted selection.

The present invention broadly relates to defining a gene expression profile for SEQ ID NO. 1-203 that facilitates identification, isolation and characterization of high and low sucrose content sugarcane plants. The present invention also relates to defining a gene expression profile for SEQ ID NO:s 1-203 and SEQ ID NO:s 229-373 that is associated with sucrose content indicating genes that may be useful in the generation of sucrose enriched plants. Gene expression data can be determined for plants that can be a progeny derived from crossings (A), commercial varieties or cultivars (B), or transgenic plants (C).

With the purpose of selecting plants with high brix (soluble sugar content), a series of crossings involving *Saccharum officinarum* and *Saccharum spontaneum* genotypes were performed. First, intra-specific polycrosses were performed among 21 *Saccharum officinarum* genotypes and 13 *Saccharum spontaneum* genotypes (Table 1). Subsequently, the progenies of these independent crossings were evaluated for their sugar content and the most extreme individuals intercrossed. A series of recombination and selection events was promoted thereafter to select two populations with contrasting sugar accumulation capacities (FIG. 1). Eight genotypes with high brix (HB) content and eight with low brix (LB) were selected from the F3 progeny. In the context of the present invention, but not limited to, the brix difference ranges from 3 to 16. Table II shows the brix values for the sixteen individuals selected. Leaf+1 and internodes 1, 5 and 9 were collected. As used herein, leaf+1 is the first leaf with a visible dewlap and internodes are the plant parts above ground, with the exception of leaves. Tissues were pooled for HB and LB independently and total RNA was extracted.

TABLE I

<i>S. officinarum</i> and <i>S. spontaneum</i> genotypes used for the polycrosses.		
	<i>S. officinarum</i>	<i>S. spontaneum</i>
	Caiana Fita	IN8458
	IK76108	IN8488
	Lahaina	Krakatau
	MZ151	SES 147b
	MZ151 roxa	US56158
	Sabura	US7440
	Salangor	US851008
	Sinimbu	UM721
	NG213	UM691
	Fiji 47	SES 194
	Hinahina 18	IK7686
	Manjri Red	US56193
	Muntok Java	US571723
	NG77142	
	Soff 8268	
	SS601	
	Sylva	
	NG2880	
	Vae Vae Ula	
	IJ76315	
	IN8425	

TABLE II

Brix measurements of the 16 individuals (genotypes) selected for gene expression profiling.		
Classification	Genotype	Brix
High Brix	CTC98-241	23.00
	CTC98-242	23.90
	CTC98-243	22.90
	CTC98-244	23.40
	CTC98-246	22.60
	CTC98-252	22.20
	CTC98-253	22.50
	CTC98-258	22.10
Low Brix	CTC98-261	8.60
	CTC98-262	9.10
	CTC98-265	9.10
	CTC98-268	9.35
	CTC98-271	10.60
	CTC98-272	10.80
	CTC98-277	10.60
	CTC98-279	10.60

In a similar experiment, a field-grown F<sub>1</sub> progeny selected from a cross between the sugarcane varieties SP 80-180 and SP 80-4966 was characterized. From a total of 500 individuals, we picked out seven plants with the highest (7HB) and seven with the lowest (7LB) sugar content. FIG. 2 shows the average values and standard deviations for soluble solids level (Brix) of the most mature internode of these two groups of plants along the growing season (6, 7, 9, 11 and 13 months after planting).

Additionally, the F<sub>1</sub> progeny from a cross between the sugarcane varieties SP80-144 and SP85-7215 (selected as described for the cross between varieties SP 80-180 and SP 80-4966), two varieties precocious and rich in sucrose production (SP91-1049 and SP94-3166) and two varieties late and poor in sucrose production (SP83-2847 and SP89-1115) were also analysed. FIG. 6 shows the sugar content during the growing season in the two sugarcane cultivars poor and late in sucrose accumulation (SP83-2847 and SP94-3116) and the two sugarcane cultivars rich and precocious in sucrose accumulation (SP91-1049 and SP89-1115). For all of these, brix measures from field-grown plants were taken, leaf tissues were collected and total RNA was extracted. Table III lists all the progenies and varieties used in the present invention.

TABLE III

<u>Sugarcane Progenies and varieties used for molecular marker identification</u>		
Tissue	Plant Age	Origin of High Brix and Low Brix Plants
Internode 1	7 months	SP80-180 vs SP80-4966 progenies
Internode 5	7 months	SP80-180 vs SP80-4966 progenies
Internode 9	7 months	SP80-180 vs SP80-4966 progenies
Internode 1	11 months	SP80-180 vs SP80-4966 progenies
Internode 5	11 months	SP80-180 vs SP80-4966 progenies
Internode 9	11 months	SP80-180 vs SP80-4966 progenies
Internode 1	10 months	<i>S. spontaneum</i> vs <i>S. officinarum</i> progenies
Internode 5	10 months	<i>S. spontaneum</i> vs <i>S. officinarum</i> progenies
Internode 9	10 months	<i>S. spontaneum</i> vs <i>S. officinarum</i> progenies
Leaf	10 months	SP80-144 vs SP85-7215 progenies
Leaf	9 months	SP80-180 vs SP80-4966 progenies
Leaf	10 months	<i>S. spontaneum</i> vs <i>S. officinarum</i> progenies
Leaf	7 months	SP83-2847 varieties
Leaf	7 months	SP91-1049 varieties
Leaf	7 months	SP94-3116 varieties
Leaf	7 months	SP89-1115 varieties
Leaf	12 months	SP83-2847 variety
Leaf	14 months	SP83-2847 variety
Leaf	16 months	SP83-2847 variety
Leaf	18 months	SP83-2847 variety
Internode 1	12 months	SP83-2847 variety
Internode 1	14 months	SP83-2847 variety
Internode 1	16 months	SP83-2847 variety
Internode 1	18 months	SP83-2847 variety
Leaf	12 months	SP94-3116 variety
Leaf	14 months	SP94-3116 variety
Leaf	16 months	SP94-3116 variety
Leaf	18 months	SP94-3116 variety
Internode 1	12 months	SP94-3116 variety
Internode 1	14 months	SP94-3116 variety
Internode 1	16 months	SP94-3116 variety
Internode 1	18 months	SP94-3116 variety
Leaf	12 months	SP91-1049 variety
Leaf	14 months	SP91-1049 variety
Leaf	16 months	SP91-1049 variety
Leaf	18 months	SP91-1049 variety
Internode 1	12 months	SP91-1049 variety
Internode 1	14 months	SP91-1049 variety
Internode 1	16 months	SP91-1049 variety
Internode 1	18 months	SP91-1049 variety

TABLE III-continued

<u>Sugarcane Progenies and varieties used for molecular marker identification</u>		
Tissue	Plant Age	Origin of High Brix and Low Brix Plants
Leaf	12 months	SP89-1115 variety
Leaf	14 months	SP89-1115 variety
Leaf	16 months	SP89-1115 variety
Leaf	18 months	SP89-1115 variety
Internode 1	12 months	SP89-1115 variety
Internode 1	14 months	SP89-1115 variety
Internode 1	16 months	SP89-1115 variety
Internode 1	18 months	SP89-1115 variety

In parallel, cDNA microarrays were constructed with PCR products derived from 1857 polynucleotides representing sugarcane genes from the cDNA libraries produced by the Sugarcane EST Consortium (SUCEST), providing a platform for comparisons of gene expression profile. Approximately half of all the signal transduction genes identified by the Sugarcane Signal Transduction (SUCAST) project are represented in these arrays (Papini-Terzi et al., 2005), as well as genes related to general metabolism, stress, pathogen responses and transcription. The HB (High Brix) and LB (Low Brix) samples from each progeny or variety tissue were compared by hybridizing to the arrayed genes. Two replicate hybridizations were made for each comparison with the dye-swapped in the second hybridization. To reveal molecular markers of brix content, hybridizations were done to compare a tissue from the high brix plant to the same tissue in a low brix plant (Design I). Also, two high brix varieties and two low brix varieties were compared (Design II) by performing hybridizations against a common reference composed of an equimolar mixture of RNA samples from all four cultivars. Two replicate hybridizations were made for each comparison with the dye-swapped in the second hybridization. Additionally, mature and intermediately mature internodes were compared to immature internodes from both the high brix and the low brix plants (Design III). Again, two replicate hybridizations were made for each comparison with the dye-swapped in the second hybridization. Data analysis was done essentially as described by Papini-Terzi et al. (2005). Briefly, cut-off limits that define “differential expression” were calculated based on “self-self” hybridizations (Vencio and Koide, 2005). To improve data reliability, only genes with at least 70% consistency in replicate experiments were considered differentially expressed. A total of 208 SAS (SEQ ID Nos 1-203) were found differentially expressed in at least one sample when tissues from HB and LB plants were contrasted. When mature and immature internodes were compared a total of 140 differentially expressed genes were identified (SEQ ID Nos 229 to 373). Tables IV and XIII list all of the ESTs corresponding to each SAS (sugarcane assembled sequence) predicted to correspond to the same transcript as assembled by the CAP3 program (Vettore et al., 2003) and the predicted assembled sequence. The ratio values for the microarray signals for each SAS in each sample is presented in Tables V to IX and Table XIV to XX. The tables also show the categories and gene functions for each sequence.

TABLE IV

List of Sugarcane Assembled Sequences (SAS) and their SEQ ID Nos.

The EST Genbank accession numbers are in parentheses. The SEQ ID No. refers to the sequence identifiers in the sequence listings. The listed ESTs assembled to the indicated sequence and should be considered one transcript. Each SAS is differentially expressed between plants with low and high sucrose content.

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SEQ ID No. 1: SCAGFL1089G08.g  
(CA199089, CA224271, CA224272)

SEQ ID No. 2: SCCCLR2C01G07.g  
(CA185584, CA166776, CA134755, CA081538, CA166739, CA155955, CA084974, CA157742, CA270171, CA159531, CA187781, CA159517, CA089886, CA084049, CA159619, CA140397, CA087051, CA262468, CA159606, CA089976, CA183396, CA129456, CA066628, CA166690, CA140819, CA190385, CA187438, CA208612, CA190989, CA127354, CA140895, CA106597, CA158530, CA165616, CA157955, CA158357, CA163017, CA180366, CA156493, CA156721, CA110716, CA162841, CA088522)

SEQ ID No. 3: SCCCRZ1001C01.g  
(CA186259, CA147312, CA107529, CA283111, CA275744, CA245497, CA240766, CA217267, CA129544, CA232142, CA186319, CA132949, CA266299, CA279493, CA239038, CA069036, CA279491, CA081552, CA172945, CA270762, CA214162, CA155441, CA208908, CA077560, CA094623, CA080165, CA281654, CA068431, CA080252, CA253608, CA280034, CA146798, CA149332, CA286419, CA149406, CA208282, CA168868, CA167581, CA247594, CA245731, CA264236, CA256980, CA196120, CA166139, CA256260, CA133068, CA216602, CA096037, CA133422, CA209478, CA172392, CA196703, CA148592, CA107794, CA078322, CA069441, CA262406, CA164639, CA117241, CA291436, CA272137, CA156857, CA275745, CA233167, CA073173, CA294936, CA096560, CA204575, CA190808, CA294814, CA134607, CA095396, CA294999, CA233246, CA279310, CA272172, CA121188, CA165918, CA087433, CA152584, CA163918, CA134688, CA260773, CA232223, CA134035, CA087517, CA078469, CA280895, CA147004, CA270846, CA285363, CA224721, CA300843, CA085545, CA193771, CA085617, CA152497, CA147851, CA234786, CA264280, CA190048, CA264249, CA259379, CA134846, CA284676, CA066363, CA148782, CA134929, CA094480, CA100929, CA128739, CA230006, CA257872, CA272842, CA153380, CA088481, CA199337, CA067318, CA120108, CA257959, CA068501, CA227954, CA156682, CA173310, CA064714)

SEQ ID No. 4: SCEQRT1033F01.g  
(CA184995, CA156175, CA130817, CA186778, CA296253, CA162940, CA133313, CA185329, CA117474, CA186710, CA204874)

SEQ ID No. 5: SCEZLR1031G10.g  
(CA175202, CA165752, CA167131, CA234178, CA121597, CA067987, CA118138, CA257467, CA098577)

SEQ ID No. 6: SCEZRZ1015G02.g  
(CA237872, CA095197, CA148000, CA208159)

SEQ ID No. 7: SCJFRZ2014A03.g  
(CA068448, CA182636, CA124874, CA151939)

SEQ ID No. 8: SCUTST3090E03.g  
(CA187278, CA185355, CA180421, CA184313, CA210629)

SEQ ID No. 9: SCVPCL6042B11.g  
(CA179030, CA079210, CA171761, CA167601, CA099889)

SEQ ID No. 10: SCVPFL3046C06.b  
(CA244704, CA169357, CA226883, CA279223, CA226955, CA169444)

SEQ ID No. 11: SCACCL6008H06.g  
(CA297327, CA096029, CA272424)

TABLE IV-continued

List of Sugarcane Assembled Sequences (SAS) and their SEQ ID Nos.

The EST Genbank accession numbers are in parentheses. The SEQ ID No. refers to the sequence identifiers in the sequence listings. The listed ESTs assembled to the indicated sequence and should be considered one transcript. Each SAS is differentially expressed between plants with low and high sucrose content.

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SEQ ID No. 12: SCACLR1036B06.g  
(CA116282, CA208326, CA185586, CA161943, CA208173, CA164611, CA250322, CA141763, CA248417, CA173006, CA271344, CA248060, CA295677, CA141850, CA115167, CA150326, CA263624, CA155589, CA172473, CA210572, CA212977, CA071050, CA223263, CA183780, CA182338, CA123614, CA263704, CA258818, CA227706, CA185483, CA180358, CA227787, CA183645, CA183050, CA185991, CA164775, CA187002, CA167583, CA187440, CA294229, CA247569, CA268117, CA081801, CA175295, CA294155, CA231298, CA198645, CA181860, CA091352, CA203545, CA234600, CA163160, CA258992, CA211128, CA186109, CA173482, CA185124, CA194883, CA262166, CA280273, CA169398, CA224642, CA170802, CA208174, CA195079, CA169482, CA170947, CA170731, CA279502, CA170881, CA181104, CA206750, CA294040, CA171028, CA152678, CA257305, CA293976, CA213043, CA181646, CA187605, CA182139, CA143731, CA257402, CA193572, CA180425, CA297996, CA180830, CA283968, CA183965, CA213586, CA194480, CA086671, CA208319, CA075723, CA194663, CA293330, CA184108, CA075807, CA295739, CA168382, CA167495, CA212733, CA248494, CA187062, CA182290, CA181789, CA176860, CA201177, CA081385, CA122294, CA111436, CA181610, CA081463, CA081454, CA122407, CA172507, CA217801, CA112764, CA119200, CA205047, CA177228, CA168599, CA217883)

SEQ ID No. 13: SCACLR1126E09.g  
(CA116458, CA129697, CA118229)

SEQ ID No. 14: SCACLR2007G02.g  
(CA127563, CA091213, CA254488, CA091132, CA157102)

SEQ ID No. 15: SCACLR2014E12.g  
(CA192165, CA154258, CA186575, CA158514, CA127675, CA104491, CA154264, CA097458, CA258945, CA164635, CA143359, CA186649, CA245697, CA113109, CA231117, CA271862)

SEQ ID No. 16: SCACSB1037A07.g  
(CA167445, CA204908)

SEQ ID No. 17: SCAGAM2125C01.g  
(CA082271)

SEQ ID No. 18: SCAGFL1089C03.g  
(CA232431, CA214773, CA199044, CA226812, CA251426)

SEQ ID No. 19: SCAGLB1070E01.g  
(CA111450, CA086189, CA214795, CA174551, BQ804015, CA174968, CA259932, CA072721, CA214876)

SEQ ID No. 20: SCAGLR1043E04.g  
(CA139075, CA095747, CA163740, CA287933, CA254860, CA287205, CA276681, CA163825, CA158080, CA159744, CA166834, CA089831, CA146535, CA107721, CA159823, CA163282, CA101632, CA271953, CA112877, CA165306, CA116967, CA120230, CA165312, CA186064)

SEQ ID No. 21: SCAGLR1043F02.g  
(CA290432, CA292969, CA279534, CA183060, CA183152, CA121646, CA096370, CA099981, CA192245, CA167424, CA214962, CA125300, CA267241, CA122577, CA246321, CA214857, CA261846, CA214921, CA120097, CA122234, CA158059, CA202210, CA273838, CA263626, CA205312, CA183023, CA263706, CA185079, CA116969, CA275126, CA184998)



TABLE IV-continued

List of Sugarcane Assembled Sequences (SAS) and their SEQ ID Nos.  
The EST Genbank accession numbers are in parentheses. The SEQ ID No. refers to the sequence identifiers in the sequence listings. The listed ESTs assembled to the indicated sequence and should be considered one transcript. Each SAS is differentially expressed between plants with low and high sucrose content.

SEQ ID No. 22: SCAGLR2026G12.g  
(CA282277, CA117544, CA173493, CA097993, CA123854, CA277803, CA276657, CA163057, CA089417, CA123966, CA150636, CA152810, CA105994, CA124675, CA095504, CA260199, CA124712, CA288917, CA145237, CA165000, CA167668, CA066913, CA161175, CA128073, CA128273, CA157707, CA084376, CA143727, CA143896, CA146035, CA159999, CA128260, CA123367, CA125688, CA111277, CA081486, CA239639, CA159912, CA224751, CA135227, CA277229, CA154488, CA114788, CA187359, CA183121, CA137987, CA125112)

SEQ ID No. 23: SCAGSD2042G08.g  
(CA301419, CA301408, CA282279, CA282268)

SEQ ID No. 24: SCBFFL4114B06.g  
(CA254510)

SEQ ID No. 25: SCBFFL5074C09.g  
(CA204004, CA293285, CA203956, CA244892, CA290019, CA132334, CA244976, CA235410, CA292110, CA239336)

SEQ ID No. 26: SCBFLR1039B05.g  
(CA072436, CA164922, CA219265, CA294041, CA087182, CA086094, CA133140, CA082356, CA178376, CA150762, CA091920, CA261338, CA155935, CA092012, CA084247, CA074480, CA163545, CA163534, CA264111, CA188825, CA079335, CA188476, CA087023, CA271843, CA164692, CA161125, CA161569, CA186875, CA218879, CA147374, CA086305, CA218962, CA247037, CA158661, CA089106, CA089861, CA154471, CA172672, CA155677, CA157667, CA240350, CA160822, CA085679, CA142367, CA067697, CA078551, CA165453, CA193896, CA240083, CA159199, CA117385, CA083799, CA184601, CA073646, CA087006, CA067781, CA228606, CA157128, CA165295, CA164303, CA090710, CA157426, CA218214, CA144877, CA082959, CA082212, CA092766, CA218299, CA082071, CA082361, CA166357, CA092479, CA155760, CA154412, CA157932, CA080915, CA089329, CA155569, CA084631, CA084421, CA163520, CA070855, CA267791, CA070926, CA083685, CA193867, CA164257, CA262071, CA280355, CA253389, CA151412, CA099704, CA099702, CA091852, CA103683, CA218228, CA216440, CA076652, CA218313, CA081569, CA147549, CA092093, CA092327, CA082854, CA160806, CA234098, CA081072, CA155277, CA081503, CA156306, CA228091, CA165593, CA084277, CA164984, CA085999)

SEQ ID No. 27: SCBFLR1060F03.g  
(CA117505, CA090821, CA184876, CA102138)

SEQ ID No. 28: SCBFRZ2046D07.g  
(CA150681, CA109085, CA179474, CA203314, CA174283)

SEQ ID No. 29: SCBFSB1046D04.g  
(CA167835)

SEQ ID No. 30: SCBFSB1047C02.g  
(CA170539, CA208192, CA167900, CA178739)

SEQ ID No. 31: SCBFST3136A06.g  
(CA181757, CA181841, CA204913)

SEQ ID No. 32: SCBGLR1003D06.g  
(CA222877, CA125433, CA148517, CA123170, CA124367, CA229025, CA191858, CA150470, CA137422, CA242621, CA067144, CA107570, CA077924, CA219677, CA117862, CA137913, CA260601, CA189186, CA191192, CA103772, CA149267, CA111228, CA149344, CA283660, CA154152, CA153751, CA165134, CA177823, CA228650, CA287491,

TABLE IV-continued

List of Sugarcane Assembled Sequences (SAS) and their SEQ ID Nos.  
The EST Genbank accession numbers are in parentheses. The SEQ ID No. refers to the sequence identifiers in the sequence listings. The listed ESTs assembled to the indicated sequence and should be considered one transcript. Each SAS is differentially expressed between plants with low and high sucrose content.

5  
10  
15  
SEQ ID No. 33: SCBGLR1023D05.g  
(CA193105, CA188272, CA224873, CA241264, CA300539, CA188009, CA241339, CA241331, CA133005, CA150388, CA079307, CA185891, CA079026, CA088897, CA116440, CA073525, CA117725, CA286594)

20  
SEQ ID No. 34: SCBGLR1096E06.g  
(CA131852, CA136715, CA264334, CA198772, CA181655, CA118258)

25  
SEQ ID No. 35: SCBGLR1099G02.g  
(CA118527, CA088599)

30  
SEQ ID No. 36: SCBGLR1115D10.g  
(CA236898, CA118948, CA290199, CA222803, CA247964, CA241212, CA294776, CA213997, CA223503, CA223512, CA241290, CA077364, CA223593, CA223583, CA228839, CA237054, CA200849, CA200388, CA238984, CA077442, CA079128, CA271913)

35  
SEQ ID No. 37: SCCCAD1001C08.g  
(CA213052, CA064626, CA208782)

SEQ ID No. 38: SCCCAD1004H02.g  
(CA064903, CA065602, CA196686, CA068322)

40  
SEQ ID No. 39: SCCCAM1001A03.g  
(CA224922, CA097767, CA289761, CA293310, CA072765, CA177152, CA082771, CA228990, CA200984, CA071379, CA186832, CA174514, CA299571, CA285188, CA200732, CA074444, CA070971, CA266681, CA292024)

45  
SEQ ID No. 40: SCCCAM2004G02.g  
(CA175137)

SEQ ID No. 41: SCCCAM2C04G08.g  
(CA188572, CA081398, CA083085, CA177802, CA081466)

50  
SEQ ID No. 42: SCCCCL3001F04.g  
(CA090274, CA218633, CA271564, CA072795, CA176380, CA212400, CA076605, CA292379, CA176809, CA261558, CA092442, CA082952, CA171891, CA132285, CA298117, CA136926, CA205249, CA244356, CA084659, CA174001, CA220841, CA188161, CA262641, CA084625, CA147909, CA258069, CA130594, CA268345, CA098011, CA297370, CA147196, CA232960, CA072355, CA139295, CA103872, CA161619, CA076646, CA192047, CA069119, CA269782, CA176915, CA202483, CA147582, CA142782, CA077648, CA092390, CA082458, CA266894, CA230599, CA129577, CA192875, CA205406, CA195633, CA258918, CA239390, CA195611, CA091961, CA211152, CA238101, CA082565, CA261071, CA139562, CA238798, CA267286, CA126957, CA112818, CA258847, CA097943, CA262159, CA170717, CA070245, CA192180, CA167707, CA147514, CA176991, CA076215, CA266294, CA071776, CA190170, CA261881, CA082649, CA167116, CA200225, CA166545, CA174720, CA180863, CA098735, CA078299, CA080135, CA137514, CA084364, CA146987, CA130332, CA078373, CA215588,

55  
60  
65  
SEQ ID No. 43: SCCCCL3001F04.g  
(CA179346, CA079412, CA147435, CA187943, CA179432, CA179450, CA167646, CA117675, CA147627, CA279536,

TABLE IV-continued

List of Sugarcane Assembled Sequences (SAS) and their SEQ ID Nos.  
The EST Genbank accession numbers are in parentheses. The SEQ ID No. refers to the sequence identifiers in the sequence listings. The listed ESTs assembled to the indicated sequence and should be considered one transcript. Each SAS is differentially expressed between plants with low and high sucrose content.

CA123234, CA251889, CA209472, CA094022, CA093214,  
CA235526, CA066029, CA291616, CA270178, CA088732,  
CA079067, CA210802, CA173849, CA208418, CA147384,  
CA249228, CA205005)

SEQ ID No. 43: SCCCCL3002C09.b  
(CA164754, CA192507, CA149213, CA260796, CA187083,  
CA101050, CA232366, CA230776, CA285317, CA299708,  
CA232454, CA168679, CA122474, CA179836, CA117294,  
CA122512, CA123772, CA254900, CA183002, CA127885,  
CA168911, CA071983, CA236670, CA266142, CA109668,  
CA168996, CA094485, CA273741, CA182273, CA300109,  
CA259484, CA109752, CA266217, CA095537, CA105282,  
CA190305, CA273812, CA095612, CA174112, CA102333,  
CA222873, CA241526, CA234235, CA169388, CA138129,  
CA247699, CA259138, CA169473, CA189915, CA232514,  
CA174741, CA221599, CA174821, CA195129, CA205165,  
CA136996, CA078205, CA189405, CA235587, CA098138,  
CA116327, CA114878, CA191259, CA300967, CA191089,  
CA235666, CA183278, CA145262, CA137898, CA156970,  
CA121379, CA095453, CA134465, CA138724, CA129675,  
CA134544, CA174648, CA123308, CA137470, CA228406,  
CA125187, CA179729, CA145327, CA179613, CA116680,  
CA134096, CA185020, CA097986, CA241590, CA120065,  
CA098133, CA300763, CA248222, CA114920, CA140135,  
CA260971, CA206920, CA069768, CA135583, CA241001,  
CA126239, CA254670, CA104750, CA225281, CA205773,  
CA158716, CA177253, CA135668, CA069844, CA176685,  
CA104833, CA179725, CA175015, CA093273, CA156663,  
CA144277, CA077356, CA139207, CA077433, CA156162,  
CA233672, CA289617, CA136244, CA092631, CA121367,  
CA166600, CA285273, CA096245, CA174136, CA131526,  
CA127387, CA243490, CA107152, CA130718, CA234183,  
CA139986, CA242827, CA295952, CA127931, CA130008,  
CA134095, CA138704, CA083624, CA291487, CA217158,  
CA140705, CA176381, CA300124, CA225694, CA269792,  
CA142766, CA244765, CA072024, CA208843, CA140774,  
CA142408, CA244840, CA240123, CA294166, CA131496,  
CA242966, CA183794, CA078230, CA294108, CA171510,  
CA070363, CA084393, CA243058, CA238566, CA130322,  
CA275283, CA149534, CA070447, CA086950, CA275350,  
CA145273, CA103468, CA186854, CA101246, CA127499,  
CA113173, CA255273, CA228952, CA180533, CA188382,  
CA280222, CA179960, CA145293, CA205177, CA301035,  
CA127828)

SEQ ID No. 44: SCCCCL3080A11.b  
(CA195011, CA186362, CA296480, CA296654, CA275397,  
CA290669, CA282198, CA221529, CA275467, CA135001,  
CA167417, CA290056, CA148875, CA076391, CA242540,  
CA141300, CA287167, CA076476, CA176410, CA080697,  
CA252988, CA184697, CA242340, CA200871, CA179397,  
CA253071, CA185063, CA159627, CA284239, CA185199,  
CA159286, CA291109, CA179461, CA248226, CA086290,  
CA176240, CA191934, CA245914, CA278165, CA103412,  
CA152746, CA230916, CA245835, CA242649, CA230990,  
CA132349, CA287873, CA166292, CA273797, CA160174,  
CA274023, CA122335, CA273788, CA092884, CA091203,  
CA154817, CA276231, CA136820, CA287241, CA207749,  
CA276377, CA066806, CA122402, CA159765, CA276035,  
CA296496, CA279832, CA271356, CA091503, CA215068,  
CA129109, CA116743, CA121331, CA290328, CA285668,  
CA287690, CA232825, CA069961, CA076390, CA101186,  
CA240902, CA180980, CA076475, CA226125, CA283780,  
CA283709, CA159661, CA182917, CA202160, CA065119,  
CA155633, CA218498, CA217558, CA288910, CA130058,  
CA169110, CA249436, CA190722, CA282286, CA169189,  
CA149394, CA176923, CA148689, CA123410, CA197169,  
CA174886, CA202258, CA181623, CA153982, CA263764,

TABLE IV-continued

List of Sugarcane Assembled Sequences (SAS) and their SEQ ID Nos.  
The EST Genbank accession numbers are in parentheses. The SEQ ID No. refers to the sequence identifiers in the sequence listings. The listed ESTs assembled to the indicated sequence and should be considered one transcript. Each SAS is differentially expressed between plants with low and high sucrose content.

CA274086, CA111644, CA093560, CA273768, CA112839,  
CA093040, CA065124, CA137999, CA264537)

SEQ ID No. 45: SCCCCL3120C09.g  
(CA164701, CA224926, CA093647, CA083169, CA111541,  
CA083168, CA093732, CA122320, CA265053, CA157947,  
CA122415, CA122420, CA273041, CA164238, CA130292,  
CA121753, CA161184, CA087082, CA090483, CA072914)

SEQ ID No. 46: SCCCCL3120G07.g  
(CA126728, CA185585, CA206387, CA125243, CA265002,  
CA185315, CA245734, CA180717, CA067294, CA091012,  
CA181272, CA244870, CA264526, CA106164, CA199596,  
CA180607, CA236822, CA104054, CA244956, CA125117,  
CA180803, CA067314, CA104139, CA224603, CA279337,  
CA099590, CA142258, CA168155, CA094223, CA266351,  
CA180794, CA231617, CA209380, CA093688, CA125829,  
CA187261, CA187424, CA261208, CA067342, CA226296,  
CA189470, CA067295, CA168751, CA090956, CA184722,  
CA178676, CA211245, CA239943, CA107492)

SEQ ID No. 47: SCCCCL4002E02.g  
(CA116501, CA215472, CA157057, CA272126, CA132749,  
CA282608, CA185323, CA134724, CA131522, CA298731,  
CA172476, CA093967, CA157851, CA177663, CA265966,  
CA164160, CA157052, CA145182, CA184790, CA069776,  
CA222319, CA156078, CA190828, CA140192, CA133240,  
CA211567, CA166155, CA067205, CA195541, CA091963,  
CA172143, CA089803, CA163027, CA090747, CA191514,  
CA139123, CA162363, CA225047, CA109794)

SEQ ID No. 48: SCCCCL4005F05.g  
(CA280584, CA301445, CA101272, CA094199, CA251241,  
CA287651, CA277095, CA217700)

SEQ ID No. 49: SCCCCL6002B05.g  
(CA235513, CA140487, CA095693, CA183575, CA187535,  
CA270075, CA259493, CA262265, CA181192, CA279039)

SEQ ID No. 50: SCCCCL6003D08.g  
(CA261317, CA207685, CA249487, CA295361, CA295292,  
CA176975, CA249563, CA259708, CA096709)

SEQ ID No. 51: SCCCFL4094H12.g  
(CA235328, CA253578)

SEQ ID No. 52: SCCCCLB1001D03.g  
(CA070103, CA233451, CA280144, CA161397, CA073973,  
CA246052, CA266278, CA187448, CA087616, CA105439,  
CA292489, CA289895, CA251852, CA112903, CA217956,  
CA110778, CA193638, CA079528, CA109891, CA157072)

SEQ ID No. 53: SCCCCLB1003E11.g  
(CA183789, CA280103, CA133961, CA139899, CA070532,  
CA110960, CA153393, CA133885, CA263460, CA115969,  
CA153912, CA115964, CA271209, CA135793, CA271124,  
CA186641, CA170726, CA186568)

SEQ ID No. 54: SCCCCLR1001A06.g  
(CA190346, CA248924, CA092763, CA083592, CA188740,  
CA077113, CA116115, CA158015, CA121535, CA204604,  
CA216472, CA105973)

SEQ ID No. 55: SCCCCLR1001E04.g  
(CA286692, CA185203, CA283556, CA297496, CA283763,  
CA107947, CA281797, CA273397, CA288055, CA182167,  
CA272567, CA275912, CA115183, CA261160, CA169335,  
CA275587, CA116155, CA276409, CA275516, CA113912,  
CA180802, CA281743, CA169255, CA275068, CA283676,

TABLE IV-continued

List of Sugarcane Assembled Sequences (SAS) and their SEQ ID Nos.  
The EST Genbank accession numbers are in parentheses. The SEQ ID No. refers to the sequence identifiers in the sequence listings. The listed ESTs assembled to the indicated sequence and should be considered one transcript. Each SAS is differentially expressed between plants with low and high sucrose content.

CA274801, CA185414, CA288928, CA297998, CA276051,  
CA247335, CA278026, CA276440, CA295185, CA110175,  
CA182175, CA281251, CA287476, CA277138, CA277597,  
CA281255, CA277512, CA170522, CA282815, CA216931,  
CA208645, CA208714, CA117824, CA119303, CA295245,  
CA210512, CA297891, CA180801, CA284125, CA275675,  
CA301424, CA285422, CA182158, CA286170, CA182550,  
CA284723, CA286095, CA282404, CA274292, CA183110)

SEQ ID No. 56: SCCCLR1022B11.g  
(CA262370, CA175573, CA283139, CA282225, CA175736,  
CA098979, CA274092, CA283705, CA234778, CA090105,  
CA291719, CA234765, CA149808, CA156650, CA184954,  
CA162473, CA165344, CA283982, CA145397, CA227663,  
CA217233, CA193153, CA098173, CA170572, CA168929,  
CA133676, CA119647, CA096824, CA169015, CA181636,  
CA176861, CA108797, CA095801, CA102799, CA168953,  
CA142627, CA140623, CA150372, CA211448, CA065362,  
CA283916, CA262588, CA296130, CA137717, CA144579,  
CA281526, CA097927, CA260822, CA178228, CA099128,  
CA192194, CA301126, CA135072, CA179839, CA150376,  
CA234766, CA297660, CA281655, CA176409, CA273865,  
CA297545, CA284140, CA297734, CA098177, CA073430,  
CA259653, CA136165, CA135273, CA153599, CA181778,  
CA282925, CA153678, CA070825, CA144282, CA296412,  
CA097932)

SEQ ID No. 57: SCCCLR1022F10.g  
(CA233639, CA260053, CA185523, CA222669, CA095561,  
CA167708, CA222802, CA278697, CA175743, CA221789,  
CA121319, CA177308, CA299149, CA273209, CA244627,  
CA215981, CA178001, CA066057, CA244686, CA234654,  
CA297895, CA179682, CA207766, CA186315, CA194047,  
CA233580, CA186380, CA269743, CA186727, CA179261,  
CA186798, CA146095, CA229185, CA239458, CA240513,  
CA221284, CA118249, CA276970, CA253631, CA163389,  
CA194377, CA184587, CA138682, CA083453, CA186061,  
CA168226, CA289825, CA261002, CA279246, CA099796,  
CA254874, CA222389, CA269896, CA133477, CA221786,  
CA298984, CA256819, CA167056, CA181465, CA164471,  
CA222384, CA178907, CA244604, CA118336, CA266032,  
CA118095, CA084230, CA280986, CA258373, CA266089,  
CA250738, CA193208, CA122349, CA185474, CA119690,  
CA175851, CA103705, CA099948, CA299982, CA276941,  
CA298487, CA148104, CA187876, CA107311, CA066053,  
CA273213, CA173497, CA222054, CA182618, CA244395,  
CA273241, CA244475, CA257856, CA205271, CA085415,  
CA192092, CA097961)

SEQ ID No. 58: SCCCLR1024A02.g  
(CA177199, CA178859, CA148547, CA271595, CA165098,  
CA191796, CA284535, CA119371, CA257923, CA284457,  
CA139287)

SEQ ID No. 59: SCCCLR1024C03.g  
(CA214530, CA092678, CA259139, CA119392, CA138689,  
CA142234, CA110468, CA166793, CA235001, CA239014,  
CA187582, CA153171, CA166778, CA229316, CA108240,  
CA142532, CA231084, CA122112, CA249179, CA267413,  
CA116485, CA188769, CA130021, CA193695, CA073718,  
CA205841, CA183536, CA161063, CA206262, CA235000,  
CA190341, CA202723, CA090059, CA090058, CA236017,  
CA082031, CA187867, CA155918, CA103108, CA070579,  
CA079479, CA110879, CA119822)

SEQ ID No. 60: SCCCLR1048D07.g  
(CA147475, CA291066, CA096819, CA204869, CA181487,  
CA192930, CA209156, CA067272, CA147995, CA244339,  
CA180480, CA171800, CA284134, CA196820, CA244421,

TABLE IV-continued

List of Sugarcane Assembled Sequences (SAS) and their SEQ ID Nos.  
The EST Genbank accession numbers are in parentheses. The SEQ ID No. refers to the sequence identifiers in the sequence listings. The listed ESTs assembled to the indicated sequence and should be considered one transcript. Each SAS is differentially expressed between plants with low and high sucrose content.

5 CA243578, CA182300, CA186405, CA186430, CA283235,  
CA179955, CA184880, CA186482, CA145597, CA186507,  
CA208666, CA197511, CA175966, CA145686, CA256333,  
CA204958, CA209389, CA101793, CA101156, CA221552,  
15 CA181039, CA166999, CA180658, CA256408, CA253875,  
CA192877, CA197390, CA166969, CA093997, CA240271,  
CA205247, CA182628, CA181383, CA099255, CA146394,  
CA070562, CA213081, CA185160, CA070652, CA070769,  
CA180031, CA291102, CA170929, CA204905, CA132911,  
CA218801, CA134618, CA171253, CA206709, CA167078,  
CA222191, CA134393, CA244769, CA298008, CA133579,  
20 CA140427, CA221930, CA171805, CA147956, CA145072,  
CA115358, CA168857, CA145152, CA221551, CA254585,  
CA222208, CA193664, CA168945, CA135732, CA106240,  
CA288063, CA067331, CA105045, CA182416, CA253889,  
CA267756, CA211247, CA197638, CA122733, CA220849,  
CA217920, CA217294, CA159483, CA267841, CA122809,  
25 CA064754, CA168537, CA205015, CA217367, CA121248,  
CA195018, CA141826, CA173132, CA185041, CA152829,  
CA183112, CA222487, CA066599, CA244066, CA165764,  
CA096242, CA207168, CA187102, CA121886, CA172779,  
CA232513, CA221622, CA163385, CA187635, CA165823,  
CA108173, CA216201, CA196736, CA145978, CA253253,  
30 CA143737, CA220822, CA066971, CA137693, CA192288,  
CA169323, CA149105, CA235200, CA133460, CA231421,  
CA256401, CA155413, CA115687, CA231501, CA065787,  
CA066028, CA130814, CA166921, CA195510, CA065872,  
CA119495, CA211215, CA234020, CA097049, CA110451,  
CA219727, CA130446, CA107579, CA104154, CA170754,  
35 CA169355, CA138200, CA167435, CA192429, CA190819,  
CA138088, CA170937, CA187379, CA222270, CA169442,  
CA256336, CA171875, CA289972, CA204877, CA133091,  
CA253873, CA146649, CA171683, CA174259, CA182738,  
CA180326, CA146716, CA132203, CA157422, CA192841,  
CA257875, CA180828, CA157372, CA234853, CA121786,  
40 CA181526, CA205074, CA186020, CA194299, CA217863,  
CA185113, CA211872, CA121463, CA133052, CA173016,  
CA068878, CA195370, CA170626, CA070371, CA216657,  
CA068962, CA243574, CA171193, CA216340, CA297779,  
CA182680, CA067729, CA180065, CA207908, CA067811,  
CA180150)

45 SEQ ID No. 61: SCCCLR1048F03.g  
(CA127113, CA065075, CA127212, CA277499, CA129554,  
CA121603, CA121408, CA125178, CA127440, CA276807,  
CA126903, CA283043, CA236098, CA097364, CA118155,  
CA281809, CA070362, CA297080, CA278048, CA121485,  
CA301525, CA116435, CA120637, CA284860, CA277432,  
50 CA276771, CA189482, CA124010, CA276938, CA120532,  
CA288405, CA122385, CA276469, CA215504, CA065010,  
CA275948, CA126086, CA208335, CA209295, CA210653,  
CA126762, CA219057, CA127157, CA072321, CA125785,  
CA206577, CA190063, CA284449, CA070651, CA285051,  
CA065024, CA120482, CA117975, CA208190, CA129193,  
55 CA289201, CA168876, CA289063, CA096730, CA128766,  
CA282961, CA189708, CA285413, CA067943, CA275056,  
CA065005, CA274114, CA276236, CA067075, CA126585,  
CA126946, CA193276, CA177371, CA286524, CA281416,  
CA176878, CA301261, CA120733, CA267336, CA190241,  
CA119190, CA297298, CA116632, CA117265, CA276973,  
CA125066, CA119744, CA227317, CA279870, CA124816,  
60 CA285933, CA121585, CA212660, CA173116, CA125319,  
CA282719, CA212404, CA284489, CA066031, CA285534,  
CA285189, CA118289, CA284558, CA119511, CA274189,  
CA065095, CA129555, CA283138, CA283217, CA285867,  
CA124018, CA281823, CA296966, CA288144, CA123645,  
CA126639, CA278851, CA297029, CA117985, CA296567,  
65 CA195886, CA068236, CA219344, CA065081, CA208255,  
CA129812, CA296642, CA126079, CA068319, CA129203,

TABLE IV-continued

List of Sugarcane Assembled Sequences (SAS) and their SEQ ID Nos.  
The EST Genbank accession numbers are in parentheses. The SEQ ID No. refers to the sequence identifiers in the sequence listings. The listed ESTs assembled to the indicated sequence and should be considered one transcript. Each SAS is differentially expressed between plants with low and high sucrose content.

CA125738, CA276707, CA194608, CA282969, CA122439, CA122553, CA276334, CA281049, CA281213, CA208478, CA265249)

SEQ ID No. 62: SCCCLR1065F03.g  
(CA119768, CA180227)

SEQ ID No. 63: SCCCLR1066G08.g  
(CA130183, CA119863, CA190094, CA189956, CA118906, CA129694)

SEQ ID No. 64: SCCCLR1068D03.g  
(CA131141, CA282509, CA101490, CA156675, CA119997, CA266674, CA131210, CA107609, CA265499)

SEQ ID No. 65: SCCCLR102F07.g  
(CA288961, CA273685, CA256939, CA112913, CA107999, CA276603, CA241855, CA085479, CA193799, CA252891, CA097052, CA257482, CA203818, CA239070, CA266548, CA099488, CA252672, CA202292, CA279439, CA187630, CA298704, CA125723, CA251524, CA179558, CA177714, CA119975, CA276149, CA128085, CA264406, CA124059, CA247506, CA246266, CA222791, CA100437, CA252417, CA189608, CA225806)

SEQ ID No. 66: SCCCLR103G01.g  
(CA114535, CA287070, CA203793, CA113049, CA227918, CA143767, CA239356, CA111397, CA177088, CA130728, CA189457, CA164190, CA236768, CA141069, CA122177, CA110741, CA276010, CA072413, CA272629, CA174772, CA256494, CA077651, CA269728, CA178457, CA115111, CA287055, CA126217, CA193225, CA178389, CA247689, CA228551, CA138141, CA227995, CA286643, CA189695, CA256499, CA228805, CA106329, CA202331, CA141201, CA142188, CA123003, CA256606, CA097345, CA167647, CA290389, CA154610, CA081435, CA256686, CA126629, CA115110, CA151805, CA081363, CA167055, CA235116, CA133295, CA148899, CA173127, CA099540, CA148811, CA192344, CA235424, CA272042, CA147268)

SEQ ID No. 67: SCCCLR103H09.g  
(CA194061, CA211639, CA280503, CA116278, CA077744, CA211491, CA209038, CA100317, CA072278, CA096295, CA132466, CA250830, CA292901, CA255776, CA065950, CA160220, CA106513, CA097514, CA098595, CA104618, CA131327, CA119740, CA264663, CA299848, CA218570, CA183289, CA097825, CA158831, CA135080, CA100314, CA132712, CA100433, CA193691, CA138566, CA103770, CA189715, CA160835, CA134664, CA167292, CA196381, CA172852, CA155853, CA084870, CA180963, CA155411, CA156712, CA154796, CA139279, CA163490, CA284118, CA156681, CA110548, CA248342, CA208017, CA169428, CA233919, CA204384, CA295171, CA179262, CA275173, CA100318, CA272098, CA196446, CA244403, CA220478, CA210201, CA218571, CA117867, CA096983, CA132497, CA122468, CA251047, CA136481, CA138022, CA211494, CA190471, CA175863, CA209234, CA143825, CA133828, CA067734, CA180756, CA137429, CA103045, CA100994, CA068413, CA234182, CA227939, CA263768, CA273411, CA205106)

SEQ ID No. 68: SCCCLR104C02.g  
(CA125668, CA125865, CA189739, CA125492)

SEQ ID No. 69: SCCCLR104G08.g  
(CA244725, CA238883, CA238483, CA199706, CA117832, CA204153, CA261571, CA167779, CA176803, CA189784, CA193796, CA276132)

TABLE IV-continued

List of Sugarcane Assembled Sequences (SAS) and their SEQ ID Nos.

The EST Genbank accession numbers are in parentheses. The SEQ ID No. refers to the sequence identifiers in the sequence listings. The listed ESTs assembled to the indicated sequence and should be considered one transcript. Each SAS is differentially expressed between plants with low and high sucrose content.

5 SEQ ID No. 70: SCCCLR1C05B03.g  
(CA143788, CA143875, CA143787, CA143708, CA101128, CA143785, CA157761, CA250652, CA185977, CA183646, CA120887, CA189812, CA287301)

10 15 SEQ ID No. 71: SCCCLR1C05B07.g  
(CA165238, CA208083, CA066000, CA126133, CA201529, CA116306, CA122356, CA295947, CA160571, CA120466, CA122884, CA211355, CA071582, CA264046, CA155655, CA085182, CA225540, CA066152, CA122081, CA177997, CA176532, CA071498, CA221498, CA171047, CA279593, CA189816, CA242630, CA092278, CA125314, CA170969, CA281472, CA081806, CA160840, CA272348, CA233103, CA204708, CA280170, CA198137, CA233033, CA189599, CA165234, CA086800, CA123824, CA258260, CA128698, CA140416, CA284775, CA201691, CA192826, CA189953, CA132444, CA198335, CA091105, CA091933, CA201610, 25 CA121611, CA207356, CA259590)

SEQ ID No. 72: SCCCLR1C05G07.g  
(CA297138, CA290571, CA262529, CA220559, CA204203, CA069404, CA115586, CA193158, CA121039, CA174217, CA115870, CA174293, CA104946, CA274619, CA220266, 30 CA142369, CA242315, CA160721, CA158160, CA210774, CA218047, CA233747, CA278657, CA128109, CA152442, CA184091, CA100098, CA097713, CA103537, CA217191, CA196047, CA274571, CA272485, CA069076, CA196586, CA261588, CA142478, CA202565, CA108110, CA084880, CA257882, CA229994, CA196659, CA066247, CA133689, 35 CA297542, CA173977, CA182109, CA202628, CA230076, CA086869, CA219503, CA073403, CA098116, CA173463, CA204754, CA186033, CA233775, CA101254, CA124205, CA095524, CA069310, CA128718, CA069189, CA203720, CA243929, CA287679, CA284184, CA262863, CA261604, CA123605, CA119184, CA284257, CA202222, CA119783, 40 CA196568, CA259819, CA172217, CA196643, CA068643, CA104586, CA271898, CA222538, CA091523, CA264674, CA193641, CA104655, CA132878, CA125332, CA156254, CA069514, CA300556, CA176289, CA070284, CA189868, CA070369, CA195256, CA147140, CA089091, CA234689, CA066214, CA067046, CA192673, CA269296, CA243676, CA067124, CA264162, CA263530, CA160302, CA157527, 45 CA207879, CA249440, CA104497, CA193097, CA104395, CA294629, CA117002, CA104480, CA211739, CA261852, CA126214, CA108276, CA099770, CA111230, CA166005, CA254045, CA132264, CA268441, CA132728, CA290796, CA173401, CA196261, CA272490, CA233980, CA260947, CA193010, CA225272, CA290862, CA252690, CA070750, 50 CA114221, CA070826, CA066738, CA172334, CA229793, CA267884, CA224989, CA207706, CA229890, CA156552, CA192222, CA190669, CA160369, CA275764, CA066572, CA216926, CA165930, CA244384, CA291738, CA223497, CA286984, CA178039, CA244462, CA208957, CA240296, CA067855, CA263436, CA181579, CA223577, CA146490, 55 CA249333, CA185057, CA201456, CA211242, CA144460, CA157071, CA193340, CA097777, CA194601, CA214431, CA098121, CA295608, CA127853, CA138257, CA138018, CA218660, CA141681, CA221859, CA218738, CA185406, CA197336, CA100940, CA197241, CA284997, CA291940, CA159153, CA240718, CA215992, CA225524, CA210365, CA159221, CA264160, CA235294, CA159304, CA248608, CA186071, CA211758, CA069425, CA110260, CA072797, CA105702, CA120991, CA100099, CA105781, CA244089, CA266283, CA208917, CA177938, CA167214, CA181492, CA146602, CA065458, CA183802, CA295110, CA183809, CA104306, CA227708, CA183876, CA267695, CA181557, 60 CA158128, CA104378, CA267781, CA183921, CA227789, CA147775, CA262173, CA147225, CA164441, CA186580, CA300171, CA264964, CA166300, CA186652, CA204896,

TABLE IV-continued

List of Sugarcane Assembled Sequences (SAS) and their SEQ ID Nos.  
The EST Genbank accession numbers are in parentheses. The SEQ ID No. refers to the sequence identifiers in the sequence listings. The listed ESTs assembled to the indicated sequence and should be considered one transcript. Each SAS is differentially expressed between plants with low and high sucrose content.

CA285255, CA226022, CA217982, CA224315, CA105942,  
CA158616, CA297551, CA117447, CA220364, CA168851,  
CA276987, CA190237, CA106022, CA116056, CA264622,  
CA184486, CA271818, CA168430, CA189345, CA233898,  
CA172815, CA155992, CA206379, CA166234, CA187152,  
CA212298, CA099983, CA204961, CA273020, CA169701,  
CA284310, CA180342, CA064888, CA183975, CA284388,  
CA262319, CA186021, CA248789, CA262273, CA282426,  
CA177536, CA248866, CA212699, CA110479, CA176162,  
CA144804, CA141216, CA275881, CA176238, CA184086,  
CA141296, CA224239, CA204895, CA276923, CA197046,  
CA221422, CA068719, CA068789, CA144258, CA183632,  
CA130681, CA136685, CA184391, CA112468, CA183495,  
CA103881, CA211815, CA204894, CA293260, CA099929,  
CA094118, CA284494, CA254873, CA135620, CA190021,  
CA284622, CA192812, CA135705, CA068304, CA103086,  
CA155097, CA173863, CA068377, CA110653, CA255712,  
CA209951, CA185502, CA278212, CA117995, CA255796,  
CA168934, CA098017, CA219302, CA257679, CA169019,  
CA278196, CA105166, CA101795, CA087846, CA193447,  
CA270003, CA105242, CA191196, CA266313, CA288753,  
CA257281, CA282991, CA096227, CA068749, CA197855,  
CA065529, CA222362, CA243507, CA068817, CA065600,  
CA118181, CA068718, CA238905, CA273579, CA213371,  
CA166910, CA185022, CA122534, CA158024, CA068788,  
CA070547, CA065590, CA064671, CA183774, CA164793,  
CA119888, CA091778, CA202473, CA082838, CA138229,  
CA099466, CA191901, CA124125, CA164484, CA261289,  
CA243775, CA172637, CA253160, CA067154, CA172720,  
CA097408, CA160296, CA253234, CA273519, CA067231,  
CA129930, CA097192, CA126132, CA126138, CA271899,  
CA295338, CA206463, CA067398, CA099677, CA097714,  
CA124424, CA294414, CA180655, CA294483, CA268542,  
CA211287, CA168728, CA268608, CA147090, CA117060,  
CA297065, CA193107, CA195812)

SEQ ID No. 73: SCCCLR1C08G10.g  
(CA242767, CA121427, CA190110, CA265913, CA256539, CA230257)

SEQ ID No. 74: SCCCLR2001H09.g  
(CA296017, CA073224, CA150710, CA161861, CA275518,  
CA121510, CA236217, CA121324, CA106856, CA275589,  
CA105456, CA186919, CA115199, CA072158, CA105535,  
CA198312, CA279139, CA267315, CA088244, CA228873,  
CA199179, CA117254, CA110928, CA120536, CA172530,  
CA188752, CA127047, CA079583, CA114477, CA074802,  
CA236212, CA208088, CA074878, CA214679, CA152717,  
CA292362, CA109321, CA121262, CA236850, CA257917,  
CA109407, CA131450, CA170188, CA117821, CA249112,  
CA073701, CA165055, CA280305)

SEQ ID No. 75: SCCCLR2002E04.g  
(CA189063, CA103400, CA105310, CA257545, CA074280,  
CA081249, CA225565, CA111480, CA200578, CA205658,  
CA172577, CA107282, CA203202, CA110134, CA086789,  
CA075665, CA119351, CA175412, CA278217, CA262185,  
CA289641, CA297337, CA178188, CA110401, CA071940,  
CA256334, CA073443, CA271459, CA114734, CA214806,  
CA277079, CA150950, CA112857, CA201428, CA190220,  
CA290653, CA189454, CA115238, CA127110, CA112237,  
CA300604, CA178184, CA129133, CA178175, CA286335,  
CA212524, CA213221, CA223367, CA077677, CA210590,  
CA251136, CA223442, CA255159, CA124471, CA104032,  
CA206849, CA200562, CA278797, CA278234, CA121278,  
CA295565, CA207628, CA249525, CA091812, CA187657,  
CA216232, CA124525, CA177704, CA211004, CA238405,  
CA220308)

TABLE IV-continued

List of Sugarcane Assembled Sequences (SAS) and their SEQ ID Nos.  
The EST Genbank accession numbers are in parentheses. The SEQ ID No. refers to the sequence identifiers in the sequence listings. The listed ESTs assembled to the indicated sequence and should be considered one transcript. Each SAS is differentially expressed between plants with low and high sucrose content.

5 SEQ ID No. 76: SCCCLR2002F08.g  
(CA211650, CA110492, CA148400, CA300475, CA150508,  
CA150497, CA300102, CA300257, CA095819, CA104906,  
CA091149, CA153754, CA258870, CA269965, CA297954,  
15 CA065422, CA174959, CA194403, CA106313, CA139292,  
CA248471, CA282371, CA168458, CA300988, CA166296,  
CA067041, CA288473, CA180947, CA067119, CA065892,  
CA162857, CA272827, CA296238, CA274958, CA114610,  
CA273634, CA127125, CA260192, CA300615, CA285686,  
CA152730, CA082206, CA105905, CA285436, CA070842,  
CA218583, CA168512, CA070916, CA101647, CA295802,  
20 CA211573, CA262162, CA132706, CA287764, CA285726,  
CA272603, CA196573, CA273889, CA105900, CA296728,  
CA262057, CA162541, CA064764, CA297035, CA297113,  
CA225722, CA125625, CA281507, CA129167, CA288837,  
CA106118, CA287900, CA177953, CA124483, CA128800,  
CA218582, CA276318, CA287392, CA278517, CA218499,  
25 CA218007, CA299081, CA295773, CA207196, CA145252,  
CA150651, CA261878, CA107256, CA155204, CA155181,  
CA296047, CA085447, CA127248, CA171611, CA300905,  
CA274697, CA184257, CA278069, CA275866, CA070109,  
CA141467, CA070191, CA152802, CA287858, CA190605,  
CA154302, CA199564, CA283532, CA209584, CA296251,  
30 CA291158, CA064871, CA102133, CA275969, CA141502,  
CA275504, CA141819, CA275580, CA106944, CA120936,  
CA150645, CA118413, CA274736, CA296185, CA223170,  
CA208853, CA283624, CA067879, CA107873, CA264649,  
CA288282, CA138280, CA148571, CA276218, CA260193)

35 SEQ ID No. 77: SCCCLR2002H11.g  
(CA127148, CA113376, CA090822, CA175277, CA144706,  
CA191342, CA249121, CA112140)

40 SEQ ID No. 78: SCCCLR2003E10.g  
(CA261916, CA072670, CA127180, CA082686, CA098222,  
CA072679, CA227230, CA230364, CA102583, CA131720)

SEQ ID No. 79: SCCCLR2C01F06.g  
(CA125903, CA130165, CA127342, CA123725)

45 SEQ ID No. 80: SCCCLR2C02A05.g  
(CA116671, CA130253)

50 SEQ ID No. 81: SCCCLR2C02D03.g  
(CA262689, CA083750, CA101533, CA177058, CA236874,  
CA100362, CA128908, CA171906, CA102805, CA115056,  
CA127401, CA146627, CA158448, CA098804, CA146619,  
CA258980, CA215587, CA265819, CA265880, CA212035,  
CA261941, CA071913, CA267912, CA154469, CA079309,  
CA174463, CA118147, CA146622, CA273451, CA117370,  
CA267710, CA188407, CA122342)

60 SEQ ID No. 82: SCCCRT1001E01.g  
(CA145556, CA265124, CA140467, CA259428, CA269652,  
55 CA132841, CA253363, CA298816, CA258474, CA265609,  
CA240255, CA185830, CA130669, CA139431, CA130399,  
CA260672, CA138292, CA218105, CA266538, CA269994,  
CA218177, CA258974, CA145910, CA190685, CA221999,  
CA190860, CA259945, CA080912, CA278886, CA264789,  
CA145914, CA107290, CA273194, CA260082, CA137145,  
CA265723, CA145474, CA131856, CA265716)

65 SEQ ID No. 83: SCCCRT2002G11.g  
(CA098113, CA259292, CA167710, CA160985, CA167765,  
CA277212, CA301138, CA252372, CA264993, CA166058,  
CA174697, CA080916, CA298478, CA108271, CA213368,  
CA173993, CA211356, CA158908, CA162533, CA194961,  
CA184093, CA096644, CA161001, CA300513, CA144742,  
CA229700, CA266477, CA092549, CA193396, CA197153,

TABLE IV-continued

List of Sugarcane Assembled Sequences (SAS) and their SEQ ID Nos.

The EST Genbank accession numbers are in parentheses. The SEQ ID No. refers to the sequence identifiers in the sequence listings. The listed ESTs assembled to the indicated sequence and should be considered one transcript. Each SAS is differentially expressed between plants with low and high sucrose content.

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CA096270, CA267077, CA174874, CA298338, CA158349, CA214804, CA136971, CA263769, CA225513, CA214883, CA157020, CA263846, CA281339, CA164770, CA160919, CA203458, CA290101, CA161006, CA114942, CA289802, CA195261, CA298479, CA198016, CA197064, CA298238, CA171959, CA172546, CA273048, CA299633, CA137199, CA156278, CA160900, CA194153, CA265809, CA160988, CA247104, CA174172, CA265871, CA191620, CA198789, CA175182, CA141419, CA174246, CA256737, CA123842, CA171971, CA172544, CA109630, CA163657, CA174143, CA256660, CA217966, CA109716, CA268027, CA157316, CA295099)

SEQ ID No. 84: SCCCZRZ1001F02.g  
(CA103948, CA150083, CA259661, CA300458, CA260819, CA115748, CA132394, CA139574, CA150333, CA137265, CA174881, CA276459, CA187808, CA162788, CA225541, CA236121, CA272799, CA143215, CA086510, CA126049, CA140320, CA190692, CA214128, CA293279, CA232739, CA288829, CA232827, CA205598, CA154561, CA258276, CA137338, CA285532, CA128190, CA142456, CA201134, CA132162, CA228245, CA126555, CA071690, CA209954, CA143470, CA248359, CA200342, CA115266, CA136159, CA207491, CA279420, CA272494, CA229717, CA287861, CA289897, CA292215, CA288557, CA123136, CA106015, CA109649, CA124195, CA256039, CA106083, CA259023, CA109734, CA182936, CA146835, CA267500, CA260093, CA161128, CA213896, CA260715, CA247923, CA260696, CA232980, CA235230, CA161214, CA233046, CA183253, CA106339, CA205597, CA226389, CA213070, CA085049, CA118942, CA065078, CA265611, CA065008, CA284023)

SEQ ID No. 85: SCCCZRZ1001H05.g  
(CA145736, CA287892, CA192135, CA146862, CA234792, CA101303, CA204402, CA151180, CA119789, CA288119, CA151262, CA080448, CA145653, CA095725)

SEQ ID No. 86: SCCCZRZ1002E08.g  
(CA179035, CA191340, CA233483, CA300253, CA085975, CA269763, CA262601, CA236263, CA070203, CA086063, CA190618, CA085969, CA300380, CA120960, CA294874, CA180727, CA292085, CA301489, CA086058, CA273085, CA131694, CA285350, CA182564, CA244750, CA238660, CA244829, CA243124, CA180028, CA144527, CA228073, CA159113, CA260317, CA161623, CA185003, CA184781, CA101457, CA136411, CA287945, CA269808, CA299418, CA142515, CA174197, CA128767, CA268523, CA174275, CA282823, CA146924, CA251224, CA172558, CA131340, CA200210, CA228169, CA184495, CA201598, CA178951, CA130651, CA183353)

SEQ ID No. 87: SCCCZRZ1002H08.g  
(CA279826, CA135036, CA124184, CA076729, CA240511, CA076725, CA146959, CA291640, CA146710, CA066324, CA122936, CA203952, CA156670, CA162985, CA245296, CA278468, CA117478, CA184525, CA207771, CA116304, CA240781)

SEQ ID No. 88: SCCCZRZ1004H12.g  
(CA216874, CA081561, CA106731, CA251585, CA066538, CA114810, CA148014, CA114649, CA267565, CA267650, CA088912, CA149128, CA227151, CA105454, CA125437, CA269856, CA187518, CA066036, CA286910, CA265042, CA234010, CA160780, CA185108, CA149229, CA110623, CA264544, CA095591, CA150496, CA111584, CA176699, CA140671, CA108165, CA123092, CA283700, CA287402, CA167981, CA064988, CA275544, CA177425, CA141224, CA275615, CA211803, CA125932, CA212296, CA141306, CA191643, CA140689, CA279161, CA079659, CA240039,

TABLE IV-continued

List of Sugarcane Assembled Sequences (SAS) and their SEQ ID Nos.

The EST Genbank accession numbers are in parentheses. The SEQ ID No. refers to the sequence identifiers in the sequence listings. The listed ESTs assembled to the indicated sequence and should be considered one transcript. Each SAS is differentially expressed between plants with low and high sucrose content.

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CA159148, CA174083, CA067685, CA198561, CA143599, CA267523, CA097307, CA067769, CA267610, CA101896, CA096607, CA124965, CA248186, CA124435, CA108814, CA134608, CA192137, CA108989, CA134689, CA166683, CA094488, CA291849, CA109073, CA153798, CA147144, CA299990, CA173707, CA267553, CA225467, CA273321, CA110109, CA267638, CA104185, CA161871, CA290349, CA270432, CA163555, CA154762, CA222553, CA270296, CA166573, CA108407, CA182036, CA164299, CA202506, CA075284, CA225393, CA277703, CA202590, CA102086, CA110611, CA065056, CA233782, CA197286, CA229575, CA277050, CA157909, CA277094, CA140749, CA137396, CA196896, CA282885, CA239918, CA301434, CA196962, CA164275, CA084201, CA275533, CA145361, CA234812, CA275603, CA081143, CA186963, CA195293, CA131246, CA163061, CA180624, CA120533, CA181897, CA192846, CA159009, CA067687, CA225503, CA193928, CA170449, CA067771, CA156228, CA157265)

SEQ ID No. 89: SCCCZRZ2001A10.g  
(CA083266, CA170546, CA213983, CA240546, CA214055, CA068172, CA243400, CA112026, CA159624, CA178417, CA149593, CA195353)

SEQ ID No. 90: SCCCZRZ2001E12.g  
(CA220407, CA069786, CA266584, CA117131, CA149640, CA102694, CA107051, CA126788, CA178629, CA116298, CA189528)

SEQ ID No. 91: SCCCZRZ2003E12.g  
(CA290451, CA171106, CA257067, CA126312, CA285909, CA191695, CA175249, CA277181, CA198875, CA264876, CA228763, CA257385, CA149818, CA268790, CA228758, CA239922, CA147478)

SEQ ID No. 92: SCCCZRZ2C01F09.g  
(CA238345, CA110244, CA292133, CA226215, CA290161, CA089133, CA225941, CA087675, CA081960, CA263629, CA263709, CA271851, CA098120, CA103239, CA241010, CA081617, CA127228, CA241092, CA249515, CA289050, CA081621, CA285377, CA149903, CA084191, CA237910, CA287616, CA170459, CA180444, CA241705, CA072646, CA198212, CA140343, CA074071, CA260574, CA275241, CA219063, CA230826, CA216366, CA284463, CA231731, CA275313, CA277199, CA284538, CA085114, CA146451, CA238575, CA170457, CA241499, CA276966, CA150000, CA194018, CA282348, CA151656, CA292177, CA151735, CA081964, CA276948, CA281247, CA148593, CA127998, CA297924, CA098115, CA225142, CA104406)

SEQ ID No. 93: SCCCSD1003E02.g  
(CA284001, CA285612, CA291203, CA278558, CA277223, CA285546, CA272455, CA284812, CA288109, CA285276, CA274083, CA274097, CA282761, CA284853, CA282957, CA276485, CA288135, CA282680, CA287028, CA288317, CA301448, CA281013, CA278500, CA287354)

SEQ ID No. 94: SCCCSD1092A08.g  
(CA284222, CA275878, CA276919, CA284291, CA284297, CA281361, CA273485, CA285647, CA286280, CA287406)

SEQ ID No. 95: SCCCSD2001E05.g  
(CA282080, CA282487, CA278050, CA284383, CA274256)

SEQ ID No. 96: SCCCSD2C03G12.g  
(CA301232, CA297876, CA297283)

TABLE IV-continued

List of Sugarcane Assembled Sequences (SAS) and their SEQ ID Nos.

The EST Genbank accession numbers are in parentheses. The SEQ ID No. refers to the sequence identifiers in the sequence listings. The listed ESTs assembled to the indicated sequence and should be considered one transcript. Each SAS is differentially expressed between plants with low and high sucrose content.

SEQ ID No. 97: SCCCST1001C04.g  
(CA096261, CA241976, CA265094, CA217159, CA169670, CA085862, CA103281, CA236141, CA230822, CA166981, CA178741, CA173538)

SEQ ID No. 98: SCCCST1006B11.g  
(CA211361, CA070492, CA219037, CA070499, CA178358, CA173923, CA217421, CA217710)

SEQ ID No. 99: SCCCST3001H12.g  
(CA182157, CA090806, CA135450, CA192177, CA157038, CA180203, CA186190, CA185139, CA088464, CA107032, CA186187)

SEQ ID No. 100: SCEPAM1020A03.g  
(CA298761, CA238039, CA072781, CA202979, CA265514, CA203056, CA216879, CA274267, CA154767, CA072753, CA232137, CA272619)

SEQ ID No. 101: SCEPLR1030B03.g  
(CA284018, CA296786, CA191311, CA135484, CA132970, CA260298, CA293358, CA232052, CA145338, CA296858, CA300403, CA289136, CA190455, CA256928, CA276730, CA114900, CA151879, CA131612, CA285822, CA281761, CA277035, CA131569, CA256849, CA139403, CA120776, CA111640, CA144584, CA109836, CA163350, CA103723, CA138138)

SEQ ID No. 102: SCEPLR1030E06.g  
(CA120812, CA166500, CA121058, CA157792, CA147349)

SEQ ID No. 103: SCEPRZ1008F02.g  
(CA084261, CA147347, CA090873, CA152001, CA234969, CA091560, CA150615, CA253916, CA204783, CA205748, CA192626, CA201996, CA202076, CA280863, CA162916, CA088703, CA085702, CA175387, CA269587, CA152933, CA092690, CA229677, CA152922, CA200559, CA156055, CA170331, CA140801, CA256055, CA152711, CA153264, CA199353, CA091994, CA151595, CA221404, CA153337, CA198274, CA151680, CA273193, CA214750, CA249251, CA084265, CA113829)

SEQ ID No. 104: SCEPRZ1010E06.g  
(CA153095, CA171009, CA300383, CA134779, CA147516, CA171086, CA290145, CA187047, CA190622, CA249955, CA131632, CA285405, CA195540, CA146683, CA255486, CA274214, CA143354, CA262861, CA250035, CA196569, CA205156, CA196644, CA296007, CA172028, CA184943, CA117936, CA257643)

SEQ ID No. 105: SCEPRZ3087C08.g  
(CA160294, CA160210)

SEQ ID No. 106: SCEQLB2019B08.g  
(CA279976, CA272048)

SEQ ID No. 107: SCEQLR1007G03.g  
(CA140431, CA259456, CA211527, CA271749, CA266277, CA141614, CA215266, CA220502, CA201033, CA142803, CA094784, CA172036, CA107212, CA194369, CA295096, CA065513, CA157629, CA181854, CA099236, CA296097, CA068795, CA145592, CA157045, CA169225, CA195900, CA289800, CA083770, CA103698, CA196336, CA066685, CA279318, CA134272, CA169306, CA144849, CA173189, CA190898, CA206313, CA176452, CA257180, CA084874, CA101125, CA249765, CA284335, CA162053, CA180997, CA197651, CA143812, CA188901, CA194298, CA234171, CA085641, CA267721, CA123786, CA267873, CA139542, CA208084, CA097722, CA158840, CA103745, CA232413,

TABLE IV-continued

List of Sugarcane Assembled Sequences (SAS) and their SEQ ID Nos.

The EST Genbank accession numbers are in parentheses. The SEQ ID No. refers to the sequence identifiers in the sequence listings. The listed ESTs assembled to the indicated sequence and should be considered one transcript. Each SAS is differentially expressed between plants with low and high sucrose content.

5  
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15  
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SEQ ID No. 108: SCEQLR1091A10.g  
(CA114539, CA257837, CA077076, CA262215, CA274238, CA211402, CA274108, CA230959, CA121144, CA256388, CA288382, CA079882, CA230878, CA241079, CA256311, CA237783, CA240995, CA073200, CA235765, CA113590, CA126147, CA077764, CA118720, CA123712, CA286990, CA281182, CA111839, CA124521, CA077641, CA255256, CA111725, CA129312, CA216352, CA209624, CA111908, CA155939, CA189115, CA135189, CA235762, CA291159, CA238370)

SEQ ID No. 109: SCEQRT1024B02.g  
(CA216940, CA225607, CA179965, CA204515, CA132482, CA185736)

SEQ ID No. 110: SCEQRT1024E12.g  
(CA295147, CA260615, CA254686, CA132523, CA197622, CA204899, CA190453, CA212246, CA197604, CA270758, CA270346, CA130936, CA269290, CA256715, CA132252, CA182867, CA107713, CA256638, CA258402, CA217358, CA184651, CA109919, CA185468, CA217428, CA156179, CA220042, CA109994, CA284009, CA2214271, CA139017, CA135234, CA260181, CA234511, CA161112, CA102825, CA183055, CA103445, CA192331, CA107252, CA161202, CA288819, CA107320, CA258917, CA244198, CA220062, CA259939, CA069469, CA244275, CA220141, CA185728, CA284013)

SEQ ID No. 111: SCEQRT1025D04.g  
(CA210404, CA217344, CA296134, CA217415, CA187015)

SEQ ID No. 112: SCEQRT1025D06.g  
(CA132593, CA141785, CA141018, CA215251)

SEQ ID No. 113: SCEQRT1026H08.g  
(CA145460, CA069364, CA140129, CA250315, CA145544, CA141404, CA293054, CA282922, CA163907, CA261070, CA163990, CA205321, CA173746, CA283810, CA134025,

TABLE IV-continued

List of Sugarcane Assembled Sequences (SAS) and their SEQ ID Nos.

The EST Genbank accession numbers are in parentheses. The SEQ ID No. refers to the sequence identifiers in the sequence listings. The listed ESTs assembled to the indicated sequence and should be considered one transcript. Each SAS is differentially expressed between plants with low and high sucrose content.

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CA170490, CA240108, CA069401, CA280554, CA277690, CA168030, CA240167, CA222954, CA132730, CA217518, CA277435, CA191682, CA190599, CA133625, CA264946, CA277153, CA070912, CA217975, CA146562, CA284169, CA143199, CA087655, CA287350, CA273405, CA084518, CA301511, CA143266, CA290482)

SEQ ID No. 114: SCEQRT1028C03.g  
(CA139365, CA286665, CA260598, CA139023, CA285888, CA274666, CA137906, CA281362, CA285687, CA136311, CA141788, CA103170, CA133136, CA269938, CA284682, CA288527, CA141870, CA285073, CA285465, CA284318, CA287456, CA130761, CA137490, CA144380, CA297849, CA131873, CA143782, CA281126, CA143182, CA191432, CA284091, CA278152, CA164514, CA139044, CA138535, CA283285, CA106682, CA102643, CA136156, CA132845, CA276716, CA275759, CA284563, CA268586, CA268592, CA143781, CA268641, CA284432, CA273135, CA139564, CA297995, CA268645, CA287370, CA143142, CA138952, CA143227, CA297005, CA101363, CA142135, CA115501, CA278630, CA138496, CA101781, CA286567, CA141623, CA136320, CA136240, CA288341, CA288312, CA104716, CA288071, CA193582, CA130778, CA297953, CA104799, CA143442, CA274724, CA104459, CA104545, CA274625, CA290645, CA278030, CA275085, CA138291, CA145190, CA144775, CA290713, CA133241, CA141076, CA272524, CA146265, CA293757, CA135230, CA139625, CA277500, CA131620, CA269954, CA131757, CA106126, CA268581, CA273592, CA106187, CA136999, CA288204, CA277749, CA143039, CA278287, CA139806)

SEQ ID No. 115: SCEQRT1031D02.g  
(CA074042, CA088825, CA075266, CA271676, CA295638, CA133114, CA268786, CA112006, CA291853, CA269112, CA089768, CA292656, CA273097, CA078197, CA073875, CA074037, CA189360, CA260450)

SEQ ID No. 116: SCEQRT1033H06.g  
(CA101392, CA115952, CA155650, CA133340, CA213648, CA215953, CA108139, CA102933, CA163612)

SEQ ID No. 117: SCEQRT2098H06.g  
(CA172591, CA163271, CA229649, CA139483)

SEQ ID No. 118: SCEQRT2099H01.g  
(CA086208, CA264357, CA086287, CA080644, CA266323, CA161194, CA300091, CA287964, CA221671, CA131618, CA251982, CA221152, CA159591, CA221951, CA156418, CA240390, CA161187, CA159676, CA139559, CA077881, CA161261, CA110139, CA077863)

SEQ ID No. 119: SCEQRT2100B02.g  
(CA217945, CA139573, CA204327, CA260706, CA204248, CA269222, CA269284)

SEQ ID No. 120: SCEQRZ3020C02.g  
(CA250725, CA161134, CA165966, CA160060, CA156919, CA164968, CA251491, CA069428)

SEQ ID No. 121: SCEZAM2058E08.g  
(CA188635, CA183792, CA195687, CA084907, CA081270, CA081191, CA173384)

SEQ ID No. 122: SCEZHR1047A01.g  
(CA103161, CA101776)

SEQ ID No. 123: SCEZHR1087F06.g  
(CA253395, CA197374, CA287472, CA103877, CA278023)

TABLE IV-continued

List of Sugarcane Assembled Sequences (SAS) and their SEQ ID Nos.

The EST Genbank accession numbers are in parentheses. The SEQ ID No. refers to the sequence identifiers in the sequence listings. The listed ESTs assembled to the indicated sequence and should be considered one transcript. Each SAS is differentially expressed between plants with low and high sucrose content.

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SEQ ID No. 124: SCEZHR1088E02.g  
(CA301005, CA296733, CA247972, CA103945, CA243569, CA251930)

SEQ ID No. 125: SCEZLB1009A09.g  
(CA281626, CA244568, CA116483, CA237705, CA298353, CA298000, CA113117, CA284416, CA277289, CA284348, CA276706, CA290833, CA203091, CA101727, CA176398, CA132760, CA096672, CA290760, CA282167)

SEQ ID No. 126: SCEZLB1010E10.g  
(CA111286, CA201293, CA292534, CA113224, CA078624)

SEQ ID No. 127: SCEZLB1012F10.g  
(CA174564, CA069051, CA216445, CA163915, CA198521, CA068371, CA296305, CA113392, CA099142, CA163996, CA166390, CA116217, CA210122, CA074493, CA114992, CA275989)

SEQ ID No. 128: SCEZLR1052E07.g  
(CA121650, CA116831, CA120886)

SEQ ID No. 129: SCEZRZ3098G10.g  
(CA296471, CA160526, CA273318, CA275478, CA283208, CA160609, CA285866, CA277278, CA158745, CA283693, CA285324, CA285071, CA284153, CA274955, CA285128, CA297181, CA278664, CA272542, CA273750, CA294380, CA287923, CA273821, CA294450, CA297756, CA274726, CA296701, CA277926, CA296395, CA286712, CA286723, CA286722, CA275718, CA275927, CA283291, CA275408)

SEQ ID No. 130: SCEZST3147A10.g  
(CA194007, CA182656)

SEQ ID No. 131: SCJFFL3C03C02.g  
(CA230214, CA230128, CA229489)

SEQ ID No. 132: SCJFLR1035E04.g  
(CA086527, CA195068, CA069060, CA083548, CA295865, CA177350, CA177349, CA277098, CA276954, CA155838, CA197797, CA244043, CA088503, CA121818, CA080812, CA155548, CA078754, CA089206, CA163208, CA129874, CA211416, CA276961, CA144131, CA158866, CA155542, CA199612, CA263981)

SEQ ID No. 133: SCJFLR1074E09.g  
(CA262344, CA266655, CA176711, CA133325, CA122163, CA131810, CA082004, CA181680, CA180565, CA078933, CA085138, CA210263, CA210980, CA184457, CA262635, CA176142, CA234269, CA176141, CA178297, CA183158, CA082635, CA082991, CA198762, CA190715, CA190706, CA274415, CA081600, CA279078, CA181928, CA081942, CA267908, CA089450, CA084567, CA186427, CA078935)

SEQ ID No. 134: SCJFRT1005C11.g  
(CA177520, CA225223, CA106003, CA253319, CA171361, CA209379, CA270001, CA185425, CA155754, CA167026, CA270006, CA106095, CA213061, CA170199, CA287881, CA132140, CA204757, CA155038, CA133369, CA254157, CA280727, CA260033, CA146511, CA186031, CA161879, CA296036, CA220424, CA220423, CA102390, CA184239)

SEQ ID No. 135: SCJFRT1007E01.g  
(CA267659, CA267574, CA259232, CA265484, CA145383, SCJLLB2077E09.b)

SEQ ID No. 136: SCJFRT1007H07.g  
(CA232046, CA260877, CA092783, CA231963, CA204189, CA133468, CA244788, CA244787, CA254691, CA244858,



TABLE IV-continued

List of Sugarcane Assembled Sequences (SAS) and their SEQ ID Nos.

The EST Genbank accession numbers are in parentheses. The SEQ ID No. refers to the sequence identifiers in the sequence listings. The listed ESTs assembled to the indicated sequence and should be considered one transcript. Each SAS is differentially expressed between plants with low and high sucrose content.

CA204513, CA230346, CA256769, CA108120, CA089835, CA204647, CA264840, CA230425, CA268306, CA258270, CA222112, CA165049, CA222037, CA259725, CA114043, CA233931, CA259471)

SEQ ID No. 137: SCJFRT2055G07.g  
(CA096216, CA243260, CA285937, CA230920, CA140859, CA083416)

SEQ ID No. 138: SCJFRZ2007F10.g  
(CA162683, CA160048, CA279259, CA151224, CA159697, CA156537, CA162591, CA113918, CA160134, CA162626, CA081758, CA165192, CA159782, CA162706, CA151304, CA266640)

SEQ ID No. 139: SCJFRZ2012F04.g  
(CA151819, CA226484, CA196727, CA176517, CA200020)

SEQ ID No. 140: SCJFRZ2034D04.g  
(CA293545, CA237627, CA152997)

SEQ ID No. 141: SCJFRZ3C03H08.g  
(CA159498, CA159411)

SEQ ID No. 142: SCJFST1009H11.g  
(CA176832, CA174223, CA174300)

SEQ ID No. 143: SCJLLR1054C03.g  
(CA072193, CA122571, CA137632, CA070187, CA191143, CA188078, CA249372, CA249371, CA077923, CA208829, CA208828, CA070105, CA261620)

SEQ ID No. 144: SCJLRT1016G06.g  
(CA135201, CA141549)

SEQ ID No. 145: SCJLRT1021D12.g  
(CA169233, CA144275, CA169232, CA076021, CA075936, CA184045, CA135772, CA095372, CA216051, CA168410)

SEQ ID No. 146: SCJLRT1023A09.g  
(SCJLRT1023A09.g, CA182963, CA250841, CA248659)

SEQ ID No. 147: SCJLRZ1021D12.g  
(CA242041, CA249059, CA254109, CA213847, CA137917, CA148975, CA118183, CA214586, CA197889, CA144551, CA196585, CA262465)

SEQ ID No. 148: SCJLST1022A12.g  
(CA212757, CA175747, CA184421)

SEQ ID No. 149: SCMCLR1123E10.g  
(CA123814, CA077430, CA225563)

SEQ ID No. 150: SCMCR2103B04.g  
(CA172001, CA142458, CA218053)

SEQ ID No. 151: SCMCS2061D05.g  
(CA281642, CA278782, CA287422)

SEQ ID No. 152: SCQGHR1010D02.g  
(CA106316)

SEQ ID No. 153: SCQGHR1012B09.g  
(CA287612, CA106449)

SEQ ID No. 154: SCQGLR1085F11.g  
(CA264338, CA126544, CA192941, CA167483, CA123056, CA124270, CA272314, CA261490, CA279307, CA265550, CA271792, CA122975, CA264343, CA270329, CA273106)

TABLE IV-continued

List of Sugarcane Assembled Sequences (SAS) and their SEQ ID Nos.

The EST Genbank accession numbers are in parentheses. The SEQ ID No. refers to the sequence identifiers in the sequence listings. The listed ESTs assembled to the indicated sequence and should be considered one transcript. Each SAS is differentially expressed between plants with low and high sucrose content.

SEQ ID No. 155: SCQGR1040G03.g  
(CA142863, CA142796, CA136289)

SEQ ID No. 156: SCQGSB1082E12.g  
(CA170065)

SEQ ID No. 157: SCQSRT1036D03.g  
(CA136902, CA135021, CA287878, CA274443, CA296937, CA138673, CA191058)

SEQ ID No. 158: SCQSSB1077D06.g  
(CA170725)

SEQ ID No. 159: SCRFHR1009G06.g  
(CA217470, CA107403, CA198006, CA217550)

SEQ ID No. 160: SCRFRLR1012D12.g  
(CA215552, CA192043, CA124962, CA125195, CA145888, CA121817, CA278865, CA174653, CA248262, CA272947, CA260358, CA291459, CA203303, CA1433179, CA141645, CA178853, CA187649, CA206782, CA090093, CA143252, CA278919)

SEQ ID No. 161: SCRFRLR1012F12.g  
(CA145277, CA176384, CA102865, CA218229, CA171925, CA191792, CA195660, CA218314, CA240492, CA198659, CA244914, CA182463, CA131724, CA244997, CA171817, CA194382, CA205344, CA170805, CA205416, CA173212, CA170885, CA181179, CA170637, CA183044, CA195239, CA206962, CA185418, CA139670, CA195249, CA176430, CA181413, CA181342, CA091964, CA183864, CA222085, CA258352, CA140506, CA180474, CA119811, CA222017, CA195130, CA185570, CA296593, CA194982, CA183360, CA173154, CA186079, CA296664, CA171270, CA195468, CA183252, CA294806, CA132456, CA195394, CA206688, CA256506, CA131509, CA187503, CA256594, CA108050, CA159196, CA240650, CA177662, CA159279, CA177742, CA239913, CA171438, CA156947, CA173255, CA256346, CA235445, CA256418, CA186679, CA219554, CA187631, CA186748, CA245097, CA185375, CA219625, CA181621, CA187266, CA123999, CA244218, CA245173, CA182407, CA253693, CA184655, CA143210, CA180512, CA256622, CA244292, CA185011, CA143274, CA168051, CA130540, CA207436, CA219682, CA066624, CA216694, CA178229, CA256208, CA213213, CA171923, CA189901, CA181034, CA102783, CA146612, CA118091, CA130413, CA185759, CA180234, CA184401, CA069670, CA186382, CA186701, CA164112, CA186458, CA186769, CA191147, CA181041, CA191952, CA298549, CA187520, CA155473, CA111918, CA181356, CA215886, CA145798, CA143022, CA249269, CA168083, CA215375, CA073688, CA161824, CA216676, CA198787, CA145199, CA254628, CA186888, CA213066, CA091970, CA215884, CA143890, CA222334, CA220813, CA171807, CA181203, CA130692, CA186145, CA260159, CA158846, CA064841, CA295391, CA192487, CA132539, CA300897, CA141052, CA155506, CA182241, CA187303, CA258020, CA066321, CA125200, CA170189, CA108039, CA159362, CA173331, CA298200, CA101575, CA159451, CA116648, CA183460, CA107663, CA240851, CA289373, CA185342, CA240929, CA216040, CA186847, CA181218, CA172612, CA180663, CA136914, CA217359, CA163192, CA172697, CA228382, CA217429, CA159166, CA185025, CA192456, CA102223, CA156933, CA101474, CA183302, CA186227, CA159239, CA269601, CA181346, CA102790, CA187044, CA184058, CA195530, CA255719, CA136787, CA255803, CA140448, CA247100, CA183704, CA222949, CA183064, CA168215, CA292284, CA272087, CA174156, CA131207, CA203204, CA181678, CA195537, CA174230,

TABLE IV-continued

List of Sugarcane Assembled Sequences (SAS) and their SEQ ID Nos.

The EST Genbank accession numbers are in parentheses. The SEQ ID No. refers to the sequence identifiers in the sequence listings. The listed ESTs assembled to the indicated sequence and should be considered one transcript. Each SAS is differentially expressed between plants with low and high sucrose content.

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CA113053, CA213323, CA181745, CA183105, CA137679,  
 CA221917, CA234916, CA191379, CA207396, CA249902,  
 CA203603, CA257333, CA192868, CA108462, CA131411,  
 CA272376, CA194489, CA249816, CA257417, CA207923,  
 CA183017, CA194671, CA163065, CA185665, CA257591,  
 CA182994, CA279934, CA208015, CA186256, CA177351,  
 CA132757, CA146153, CA172253, CA181813, CA182473,  
 CA181263, CA182486, CA185227, CA144437, CA210632,  
 CA179930, CA163280, CA178697, CA187150, CA102845,  
 CA183295, CA203119, CA167619, CA183126, CA240601,  
 CA167572, CA197131, CA187498, CA187269, CA181877,  
 CA154563, CA166216, CA198634, CA255532, CA221973,  
 CA205215, CA165092, CA211170, CA179824, CA185664,  
 CA162302, CA185103, CA138255, CA173288, CA168237,  
 CA234213, CA138061, CA256349, CA170955, CA162207,  
 CA168159, CA134163, CA181092, CA256421, CA081501,  
 CA134612, CA216664, CA171033, CA180502, CA108052,  
 CA134694, CA242240, CA185226, CA193845, CA210899,  
 CA159347, CA266029, CA159436, CA171415, CA135255,  
 CA233811, CA171999, CA187597, CA180638, CA135773,  
 CA253334, CA131134, CA182234, CA184039, CA166175,  
 CA180410, CA280449, CA297478, CA194983, CA215483,  
 CA264565, CA107740)

SEQ ID No. 162: SCRFLR1034G06.g  
 (CA241449, CA235335, CA117136, CA164653, CA178183,  
 CA254415, CA125238, CA164095, CA222593, CA230775,  
 CA129494, CA187277, CA096098, CA163037, CA217349,  
 CA216252, CA163492)

SEQ ID No. 163: SCRFLR2037F09.g  
 (CA209741, CA268887, CA178192, CA261014, CA242867,  
 CA265801, CA197228, CA129199, CA263453, CA263426,  
 CA146361, CA212193, CA198338, CA263428, CA292726)

SEQ ID No. 164: SCRUD1063D03.g  
 (CA068586, CA068642, CA209109, CA068658, CA068557)

SEQ ID No. 165: SCRUD1064B08.g  
 (CA068774, CA209078, CA068700)

SEQ ID No. 166: SCRUF11112F04.b  
 (CA249652, CA097438, CA097351)

SEQ ID No. 167: SCRULB1060F05.g  
 (CA173325, CA260726, CA086474, CA255253, CA258837,  
 CA166401, CA075394, CA076741, CA220439, CA079619,  
 CA202888, CA275737, CA272422, CA086576, CA261359,  
 CA115018, CA176599)

SEQ ID No. 168: SCRULB2065G10.g  
 (CA271141, CA266659, CA271226)

SEQ ID No. 169: SCRUSB1062E12.g  
 (CA169672, CA208550, CA182671, CA171140, CA184190)

SEQ ID No. 170: SCSBAD1084C01.g  
 (CA104637, CA090516, CA196055, CA105810, CA069997,  
 CA104732, CA225658, CA250072, CA255717, CA256367,  
 CA256852, CA104815, CA255801, CA223408, CA217811,  
 CA230204, CA222042, CA266094, CA202055)

SEQ ID No. 171: SCSBAM1084E01.g  
 (CA134918, CA160648, CA271201, CA163376, CA159473,  
 CA079123, CA287106)

SEQ ID No. 172: SCSBAM1085B06.g  
 (CA155118, CA160431, CA238835, CA164387, CA159328,  
 CA079174, CA166634, CA111526)

TABLE IV-continued

List of Sugarcane Assembled Sequences (SAS) and their SEQ ID Nos.

The EST Genbank accession numbers are in parentheses. The SEQ ID No. refers to the sequence identifiers in the sequence listings. The listed ESTs assembled to the indicated sequence and should be considered one transcript. Each SAS is differentially expressed between plants with low and high sucrose content.

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SEQ ID No. 173: SCSBAM1086F04.g  
 (CA079296)

SEQ ID No. 174: SCSBHR1050B11.g  
 (CA210645, CA170681, CA167697, CA107340, CA215631,  
 CA206834, CA108412, CA182286, CA197994, CA277167,  
 CA163113, CA192646, CA276916, CA265467, CA181920,  
 CA184384, CA273323, CA211222, CA211754, CA185581,  
 CA219190, CA260157, CA102243, CA286611, CA185579,  
 CA218411, CA288879, CA193027, CA229712, CA196151,  
 CA218111, CA212330, CA256722, CA283661, CA195272,  
 CA206786, CA197939, CA102985, CA182506, CA284298,  
 CA268890, CA068317, CA213471, CA211376, CA124505,  
 CA068559, CA110532, CA110645, CA196292, CA274987,  
 CA291082)

SEQ ID No. 175: SCSBHR1052E03.g  
 (CA109838, CA103669, CA108022)

SEQ ID No. 176: SCSBSD2029D11.g  
 (CA273475, CA291058, CA296853, SCEPSD1006B07.g,  
 CA296781)

SEQ ID No. 177: SCSBSD2029F05.g  
 (CA277625, CA286610, CA287004, CA286219)

SEQ ID No. 178: SCSBST3096H04.g  
 (CA250727, CA185029, CA081571, CA209300, CA099207)

SEQ ID No. 179: SCSFAD1125C08.g  
 (CA218816, CA217232, CA265904)

SEQ ID No. 180: SCSGAM1094D05.g  
 (CA162116, CA086160, CA079959, CA166087, CA164634,  
 CA259450, CA162089, CA268215, CA162088, CA088600,  
 CA268472, CA260072, CA265273, CA155162)

SEQ ID No. 181: SCSGFL4193B05.g  
 (CA256924, CA227764, CA065586)

SEQ ID No. 182: SCSGHR1069F04.b  
 (CA068965, CA109244)

SEQ ID No. 183: SCSGLR1045F05.g  
 (CA227916, CA126326, CA235027, CA271367, CA096003,  
 CA217599, CA092647, CA123937, CA126293, CA212141,  
 CA184768, CA103141, CA109865, CA103057, CA198702,  
 CA103058)

SEQ ID No. 184: SCSGSB1009D11.g  
 (CA172723, CA195396, CA172640)

SEQ ID No. 185: SCUTAM2005B03.g  
 (CA090809, CA245425)

SEQ ID No. 186: SCUTAM2115C12.g  
 (CA086564, CA086570, CA092157)

SEQ ID No. 187: SCUTLR2023D06.g  
 (CA243852, CA300860, CA067973, CA111863, CA261222,  
 CA116646, CA107988, CA176922, CA173185, CA085544,  
 CA264052, CA129911, CA208820, CA070339)

SEQ ID No. 188: SCUTRZ2022G04.g  
 (CA282192, CA102010, CA299087, CA217805, CA162851,  
 CA237908, CA101358, CA289898, CA293565, CA122383,  
 CA070388, CA177777, CA069853, CA153426, CA248297,  
 CA159447)

TABLE IV-continued

List of Sugarcane Assembled Sequences (SAS) and their SEQ ID Nos.

The EST Genbank accession numbers are in parentheses. The SEQ ID No. refers to the sequence identifiers in the sequence listings. The listed ESTs assembled to the indicated sequence and should be considered one transcript. Each SAS is differentially expressed between plants with low and high sucrose content.

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SEQ ID No. 189: SCUTST3084F06.g  
(CA186860, CA273919, CA181491, CA213324, CA181556)

SEQ ID No. 190: SCUTST3152C08.g  
(CA209403, CA181973, CA187843)

SEQ ID No. 191: SCVPAM1055A12.g  
(CA099145, CA234768, CA279908, CA080282, CA243494, CA065806, CA162304, CA074300, CA198499, CA234769, CA099202, CA218059)

SEQ ID No. 192: SCVPC16041F01.g  
(CA233726, CA099858, CA222285)

SEQ ID No. 193: SCVPL3040D12.g  
(CA246849, CA247391, CA225824)

SEQ ID No. 194: SCVPL3045B09.g  
(CA244206, CA242703, CA242545, CA227029, CA254139, CA255498, CA243610, CA228891, CA256240, CA241190, CA226680, CA230797, CA241549)

SEQ ID No. 195: SCVPLR1049B12.g  
(CA128277, CA128268, CA113688, CA280120, CA201390, CA126944, CA263569, CA111798, CA142645, CA117891)

SEQ ID No. 196: SCVPLR2005G05.g  
(CA115417, CA269672, CA275150, CA196175, CA136519, CA150580, CA111903, CA181691, CA285411, CA071020, CA199358, CA253634, CA100886, CA199448, CA229814, CA164912, CA205467, CA104448, CA274931, CA238127, CA130082, CA265998, CA104535, CA110496, CA229735, CA266059, CA151909, CA215144, CA214637, CA175326, CA277166, CA095092, CA166114, CA197942, CA200312, CA187461, CA214780, CA273212, CA110942, CA180970, CA254976, CA243592, CA219837, CA214623)

SEQ ID No. 197: SCVPLR2012A10.g  
(CA128947, CA084780, CA130173, CA112670, CA081361, CA091553, CA189411, CA074286)

SEQ ID No. 198: SCVPLR2027D02.g  
(CA139889, CA281733, CA276600, CA137157, CA287148, CA196795, CA121234, CA190870, CA121263, CA285555,

TABLE IV-continued

List of Sugarcane Assembled Sequences (SAS) and their SEQ ID Nos.

The EST Genbank accession numbers are in parentheses. The SEQ ID No. refers to the sequence identifiers in the sequence listings. The listed ESTs assembled to the indicated sequence and should be considered one transcript. Each SAS is differentially expressed between plants with low and high sucrose content.

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5 SEQ ID No. 199: SCVPRT2074D04.g  
(CA216242, CA101435, CA136611, CA237797, CA108537, CA090875, CA145883, CA175433, CA177864, CA145938, CA164642)

10 SEQ ID No. 200: SCVPRT2081G05.g  
(CA146516)

15 SEQ ID No. 201: SCVPRZ2038C12.g  
(CA116869, CA116232, CA246884, CA229323, CA101842, CA138831, CA095760, CA069655, CA170285, CA195638, CA133601, CA067592, CA291694, CA112695, CA217972, CA273837, CA067665, CA247936, CA144990, CA136455, CA278472, CA142261, CA247884, CA169426, CA136187, CA140235, CA294606, CA290785, CA138166, CA095965, CA169509, CA289245, CA290853, CA238260, CA284373, CA253974, CA274756, CA174589, CA197138, CA089467, CA176404, CA301325, CA176402, CA108223, CA263499, CA089556, CA085065, CA145765, CA209854, CA078829, CA185533, CA284004, CA223109, CA184146, CA196166, CA229320, CA133147, CA231712, CA287218, CA221504, 35 CA153992, CA088034, CA267926, CA178000, CA237734, CA225054, CA203790, CA232984, CA300291, CA278621, CA204937, CA226326, CA100069, CA254749, CA096038, CA129441, CA096280, CA298558, CA246279, CA242469, CA199423, CA299287, CA122008, CA187480, CA240020, CA283618, CA277794, CA273434, CA207921, CA205591, 40 CA138290, CA265687, CA246929, CA084012, CA102242)

SEQ ID No. 202: SCVPRZ2043F09.g  
(CA154468, CA276289)

SEQ ID No. 203: SCVPRZ3025G09.g  
(CA166458, CA215142, CA219273, CA067980, CA219244)

TABLE V

Genes differentially expressed between a high brix pool of eight plants and a low brix pool of eight plants.

The individuals were selected from an F3 progeny of a cross between *Saccharum officinarum* and *Saccharum spontaneum* genotypes. RNA samples from the indicated tissues were used to generate probes for cDNA microarray hybridizations. The fifth column indicates the average ratios (fold induction) in high against low brix comparisons. The last column indicates the average ratios (fold induction) in low against high brix comparisons. The average brix in the high brix population was 22.82. The average brix in the low population was 9.84.

Tissue	SAS	Category	Description of homologue	High Brix	Low Brix
Intermode 1	SCJFST1009H11.g	No matches		2.03165	
	SCCCCL3001F04.g	No matches		4.26102	
	SCRFLR2037F09.g	Calcium	Calreticulin		1.58339
	SCCCRZ1001H05.g	Transcription	HLH (helix-loop-helix)	2.19048	
Intermode 5	SCSBHR1050B11.g	Others	Putative senescence-associated protein	4.01392	
	SCEZST3147A10.g	Transcription	Zinc finger proteins C3H	2.13461	
	SCCCCL3080A11.b	Ubiquitination	Polyubiquitin		1.70138
	SCCCCL3001F04.g	No matches		3.88735	

TABLE V-continued

Genes differentially expressed between a high brix pool of eight plants and a low brix pool of eight plants.					
The individuals were selected from an F3 progeny of a cross between <i>Saccharum officinarum</i> and <i>Saccharum spontaneum</i> genotypes. RNA samples from the indicated tissues were used to generate probes for cDNA microarray hybridizations. The fifth column indicates the average ratios (fold induction) in high against low brix comparisons. The last column indicates the average ratios (fold induction) in low against high brix comparisons. The average brix in the high brix population was 22.82. The average brix in the low population was 9.84.					
Tissue	SAS	Category	Description of homologue	High Brix	Low Brix
Internode 9	SCSBHR1050B11.g	Others	Putative senescence-associated protein	3.99269	
	SCCCLR1048F03.g	Unknown protein			1.5888
	SCQGHR1012B09.g	Stress	Probable cytochrome P450 monooxygenase	6.70883	
	SCEQRT1033F01.g		Zinc finger proteins C2C2/Dof	4.19139	
	SCCCLR1C03H09.g	Ubiquitination	Polyubiquitin		1.76444
	SCVPRZ2038C12.g	Ubiquitination	Polyubiquitin		1.68302
	SCJLLR1054C03.g	Protein kinases	Undefined	2.81512	
	SCEZRZ3098G10.g	Pathogenicity	Protease inhibitors thaumatin	2.44691	
	SCVPFL3046C06.b	Protein Phosphatases	Serine/Threonine - PPM Family PP2C Catalytic Subunit	2.84969	
	SCJFRZ2007F10.g	Development	ARC1 (arm repeat protein)		3.02837
	SCCCRZ1004H12.g	Transcription	EIL (ethylene-insensitive3-like)		2.47389
	SCCCLR1C03H09.g	Ubiquitination	Polyubiquitin		3.36544
	SCVPRZ2038C12.g	Ubiquitination	Polyubiquitin		2.93819
	SCBFSB1046D04.g	Protein kinases	Calcium-related CBL-interacting	2.48022	
	SCJFRZ2012F04.g	Receptors	Receptor Ser/Thr kinase RLK Undefined	2.471	
	SCCCRZ1002E08.g	Stress	Drought and cold response putative aquaporin		2.95528
	SCAGLR1043E04.g	Stress	Cytochrome P450 CYP74A		2.77448
	SCCCLR2003E10.g	Transcription	NAM NAC		2.61186
	SCCCLR1048F03.g	Unknown protein			4.17702
	Leaf	SCBGLR1115D10.g	No matches		2.14401
SCCCAM1001A03.g		Calcium	Calmodulin-binding proteins Multidrug resistant-like	2.16906	
SCUTAM2005B03.g		Stress	Cytochrome P450 CYP90	2.27431	
SCVPCL6041F01.g		Receptors	Receptor Ser/Thr kinase RLK with lectin domain		1.82155
SCCCRZ1001F02.g		Stress	Drought and cold response putative aquaporin		2.01257
SCRUFL1112F04.b		Others	RNA stability UDP-GlcNAc		2.45556
SCACLR1036B06.g		Protein kinases	Calcium-related CBL-interacting		1.98763
SCEPLR1030B03.g		Pathogenicity	R-genes (receptors) With LRR/Tomato LRP protein		1.56394
SCBGLR1099G02.g		Transcription	AP2/EREBP DREB1	2.17826	
SCCCL3120C09.g		Receptors	Receptor Ser/Thr kinase RLK with Lys domain		1.96465
SCJFLR1035E04.g		Transcription	Scarecrow		1.53914
SCACLR2014E12.g		Ubiquitination	E2		1.66079
SCCCSD2001E05.g		Pathogenicity	Protease inhibitors thaumatin		2.19065
SCCCLR1068D03.g		Small GTPases	Rab		1.83141
SCAGLR1043E04.g		Stress	Cytochrome P450 CYP74A		1.88887
SCEQRT1024E12.g		Hormone biosynthesis	Salicylic Acid		2.01108
SCSGFL4193B05.g		Stress	Cytochrome P450 CYP73		1.98329
SCCCCL3001F04.g		No matches		2.18921	
SCCCLR1001E04.g		House keeping/controls	Rubisco small subunit		2.33399
SCBGLR1003D06.g		Ubiquitination	E2		1.97415
SCEQRT2099H01.g	Protein kinases	Calcium-related CDPK		1.62919	
SCACCL6008H06.g	Stress	Drought and cold response Low temperature induced (L\$S		1.87927	
SCCCRZ1002E08.g	Stress	Drought and cold response putative aquaporin		1.76115	
SCBFAST3136A06.g	No matches			2.23606	
SCEQRT1026H08.g	Stress	Cytochrome P450 CYP75		1.88583	
SCVPFL3045B09.g	Stress	Metallothionein		2.01704	
SCSGHR1069F04.b	Stress	Cytochrome P450	2.51921		
SCQSRT1036D03.g	Pathogenicity	R-genes transduction PR		1.87037	
SCAGLR2026G12.g	No matches			1.94474	
SCEQRT1028C03.g	Pathogenicity	R-genes transduction PR		2.41575	
SCUTRZ2022G04.g	Others	Heat shock protein		2.3825	
SCQGSB1082E12.g	Receptors	Receptor Ser/Thr kinase RLK Undefined		2.41928	

TABLE VI

Genes differentially expressed between a high brix pool of eight plants and a low brix pool of eight plants.

The individuals were selected from an F1 progeny of a cross between two commercial varieties, SP80-144 and SP85-7215. RNA samples from the indicated tissues were used to generate probes for cDNA microarray hybridizations. The fifth column indicates the average ratios (fold induction) in high against low brix comparisons. The last column indicates the average ratios (fold induction) in low against high brix comparisons. The average brix in the high brix population was 14.36. The average brix in the low population was 8.87.

Tissue	SAS	Category	Description of homologue	High Brix	Low Brix
Leaf	SCVPRZ2043F09.g	Receptors	Receptor Ser/Thr kinase RLK Undefined		2.94471
	SCCCSD2C03G12.g	Pathogenicity	Fungal resistance Undefined		4.43542
	SCJFRT1007E01.g	Stress	Dioxygenases		1.94338
	SCUTAM2115C12.g	Unknown protein			2.21849
	SCSBAM1086F04.g	Receptors	Receptor Ser/Thr kinase RLK Undefined		2.77975
	SCCCSD1092A08.g	No matches			3.85136
	SCVPRZ3025G09.g	Hormone biosynthesis	Jasmonic Acid 12-oxo-phytodienoate reductase		5.65617
	SCAGAM2125C01.g	Receptors	Receptor Ser/Thr kinase RLK Undefined		1.59055
	SCCCST1006B11.g	Protein kinases	SNF1-related		2.62841
	SCJLST1022A12.g	Receptors	Receptor Ser/Thr kinase RLK undefined with LRR		2.81094
	SCRULB1060F05.g	Inositol	Inositol kinases 1-Phosphatidylinositol 4-kinase		7.28074
	SCJFFL3C03C02.g	No matches			2.07492
	SCCCCL4005F05.g	Protein kinases	Undefined		2.29254
	SCVPFL3040D12.g	Transcription	CREB-binding/acetyltransferase-related		3.10639
	SCSGLR1045F05.g	Unknown protein		1.69705	
	SCMCLR1123E10.g	Others	T-complex protein (chaperonin)	3.08493	
	SCCCRZ1001C01.g	Stress	Drought-induced	2.21354	
	SCCCLR1C05B03.g	Transcription	Myb	2.39082	
	SCBFLR1039B05.g	Others	Xyloglucan endotransglycosylase	2.72608	
	SCSBSD2029D11.g	No matches		2.0015	
	SCVPCL6041F01.g	Receptors	Receptor Ser/Thr kinase RLK with lectin domain	3.02993	
	SCCCLR2001H09.g	Stress	Thioredoxin	1.82511	
	SCBGLR1096E06.g	Others	Putative inosine monophosphate dehydrogenase	2.29479	
	SCQSSB1077D06.g	Receptors	Receptor Ser/Thr kinase RLK Undefined	1.95563	
	SCEZLB1009A09.g	Hormone related	Similar to BLE1 protein	2.29938	
	SCEZLR1052E07.g	No matches		2.98578	
	SCCCCL4002E02.g	Others	Extensin	1.87858	
	SCCCRZ2003E12.g	Transcription	bZIP	2.41759	
	SCCCLB1001D03.g	Protein Phosphatases	Serine/Threonine - PPP Family PP2A/Catalytic Subunit	1.88391	
	SCAGLB1070E01.g	Receptors	Receptor Ser/Thr kinase RLK Undefined	7.40783	
	SCJLRZ1021D12.g	Receptors	Receptor Ser/Thr kinase RLK undefined with LRR	3.33105	
	SCCART2002G11.g	Protein kinase	Cell cycle-related MHK (male germ cell associated)	3.57013	
	SCCCLR2C02D03.g	Calcium	Calmodulin-binding proteins Chaperonin 10	1.94335	
	SCCART2002G11.g	Protein kinase	Cell cycle-related MHK (male germ cell associated)	3.77176	

TABLE VII

Genes differentially expressed between a high brix variety and a low brix variety.

Two individuals were selected from SP83-2847 and two individuals from SP91-1049. RNA samples from the indicated tissues were used to generate probes for cDNA microarray hybridizations. The fifth column indicates the average ratios (fold induction) in high against low brix comparisons. The last column indicates the average ratios (fold induction) in low against high brix comparisons. The average brix in SP91-1049 was 20.2. The average brix in SP83-2847 was 16.2.

Tissue	SAS	Category	Description of homologue	High Brix	Low Brix
Leaf	SCCCLR2002F08.g	Hormone related	Auxin auxin repressed		2.48663
	SCRUAD1064B08.g	No matches			6.06841
	SCEQRT1024E12.g	Hormone biosynthesis	Salicylic Acid	1.58685	
	SCBFST3136A06.g	No matches		2.2018	
	SCSGSB1009D11.g	Unknown protein		4.54795	
	SCACCL6008H06.g	Stress	Drought and cold response Low temperature induced (LTI)	4.15788	
	SCSBAM1085B06.g	Hormone biosynthesis	Jasmonic Acid Linoleic acid desaturase	2.43754	
	SCJLRT1016G06.g	Stress	Wound-Induced Ribonuclease	4.45431	
	SCCCLR1024C03.g	Stress	Drought and cold response putative aquaporin	1.72509	
	SCCCLR1001E04.g	House keeping/controls	Rubisco small subunit	3.10813	

TABLE VIII

Genes differentially expressed between a high brix variety and a low brix variety.  
Two individuals were selected from SP89-1115 and two individuals from SP94-3116.  
RNA samples from the indicated tissues were used to generate probes for cDNA microarray hybridizations. The fifth column indicates the average ratios (fold induction) in high against low brix comparisons. The last column indicates the average ratios (fold induction) in low against high brix comparisons. The average brix in SP89-1115 was 19.9. The average brix in SP94-3116 was 14.2.

Tissue	SAS	Category	Description of homologue	High Brix	Low Brix
Leaf	SCAGSD2042G08.g	No matches			2.56194
	SCEQRT1033H06.g	Receptors	Receptor Ser/Thr kinase RLK undefined with LRR		2.58749
	SCJLRT1016G06.g	Stress	Wound-induced Ribonuclease		2.4137
	SCEQRT1024B02.g	Protein kinases	Undefined (with insertion domain)	5.41746	
	SCCCRZ2001A10.g	Inositol	Inositol kinases 1-Phosphatidylinositol 4-kinase		3.90421
	SCCCLR1022B11.g	Stress	Drought and cold response Cysteine proteinase RD19A precursor		1.74873
	SCBFLR1060F03.g	Receptors	Receptor Ser/Thr kinase RLK undefined with LRR		3.23768

TABLE IX

Genes differentially expressed between a high brix pool of eight plants and a low brix pool of eight plants.  
The individuals were selected from an F1 progeny of a cross between two commercial varieties, SP80-180 and SP80-4966. RNA samples from the indicated tissues were collected from March to July and used to generate probes for cDNA microarray hybridizations. The fifth column indicates the average ratios (fold induction) in high against low brix comparisons. The last column indicates the average ratios (fold induction) in low against high brix comparisons. The average brix in the high brix population was 18.47 in March, 21.79 in May and 22.63 in July. The average brix in the low population was 13.66 in March, 17.59 in May and 18.96 in July.

Tissue	SAS	Category	Description of homologue	High Brix	Low Brix
Internode 1 march	SCEPLR1030E06.g	Receptors	Receptor Ser/Thr kinase RLK undefined with LRR	1.87064	
	SCACLR2007G02.g	Protein kinases	Others Abscisic acid-inducible		1.90147
	SCEZLB1012F10.g	Calcium	Calmodulin-binding proteins GNGC family		1.88909
	SCEQRT1024E12.g	Hormone biosynthesis	Salicylic Acid		1.85544
	SCJLRT1016G06.g	Stress	Wound-induced Ribonuclease		2.07306
	SCJFRT1005C11.g	Hormone biosynthesis	Ethylene ACC oxidase		3.48319
	SCVPLR2005G05.g	Others	Putative Mob1/phoecin family protein		1.6251
	SCEQRT1026H08.g	Stress	Cytochrome P450 CYP75		2.40851
	SCCCLR1C04C02.g	No matches			2.07835
	SCQGHR1010D02.g	Others	Putative terpene synthase		3.02686
	SCBGLR1023D05.g	Pathogenicity	R-genes transduction LSD1	2.21144	
	SCUTRZ2022G04.g	Others	Heat shock protein		1.71301
	SCCCLR1C02F07.g	Inositol	Others myo-Inositol-1-phosphate synthase		1.83045
	SCEQRT1028C03.g	Pathogenicity	R-genes transduction PR		2.46157
	SCVPLR1049B12.g	Unknown protein			2.59241
	SCSBAM1084E01.g	Protein kinases	MAPK/MAPKK/MAPKKK MAPK		1.98747
	SCCCLR2002E04.g	Others	Putative Bet v I pollen allergen		2.2259
	SCCCCL6002B05.g	Hormone biosynthesis	Auxin Nitrilase		1.67598
	SCJLRT1021D12.g	Stress	Wound-Induced Chalcone synthase		3.6397
	SCVPLR2027D02.g	Stress	Wound-Induced Chalcone synthase		1.73982
	SCEZLB1010E10.g	Transcription	Other Auxin-response factors With B3 domain		1.62134
	SCRFLR1012D12.g	Hormone biosynthesis	Auxin Nitrilase	1.76443	
	SCCCLR1C05G07.g	Others	S-adenosylmethionine decarboxylase		1.93684
	SCSBHR1052E03.g	Stress	ABA and stress induced		2.27594
	SCRFLR1012F12.g	Others	caffeic acid 3-O-methyltransferase		2.22106
	SCCCAM2C04G08.g	Receptors	Receptor Ser/Thr kinase leucine-rich transmembrane kinase (LTK1)		1.67218
	SCACCL6008H06.g	Stress	Drought and cold response Low temperature induced (LTI)		1.91951
	SCRFLR1034G06.g	Protein kinases	Undefined		1.76667
	SCUTST3084F06.g	Stress	Drought and cold response Low temperature induced (LTI)		1.73383
	SCAGLR1043E04.g	Stress	Cytochrome P450 CYP74A		2.05809
	SCJFRT1007H07.g	Hormone biosynthesis	Jasmonic Acid Lipoxigenase		3.99155
	SCCCRT1001E01.g	Hormone biosynthesis	Jasmonic Acid Lipoxigenase		2.71944
	SCCCLR2C01F06.g	Stress	Wound-induced		1.78615
SCVPLR1010E06.g	Protein Phosphatases	Serine/Threonine - PPM Family PP2C-like		1.55514	
SCCCLR2002F08.g	Hormone related	Auxin auxin repressed		1.60673	
SCJFRZ3C03H08.g	Pathogenicity	R-genes (receptors) With LRR		1.75681	
SCEQRT2098H06.g	Pathogenicity	R-genes (receptors) With LRR/NBS-LRR		1.68827	
SCEZAM2058E08.g	Receptors	Receptor Ser/Thr kinase RLK Undefined		1.60291	
SCACSB1037A07.g	Stress	Cytochrome P450 CYP98A		1.63	
SCAGLR1043F02.g	Calcium	Calmodulin-binding proteins HSP70s (heat shock)		2.03737	
SCJFRZ2007F10.g	Development	ARC1 (arm repeat protein)		1.82989	
Internode 1 July					

TABLE IX-continued

Genes differentially expressed between a high brix pool of eight plants and a low brix pool of eight plants.					
The individuals were selected from an F1 progeny of a cross between two commercial varieties, SP80-180 and SP80-4966. RNA samples from the indicated tissues were collected from March to July and used to generate probes for cDNA microarray hybridizations. The fifth column indicates the average ratios (fold induction) in high against low brix comparisons. The last column indicates the average ratios (fold induction) in low against high brix comparisons. The average brix in the high brix population was 18.47 in March, 21.79 in May and 22.63 in July. The average brix in the low population was 13.66 in March, 17.59 in May and 18.96 in July.					
Tissue	SAS	Category	Description of homologue	High Brix	Low Brix
	SCRUSB1062E12.g	Others	Putative triacylglycerol lipase		1.49831
	SCCCRZ1001C01.g	Stress	Drought-induced		1.52895
	SCEZHR1088E02.g	Protein Phosphatases	Tyrosine Phosphatases Dual Specificity Protein Phosphatases (DSPP)	1.87674	
Internode 5 march	SCCCLR1066G08.g	Transcription	HGM (High mobility group protein)	1.57463	
	SCEZRZ1015G02.g	Unknown protein	Putative protein kinase Casein kinase I	1.91199	
	SCAGFL1089C03.g	Stress	Glutathione S-transferases	2.10704	
	SCEZLR1031G10.g	Protein kinases	Cell cycle-related CDC2/CRK2	2.14401	
	SCSGSB1009D11.g	Unknown protein		2.09248	
	SCCCFL4094H12.g	Receptors	Receptor Ser/Thr kinase RLK Undefined	1.76665	
	SCRULB2065G10.g	No matches			2.15317
	SCQGLR1085F11.g	Stress	Drought-Induced		2.7353
	SCJFRZ2034D04.g	Others	SET-domain protein		2.69909
	SCBFFL4114B06.g	Receptors	Receptor Ser/Thr kinase RLK Undefined		3.67808
	SCEPRZ3087C08.g	Stress	Drought and cold response Low temperature induced (LTI)		1.78187
	SCCCLR1065F03.g	Pathogenicity	R-genes (receptors) With LRR/NBS-LRR		1.7714
	SCCCLR2C01F06.g	Stress	Wound-Induced	2.334	
	SCUTLR2023D06.g	Transcription	CCAAT Hap	1.68942	
	SCEQLR1007G03.g	Calcium	Calmodulin-binding proteins EF-1 alpha	1.64492	
	SCACLR2007G02.g	Protein kinases	Others Abscisic acid-Inducible	1.57037	
	SCUTRZ2022G04.g	Others	Heat shock protein	2.11424	
	SCQGRT1040G03.g	Development	Expansin	1.7436	
	SCEQRT1026H08.g	Stress	Cytochrome P450 CYP75	1.59596	
	SCAGFL1089G08.g	no match			2.06063
	SCJFRZ3C03H08.g	Pathogenicity	R-genes (receptors) With LRR		2.76853
	SCEQRT2098H06.g	Pathogenicity	R-genes (receptors) With LRR/NBS-LRR		2.6343
	SCCCLR2002H11.g	Unknown protein			1.64637
	SCVPRT2081G05.g	Protein kinases	Cell cycle-related CDK		2.15674
	SCCCLR1022F10.g	Others	Glycine hydroxymethyltransferase	2.02802	
	SCBFSB1047C02.g	Others	Hypothetical protein	2.58471	
	SCRULB1060F05.g	Inositol	Inositol kinases 1-Phosphatidylinositol 4-kinase	1.65757	
	SCCCLR1024A02.g	Receptors	Receptor Ser/Thr kinase RLK Undefined	1.60332	
	SCEPRZ1008F02.g	Transcription	LIM (protein-protein Interaction)	1.833	
	SCCCFL4094H12.g	Receptors	Receptor Ser/Thr kinase RLK Undefined	1.84294	
	SCACCL6008H06.g	Stress	Drought and cold response Low temperature Induced (LTI)		1.92651
	SCJLRT1016G06.g	Stress	Wound-induced Ribonuclease		3.13455
	SCEZST3147A10.g	Transcription	Zinc finger proteins C3H		2.21445
	SCCCRZ1002H08.g	Others	Sapoin B domain-containing protein		2.32254
	SCCCLB1003E11.g	Protein kinases	Others REK-like		3.07187
	SCSFAD1125C08.g	Pathogenicity	Polygalacturonase-Inhibiting		2.31427
Internode 5 July	SCCCLR1C04G08.g	Protein kinases	Casein kinase Casein kinases I	1.76524	
	SCVPRT2074D04.g	Others	unkown protein	1.75747	
	SCJFRZ3C03H08.g	Pathogenicity	R-genes (receptors) With LRR	2.52658	
	SCRFLR1012F12.g	Others	caffeic acid 3-O-methyltransferase		1.63946
	SCCCLR1024C03.g	Stress	Drought and cold response putative aquaporin		2.50238
	SCEQLR1091A10.g	Others	60S Ribosomal protein L23		1.74167
	SCCCRZ2C01F09.g	Ubiquitination	E2		1.62723
	SCEPAM1020A03.g	Protein kinases	Others ATN1-like		1.9435
	SCSBHR1050B11.g	Others	Putative senescence-associated protein	3.83889	
	SCJFRZ2007F10.g	Development	ARC1 (arm repeat protein)	2.38995	
	SCCCRZ1001H05.g	Transcription	HLH (helix-loop-helix)	4.15387	
	SCEQRT1033F01.g	.	Zinc finger proteins C2C2/Dof	3.65977	
	SCCCLR1048D07.g	Hormone biosynthesis	Salicylic Acid	4.58868	
	SCSBHR1050B11.g	Others	Putative senescence-associated protein	2.34488	
	SCSBSD2029F05.g	Unknown protein			2.73215
	SCCCLR2003E10.g	Transcription	NAM NAC		2.44948
	SCCCLR2C02A05.g	Development	Expansin		1.58639
	SCACSB1037A07.g	Stress	Cytochrome P450 CYP98A		1.85253
	SCCCLR1C03G01.g	Hormone biosynthesis	Jasmonic Acid Linoleic acid desaturase		1.47918
	SCCCLR1C05B07.g	Protein kinases	Calcium-related CBL-Interacting	2.71519	
	SCSBHR1050B11.g	Others	Putative senescence-associated protein	2.45088	
	SCMCRZ2103B04.g	Protein kinases	Undefined	1.73105	
	SCCCLB1003E11.g	Protein kinases	Others REK-like	3.30364	
	SCVPAM1055A12.g	Protein kinases	Casein kinases Casein kinase I	1.67698	
	SCEZHR1088E02.g	Protein Phosphatases	Tyrosine Phosphatases Dual Specificity Protein Phosphatases (DSPP)	3.28753	

TABLE IX-continued

Genes differentially expressed between a high brix pool of eight plants and a low brix pool of eight plants.					
The individuals were selected from an F1 progeny of a cross between two commercial varieties, SP80-180 and SP80-4966. RNA samples from the indicated tissues were collected from March to July and used to generate probes for cDNA microarray hybridizations. The fifth column indicates the average ratios (fold induction) in high against low brix comparisons. The last column indicates the average ratios (fold induction) in low against high brix comparisons. The average brix in the high brix population was 18.47 in March, 21.79 in May and 22.63 in July. The average brix in the low population was 13.66 in March, 17.59 in May and 18.96 in July.					
Tissue	SAS	Category	Description of homologue	High Brix	Low Brix
Internode 9 march	SCCCRZ1001F02.g	Stress	Drought and cold response putative aquaporin		2.29254
	SCEZHR1087F06.g	Stress	Cytochrome P450 CYP84		2.3784
	SCBFRZ2046D07.g	Protein kinases	RLCK NAK-like		2.13676
	SCRUAD1063D03.g	No matches			1.93091
	SCSGFL4193B05.g	Stress	Cytochrome P450 CYP73		1.58639
	SCJFRZ2014A03.g	.	R-genes (receptors) With LRR/NBS-LRR		2.52532
	SCCCLR1048F03.g	Unknown protein			2.10185
	SCSBHR1050B11.g	Others	Putative senescence-associated protein		3.73288
	SCVPLR2012A10.g	Hormone biosynthesis	Ethylene ACC oxidase		1.78441
	SCEQRT2100B02.g	Stress	Drought and cold response putative aquaporin		2.00347
	SCCCRZ1001F02.g	Stress	Drought and cold response putative aquaporin		1.7121
	SCMCRT2103B04.g	Protein kinases	Undefined		1.80135
	SCAGLR1043F02.g	Calcium	Calmodulin-binding proteins HSP70s (heat shock)		2.89959
	SCEZHR1088E02.g	Protein Phosphatases	Tyrosine Phosphatases Dual Specificity Protein Phosphatases (DSPP)		2.79028
	SCCST3001H12.g	Stress	Drought and cold response putative aquaporin		2.0084
	SCCCRZ1002E08.g	Stress	Drought and cold response putative aquaporin		1.79386
	SCCCLR1024C03.g	Stress	Drought and cold response putative aquaporin		1.80152
	SCJFRT2055G07.g	Ubiquitination	Polyubiquitin		1.60639
	SCCEPRZ1010E06.g	Protein Phosphatases	Serine/Threonine - PPM Family PP2C-like		1.53961
	SCCCCL3002C09.b	Stress	Glutathione S-transferases		1.55841
	SCEZRZ1015G02.g	Unknown protein	Putative protein kinase Casein kinase I		1.85411
	SCCCSD2001E05.g	Pathogenicity	Protease inhibitors thaumatin		6.05847
	SCUTST3090E03.g	Unknown protein			1.56216
	SCBFL5074C09.g	Stress	Drought and cold response reversibly glycosylated polypeptide		1.79364
	SCAGFL1089C03.g	Stress	Glutathione S-transferases		1.6557
	SCSGSB1009D11.g	Unknown protein			2.4264
	SCCCSD1003E02.g	Pathogenicity	Protease inhibitors thaumatin		4.87282
	SCCCLR2C01F06.g	Stress	Wound-induced		3.40039
	SCCCAD1001C08.g	Stress	Peroxidases P7X		1.97943
	SCCCAM2004G02.g	Hormone related	Auxin Auxin transport/auxin efflux carrier		1.78676
	SCSFAD1125C08.g	Pathogenicity	Polygalacturonase-inhibiting		1.60435
	SCCCLR1001A06.g	Others	Extensin-like protein		1.57973
	SCAGLR1043E04.g	Stress	Cytochrome P450 CYP74A		1.9974
	SCBFSB1047C02.g	Others	Hypothetical protein		2.05746
	SCCCLR2C01G07.g	Protein kinases	SNF1-related		1.76015
	SCEZHR1047A01.g	Receptors	Receptor Ser/Thr kinase RLK undefined with LRR		1.60061
	SCVPCL6041F01.g	Receptors	Receptor Ser/Thr kinase RLK with lectin domain		1.59157
	SCEQRT1028C03.g	Pathogenicity	R-genes transduction PR		4.96024
	SCCCST1001C04.g	No matches			1.67914
	SCRFRH1009G06.g	Stress	Infected libraries		2.02309
	SCCCCL3120G07.g	Calcium	Calmodulin-binding proteins HSP70s (heat shock)		1.67313
	SCRFLR1012F12.g	Others	caffeic acid 3-O-methyltransferase		1.76972
	SCMCSD2061D05.g	Protein kinases	Undefined		2.00471
	SCRFLR1012F12.g	Others	caffeic acid 3-O-methyltransferase		1.73901
	SCCCLR1022F10.g	Others	Glycine hydroxymethyltransferase		1.93433
SCSGAM1094D05.g	Hormone biosynthesis	Salicylic Acid		1.62394	
SCSBAD1084C01.g	Others	Tubulin alpha-1 chain		1.7221	
SCSBAD1084C01.g	Others	Tubulin alpha-1 chain		1.70571	
SCEPRZ1008F02.g	Transcription	LIM (protein-protein interaction)		2.3459	
SCCCAD1004H02.g	Stress	Catalases		2.34832	
SCVPCL6042B11.g	Receptors	Receptor Ser/Thr kinase RLK Undefined		2.05874	
SCCCLR2C01F06.g	Stress	Wound-induced		1.68028	
SCUTST3084F06.g	Stress	Drought and cold response Low temperature induced (LTI)		2.65146	
SCJFLR1074E09.g	Stress	Drought and cold response Low temperature induced (LTI)		1.7881	
SCCCLR1C08G10.g	Transcription	Myb LH1/CY1		1.7247	
SCACLR1126E09.g	No matches			1.88699	
SCCCLR2C01F06.g	Stress	Wound-induced		1.98605	
SCEQLB2019B08.g	Protein kinases	SNF1-related		2.27361	
SCEQRT1031D02.g	Adapters	14-3-3 proteins		1.89991	
SCCCRZ1002E08.g	Stress	Drought and cold response putative aquaporin		2.22348	
SCQGLR1085F11.g	Stress	Drought-induced		2.57185	
SCJLRT1023A09.g	Transcription	HLH (helix-loop-helix)		2.21673	
SCSBAM1085B06.g	Hormone biosynthesis	Jasmonic Acid Unoleic acid desaturase		1.87983	
SCEPRZ3087C08.g	Stress	Drought and cold response Low temperature induced (LTI)		2.40687	



TABLE IX-continued

Genes differentially expressed between a high brix pool of eight plants and a low brix pool of eight plants.					
The individuals were selected from an F1 progeny of a cross between two commercial varieties, SP80-180 and SP80-4966. RNA samples from the indicated tissues were collected from March to July and used to generate probes for cDNA microarray hybridizations. The fifth column indicates the average ratios (fold induction) in high against low brix comparisons. The last column indicates the average ratios (fold induction) in low against high brix comparisons. The average brix in the high brix population was 18.47 in March, 21.79 in May and 22.63 in July. The average brix in the low population was 13.66 in March, 17.59 in May and 18.96 in July.					
Tissue	SAS	Category	Description of homologue	High Brix	Low Brix
	SCEQRT1025D06.g	Adapters	14-3-3 proteins		2.23722
	SCCCRZ2001E12.g	Transcription	HLH (helix-loop-helix) PIF-like		2.17995
	SCUTST3152C08.g	Calcium	Calmodulin		1.78114
	SCACCL6008H06.g	Stress	Drought and cold response Low temperature induced (LTI)		3.24015
	SCSBST3096H04.g	Inositol	Inositol phosphatases		2.8703
			Inositol-1,4,5-trisphosphate 5-Phosphatase		
	SCEQRZ3020C02.g	Receptors	Receptor Ser/Thr kinase RLK undefined with LRR	1.70665	
	SCCCCL6003D08.g	Ubiquitination	F-box protein		1.9614
	SCEQRT1025D04.g	Receptors	G-protein coupled		1.78293
	SCEPRZ1010E06.g	Protein Phosphatases	Serine/Threonine - PPM Family PP2C-like		2.54771

#### Confirmation of Expression Data

Real-time PCR reactions were performed to confirm the expression data obtained. cDNA templates were generated from a pool of 8 individuals from the cross between commercial varieties (SP80-180 and SP80-4966), from the multiple crossings among *S. officinarum* and *S. spontaneum* genotypes or from individual tissue samples. Leaf or internode RNA derived from three HB genotypes (CTC98-243, CTC98-246, CTC98-253) and three LB genotypes (CTC98-261, CTC98-265, CTC98-272) (FIG. 3). The mRNA levels for nine SAS show some variation in the different genotypes and pools but all transcript levels are in agreement with the expected based on microarray results.

The differential expression of the genes in high and low sugar content plants could also be confirmed by northern blot hybridization. Four genes with greater expression in the high sugar content plants from the SP80-180 vs. SP80-4966 progenies (SCSBAM1085B06.g, SCACLR1126E09.g, SCEQRZ3020C02.g and SCCLLR1C08G10.g) and three with increased expression in the low sugar content plants (SCSBST3096H04.g, SCEQLB2019B08.g and SCQGLR1085F11.g) were analyzed by RNA-blotting using total RNA from three sugarcane individuals to provide replication for gene expression trends. FIG. 4 shows that the microarray data was confirmed in at least two of the three independent samples collected nine months after planting, indicating a high consistency between the two data sets.

To confirm gene expression trends along the growing season we determined the mRNA levels for the same seven genes in the 7HS (high sugar) and 7LS (low sugar) pools collected 6, 7, 9, 11 and 13 months after planting (FIG. 5). The inset graph represents the expression profile of each gene plotted for each population. The four genes found to be enriched in the high sugar content plants were consistently differentially expressed along the growing season (FIG. 5 a-d). These genes are possibly involved in the control of sucrose synthesis, accounting for the higher sugar content in these segregant plants. The genes with more transcripts in the low sugar content plants showed a less consistent pattern (FIG. 5 e-g). All of them were differentially expressed in the plants at nine months after planting, confirming the expression observed by

microarrays, but only the one encoding dehydrin, a stress-related protein (FIG. 5g) had a more consistent pattern along the growing season.

Identity/Function of Differentially Expressed Genes The SAS represented in our array were chosen from 7381 genes catalogued by the SUCAST project (Papini-Terzi et al., 2005; Souza et al., 2001) and from the SUCAMET Catalogue of sugarcane metabolism genes available on the World Wide Web at [sucast-fun.org](http://sucast-fun.org). The SUCAST Catalogue includes Protein and Functional categories such as Receptors, Protein Kinases, Protein Phosphatases, Small GTPases, Transcription Factors, Calcium, Inositol, Ubiquitination, Hormone Biosynthesis, Development, Stress and Pathogenicity, among others. The catalogue also contains 548 SAS corresponding to hypothetical proteins or new genes for which no function can be inferred solely from the sequence or no similarity has been found to genes in public databases ('no matches'). The tissue-specificity of the selected genes has been evaluated in a previous work (Papini-Terzi et al., 2005), which revealed 217 genes with preferential expression in one of the six tissues analyzed (flowers, buds, leaves, roots, mature and immature internodes) and 153 highly ubiquitous genes.

Leaf mesophyll cells are the primary photosynthetic tissue, and photosynthate, mainly in the form of sucrose, is transported to meristems and developing organs. In sugarcane, growing young leaves and stem are the main carbohydrate-importing tissues. Source and sink tissues must be co-ordinately regulated at the level of gene expression and enzyme activity to produce rapid growth and efficient sucrose accumulation. Light and sugars regulate growth activities by a coordinated modulation of gene expression and enzyme activities in both, carbohydrate-exporting (source) and carbohydrate-importing (sink) tissues. Gene regulation is based on sensing different signals or stimuli, which then is transmitted through a signaling pathway that in the end leads to an increase or decrease of transcription. In sugar signaling, the first step is to sense the nature and level of the specific sugar. While elevated cellular levels of sugar up regulate genes involved in the synthesis of polysaccharides, storage proteins, pigments, as well as genes associated with defense responses and respiration, sugar deprivation enhances the expression of genes involved in photosynthesis and resource remobilization, such as the degradation of starch, lipid, and protein

(Koch, 1996; Yu, 1999; Ho et al., 2001). Although the regulatory effect of sugars on photosynthetic activity and plant metabolism has long been recognized, the concept of sugars as central signaling molecules is relatively new (reviewed by Rolland et al., 2002).

In this work, we evaluated the expression levels of SUCAST and SUCAMET genes in four tissues (leaf, internodes 1, 5 and 9) from three sugarcane populations with contrasting sugar accumulation capacities and four commercial varieties. We describe a total of 203 SAS (Sequence ID Nos 1-203) differentially expressed between the high and low brix populations in at least one of the tissues analyzed (Tables V to IX). Two of them appeared differentially expressed in five of the samples analyzed, four in four, fourteen in three and thirty in two, totalling 50 genes for which transcripts are altered in more than one sample (Table X). The differentially expressed genes belong to several functional categories including calcium signalling, stress responses, transcription and ubiquitination. These genes and their variants can be used to predict sugar content from plants or generate plants with higher sucrose content.

TABLE X

Number of occurrences of differential expression for each SAS in all the samples analyzed.	
Occurrences	Number of SAS
5	2
4	4
3	14
2	30
1	153

Since significant number of genes encoding SNF1 related-kinases were found differentially expressed (see below) we looked for differentially expressed genes encoding SNF1s and their regulators in commercial varieties that varied in sucrose content. Table XIV list several members of this family of proteins whose expression was found to be associated to sucrose content.

In an alternate approach, mature (Internode 9), intermediately mature (Internode 5) and immature (Internode 1) culm samples were compared. The aim of these comparisons was to reveal genes differentially expressed when internodes rich in sucrose were compared to the first internodes poor in sucrose. A total of 186 genes were identified as developmentally regulated during culm maturation (Tables XV to XX). Forty-six of them were also found to be differentially expressed in the direct comparisons between high and low brix and eighteen of them were altered in up to 5 of the samples analysed. Table XXI shows the 18 SAS found differentially expressed in at least two of the biological samples considered (the data regarding 14 of them were retrieved from Felix, 2006 as indicated in the Table). SEQ ID Nos: 229-373 relate to the 140 SAS whose expression was altered in high sugar internodes which are not contained in the SEQs Nos 1-203 group. The data revealed by this experimental design indicates that the genes differentially expressed in high vs. low brix plants may have a role in culm maturation and may improve this process and consequently alter sucrose content if altered in transgenic plants.

There are several genes encoding protein kinases involved with the calcium signalling pathway altered in association with sucrose content. One (SCEQRT2099H01.g) is similar to members of the CDPK family (Calcium-dependent Protein Kinase) and nine others (SCACLR1036B06.g,

SCBFSB1046D04.g, SCCCLR1C05B07.g,  
SCEQLB2019B08.g, SCMCRT2103B04.g,  
SCCCLR2C01G07.g, SCCCLR1002D12.g,  
SCEQRT2030G04.g, SCSGHR1070F12.g) to CIPKs (CBL-  
interacting protein kinases) from the SnRK3 subgroup of  
plant DNF-like protein kinases (Hrabak et al., 2000). An  
*Arabidopsis* CIPK14 has been shown to be induced by  
sucrose, and sucrose-responsive elements in its promoter  
have been identified (Lee et al., 2005). Several studies  
have reported that some CDPKs and SNRK (SNF1-related  
kinases) are able to phosphorylate and regulate the enzyme  
sucrose synthase (Hardin et al., 2003; Hardin et al., 2004;  
Huber et al., 1996; Zhang et al., 1999). Plant SNF1-related  
kinases are regulated by regulatory subunits AKINbetagamma  
(Lumbreras et al., 2001). We found two SAS coding for  
such SnRK putative regulatory subunits, SCEQLR1092H10.g  
and SCJFST1011B06.g, the latter being differentially  
expressed in seven of the samples analyzed. We also found  
a gene encoding a SnRK1 (SCJFRZ2032G01.g) down-regulated  
in mature internodes in relation to immature internodes.  
SnRK1 (SNF1-Related Protein Kinase-1) is a plant protein  
kinase with a catalytic domain similar to that of SNF1  
(Sucrose Non-fermenting-1) of yeast and AMPK (AM-  
Pactivated protein kinase) of animals (Halford et al., 2003).  
Carraro et al., (2001) identified at least 22 sugarcane  
expressed sequence tag (EST) contigs encoding putative  
SnRKs in the SUCEST database. Studies led to the hypothesis  
that SnRK1 is activated in response to high intracellular  
sucrose and/or low intracellular glucose levels (Halford et al.,  
2003). The first plant protein to be identified as a substrate  
for SnRK1 was a HMG-CoA reductase in *A. thaliana* (Dale et al.,  
1995). Subsequently, two other important enzymes, SPS and  
NR were shown to be substrates for SnRK1 phosphorylation  
in Ser-binding sites. In both cases, phosphorylation results  
in inactivation of the enzyme, although the inactivation of NR  
and SPS also requires the binding of a 14-3-3 protein to the  
phosphorylation site (Bachmann et al., 1996; Moorhead et al.,  
1999).

Four genes encoding CIPKs were found to be differentially  
expressed when mature and immature internodes were compared  
(SCJFRZ2032C08.g, SCJLRT1023G09.g,  
SCCCLR1C05B07.g, SCJLRZ1023H04.g). Our published  
studies have also identified two additional genes encoding  
SNF1-related SnRK3 CIPKs (SCCCLR2C01G07.g and  
SCMCRT2103B04.g) that are differentially regulated when  
mature and immature sugarcane internodes are compared that  
corroborate the present data and confirm a role for SNF-  
related kinases and their regulators in sucrose synthesis and  
accumulation (Felix, 2006). Additionally, three genes encoding  
SNF1-related kinases similar to osmotic stress-related  
kinases (SCCCST1004A07.g, SCEPRZ1009C10.g and  
SCCCST1006B11.g) were also found to be differentially  
expressed.

CIPKs interact with Calcineurin B-like proteins (CBL)  
(Shi et al., 1999). We found six genes encoding CBLs in the  
SUCEST database and thirty-one CIPKs, twenty-four of  
which were analyzed in this work. A calreticulin  
(SCRFLR2037F09.g) and a calmodulin  
(SCUTST3152C08.g) were found to be enriched in LB  
immature internodes and leaves respectively, and five cal-  
modulin-binding proteins to be up-regulated  
(SCCCAM0001A03.g, SCCCLR2C02D03.g,  
SCEZLB1012F10.g, SCAGLR1043F02.g,  
SCEQLR1007G03.g, SCCCCL3120G07.g). Calcium sig-  
nalling is effected via changes of calcium concentration and  
calcium sensing proteins such as calmodulin, calcineurin and  
calreticulin (Sanders et al., 2002). The latter relay the signal

downstream through phosphorylation cascades and changes in gene expression. Studies with the sucrose synthase from maize showed that phosphorylation of this enzyme at the residue Ser-15 by CDPKs stimulates its sucrose cleavage activity (Hardin et al., 2003; Huber et al., 1996). Moreover, CDPKs may phosphorylate at Ser-170 and target this enzyme for 26S-proteasome-dependent degradation (Hardin et al., 2003; Hardin & Huber, 1999). Sucrose synthase is related to several physiological processes, including sink/source relationships within the plant (Hanggi & Fleming, 2001; Zrenner et al., 1995) and may contribute to sucrose accumulation in sugarcane. Additionally, it has been shown that some calcium-dependent kinases can phosphorylate and inactivate sucrose-phosphate synthase, which has a key role in sucrose biosynthesis (McMichael et al., 1995; Pagnussat et al., 2002). Taken together, these results suggest that, as sucrose biosynthesis seems to be (at least partially) a SNF1- and calcium-regulated process, genes encoding the calcium-dependent kinases and SNF1-related protein kinases and their modulators differentially expressed in our study may represent critical points in the control of sucrose synthesis and accumulation in sugarcane. Consequently, these sugarcane genes can be used to increase sucrose content in transgenic plants.

To confirm that differential gene expression associated to sucrose content was indeed reflecting a role for these genes in sucrose synthesis or accumulation we obtained sugarcane transgenic plants where the gene encoding CIPK-8 (SAS SCEQLB2019B08.g) was silenced by RNAi interference. Sugarcane embryonic callus from the cultivars SP80-185, SP94-3116, CTC1, SP83-2847, SP80-1842 and SP91-1049 were bombarded by biolistics with a construct where 331 bp of SAS SCEQLB2019B08.g (SEQ ID No. 378) was cloned in the sense and antisense orientation. The 331 bp fragment was obtained by PCR using the primers SNFL1 (SEQ ID No. 374): 5'-CCCTCTAGACTCGAG CATTTCATTCCATTC-CGTTCC-3' and SNFL2 (SEQ ID No. 375): 5'-CCCAAGCT-TGAATC CGCCACCAGTAGCAAATTCT-3'. The fragment was digested with the enzymes XhoI and EcoRI and cloned in the pHannibal vector (Wesley et al., 2001) digested with the same enzymes for the sense orientation. The same fragment was then digested with HindIII and XbaI and cloned in the vector already containing the sense construct digested with the same enzymes for the antisense orientation. FIG. 7 shows an alignment to two additional EST sequences encoding CIPKs (CIPK-29 SCSGHR1070F12.g and CIPK-1 SCCCCL5001D11.g) that are 95 and 85% identical, respectively, to the CIPK-8 fragment region amplified (red line) and show 65% overall identity when the three complete sequences are considered. CIPK-29 has also been identified as differentially expressed when high brix and low brix plants were compared using, cDNA microarrays. CIPK-1 was not detected by our array experiments as a differentially expressed gene. Transgenic plants were generated by co-transformation of the pHannibal-CIPK RNAi construct and the pHA9 vector (Wei and Albert, U.S. Pat. No. 6,706,948) which contains the maize ubi1 promoter driving a neomycin phosphotransferase II gene and NOS terminator. To verify that CIPK-8 mRNA levels were decreased in the transgenic plants obtained CIPK-8 mRNA levels were quantitated by Real-time PCR. 8 shows the mRNA levels for CIPK-8 in relation to the reference gene GAPDH. The real-time PCR primers used are listed in Table XII. Since CIPK-29 and CIPK-1 were very similar to CIPK-8 their mRNA levels were also measured in the transgenic plants. Leaves from four plants from cultivar SP94-3116 transformed with the CIPK-8 RNAi construct and four construct plants transformed with the empty vectors alone are shown. The data indicates suc-

cessful silencing for the CIPK-8 gene when control and RNAi CIPK-8 plants are compared. The data also indicates that the construct introduced was able to silence the CIPK-29 and CIPK-1 genes as well. To confirm the increased sucrose content due to the silencing of the genes total and reductive sugar levels were determined by HPLC (high performance liquid chromatography). FIG. 8 indicates the sucrose levels in control and CIPK silenced plants as well as the ratio between sucrose to glucose+fructose. Silenced plants presented in average 64.18 µg of sucrose/mg of leaf dried weight while control plants presented 21.95 µg/mg. The ratio of sucrose/glucose+fructose was also altered. CIPK silenced plants presented a ratio of 6.81 of sucrose over the monosaccharides while the control plants showed an average ratio of 0.57. This may possibly indicate an overall 12 fold more efficient conversion of the monosaccharides glucose and fructose into sucrose in the leaves of silenced plants.

Since both CIPK-8 and CIPK-29 were found to be differentially expressed in sugarcane leaves we postulate that CIPK kinases regulate sucrose synthesis in sugarcane. Additionally, CIPKs may have a role in regulating sugar accumulation in the internode tissues since several of them were detected as differentially expressed in these organs. Since the fragment used to silence the differentially expressed CIPK-8 and CIPK-29 was also efficient in silencing CIPK-1, which has an overall identity to CIPK-8 and CIPK-29 of 65%, it is possible that the use of SNF1-related genes with identity to the genes protected in this patent, either to the whole genes, or fragments of the genes, of at least 65%, but not restricted to 65%, may also be able to silence the protected genes. The reverse scenario is also plausible. Since CIPK-1, a gene that was not detected in our microarray data as associated to sucrose content, was silenced by the CIPK-8 construct even though it presented only 65% sequence identity to its overall available sequence, it is possible to silence sucrose associated genes by using sequences from similar sucrose-unrelated genes.

Additional genes that may contribute to sucrose synthesis and accumulation are described below. We identified five genes encoding aquaporins among the differentially expressed genes when high brix and low brix plants were compared (SCCCLR1024C03.g, SCCCZR1001F02.g, SCCCZR1002E08.g, SCCCST3001H12.g, SCEQRT2100B02.g). In a previous work they were demonstrated to be down-regulated in the mature internodes (Felix, 2006). This large and diverse family of membrane proteins, also known as MIPs (Major Intrinsic Proteins) is primarily involved in the regulation of water movement between cells and cell compartments, although many of them also facilitate the passage of small solutes (rev. Maurel and Chrispeels, 2001; Chaumont et al, 2005). According to their subcellular localization, aquaporins can be classified as plasma membrane intrinsic proteins (PIPs) or tonoplast intrinsic proteins (TIPs). The aquaporins genes we identified as differentially expressed fall into both of these categories. The accumulation of sucrose in such high concentrations as seen in sugarcane cells certainly represents an osmotic challenge, which demands efficient control of solute compartmentation. As key players in the equilibration of water potentials via regulation of membrane permeability, aquaporins may have a fundamental role in the process of sugar storage in sugarcane vacuoles. It has been observed in *Arabidopsis* that loss of the aquaporin TIP1;1 severely affects carbohydrate metabolism and transport (Ma et al., 2004) and the authors postulate that this aquaporin could be involved in a vesicle-based routing of carbohydrates towards the central vacuole. Due to the diversity of roles described for the members of this family, additional experiments are necessary to elucidate the possible

roles of these sugarcane aquaporins in the sugar accumulation process. Sugar-signaling pathways do not operate in isolation but are part of cellular regulatory networks. Recent results clearly show cross talk between different signaling systems, especially those of sugars, phytohormones, and light. Most of the stress-related genes are cold- and drought-induced; there is also a ribonuclease that appeared altered four times and a wound-induced protein differentially expressed in 5 samples. Four sugarcane stress-related ESTs belong to a class of low-molecular-weight hydrophobic proteins (LTI) involved in maintaining the integrity of the plasma membrane during cold, dehydration and salt stress conditions. These genes are activated by environmental factors, such as dehydration and salinity and by chemical signals such as abscisic acid (ABA) (Morsy et al., 2005).

Sixteen differentially expressed genes encode transcription factors. A putative AP2/EREBP transcription factor (SCBGLR1099G02.g) was shown to have enhanced expression in leaves from plants with high sugar content. AP2/EREBP form a family of plant-specific transcription factors that contains an AP2/EREBP (ethylene responsive element binding protein) domain, a conserved region of 60 aminoacids involved in DNA binding (Jofuku et al., 1994; Okamoto et al., 1993; Riechmann and Meyerowitz, 1998). AP2 transcription factors are involved in the specification of flower organ and meristem identity, and suppression of flower meristem indeterminacy (Bowman et al., 1989; Irish and Sussex, 1990; Kunst et al., 1989; Okamoto et al., 1993). AP2 is also required for ovule and seed coat development (Jofuku et al., 1994; Leon-Kloosterziel et al., 1994; Modrusan et al., 1994). Although the most remarkable function of AP2 is in flower development, its transcripts are also detected in leaves, stems, and seedlings (Jofuku et al., 1994), opening the possibility of diverse functions for different members of the AP2 family. It was already shown that ap2 mutations cause changes in the ratio of hexose to sucrose during seed development (Ohto et al., 2005). Because of this observation, it is believed that potential targets of AP2 activity may be enzymes involved in sugar metabolism.

We found eight CYP-related genes altered among the differentially expressed genes (SCEQRT1026H08.g, SCAGLR1043E04.g, SCUTAM2005B03.g, SCSGFL4193B05.g, SCACSB1037A07.g, SCEZHR1087F06.g, SCSGHR1069F04.g, SCQGHR1012B09.g). Cytochrome P450 monooxygenases (P450s) are used widely in plant biosynthetic and detoxicative pathways including synthesis of lignins, UV protectants, pigments, defense compounds, fatty acids, hormones, signaling molecules, breakdown of endogenous and toxic compounds (Schuler and Werck-Reichhart, 2003). During sugarcane internode maturation, parenchyma cells differentiate into highly specialized sucrose-storage compartments. This process imposes cellular reorganization to cope with osmotic and oxidative stress, and involves progressive lignification and suberization of cell walls to prevent pathogen invasion and water loss (Kolattukudy, 1984; Jacobsen et al., 1992), which may explain the predominance of stress-related genes (34 SAS) among the genes described in this work.

Eighteen differentially expressed SAS encode for hormone biosynthesis or hormone-related genes either when comparing the high brix against low brix plants or the high brix against low brix internodes (SCCCAM2004G02.g, SCCCCL6002B05.g, SCCCFL4091A07.g, SCCCLR1048D07.g, SCCCLR1C03G01.g, SCCCLR2002F08.g, SCCCRT1001E01.g, SCEQRT1024E12.g, SCEQRT1028H06.g, SCEZLB1009A09.g, SCJFRT1005C11.g,

SCJFRT1007H07.g, SCRFLR1012D12.g, SCSBAM1085B06.g, SCSGAM1094D05.g, SCVPLR2012A10.g, SCVPRZ2038F04.g, SCVPRZ3025G09.g). Three encode for salicylic acid biosynthesis and six of them code for jasmonate biosynthesis genes. Two ESTs that were up regulated in high sugar content (HS) mature leaves codes for an omega-3 fatty acid desaturase-FAD8. In higher plants, the membrane lipids contain a high proportion of trienoic fatty acids (TAs). It has been suggested that these fatty acids, especially linolenic acid, are precursors of a defense-related signal molecule, jasmonate (JA). In *Arabidopsis*, three genes encoding the omega-3 fatty acid desaturase, namely FAD3, FAD7 and FAD8, are responsible for the production of TAs. Environmental stimuli, such as wounding, salt stress and pathogen invasion, which lead to a rapid increase in JA production, significantly induce expression of the FAD7 and FAD8 genes (Nishiuchi and Iba, 1998). The data points to a role of JA and salicylic acid synthesis in sucrose metabolism. This is the first report of the involvement of these hormones in sucrose synthesis.

Recent evidence suggests that plants have many different types of receptor-like protein kinases (RLKs) that may transduce extra cellular information into the cell. Twenty-one sugarcane SAS encoding for a RLK were found to be differentially enriched in the high sugar content plants and seventeen when mature and immature internodes were compared. RLKs have been identified from a number of plants and have been categorized into classes based on different structural motifs found in their extra cellular domains. The physiological functions of most RLKs are unknown, but some of them are involved in disease resistance and plant development (Becraft, 2002).

A SAS homologous to a gene encoding a Myb-repeat transcription factor (SCCCLR1C08G10.g), similar to CIRCADIAN CLOCK ASSOCIATED (CCA1) or LATE ELONGATED HYPOCOTYL (LHY), was up regulated in High Sugar mature leaves. CCA1/LHY and the TIMING OF CAB EXPRESSION 1 (TOC1) are thought to participate in a negative feedback loop, which is part of a model for the central oscillator in the *Arabidopsis* circadian clock. In higher plants the circadian clock controls hypocotyl elongation, daily leaf movements, flowering time and the rhythm of CO<sub>2</sub> fixation (McClung, 2001). A sugarcane LHY/CCA1 was found to be enriched in the high sugar content individuals and this expression profile was also observed throughout the growing season. In tomato, Jones and Ort (1997) have demonstrated that the circadian rhythm controls the timing of sucrose-phosphate synthase phosphatase activity, which in turn, determines the activation of sucrose phosphate synthase (SPS). SPS catalyses the conversion of UDP-glucose and fructose-6-phosphate to sucrose-6-phosphate, the second last step in sucrose biosynthesis (Huber and Huber, 1996). Pathre et al., (2004) demonstrated that the diurnal variation observed in the activity of SPS was not due to any intrinsic rhythm, but due to the transient changes in environmental conditions, like irradiance and temperature. When the circadian clock was correctly tuned with the environment, *Arabidopsis* plants presented increased photosynthesis and growth (Dodd et al., 2005). The sugarcane EST was mainly expressed in mature and immature leaves, lateral bud and flower, but also presented a weak expression in immature internodes and roots (not shown). We hypothesize that the expression profile of LHY/CCA1 transcripts in HS plants could be related to a photosynthetic advantage and, consequently, an enhanced carbon fixation. LHY/CCA1 may control the transcription of a protein phosphatase that subsequently activates the SPS enzyme, increasing sucrose synthesis.

Two SAS encoding for 14-3-3 proteins (SCEQRT1025D06.g and SCEQRT1031D02.g) were found to be more expressed in mature leaves from the Low Sugar population and four to be down-regulated in mature internodes ((SCCCRZ1001D02.g, SCCCLR1022D05.g, SCEQRT1025D06.g, SCEQRT1031D02.g). Recent reports pointed out the importance of these adapter proteins in plant metabolic pathways (Ferl, 2004). It was suggested that the members of this family affect nitrate fixation by regulating nitrate reductase (NR) and carbohydrate metabolism by binding to SPS. This enzyme has several putative phosphorylation sites that regulate its activity by 14-3-3 dependent and independent mechanisms. Non-14-3-3 events include phosphorylation of SPS on Ser-424 and Ser-158 which is thought to be responsible for light/dark modulation and osmotic stress activation of the enzyme (McMichael et al., 1993; Toroser and Huber, 1997). However, there is a site-specific regulatory interaction between 14-3-3 proteins and Ser-229 of spinach SPS, which inhibits SPS activity (Toroser et al., 1998). This regulatory node is likely to be the same that occurs in the NR regulation. In its unphosphorylated state, SPS is active. Phosphorylation by a kinase (e.g. SNF1, Bachmann et al., 1996; Moorhead et al., 1999) does not inactivate SPS, but tags the enzyme for 14-3-3 binding, which completes the signal-induced transition toward inactivation. SPS that is phosphorylated and bound by 14-3-3s may be inactivated directly in a reversible manner or may be destabilized and subjected to proteolysis (Sehnke et al., 2002; Comparot et al., 2003). It has been reported that during sugar starvation targets for 14-3-3 proteins are degraded by proteases; the function of this is not clear but it was suggested to represent a safety valve for metabolic regulation (Cotelle et al., 2000). Various research groups reported the impact of 14-3-3 proteins on metabolism. Overexpression of 14-3-3 proteins in potato induced an increase in catecholamine and soluble sugars contents in leaves, whilst a 14-3-3 antisense experiment increased the tuber starch content, NR activity and amino acid composition (Prescha et al., 2001; Swiedrych et al., 2002). In addition, Zuk et al., (2003) observed a significant increase in potato SPS and NR activities when all of the six 14-3-3 isoforms were repressed.

There are three enzymes involved on the biosynthetic pathway of lignin: cinnamoyl-coenzyme A reductase (CCR), cinnamyl alcohol dehydrogenase (CAD) and caffeic acid 3-O-methyltransferase (COMT). A SAS coding for a COMT (SCRFLR1012F12.g) was found to be differentially expressed in four different samples. Lignins are phenolic polymers found in the secondary cell walls of vascular plants. They play an important role by reducing the permeability of the cell wall to water and provide mechanical strength and defense against wounding and infection (Lewis and Yamamoto, 1990). The importance of lignin biosynthesis as dominant process in maturing sugarcane stems was observed by Casu et al., (2004). The storage parenchyma of the sugarcane maturing stem internodes is extensively lignified and Jacobsen et al., (1992) proposed that this process parallels to the increase in sucrose content observed in matures internodes. This lignification could provide defense against wounding and infection for these plants. Low lignin levels could, on the other hand, lead to high sucrose accumulation, or COMT could have an additional function in sucrose synthesis or accumulation that has not been previously identified. To test for this hypothesis and confirm that COMT differential gene expression associated to sucrose content was indeed reflecting a role for these genes in sucrose synthesis or accumulation we obtained sugarcane transgenic plants where SAS SCRFLR1012F12.g was silenced by antisense expression.

Sugarcane embryonic callus from the cultivars SP83-2847, SP91-1049, SP80-185, CTC1 and CTC5 were bombarded by biolistics with a construct where a 535 bp fragment of SAS SCRFLR1012F12.g (SEQ ID No. 380) was cloned in the antisense orientation in the BamHI site of vector pAHC17. The 535 bp fragment was obtained by PCR using the primers COMT(AS)pAHC17 forward (SEQ ID No. 376): 5'CGCGGATCCGACGTCGTCAAGTGCCAGAT3' and COMT(AS)pAHC17 reverse (SEQ ID No. 377): 5'CGGGATCCGCGTTGGCGTAGATGTAGGT3'. The fragment was digested with the enzyme BamHI, cloned in the pAHC17 vector (Christensen and Quail, 1996) digested with the same enzyme and clones were sequenced to identify a construct where the insert was in the antisense orientation. Transgenic plants were generated by co-transformation of COMT(AS)/pAHC17 construct and the pHA9 vector (Wei and Albert, U.S. Pat. No. 6,706,948). To verify that COMT SCRFLR1012F12.g mRNA levels were decreased in the transgenic plants obtained COMT mRNA levels were quantitated by Real-time PCR. FIG. 9 shows the mRNA levels for SCRFLR012F12.g in relation to the reference gene GAPDH in plants of variety SP83-2847 transformed with the COMT (AS)/pAHC17 construct. The real-time PCR primers used are listed in Table XII. Leaves from five plants transformed with the COMT antisense construct and five plants transformed with the vectors alone are shown. The data indicates successful silencing for the COMT gene when control and antisense plants are compared. To check if silencing of the genes would lead to increased sucrose content, total and reductive sugar levels were determined by HPLC (high performance liquid chromatography). FIG. 9 indicates the sucrose levels in control and COMT silenced plants as well as the ratio between sucrose to glucose+fructose. Silenced plants presented in average 29.34 µg of sucrose/mg of leaf dried weight while control plants presented 20.7 µg/mg. The ratio of sucrose/glucose+fructose was also altered. COMT silenced plants presented a ratio of 1.74 of sucrose over the monosaccharides while the control plants showed an average ratio of 0.71. This may possibly indicate an overall 2.4 fold more efficient conversion of the monosaccharides glucose and fructose into sucrose in the leaves of silenced plants.

Signals can be perceived and amplified at the cell membrane by receptors coupled to a variety of signaling pathways, including the inositol 1,4,5-trisphosphate (IP3) pathway. This second messenger is produced from the hydrolysis of phosphatidylinositol 4,5 bisphosphate and raises Ca<sup>2+</sup> levels in the cytosol (Berridge, 1993). The inositol-polyphosphate 5-phosphatase (5Ptases) comprise a large group of enzymes that can hydrolyze 5-phosphates from a variety of inositol phosphates, like IP3 (Majerus et al., 1999). There are four genes encoding inositol metabolism enzymes altered in our data (SCRULB1060F05.g, SCSBST3096H04.g, SCCCLR1C02F07.g, SCCCRZ2001A10.g) when high brix and low brix plants were compared and a Phospholipase C(SCSBHR1052C05.g) down-regulated in sugar-rich internodes. Inositol derivatives may be involved in the modulation of Ca<sup>2+</sup> levels and there are many evidences for a role of Ca<sup>2+</sup> in sugar signaling (reviewed by Rolland et al., 2002, see above).

In sugarcane, the use of wild ancestors as a means to incorporate new traits or to improve variability in a well established breeding program is something that requires a lot of attention and caution from the breeder. Such parents can carry a large proportion of variation inferior to current commercial hybrids, and sugar content is likely to be poor. The crosses and selections done in this study aimed to produce sugar content variability, introducing new genes that exist in

wild ancestors and that had never been explored in the development of hybrid commercial varieties. The final objective was, once a large variability was created from the introgression studies, to perform bulk segregation analysis in extremes of the population to eventually identify genes that could be linked to sugar content. The markers identified in this work have been shown to be useful to analyze crosses between individuals from the introgression study and elite cultivars and follow the sugar content genes coming from wild ancestors.

It is worth to mention that the use of wild germplasm from 21 *S. officinarum* and 13 *S. spontaneum* genotypes allowed the selection of more divergent materials than the crosses between the commercial varieties. The range of brix content from 8.6 (the extreme individual for LB) to 23.9 (the extreme individual for HB) could never be reached using progeny derived from conventional crosses. This is a valuable population for using in sucrose accumulation studies. The results produced are probably different from the ones that could be obtained with populations derived from crosses between commercial varieties, with higher brix content but not so contrasting phenotypes.

The approach described produced data and molecular markers to be used in breeding programs, in the characterization of transgenic plants designed to contain more sucrose, and/or used as candidate genes for genetic manipulation in transgenic plants or non-transgenic plants in order to improve the sugar content of commercial varieties. Changes in more than one gene expression are more significant while changes in three or a higher number of genes are highly significant when searching for molecular markers but a pattern of expression of just one gene was shown to be useful in characterizing a plant or population of plants in regards to sucrose content. Additionally, silencing of two genes differentially expressed by RNA interference and antisense expression proved useful in the development of transgenic plants with increased sucrose content. It is very likely that changes in transcript levels are accompanied by changes in the protein levels encoded by the genes, thus quantification of the corresponding proteins may also be used to identify plants with contrasting sucrose accumulation capacities. Measures of sucrose content can accompany gene expression measures and be complementary in defining plants with gene expression favorable to sucrose accumulation. These individuals may be crossed and rounds of selection with the aid of the markers can follow each generation to yield better sucrose producing plants.

TABLE XIII

List of Sugarcane Assembled Sequences (SAS) and their SEQ ID Nos.	
The EST Genbank accession number is in parentheses. The SEQ ID No. refers to the sequence identifiers in the sequence listing. The listed ESTs assembled to the indicated sequence and should be considered one transcript. Each SAS is differentially expressed between plants with low and high sucrose content or between internode tissues of high and low sucrose content.	
SEQ ID No. 229: SCACLR1057C07.g	(CA073791, CA220104, CA175807, CA173305, CA161664, CA208707, CA275831, CA082360, CA232127, CA208522, CA082500, CA158772, CA254078, CA154812, CA168711, CA265487, CA216423, CA082097, CA282869, CA163131, CA242148, CA116387, CA088301, CA205272, CA216758, CA083652, CA178498, CA275830, CA164981, CA173335, CA257615, CA239707, CA164577, CA085299, CA209305, CA191774, CA082901, CA206163, CA219544, CA256136,

TABLE XIII-continued

List of Sugarcane Assembled Sequences (SAS) and their SEQ ID Nos.	
The EST Genbank accession number is in parentheses. The SEQ ID No. refers to the sequence identifiers in the sequence listing. The listed ESTs assembled to the indicated sequence and should be considered one transcript. Each SAS is differentially expressed between plants with low and high sucrose content or between internode tissues of high and low sucrose content.	
CA242861, CA087944, CA219617, CA172548, CA089365, CA242929, CA296024, CA211326, CA077845, CA065159, CA220037, CA078282, CA176305, CA087014)	
SEQ ID No. 230: SCACLR1130D02.g	(CA100457, CA108544, CA104245, CA139305, CA183555, CA184261, CA075000, CA116753, CA124475, CA107618)
SEQ ID No. 231: SCACLR1130H08.g	(CA285355, CA296620, CA190345, CA236470, CA199128, CA223158, CA296543, CA237253, CA116793, CA223246, CA275687)
SEQ ID No. 232: SCACLR2022H05.g	(CA185596, CA107538, CA278239, CA142728, CA095392, CA190254, CA255382, CA118885, CA186426, CA242032, CA083853, CA088965, CA186503, CA072676, CA246552, CA088959, CA292397, CA269566, CA163748, CA243048, CA287796, CA095283, CA194496, CA285226, CA102940, CA265718, CA242052, CA194677, CA157478, CA238095, CA282663, CA127731, CA104186)
SEQ ID No. 233: SCAGLR1021G10.g	(CA184947, CA241174, CA116948, CA235280, CA148829, CA187937, CA290068, CA148916, CA253948, CA153438, CA200242, CA288775, CA242709, CA242784, CA147421, CA150935, CA110552, CA234507, CA277424, CA072428, CA220958, CA221034, CA261229, CA220980, CA225630, CA215861, CA229847, CA275017, CA229919, CA227414, CA289769, CA239844, CA184991)
SEQ ID No. 234: SCBFAD1046D01.g	(CA284358, CA285672, CA258515, CA260599, CA285724, CA284423, CA065523, CA269123)
SEQ ID No. 235: SCBGFL3095D08.g	(CA230968, CA243310, CA230887)
SEQ ID No. 236: SCBGFL4052C11.g	(CA221542, CA181746)
SEQ ID No. 237: SCBGFL4053F12.g	(CA219396, CA221898)
SEQ ID No. 238: SCBGLR1096C08.g	(CA190075, CA236012, CA290681, CA281821, CA111779, CA102557, CA224586, CA290611, CA245672, CA118621, CA219281, CA212792, CA118254, CA239357, CA123219, CA245691)
SEQ ID No. 239: SCBGLR1117A05.g	(CA069967, CA206454, CA115471, CA222775, CA300103, CA216451, CA069882, CA240610, CA121419, CA253181, CA119047)
SEQ ID No. 240: SCCCCL2001B01.b	(CA075874, CA110039, CA262153, CA138938, CA222746, CA206852, CA195629, CA065975, CA111213, CA243704, CA139758, CA067579, CA228104, CA112899, CA219971, CA159289, CA067652, CA243309, CA260244, CA136110, CA260251, CA265770, CA207439, CA141173, CA260652, CA108966, CA233446, CA109052, CA266455, CA264812, CA196943, CA065789, CA204592, CA065874, CA228837, CA267875, CA067584, CA114662, CA219472, CA219452, CA067658, CA093038, CA235273)
SEQ ID No. 241: SCCCCL4003D08.g	(CA064615, CA239044, CA246974, CA074795, CA290714,

TABLE XIII-continued

List of Sugarcane Assembled Sequences (SAS) and their SEQ ID Nos.

The EST Genbank accession number is in parentheses. The SEQ ID No. refers to the sequence identifiers in the sequence listing. The listed ESTs assembled to the indicated sequence and should be considered one transcript. Each SAS is differentially expressed between plants with low and high sucrose content or between internode tissues of high and low sucrose content.

CA074872, CA094033, CA095138, CA183882, CA249457, CA102981, CA172565, CA263531, CA183925, CA255937, CA084305, CA285149, CA085127, CA228150, CA248344, CA064616, CA290646)

SEQ ID No. 242: SCCCL4004A10.g  
(CA101534, CA147302, CA227522, CA219008, CA114047, CA177473, CA250309, CA131850, CA222728, CA096239, CA121915, CA209925, CA174118, CA158138, CA264731, CA219404, CA241947, CA239850, CA139416, CA088821, CA149323, CA075509, CA192414, CA168488, CA070307, CA191927, CA227992, CA191529, CA267246, CA213285, CA250111, CA258031, CA224522, CA122970, CA072224, CA082052, CA098902, CA098895, CA094073, CA296040, CA238636, CA098164, CA237674)

SEQ ID No. 243: SCCCL4004C06.g  
(CA184820, CA224856, CA126504, CA232891, CA206438, CA212819, CA232897, CA214257, CA101169, CA082190, CA167693, CA214057, CA300033, CA094090, CA252628, CA167758, CA111995, CA074267, CA228379, CA211130, CA249343, CA209709, CA085064, CA202861, CA119928, CA225134, CA164339, CA225122)

SEQ ID No. 244: SCCCL4007H07.g  
(CA259044, CA299572, CA172510, CA266911, CA094384, CA217028, CA119215, CA269647, CA187053, CA288923, CA172798, CA216961, CA180079, CA300646, CA298791)

SEQ ID No. 245: SCCCL5002B10.g  
(CA221338, CA161278, CA221548, CA126743, CA176053, CA095223, CA158980, CA175702, CA137305, CA108318)

SEQ ID No. 246: SCCCL5004D02.g  
(CA192143, CA236211, CA277456, CA238363, CA207316, CA083476, CA300881, CA105556, CA167444, CA195960, CA101127, CA174295, CA171982, CA179165, CA082796, CA095389, CA299706, CA235517, CA171513, CA297597, CA079747, CA159787, CA097371, CA079116)

SEQ ID No. 247: SCCFL4091A07.g  
(CA223439, CA251804, CA235024)

SEQ ID No. 248: SCCCHR1004D03.g  
(CA286507, CA215612, CA183433, CA065784, CA175929, CA102729, CA205573, CA264021, CA158422)

SEQ ID No. 249: SCCCHR1004H09.g  
(CA198695, CA218094, CA240658, CA183261, CA257018, CA185072, CA107735, CA165864, CA162193, CA280279, CA102770, CA238555, CA267028, CA131832, CA257098)

SEQ ID No. 250: SCCCLB1023E12.g  
(CA179300, CA198187, CA088499, CA224987, CA116260, CA238936, CA132328, CA210346, CA300142, CA158693, CA092253, CA271421, CA241178, CA182283, CA089207, CA194934, CA092199, CA296333, CA075354, CA224675, CA084007, CA113237, CA296334, CA066934, CA136894, CA192584, CA111805, CA067884, CA211313, CA216712, CA092778, CA066873, CA098107, CA280346, CA144921)

SEQ ID No. 251: SCCCLB2004C08.g  
(CA279906, CA261059)

SEQ ID No. 252: SCCCLR1001D10.g  
(CA249418, CA083581, CA252565, CA087780, CA126329, CA116150, CA256293, CA189955, CA208608, CA189961, CA239503, CA122010, CA180875, CA107889, CA265080,

TABLE XIII-continued

List of Sugarcane Assembled Sequences (SAS) and their SEQ ID Nos.

The EST Genbank accession number is in parentheses. The SEQ ID No. refers to the sequence identifiers in the sequence listing. The listed ESTs assembled to the indicated sequence and should be considered one transcript. Each SAS is differentially expressed between plants with low and high sucrose content or between internode tissues of high and low sucrose content.

CA154811, CA250574, CA288166, CA276490, CA203244, CA208413, CA209900, CA124777, CA289690)

5 SEQ ID No. 253: SCCCLR1022D05.g  
(CA199003, CA295779, CA243427, CA242039, CA202852, CA128804, CA079318, CA079910, CA281772, CA281793, CA250251, CA140942, CA081545, CA084937, CA074621, CA106617, CA181947, CA091378, CA247107, CA140865, CA148961, CA086118, CA235025, CA111400, CA130075, CA114483, CA193046, CA087052, CA275872, CA119131, 20 CA224651, CA240046, CA295949, CA255246, CA231690, CA222739, CA130833, CA189913, CA216812, CA152690, CA129200, CA094241, CA087758, CA001112, CA099509, CA295694, CA152604, CA289169, CA275873, CA100849, CA151157, CA278748, CA126737, CA219267, CA143476, CA217366, CA188937, CA149217, CA129933, CA230200, 25 CA088938, CA121701, CA110053, CA143403, CA217293, CA276362, CA230113, CA155717, CA228428, CA066322, CA148305, CA273294, CA125293, CA279142, CA133423, CA190364, CA241302, CA109003, CA171238, CA124306, CA288895, CA152905, CA137901, CA241224, CA171157, CA189103, CA073313, CA280288, CA222537, CA244293, 30 CA195698, CA284927, CA244221, CA240565, CA131978, CA143850, CA147045, CA116042, CA273851, CA118529, CA250276, CA114167, CA092744, CA111595, CA082835, CA283118, CA119664, CA090489, CA243388, CA139738, CA198502, CA074106, CA241811, CA193935, CA090417, CA144601, CA242944, CA263741, CA242878, CA181943, 35 CA100925, CA154899, CA255036, CA298711, CA255877, CA231477, CA301130, CA079473, CA293695, CA249587, CA201652, CA270939, CA092502, CA231391, CA142524, CA293643, CA155896, CA272121, CA148488, CA249518, CA295765, CA227150, CA169631, CA100111, CA173458, CA219272, CA067413, CA086035, CA169552, CA238069, 40 CA227079, CA101601, CA280785, CA264367, CA118824, CA220340, CA116614, CA118307, CA072726, CA255181, CA143851, CA128705, CA142362, CA230449, CA131091, CA251477, CA151152, CA192477, CA124603, CA092380, CA126294, CA071894, CA300717, CA179264, CA233938, CA126045, CA293018, CA283292, CA168278, CA162958, CA202235, CA266711, CA131176, CA119234, CA111790, 45 CA232293, CA175336, CA092372, CA232205, CA247106, CA117673, CA297133, CA073144, CA227288, CA150142, CA297060, CA139824, CA205064, CA116036, CA202889, CA215601, CA296581, CA119907, CA144265, CA192882, CA298102, CA198270, CA216807, CA182514, CA128480, CA105914, CA108571, CA177022, CA232110, CA128410, 50 CA125896, CA232195, CA289717, CA295716, CA301502)

SEQ ID No. 254: SCCCLR1022H07.g  
(CA256002, CA153512, CA119708, CA201590, CA232582, CA203039)

55 SEQ ID No. 255: SCCCLR1024E11.g  
(CA236213, CA119421, CA239312, CA087963, CA236209, CA093728, CA121529, CA144287, CA110967, CA120342, CA078164)

SEQ ID No. 256: SCCCLR1024F10.g  
(CA248370, CA191668, CA174627, CA136231, CA240508, CA146036, CA228222, CA220265, CA237574, CA268651, CA242965, CA146965, CA237607, CA243057, CA268723, CA266000, CA163172, CA150009, CA235949, CA119432, CA132957, CA153279, CA074733, CA155267, CA134767, CA153353, CA208681, CA074819, CA174997, CA294180, CA298533, CA251324, CA105997, CA066993, CA203286, 60 CA291734, CA274193, CA071109, CA071088, CA249083, CA208769, CA177604, CA106088, CA067069)

TABLE XIII-continued

List of Sugarcane Assembled Sequences (SAS) and their SEQ ID Nos.

The EST Genbank accession number is in parentheses. The SEQ ID No. refers to the sequence identifiers in the sequence listing. The listed ESTs assembled to the indicated sequence and should be considered one transcript. Each SAS is differentially expressed between plants with low and high sucrose content or between internode tissues of high and low sucrose content.

SEQ ID No. 257: SCCCLR1068G11.g  
(CA132953, CA232759, CA292317, CA213697, CA232845, CA242579, CA071844, CA133612, CA213781, CA124103, CA281045, CA243542, CA268384, CA080234, CA228260, CA112544, CA220447, CA238600, CA120333, CA130280, CA222523, CA085868, CA238048, CA289325, CA085954, CA289237, CA290116, CA252889, CA230658, CA175174, CA133538, CA246442, CA230739, CA133616, CA111266, CA080878, CA127449, CA113622, CA130344, CA225351, CA239513, CA206259, CA289382, CA246811, CA191694, CA129517, CA257025, CA108272, CA257105, CA089953, CA082439, CA285102, CA090031, CA220448, CA120037, CA296110, CA233332, CA189423, CA246856, CA247427, CA116596, CA233412, CA246807, CA224412, CA299018, CA126355, CA221362, CA298715, CA128521, CA077715, CA242434, CA071472, CA128603, CA071560, CA123524, CA236982, CA139104, CA120188, CA248016)

SEQ ID No. 258: SCCCLR1072E03.g  
(CA149803, CA140849, CA154999, CA217167, CA149970, CA197516, CA179657, CA113459, CA205466, CA299206, CA119586)

SEQ ID No. 259: SCCCLR1072H06.g  
(CA293008, CA292012, CA208082, CA212163, CA095120, CA250666, CA095061, CA250751, CA266742, CA140748, CA299559, CA221625, CA199195, CA280252, CA249305, CA283511, CA119620, CA273507, CA284119)

SEQ ID No. 260: SCCCLR1C04E03.g  
(CA295762, CA246851, CA247540, CA295704, CA250739, CA076585, CA129498, CA250812, CA189759, CA153500, CA182502, CA273004, CA180831, CA225947, CA295943, CA137602, CA283935, CA137601, CA225870, CA276088, CA239790, CA125960, CA283930, CA085833, CA236700, CA129446, CA206958, CA219091, CA204694, CA114854, CA164705, CA133070, CA264948, CA076438, CA151018, CA121378, CA288667, CA166549, CA127343, CA076524, CA120880, CA267188, CA205607, CA228116, CA137280, CA117418, CA237518, CA182380, CA235506, CA203663, CA075662, CA113908, CA202142, CA156760, CA117805, CA156119)

SEQ ID No. 261: SCCCLR1C07B07.g  
(CA281556, CA102608, CA183206, CA267464, CA216559, CA126478, CA178227, CA224781, CA220964, CA230932, CA196879, CA111576, CA159229, CA285341, CA284646, CA159313, CA267717, CA089742, CA228165, CA120559, CA267804, CA296594, CA117476, CA283020, CA291172, CA296665, CA280265, CA248548, CA090139, CA141203, CA131303, CA142862, CA269709, CA074994, CA141285, CA106243, CA141103, CA189990, CA266648, CA120035, CA134522, CA157584, CA118179, CA243432, CA210686, CA238135, CA248480, CA272949, CA290279, CA178232, CA290337, CA279227, CA148788, CA277386, CA292004, CA163922, CA248059, CA148876, CA216395, CA163999, CA249878, CA222979, CA080867, CA288178, CA267417, CA113988, CA112566, CA225163, CA249795, CA224169, CA267504, CA160144, CA199747, CA296541, CA207876, CA173201, CA127744, CA257183, CA270601, CA186974, CA244929, CA121034, CA245946, CA094024, CA249521, CA257253, CA165727, CA270682, CA109618, CA165164, CA137020, CA283548, CA274874, CA165279, CA281754, CA280871, CA079423, CA238032, CA228443, CA157012)

SEQ ID No. 262: SCCCLR2001E10.g  
(CA262799, CA127278, CA280201, CA287309, CA089562, CA078214, CA077866, CA287533, CA211102, CA180904,

TABLE XIII-continued

List of Sugarcane Assembled Sequences (SAS) and their SEQ ID Nos.

The EST Genbank accession number is in parentheses. The SEQ ID No. refers to the sequence identifiers in the sequence listing. The listed ESTs assembled to the indicated sequence and should be considered one transcript. Each SAS is differentially expressed between plants with low and high sucrose content or between internode tissues of high and low sucrose content.

5 The EST Genbank accession number is in parentheses. The SEQ ID No. refers to the sequence identifiers in the sequence listing. The listed ESTs assembled to the indicated sequence and should be considered one transcript. Each SAS is differentially expressed between plants with low and high sucrose content or between internode tissues of high and low sucrose content.

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CA089473, CA074528, CA079677, CA082818, CA118437, CA269971, CA092559, CA247542, CA285807, CA091331, CA277276, CA271301, CA072671, CA263353, CA205812, CA280164, CA116982, CA073860, CA263266, CA116704, CA089413, CA158170, CA173734, CA180319, CA163659, CA163766, CA124561, CA278597, CA072426, CA178645, CA271786, CA264556, CA120664, CA112499, CA185831, CA084497, CA160409, CA083810, CA113314, CA160061, CA187809, CA189668, CA238848, CA163843, CA114235, CA165641, CA121314, CA129676, CA263145, CA279135, CA177340, CA174900, CA152748, CA102472, CA112114, CA188798, CA077061, CA185135, CA077762, CA116858, CA178901, CA1847468, CA188663, CA177888, CA274039, CA118008, CA273237, CA174048, CA264113, CA088386, CA281646, CA157750, CA190335, CA175668, CA270524, CA154487, CA121143, CA180710, CA181093, CA091054, CA127015, CA187162, CA092675, CA291128, CA106777, CA088977)

SEQ ID No. 263: SCCCLR2002D04.g  
(CA074921, CA117323, CA243313, CA211783, CA127099, CA286494, CA075012, CA073105, CA128761, CA128376, CA128367, CA243946, CA122696, CA128446, CA230627, CA198414, CA298411, CA122974, CA238383, CA216280, CA230711, CA209970, CA118723, CA121869, CA213055, CA088133, CA241946, CA125071, CA124739, CA240999, CA119298, CA080587, CA112133, CA270423, CA241082, CA292850, CA114123, CA226786, CA257737, CA149929, CA120520, CA202694, CA120498, CA123517, CA073839)

SEQ ID No. 264: SCCCLR2002G09.g  
(CA116535, CA124657, CA116605, CA116498, CA072958, CA257354, CA247799, CA235108, CA103542, CA112157, CA224839, CA257438, CA123168, CA252080, CA080895, CA102459, CA238997, CA081185, CA236648, CA078277, CA081264, CA112560, CA112156, CA239544, CA125043, CA088777, CA248898, CA118825, CA107504, CA118646, CA248977, CA140223, CA203859, CA115827, CA103133, CA115782, CA122771, CA074515, CA229803, CA116712, CA123493, CA085075, CA122840, CA073424, CA229900, CA200897, CA073545, CA115514, CA072446, CA232187, CA072969, CA110011, CA073999, CA245664, CA298980, CA125253, CA072002, CA213810, CA190056, CA230875, CA115022, CA101040, CA230956, CA228508, CA280886, CA102455, CA245446, CA126608, CA245426, CA097164, CA243299, CA116857, CA140025, CA257680, CA101571, CA116664, CA130312, CA105336, CA129039, CA256731, CA095294, CA256654, CA110599, CA073864, CA115403, CA127390)

SEQ ID No. 265: SCCCLR2C03D05.g  
(CA147771, CA241187, CA239901, CA282278, CA280090, CA263518, CA278293, CA187784, CA242098, CA244500, CA117444, CA243119, CA220678, CA181765, CA163903, CA182831, CA154699, CA250434, CA142468, CA127482, CA115131, CA226443, CA230328, CA129679, CA250352, CA272571, CA121245, CA246334, CA263117, CA247571, CA186969, CA152166, CA198196, CA112365, CA257624, CA204733, CA194041, CA181847, CA155624, CA240278, CA201864, CA181440, CA277850, CA181770, CA230413, CA128431, CA142473, CA187851, CA163982, CA128359, CA129154, CA153759, CA163714, CA129531, CA167236, CA226189, CA287855, CA203879, CA274284, CA260310, CA127311)

SEQ ID No. 266: SCCCLR1001E12.g  
(CA262088, CA264485, CA209806, CA114408, CA194065, CA206359, CA254730, CA178254, CA166387, CA132375,



TABLE XIII-continued

List of Sugarcane Assembled Sequences (SAS) and their SEQ ID Nos.

The EST Genbank accession number is in parentheses. The SEQ ID No. refers to the sequence identifiers in the sequence listing. The listed ESTs assembled to the indicated sequence and should be considered one transcript. Each SAS is differentially expressed between plants with low and high sucrose content or between internode tissues of high and low sucrose content.

CA092696, CA092563, CA126173, CA092562, CA190880, CA170137, CA102870, CA190269, CA119262, CA089823, CA213508, CA144221, CA183640, CA130410, CA064605, CA298178)

SEQ ID No. 267: SCCCRT2001H11.g  
(CA236346, CA191174, CA300423, CA105281, CA230838, CA137439, CA200619, CA195246, CA213844, CA181724, CA108176, CA092614, CA228948, CA200693, CA203186, CA209467, CA187262, CA240256, CA241667, CA299526, CA262309, CA143552, CA295095, CA254981, CA220456, CA236075, CA235832, CA300428, CA250139, CA254632, CA243208, CA293154, CA294205, CA250212, CA269402, CA261591, CA294137, CA201093, CA243170, CA291895, CA256863, CA256942, CA166864, CA241994, CA182531, CA254163, CA196827, CA137128, CA262306, CA073149, CA245330)

SEQ ID No. 268: SCCCRT2002B03.g  
(CA220568, CA243112, CA230852, CA160770, CA180268, CA272704, CA230939, CA137141, CA244400)

SEQ ID No. 269: SCCCRZ1001A09.g  
(CA212821, CA074667, CA146782, CA272930, CA107169, CA260410)

SEQ ID No. 270: SCCCRZ1001C12.g  
(CA117861, CA182890, CA138133, CA096667, CA183036, CA276095, CA167830, CA099489, CA192252, CA137344, CA125255, CA251500, CA229153, CA082252, CA111079, CA181249, CA071519, CA298523, CA198397, CA146190, CA180974, CA071438, CA170017, CA071603, CA244468, CA086723, CA146809, CA179822, CA163106, CA139751, CA194118)

SEQ ID No. 271: SCCCRZ1001D02.g  
(CA227562, CA113855, CA074155, CA273171, CA244452, CA244374, CA144616, CA220668, CA244135, CA208913, CA197975, CA269055, CA125771, CA281706, CA285773, CA300153, CA154032, CA245267, CA239706, CA146811, CA248711, CA179814, CA194730, CA268428, CA113399, CA242036, CA227897, CA212687, CA082472, CA299324, CA082329, CA292801, CA292314, CA247082, CA260871, CA222252, CA233879, CA130465, CA140466, CA200065, CA073081, CA114463, CA192580, CA296734, CA269090, CA243519, CA078544, CA228562, CA169691, CA177628, CA112868, CA205245, CA269027, CA080412, CA240406, CA146360, CA229125, CA161211, CA230974, CA300322, CA295571, CA121414, CA151083, CA230896, CA232918, CA140354, CA167344, CA221235, CA161123, CA278179, CA092771, CA255868, CA214663, CA250421, CA260387, CA285663, CA089684, CA250336, CA254468, CA293447, CA244735, CA254392, CA292654, CA252918, CA126311, CA278803, CA076762, CA258105, CA136523, CA077192, CA225269, CA077910, CA230058, CA285260, CA229975, CA286249, CA158350, CA233369, CA243156, CA235192, CA092793, CA233280, CA269567, CA080589, CA212150, CA148111, CA117103, CA243125, CA242823, CA297617, CA070960, CA070900, CA182159, CA200781, CA082483, CA202989, CA133586, CA202917, CA166792, CA204111, CA133514, CA191341, CA229632, CA274798, CA112081, CA083506, CA087024, CA283073, CA075468, CA116699, CA117304, CA228310, CA213022, CA147101, CA280824, CA122938, CA269278, CA242644, CA286222, CA189979, CA231030, CA225697, CA216181, CA271428, CA287898, CA216319, CA249895, CA100564, CA255365, CA182292, CA090466, CA259629, CA185920, CA101429, CA130039, CA235211, CA235276, CA130053, CA090380, CA120551,

TABLE XIII-continued

List of Sugarcane Assembled Sequences (SAS) and their SEQ ID Nos.

The EST Genbank accession number is in parentheses. The SEQ ID No. refers to the sequence identifiers in the sequence listing. The listed ESTs assembled to the indicated sequence and should be considered one transcript. Each SAS is differentially expressed between plants with low and high sucrose content or between internode tissues of high and low sucrose content.

CA242902, CA216182, CA242824, CA080452, CA260017, CA081490, CA278950, CA076773, CA182164, CA209332, CA247081, CA194098, CA262165)

5 The EST Genbank accession number is in parentheses. The SEQ ID No. refers to the sequence identifiers in the sequence listing. The listed ESTs assembled to the indicated sequence and should be considered one transcript. Each SAS is differentially expressed between plants with low and high sucrose content or between internode tissues of high and low sucrose content.

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15 SEQ ID No. 272: SCCCRZ1001G10.g  
(CA222661, CA243406, CA269416, CA111447, CA122777, CA169118, CA240909, CA124462, CA122846, CA250422, CA244712, CA249447, CA287599, CA070902, CA110739, CA146855, CA256535, CA244795, CA078236, CA067840, CA070962, CA265769, CA156647, CA196108)

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SEQ ID No. 273: SCCCRZ1002F06.g  
(CA139097, CA266223, CA099736, CA191325, CA138926, CA269667, CA211498, CA224822, CA216862, CA270060, CA301136, CA287834, CA146274, CA096108, CA181984, CA202409, CA084257, CA098085, CA291642, CA240057, CA110222, CA291673, CA217925, CA224622, CA218519, CA240142, CA271896, CA124695, CA232981, CA227222, CA073020, CA209126, CA233047, CA251280, CA072868, CA206681, CA107412, CA298995, CA094500, CA195663, CA211432, CA066295, CA146933, CA220697, CA106447, CA099272, CA076956, CA069454, CA275222, CA145292,

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30 CA136184, CA179267, CA148544, CA179893, CA156981, CA114064, CA191309, CA217009, CA069184, CA212599, CA264583, CA229486, CA172986, CA096567, CA067167, CA197128, CA172767, CA253169, CA291720, CA146613, CA180633, CA212860, CA133791, CA199922, CA067244, CA262313, CA078445, CA131567, CA253243, CA074238, CA120588, CA268873, CA238585, CA219714, CA218602, CA267988, CA268534, CA070614, CA145612, CA160457, CA180428, CA268951, CA234136, CA098447, CA193324, CA136123, CA218518, CA184233, CA139019, CA145699, CA260610, CA182962, CA239591, CA099732, CA105807, CA107503, CA138654, CA212476, CA239233, CA252352, CA131278, CA085013, CA220627, CA117443, CA079490, CA238164, CA180322, CA112470, CA142140, CA075732, CA073680, CA068067, CA157313, CA179892, CA233146, CA240845, CA075816, CA068156, CA246078, CA233227, CA279126, CA240923, CA094282, CA069497, CA197493, CA182107, CA166736, CA255275, CA251326, CA198871, CA281656, CA137037, CA070883, CA296203, CA078532, CA207814, CA070947, CA199983, CA282429, CA143090, CA191565, CA189249, CA198125, CA197513, CA203121, CA264333, CA214261, CA196418, CA251452, CA171285, CA156984, CA197506, CA211996, CA100356, CA094466, CA133046, CA270062, CA249901, CA211434, CA225569, CA189822, CA093801, CA100946, CA249815, CA131571, CA2220355, CA136957, CA099350, CA064927, CA285088, CA217335, CA139813, CA146454, CA186309, CA217407, CA070684, CA268600, CA199112, CA126792, CA112223, CA265918, CA186374, CA070764, CA099737, CA226973, CA251532, CA142208, CA190634, CA279252, CA174635, CA237846, CA131296, CA224758, CA209005, CA132410, CA187486, CA230626, CA228588, CA080166, CA226226, CA131487, CA209980, CA240058, CA211052, CA230710, CA065368, CA080253, CA165083, CA129937, CA215432, CA280033, CA244591, CA065145, CA064807, CA168165, CA198439, CA218272, CA099578, CA219277, CA218353, CA096715, CA142481, CA142630, CA084917, CA100264, CA213047, CA134830, CA175003, CA121078, CA237503, CA135573, CA244608, CA134915, CA254178, CA135661, CA136819, CA069455, CA157330, CA164187, CA097370, CA067491, CA145272, CA214390, CA098535, CA097056, CA266148)

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65 SEQ ID No. 274: SCCCRZ1003A03.g  
(CA259202, CA100500, CA082076, CA122924, CA157918, CA095401, CA187294, CA090612, CA080881, CA112947,

TABLE XIII-continued

List of Sugarcane Assembled Sequences (SAS) and their SEQ ID Nos.

The EST Genbank accession number is in parentheses. The SEQ ID No. refers to the sequence identifiers in the sequence listing. The listed ESTs assembled to the indicated sequence and should be considered one transcript. Each SAS is differentially expressed between plants with low and high sucrose content or between internode tissues of high and low sucrose content.

CA090695, CA130558, CA146966, CA072719, CA296093, CA262625, CA170785, CA145446, CA178555, CA206391, CA250364, CA171994, CA145530, CA147572, CA240600, CA250453, CA095399, CA282848, CA115658, CA095183, CA237700, CA079664, CA233842, CA180299, CA262035)

SEQ ID No. 275: SCCRZ1C01H06.g  
(CA186428, CA147401, CA147396, CA102140, CA131386, CA067698, CA089218, CA174951, CA158992, CA071179, CA196935, CA190380, CA132381, CA232396, CA211475, CA270590, CA124159, CA132671, CA175342, CA300402, CA165879, CA192094, CA110028, CA118616, CA147228, CA140507, CA149523, CA117528, CA130394, CA179398, CA225915, CA187763, CA266799, CA122963, CA217785, CA232794, CA262910, CA292429, CA094522, CA232704, CA127615, CA245193)

SEQ ID No. 276: SCCRZ2001F06.g  
(CA209945, CA125138, CA089034, CA188983, CA140093, CA239385, CA128670, CA123109, CA283553, CA077454, CA149645, CA077376, CA239384, CA110981, CA289986, CA257955, CA274339, CA283333, CA285711, CA248034, CA094452, CA248046, CA119336, CA225096, CA248683, CA225120)

SEQ ID No. 277: SCCRZ2002C09.g  
(CA227904, CA086301, CA178222, CA149034, CA179328, CA164395, CA150695, CA300591, CA266120, CA214033, CA179414, CA101215, CA232117, CA266196, CA230767, CA106384, CA221659, CA077653, CA090620, CA242756, CA203337, CA104567, CA090436, CA214675, CA090702, CA182664, CA299455, CA160657, CA169652, CA115444, CA110086, CA170759, CA104628, CA090335, CA168143, CA252390, CA083307, CA256278, CA081478, CA076382, CA257169, CA205954, CA076469, CA213516, CA257243, CA192918, CA280631, CA151528, CA122818, CA122358, CA088685, CA210655, CA188323, CA253393, CA238275, CA191873, CA135967, CA150598, CA230233, CA091237, CA126923, CA188824, CA280882, CA079326, CA184911, CA173242, CA248830, CA251291, CA246358, CA131973, CA256847, CA075481, CA280627, CA244443, CA241676, CA234839, CA191350, CA132923, CA167430, CA214518, CA289890, CA129459, CA231295, CA234594, CA231360, CA122705, CA171017, CA174592, CA213097, CA203677, CA249784, CA241848, CA154628, CA084636, CA147920, CA084027, CA210274, CA085409, CA073058, CA257603, CA171251, CA235287, CA194012, CA274516, CA189176, CA205967, CA114776, CA249998, CA170208, CA200483, CA079438, CA110598, CA213534, CA081442, CA158958, CA171823, CA201301, CA113037, CA162250, CA091597, CA199925, CA105728, CA149023, CA245774, CA257029, CA294516, CA255995, CA203027, CA251151, CA257109, CA233064, CA089686, CA165671, CA206864, CA197554, CA120723, CA294637, CA195134, CA222415, CA206607, CA089770, CA082495, CA270377, CA096681, CA204010, CA084811, CA225968, CA080123, CA268286, CA177754, CA225888, CA080209, CA280835, CA075666, CA159929, CA223078, CA148574, CA186803, CA139688, CA082737, CA169610, CA071215, CA2S1920, CA071288, CA253042, CA226647, CA067362, CA149705, CA175116, CA183854, CA253113, CA194680, CA229952, CA203951, CA145489, CA183906, CA185885, CA236571, CA183894, CA229664)

SEQ ID No. 278: SCCRZ2004E04.g  
(CA265204, CA171814, CA107719, CA149900, CA193048, CA135977, CA070442)

TABLE XIII-continued

List of Sugarcane Assembled Sequences (SAS) and their SEQ ID Nos.

The EST Genbank accession number is in parentheses. The SEQ ID No. refers to the sequence identifiers in the sequence listing. The listed ESTs assembled to the indicated sequence and should be considered one transcript. Each SAS is differentially expressed between plants with low and high sucrose content or between internode tissues of high and low sucrose content.

SEQ ID No. 279: SCCRZ2C03B03.g  
(CA152461, CA091354, CA290267, CA150127, CA098420, CA160838, CA091259, CA210324, CA246275, CA160924, CA099832, CA246979)

SEQ ID No. 280: SCCRZ2C03B08.g  
(CA189326, CA128922, CA152978, CA275251, CA116757, CA206159, CA277339, CA273726, CA288950, CA288339, CA122779, CA274965, CA165128, CA149798, CA281356, CA185850, CA273473, CA083665, CA112203, CA118075, CA119323, CA258675, CA150131, CA260681, CA189332, CA183249, CA282545, CA114816, CA285606, CA284673, CA221505, CA277051, CA113469, CA274816, CA220035)

SEQ ID No. 281: SCCRZ2C03D11.g  
(CA212623, CA218773, CA234879, CA188440, CA150157, CA167123, CA160865, CA152558, CA153910, CA160953, CA292253, CA198906, CA146128, CA152637, CA253272, CA199372, CA081496, CA084800, CA210001, CA165052, CA173701, CA098184, CA198989, CA300667, CA211850, CA160948, CA207047, CA095115, CA136241, CA198430, CA256720, CA251375, CA166995, CA221307, CA110797, CA199377, CA154437, CA256643, CA237901, CA155637, CA237281, CA243431, CA199465, CA113301, CA201599, CA152440, CA186303, CA218694, CA091459, CA075606, CA102523)

SEQ ID No. 282: SCCRZ2C04A07.g  
(CA150208, CA254428, CA264432, CA109026, CA289248, CA212120, CA068378, CA269484, CA290794, CA150592, CA267114, CA108938, CA148663)

SEQ ID No. 283: SCCRZ3002D03.g  
(CA157090, CA166754, CA166468, CA081540, CA166789, CA159915, CA166748, CA158667, CA166054, CA160001, CA159544, CA158534, CA157577, CA163132, CA162955, CA159630, CA162379, CA156383, CA159213, CA156380, CA159296, CA157027, CA155724, CA166592, CA160596, CA157767, CA159130, CA159692, CA160663, CA157459, CA160591, CA162831, CA157771, CA161878, CA159777, CA157345, CA162828, CA160660, CA165592, CA157437, CA156341, CA161644, CA163699, CA166773, CA166732, CA155976, CA166749, CA166465, CA158668, CA166747, CA166717, CA156749, CA157068, CA161600, CA157110, CA155898, CA156928, CA155357, CA155731, CA155982, CA166777, CA165945, CA155803, CA166847, CA158604, CA154735, CA154876, CA157483, CA154704, CA159558, CA162867, CA156720, CA159340, CA157550, CA157322, CA156111, CA159644, CA159429)

SEQ ID No. 284: SCCRZ1004A07.g  
(CA183604, CA186275, CA243234, CA183683, CA186721, CA100350, CA187378, CA155740, CA175579, CA231947, CA228851, CA155725, CA154689, CA254179, CA172559, CA225984, CA264609, CA242994, CA158084, CA268024, CA173756, CA225902, CA163001, CA185577, CA159081, CA227411, CA139414, CA167973)

SEQ ID No. 285: SCCRZ1005H10.g  
(CA156092, CA252584, CA251786, CA095869, CA200174, CA229003, CA150731, CA267208, CA111168, CA193424, CA298858, CA284582, CA173902, CA239780, CA210407, CA253368, CA239582)

SEQ ID No. 286: SCCRZ1007H11.g  
(CA239834, CA294188, CA174066, CA294125, CA289019, CA267191, CA205751, CA247131, CA186999, CA082859, CA248451, CA197532, CA248572, CA248681, CA229903,

TABLE XIII-continued

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List of Sugarcane Assembled Sequences (SAS) and their SEQ ID Nos.

The EST Genbank accession number is in parentheses. The SEQ ID No. refers to the sequence identifiers in the sequence listing. The listed ESTs assembled to the indicated sequence and should be considered one transcript. Each SAS is differentially expressed between plants with low and high sucrose content or between internode tissues of high and low sucrose content.

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CA291504, CA223912, CA268732, CA229818, CA268664, CA177922, CA299828, CA085026, CA107150, CA270735, CA171072, CA250481, CA198295, CA224502, CA270670, CA111282, CA250414, CA170995, CA248529, CA250649, CA252343, CA115211, CA169576, CA250568, CA169653)

SEQ ID No. 287: SCCCST2004D11.g  
(CA276737, CA286409, CA290332, CA180097, CA274366, CA290274, CA276791, CA283900)

SEQ ID No. 288: SCCCST3C01D11.g  
(CA192121, CA200064)

SEQ ID No. 289: SCEPCL6019E04.g  
(CA278974, CA178777, CA258916, CA210789, CA096932, CA228505, CA292383, CA287368, CA260767, CA258913, CA067293)

SEQ ID No. 290: SCEPLB1043H04.g  
(CA112277, CA268601, CA084506, CA123703, CA130941, CA298376, CA100990, CA092352, CA111629, CA259193, CA175844, CA069065, CA236418, CA259195, CA194776, CA197355, CA285641, CA279779, CA274614, CA208294)

SEQ ID No. 291: SCEPRZ1009C10.g  
(CA216178, CA089411, CA192966, CA085572, CA147458, CA210405, CA186340, CA080065, CA195484, CA176812, CA086836, CA299623, CA186790, CA174279, CA270325)

SEQ ID No. 292: SCEQLB1065H07.g  
(CA113324, CA112585, CA112172)

SEQ ID No. 293: SCEQRT1028H06.g  
(CA185370, CA217107, CA185369, CA181686, CA144447, CA259824, CA259055, CA224656, CA132900, CA139337)

SEQ ID No. 294: SCEQRT2091B08.g  
(CA177838, CA138900, CA131473)

SEQ ID No. 295: SCEZLR1009F06.g  
(CA241512, CA233926, CA203368, CA147610, CA244100, CA143820, CA235700, CA224287, CA076822, CA136422, CA204148, CA132715, CA243514, CA121484, CA149083, CA270033, CA224204, CA235620)

SEQ ID No. 296: SCEZLR1052D02.g  
(CA290091, CA101830, CA232662, CA121616, CA136331, CA269565, CA099181, CA274273, CA261699, CA244896, CA264816, CA291831, CA244980, CA242167, CA088365, CA207802, CA164209, CA083724, CA102047, CA144138, CA287479)

SEQ ID No. 297: SCEZLR1052F07.g  
(CA074246, CA121654, CA248895, CA133812, CA282557, CA241182, CA114856, CA211933, CA248974, CA276743, CA101051, CA270608, CA276796)

SEQ ID No. 298: SCEZRZ1012A02.g  
(CA297050, CA147663, CA157700, CA105038, CA261583, CA271380, CA215641, CA159641, CA069275, CA177800, CA270487)

SEQ ID No. 299: SCJFAM1066B05.g  
(CA268766, CA074908, CA268710, CA228447, CA244764, CA274990, CA065083, CA074999)

SEQ ID No. 300: SCJFHR1C03E01.b  
(CA105064, CA292248)

TABLE XIII-continued

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List of Sugarcane Assembled Sequences (SAS) and their SEQ ID Nos.

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SEQ ID No. 301: SCJFLR1013A09.g  
(CA235310, CA282013, CA179055, CA283254, CA183161, CA290788, CA164417, CA252946, CA141957, CA096624, CA265391, CA288713, CA274581, CA190135, CA208818, CA279074, CA197553, CA228792, CA167001, CA243611, CA173593, CA132194, CA159403, CA301384, CA172463, CA157575, CA122731, CA163302, CA159490, CA122807, CA290934, CA084459, CA209937, CA276141, CA124943, CA291009, CA101340, CA219373, CA282113, CA301068, CA151204, CA155518, CA261457, CA226015, CA281400, CA277290, CA106860, CA151298, CA131594, CA209070, CA274261, CA230293, CA281699, CA102959, CA242254, CA230377, CA110744, CA297719, CA273517, CA288217, CA283872, CA069932, CA161956, CA152851, CA167994, CA279904, CA072926, CA151486, CA294369, CA285703, CA152126, CA151570, CA123278, CA294297, CA197602, CA169959, CA243645, CA301385, CA264726, CA288442, CA273556, CA139713, CA195766, CA119825, CA145652, CA101345, CA295834, CA278607, CA167657, CA145735, CA164101, CA293116, CA289163, CA284698, CA072930, CA164096, CA274175, CA199249, CA282860, CA253978, CA282859, CA277633, CA274222, CA277807, CA217957, CA066317, CA154676, CA281278, CA131869, CA121746, CA143651, CA283796, CA240378, CA276222, CA180047, CA180206, CA178970, CA280226, CA109795, CA268088)

SEQ ID No. 302: SCJFRT1062G05.g  
(CA134706, CA195808, CA245921, CA134625, CA104221)

SEQ ID No. 303: SCJFRZ2009F04.g  
(CA151389, CA159376, CA226687, CA146560, CA166765, CA197932, CA159464, CA270358, CA183354)

SEQ ID No. 304: SCJFRZ2010A09.g  
(CA151517, CA183884, CA151430)

SEQ ID No. 305: SCJFRZ2028F11.g  
(CA186745, CA152421, CA186827, CA211953, CA191943, CA198909, CA224105, CA200632, CA255362, CA066398, CA131076, CA201119, CA299210, CA299133, CA200718, CA131498, CA157938, CA205075, CA160778, CA064989, CA277477, CA281350)

SEQ ID No. 306: SCJFRZ2032C08.g  
(CA117340, CA295374, CA295303, CA152817)

SEQ ID No. 307: SCJFRZ2032G01.g  
(CA133254, CA248557, CA175553, CA290388, CA170294, CA152856, CA171924, CA205645, CA233534, CA221515, CA081654, CA171952, CA065512, CA081995, CA166558, CA065587, CA078958, CA211764, CA237388, CA258073)

SEQ ID No. 308: SCJFST1009G05.g  
(CA296907, CA174288, CA269643, CA174211, CA193249)

SEQ ID No. 309: SCJLHR1028C12.g  
(CA106176, CA106117, CA108309, CA107078)

SEQ ID No. 310: SCJLLR1054C09.g  
(CA207848, CA168087, CA168395, CA212085, CA167523, CA091873, CA122611, CA155006, CA181705, CA134394, CA225549, CA210454, CA254817, CA110775, CA178602, CA294600, CA247901, CA176250, CA191684, CA069266, CA300512, CA165622, CA155090, CA067961, CA171908, CA209040, CA173982, CA094706, CA240234, CA103017, CA122429, CA150920, CA112960, CA162575, CA122515, CA160567, CA113924, CA066919, CA160642, CA221530, CA208709, CA071863, CA214558, CA220510, CA123419,

TABLE XIII-continued

List of Sugarcane Assembled Sequences (SAS) and their SEQ ID Nos.

The EST Genbank accession number is in parentheses. The SEQ ID No. refers to the sequence identifiers in the sequence listing. The listed ESTs assembled to the indicated sequence and should be considered one transcript. Each SAS is differentially expressed between plants with low and high sucrose content or between internode tissues of high and low sucrose content.

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CA244626, CA231363, CA228474, CA111123, CA134073, CA146492, CA244685, CA219982, CA073891, CA174808, CA221075, CA262113, CA114521, CA162927, CA115467, CA161791, CA168280, CA152952, CA091868, CA233706, CA164651, CA204996, CA129415, CA172853, CA166113, CA107134, CA254985, CA159872, CA159959, CA088872, CA173464)

SEQ ID No. 311: SCJLLR1108H07.g  
(CA076625, CA161661, CA086613, CA161602, CA165554, CA245933, CA085287, CA123416, CA161598, CA175504, CA232025, CA166769, CA102997, CA076538, CA107411, CA155427, CA084502, CA106431, CA154641, CA106546, CA157227, CA154884, CA079948, CA179653, CA211436, CA121982, CA162963, CA258991, CA160716, CA243419, CA079250, CA072412, CA086508)

SEQ ID No. 312: SCJLRZ1023H04.g  
(CA265135, CA190996, CA292308, CA268081, CA256348, CA207478, CA081712, CA292758, CA256420, CA167022, CA291705, CA091971, CA179799, CA140075, CA266752, CA291699, CA258363, CA113856, CA149162, CA260595, CA140368, CA246964, CA235343, CA155907, CA140145, CA279058, CA274307, CA165644, CA278889, CA205578, CA091372, CA181941, CA166813, CA299890, CA177590, CA072486, CA156132, CA248336)

SEQ ID No. 313: SCJLRZ1026F03.g  
(CA149469, CA205387, CA289827, CA184015, CA247348, CA282029, CA187706, CA205445)

SEQ ID No. 314: SCMCL6055H06.g  
(CA183309, CA272155, CA071587, CA154790, CA236184, CA11608, CA231710, CA288208, CA098251, CA238333, CA187031, CA071503, CA293423)

SEQ ID No. 315: SCMCF5005A02.g  
(CA236668, CA293232, CA251482)

SEQ ID No. 316: SCQGLR1019A10.g  
(CA158123, CA074136, CA078695, CA202125, CA242927, CA291653, CA258225, CA223738, CA242859, CA124066, CA230103, CA120900, CA154098, CA255904, CA223648, CA129680, CA230031, CA082294, CA246357, CA262363, CA265415, CA118654, CA213833, CA125970, CA127771, CA246827, CA247296, CA087908, CA171645, CA102269, CA272756, CA137758, CA088231, CA148006, CA122701, CA187495, CA239190, CA230034, CA228513, CA074865, CA285487, CA147299, CA125885, CA236307, CA076601, CA116390, CA074785)

SEQ ID No. 317: SCQGLR1085G10.g  
(CA246799, CA299090, CA247266, CA285442, CA124279, CA092800, CA073766, CA200888, CA282968)

SEQ ID No. 318: SCQGLR2032G10.g  
(CA080092, CA073014, CA139013, CA225342, CA159885, CA165867, CA299929, CA118209, CA159972, CA108533, CA108413, CA106301, CA086875, CA086531, CA129084)

SEQ ID No. 319: SCQGRZ3011D06.g  
(CA161694, CA227205, CA245780, CA216248)

SEQ ID No. 320: SCQGSB1140F12.g  
(CA213355, CA173336)

SEQ ID No. 321: SCQGST1034G10.g  
(CA178801, CA186336, CA179790, CA176353, CA177570,

TABLE XIII-continued

List of Sugarcane Assembled Sequences (SAS) and their SEQ ID Nos.

The EST Genbank accession number is in parentheses. The SEQ ID No. refers to the sequence identifiers in the sequence listing. The listed ESTs assembled to the indicated sequence and should be considered one transcript. Each SAS is differentially expressed between plants with low and high sucrose content or between internode tissues of high and low sucrose content.

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CA236876, CA131335, CA214405, CA236124, CA186273, CA284135, CA216656, CA300978)

5 SEQ ID No. 322: SCQSHR1023F08.g  
(CA282568, CA106894, CA104925, CA211813)

SEQ ID No. 323: SCRFFL5034G07.g  
(CA292908, CA237588, CA237589)

20 SEQ ID No. 324: SCRLAD1100E08.g  
(CA218592, CA211503, CA218509)

SEQ ID No. 325: SCRLAM1010D08.g  
(CA212204, CA199909, CA248341, CA242304, CA256227, CA172929, CA220898, CA078708, CA247486, CA280865)

25 SEQ ID No. 326: SCRLFL1008C11.g  
(CA228213, CA201789, CA206320)

SEQ ID No. 327: SCRLFL1012B10.g  
(CA200156, CA199546)

30 SEQ ID No. 328: SCRLFL3007C04.g  
(CA226398)

SEQ ID No. 329: SCRLLR1111D02.g  
(CA293691, CA293635, CA125789)

35 SEQ ID No. 330: SCRLSD1012E03.g  
(CA274071, CA285380)

SEQ ID No. 331: SCRLST3166F11.g  
(CA182238, CA171790, CA184723)

40 SEQ ID No. 332: SCRUAD1063C06.g  
(CA068638, CA265707, CA068550, CA109839)

SEQ ID No. 333: SCRUAD1133D10.b  
(CA217707, CA260899, CA295151)

45 SEQ ID No. 334: SCRURT2010A10.g  
(CA144026, CA210038, CA197343, CA252900, CA067500)

SEQ ID No. 335: SCSBAM1084F08.g  
(CA198503, CA079138, CA079137)

50 SEQ ID No. 336: SCSBHR1052C05.g  
(CA196243, CA215089, CA164400, CA195955, CA108007, CA139925, CA215090, CA224796, CA098473, CA209222, CA197036, CA209253)

SEQ ID No. 337: SCSBHR1056H08.g  
(CA105333, CA108213)

55 SEQ ID No. 338: SCSBLB1035F03.g  
(CA264024, CA104540, CA115550, CA212924)

SEQ ID No. 339: SCSBSD2058D04.g  
(CA287176, CA297226, CA287175)

60 SEQ ID No. 340: SCSFAD1124E07.g  
(CA066760, CA217172, CA066828, CA217514)

SEQ ID No. 341: SCSFHR1043G09.g  
(CA108353, CA218662, CA212351)

65 SEQ ID No. 342: SCSGFL5C08F04.g  
(CA246146, CA236946, CA246999)

TABLE XIII-continued

List of Sugarcane Assembled Sequences (SAS) and their SEQ ID Nos.

The EST Genbank accession number is in parentheses. The SEQ ID No. refers to the sequence identifiers in the sequence listing. The listed ESTs assembled to the indicated sequence and should be considered one transcript. Each SAS is differentially expressed between plants with low and high sucrose content or between internode tissues of high and low sucrose content.

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SEQ ID No. 343: SCSGLR1045E07.g  
(CA168455, CA126284, CA177719, CA172031)

SEQ ID No. 344: SCSGRT2066D05.g  
(CA070717, CA175523, CA145621, CA187735)

SEQ ID No. 345: SCUTAM2088G02.g  
(CA091716, CA090231, CA091719)

SEQ ID No. 346: SCUTFL3073E12.g  
(CA257224, CA241247, CA292613)

SEQ ID No. 347: SCUTLR1037F04.g  
(CA170823, CA177197, CA279404, CA222805, CA121507, CA289444, CA282074, CA207370, CA115893, CA105265, CA226291, CA170108, CA263098, CA132119, CA107841, CA085728, CA126622, CA227826, CA227505, CA260163, CA262467, CA193720, CA219325, CA177230, CA103517, CA170340, CA170414, CA105596, CA112997, CA228100, CA234662, CA258511, CA097304, CA120418)

SEQ ID No. 348: SCUTLR1037F12.g  
(CA156611, CA293535, CA249045, CA087183, CA189165, CA086047, CA290121, CA081883, CA214139, CA229204, CA113764, CA213924, CA260485, CA126357, CA230132, CA221003, CA187849, CA273962, CA225939, CA102197, CA283956, CA183828, CA218025, CA195893, CA085608, CA263834, CA290919, CA183344, CA241008, CA104921, CA066522, CA290997, CA172858, CA095919, CA247671, CA186981, CA133280, CA245107, CA257283, CA115814, CA258330, CA212915, CA119073, CA194926, CA239944, CA104400, CA113297, CA104485, CA087184, CA069789, CA179218, CA231826, CA231159, CA086089, CA076690, CA246370, CA254495, CA091273, CA100677, CA106434, CA230786, CA253134, CA257292, CA231505, CA225180, CA241459, CA198266, CA115318, CA161747, CA103920, CA152307, CA133281, CA086095, CA231031, CA187270, CA242618, CA144012, CA111808, CA238509, CA253529, CA089266, CA157653, CA228713, CA106021, CA117820, CA126627, CA104401, CA211834, CA182929, CA104486)

SEQ ID No. 349: SCUTLR1058C02.g  
(CA262461, CA168036, CA230840, CA293241, CA281414, CA281585, CA106941, CA142008, CA151458, CA092310, CA270530, CA270458, CA225598, CA151543, CA202726, CA128347, CA241827, CA282746, CA128419, CA119915, CA204605, CA215500, CA170573, CA164411, CA134253, CA142288, CA176323, CA195642, CA255302, CA158993, CA283479, CA283473, CA126682, CA118166, CA213449, CA157587, CA207851)

SEQ ID No. 350: SCUTLR2008E01.g  
(CA123373, CA129763, CA128815)

SEQ ID No. 351: SCUTRZ2024G05.g  
(CA234849, CA204407, CA105515, CA224224, CA109551, CA143843, CA279720, CA161103, CA224302, CA299491, CA122794, CA179195, CA153592, CA105749, CA164517)

SEQ ID No. 352: SCUTST3086B02.g  
(CA213057, CA224653)

SEQ ID No. 353: SCUTST3129E01.g  
(CA172415, CA213379, CA187638)

SEQ ID No. 354: SCVPLC6041F12.g  
(CA082429, CA161720, CA139420, CA272127, CA238764,

TABLE XIII-continued

List of Sugarcane Assembled Sequences (SAS) and their SEQ ID Nos.

The EST Genbank accession number is in parentheses. The SEQ ID No. refers to the sequence identifiers in the sequence listing. The listed ESTs assembled to the indicated sequence and should be considered one transcript. Each SAS is differentially expressed between plants with low and high sucrose content or between internode tissues of high and low sucrose content.

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5 SEQ ID No. 355: SCVPLC6042B07.g  
(CA169577, CA081626, CA106612, CA099887, CA081969)

10 SEQ ID No. 356: SCVPLR1049C09.g  
(CA295256, CA300966, CA278033, CA090854, CA282609, CA121190, CA216481, CA267073, CA111152, CA126945, CA280319, CA278841, CA262278, CA287391, CA296360, CA296426, CA248739, CA287386, CA259530, CA296500, CA266143, CA216477, CA150885, CA248822, CA096454, CA099843, CA252370, CA087591, CA266218, CA071726, CA081002, CA087680, CA240033, CA219541, CA202897, CA077216, CA219614, CA066229, CA281069)

20 SEQ ID No. 357: SCVPLR1049E12.g  
(CA124363, CA107272, CA132969, CA091837, CA126955, CA122520, CA182701, CA167289)

25 SEQ ID No. 358: SCVPLR2005H03.g  
(CA107547, CA139171, CA074786, CA265130, CA268083, CA243200, CA074866, CA134745, CA100667, CA131059, CA264817, CA254269, CA268118, CA264761, CA121869, CA201866, CA220819, CA156636, CA097099, CA289841, CA222964, CA116567, CA091798, CA219374, CA138613, CA221255, CA132550, CA289940, CA251888, CA205653, CA100956, CA293549, CA243537, CA136973, CA120370,

30 CA158202, CA228366, CA260312)

35 SEQ ID No. 359: SCVPLR2012B07.g  
(CA130160, CA266175, CA077480, CA072583, CA084569, CA194404, CA278936, CA240283, CA201232, CA288279, CA077401, CA066454, CA180797, CA244848, CA266247, CA130150, CA137685, CA233499)

40 SEQ ID No. 360: SCVPLR2019B03.g  
(CA087275, CA087192, CA125068, CA101699, CA222267, CA259282, CA248553, CA223061, CA172804, CA200147, CA130990, CA225681, CA231261, CA223347, CA255228, CA273849, CA254244, CA156394, CA163312, CA117607, CA078324, CA072741, CA248475, CA212519, CA124666, CA126419, CA268138, CA105146, CA299030, CA177516, CA222789, CA105222, CA253702, CA202841, CA077031, CA077074, CA295407, CA118765, CA265852, CA289740, CA156183, CA197419, CA292775, CA207673, CA225709, CA153732, CA169731, CA102976, CA254955, CA228712, CA067636, CA264512, CA130214, CA130204, CA106807, CA207166, CA198764, CA216476, CA197293, CA103316, CA202300, CA077735, CA211185, CA067184, CA159570, CA258272, CA067264, CA159656, CA200260, CA117368, CA183438)

45 SEQ ID No. 361: SCVPLR2027A05.g  
(CA235611, CA214709, CA235691, CA229065, CA216821, CA251974, CA085301, CA101012, CA271269, CA197839, CA223162, CA118164, CA086683, CA223250, CA221375, CA188324, CA130277, CA130307, CA2291410, CA227333, CA279299, CA289704, CA167019, CA207029, CA206493, CA270388, CA176609, CA255410, CA166845, CA070734, CA073573, CA070813, CA112278, CA295884)

50 SEQ ID No. 362: SCVPRZ2038F04.g  
(CA278038, CA154019, CA185583)

55 SEQ ID No. 363: SCVPRZ3025A12.g  
(CA070455, CA292147, CA245381, CA166400, CA204294, CA242140)

TABLE XIII-continued

List of Sugarcane Assembled Sequences (SAS) and their SEQ ID Nos.

The EST Genbank accession number is in parentheses. The SEQ ID No. refers to the sequence identifiers in the sequence listing. The listed ESTs assembled to the indicated sequence and should be considered one transcript. Each SAS is differentially expressed between plants with low and high sucrose content or between internode tissues of high and low sucrose content.

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SEQ ID No. 364: SCVPRZ3029G09.g  
(CA239171, CA273853, CA166786, CA203209)

SEQ ID No. 365: SCMCST1053A06.g  
(CA110730, CA157435, CA164231, CA176670, CA079493, CA088347)

SEQ ID No. 366: SCCCLB1C06H02.g  
(CA189458, CA167345, CA115196, CA207187, CA252023)

SEQ ID No. 367: SCJLRT1023G09.g  
(CA077219, CA072472, CA136050, CA078881, CA266374, CA224918, CA162043, CA091967, CA074650)

SEQ ID No. 368: SCCST1004C05.g  
(CA098064, CA072037, CA194838, CA098063, CA173775, CA074361, CA079156, CA098059, CA084783)

SEQ ID No. 369: SCCCLB1002D12.g  
(CA092064, CA238036, CA222592, CA227487, CA110870, CA207790)

TABLE XIII-continued

List of Sugarcane Assembled Sequences (SAS) and their SEQ ID Nos.

The EST Genbank accession number is in parentheses. The SEQ ID No. refers to the sequence identifiers in the sequence listing. The listed ESTs assembled to the indicated sequence and should be considered one transcript. Each SAS is differentially expressed between plants with low and high sucrose content or between internode tissues of high and low sucrose content.

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SEQ ID No. 370: SCSGHR1070F12.g  
(CA076267, CA109334)

SEQ ID No. 371: SCEQLR1092H10.g  
(CA279813, CA186407, CA212604, CA279552, CA186484, CA135161, CA069193, CA103839, CA121281, CA153767, CA285432, CA182006, CA131451, CA285178, CA078267, CA078257, CA205885, CA136733, CA205884, CA097155, CA264106, CA279798, CA163611, CA091480, CA091191, CA187913, CA261976, CA277443, CA204843, CA273593, CA287502, CA287253, CA085398, CA222671)

SEQ ID No. 372: SCJFST1011B06.g  
(CA239247, CA174473, CA262684, CA211312, CA218557)

SEQ ID No. 373: SCEQRT2030G04.g  
(CA138771, CA145363, CA291384)

TABLE XIV

SNF-related like kinase genes and regulatory subunits differentially expressed between high brix and low brix varieties. Four individuals were selected from SP83-2847 (V1), four from SP94-3116 (V3), four from SP91-1049 (V2) and four from SP89-1115 (V4). RNA samples from the indicated tissues and collected months were used to generate probes for cDNA microarray hybridizations. The last four columns indicate the average ratios and the fold induction when the high and low brix samples were compared against an equimolar mixture of RNAs from the same varieties collected in march (when the cell is empty differential expression was not detected on the sample) The average brix measures are shown in FIG. 6.

Experiment	SAS	Category	sub category 1	sub category 2	sub category 3	High Brix		Low Brix			
						V2	V4	V1	V3		
Leaf	March	SCCCLB1002D12.g	Protein kinases	SNF-like kinases	caneCIPK-24	SNF-like/CBL-interacting Protein Kinase			3.2		
		SCSGHR1070F12.g	Protein kinases	SNF-like kinases	caneCIPK-29	SNF-like/CBL-interacting Protein Kinase			2.7		
		SCEQLR1092H10.g	Carbohydrate met	SIP homologue (AKIN gamma)	.	.			2.5		
		SCJFST1011B06.g	Carbohydrate met	Similar to AKINbetagamma	.	.	6.7		4.6		
		May	SCJFST1011B06.g	Carbohydrate met	Similar to AKINbetagamma	.	.	10.5	3.7	4.7	6.2
		September	SCEQRT2030G04.g	Protein kinases	SNF-like kinases	caneCIPK-26	SNF-like-CBL-interacting Protein Kinase			3.2	
Internode 1		SCEQLR1092H10.g	Carbohydrate met	SIP homologue (AKIN gamma)	.	.	2.7				
		SCJFST1011B06.g	Carbohydrate met	Similar to AKINbetagamma	.	.	-4.1		1.5		
	March	SCJFST1011B06.g	Carbohydrate met	Similar to AKINbetagamma	.	.	1.5	1.9	3.0		
	May	SCJFST1011B06.g	Carbohydrate met	Similar to AKINbetagamma	.	.			2.4		
	July	SCJFST1011B06.g	Carbohydrate met	Similar to AKINbetagamma	.	.	3.1	2.4	3.6	2.7	
	September	SCJFST1011B06.g	Carbohydrate met	Similar to AKINbetagamma	.	.	-3.0		-1.8		

TABLE XV

Genes differentially expressed between internode 9 (mature, rich in sugar) and internode 1 (immature, poor in sugar) from a pool of seven high brix plants. The individuals were selected from an F1 progeny of a cross between two commercial varieties, SP80-180 and SP80-4966. RNA samples from internode 9 (mature, rich in sugar) and internode 1 (immature, poor in sugar) were collected in March from the seven highest brix individuals and used to generate probes for cDNA microarray hybridizations. The column High indicates the average ratios (fold induction) of genes more expressed in internode 9 than in internode 1. The column Low indicates the average ratios (fold induction) of genes more expressed in internode 1 than in internode 9. The average brix in the highest sugar internodes was 18.47.

SAS	Category	Description of homologue	High	Low
SCCCLR1001E04.g	Carbohydrate Metabolism	Photosynthesis RUBISCO - small subunit		5.17088
SCSGFL5C08F04.g	Unknown protein			14.5502
SCCCLR1024E11.g	Stress	Superoxide dismutases Cu/Zn		3.52866
SCCCLR1068G11.g	DNA metabolism	Histone H2B		3.17131
SCEZRZ1012A02.g	Stress	Cytochrome P450 CYP9		5.68635
SCSBAD1084C01.g	Others	Tubulin alpha-1 chain		2.37024
SCCCLR2002D04.g	DNA metabolism	Histone H4		3.09739
SCJFRZ2032G01.g	Protein kinases	SNF-like kinases caneSnRK1-2		1.69948
SCCCLR2002F08.g	Hormone related	Auxin auxin repressed		2.0465
SCVPFL3045B09.g	Stress	Metallothionein		3.46187
SCJLHR1028C12.g	Stress	Infected libraries Histone H4		4.71202
SCVPLR2019B03.g	Pathogenicity	Polygalacturonase inhibitor		4.46784
SCJLRZ1023H04.g	Protein kinases	SNF-like kinases caneCIPK-9		4.32708
SCCCLR2C03D05.g	Stress	Superoxide dismutases Cu/Zn		4.75184
SCCART2001H11.g	Small GTPases	Arf		1.9028
SCCCRZ1001D02.g	Adapters	14-3-3 proteins		1.90957
SCCCRZ2C03D11.g	Transcription	Scarecrow		2.8597
SCRLLR1111D02.g	No matches (non-coding)			3.55119
SCCCRZ1002F06.g	Stress	Drought and cold response Enolase		2.15317
SCBFAD1046D01.g	Transcription	HLH (helix-loop-helix)		3.05338
SCRLST3166F11.g	No matches (non-coding)			1.7087
SCCCRZ2002C09.g	Others	Alpha tubulin		2.30795
SCCCCL3120C09.g	Receptors	Receptor Ser/Thr kinase caneRLK with LysM-1		2.72539
SCEQRT1025D06.g	Adapters	14-3-3 proteins		1.76605
SCSGLR1045E07.g	Receptors	Receptor Ser/Thr kinase caneLTK1-15 (leucine-rich transmembrane kinase)		3.27161
SCCCRZ1001A09.g	Unknown protein			3.47497
SCUTFL3073E12.g	Unknown protein			3.88751
SCJFLR1074E09.g	Stress	Drought and cold response Low temperature induced (LT1)		2.73407
SCUTST3129E01.g	Unknown protein			3.16936
SCVPLR2005H03.g	Transcription	Aux/IAA		2.96052
SCCCLR2002G09.g	DNA metabolism	Histone H4		5.40529
SCVPRT2074D04.g	Unknown protein			10.9716
SCMCST1053A06.g	Receptors	Receptor Ser/Thr kinase canePERK1-3		2.55721
SCCCRZ1001G10.g	Transcription	Aux/IAA		3.20251
SCBFLR1039B05.g	Carbohydrate Metabolism	Xyloglucan endotransglycosylase		7.23097
SCCCRZ1C01H06.g	Calcium	Calmodulin-binding proteins Apyrase		5.42483
SCSBSD2029F05.g	Unknown protein		29.3706	
SCSFHR1043G09.g	Stress	Infected libraries S-adenosylmethionine synthase		2.57568
SCEZHR1087F06.g	Stress	Cytochrome P450 CYP84		3.71447
SCJFLR1013A09.g	Stress	Drought and cold response Cysteine proteinase RD19A precursor		2.34682
SCCCAD1004H02.g	Stress	Catalase		4.81462
SCSBHR1056H08.g	Receptors	EIN2 (ethylene)		2.2665

TABLE XVI

Genes differentially expressed between Internode 9 (mature, rich in sugar) and internode 1 (immature poor in sugar) from a pool of seven high brix plants. The individuals were selected from an F1 progeny of a cross between two commercial varieties, SP80-180 and SP80-4966. RNA samples from internode 9 (mature, rich in sugar) and internode 1 (immature, poor in sugar) were collected in July from the seven highest brix individuals and used to generate probes for cDNA microarray hybridizations. The column High indicates the average ratios (fold induction) of genes more expressed in internode 9 than in internode 1. The column Low indicates the average ratios (fold induction) of genes more expressed in internode 1 than in internode 9. The average brix in the highest sugar internodes was 22.63.

SAS	Category	Description of homologue	High	Low
SCCCHR1004D03.g	Receptors	Receptor Ser/Thr kinase caneRLK-CII1		2.886
SCEQRT2091B08.g	Pathogenicity	R-genes NBS-LRR		6.61364
SCCCRZ1001D02.g	Adapters	14-3-3 proteins		4.07912
SCACLR2022H05.g	Lipid metabolism	Acyl carrier protein-like		2.62875

TABLE XVI-continued

Genes differentially expressed between Internode 9 (mature, rich in sugar) and internode 1 (immature poor in sugar) from a pool of seven high brix plants.

The individuals were selected from an F1 progeny of a cross between two commercial varieties, SP80-180 and SP80-4966. RNA samples from internode 9 (mature, rich in sugar) and internode 1 (immature, poor in sugar) were collected in July from the seven highest brix individuals and used to generate probes for cDNA microarray hybridizations. The column High indicates the average ratios (fold induction) of genes more expressed in internode 9 than in internode 1. The column Low indicates the average ratios (fold induction) of genes more expressed in internode 1 than in internode 9. The average brix in the highest sugar internodes was 22.63.

SAS	Category	Description of homologue	High	Low
SCCCLR1022D05.g	Adapters	14-3-3 proteins		2.98657
SCCCHR1004H09.g	Others	Putative cholinephosphate cytidyltransferase		1.92571
SCAGLR1021G10.g	Transcription	Homeobox knotted homeobox		2.32589
SCCCRZ1C01H06.g	Calcium	Calmodulin-binding proteins Apyrase		7.92529
SCAGLR2026G12.g	No matches			3.39302
SCCCRZ2002C09.g	Others	Alpha tubulin		4.67588
SCEZRZ1012A02.g	Stress	Cytochrome P450 CYP9		4.61871
SCUTST3129E01.g	Unknown protein			1.91148
SCRFLR2037F09.g	Calcium	Calreticulin		2.02563
SCCCLR1072H06.g	Receptors	Receptor Ser/Thr kinase caneRLK-CIII5		2.00064
SCCCRZ2C03B08.g	Unknown protein			2.91431
SCRLAM1010D08.g	Transcription	Homeobox knotted homeobox		2.79028
SCRFL3007C04.g	Receptors	Receptor Ser/Thr kinase caneRLK-D5		4.32835
SCSBAD1084C01.g	Others	Tubulin alpha-1 chain		4.77431
SCCCLR2C02A05.g	Development	Expansin		2.51264
SCBFST3136A06.g	No matches			1.64093
SCCST1005H10.g	Stress	Drought and cold response erd3-like		2.28191
SCVPRZ3025A12.g	Protein kinases	RLCK canePBS1-6		3.88743
SCBGFL4053F12.g	Receptors	Receptor Ser/Thr kinase caneRLK-DV2		3.57578
SCCST1007H11.g	Small GTPases	Rab		2.33447
SCJFRZ2009F04.g	Transcription	Aux/IAA		2.29158
SCJLLR1054C09.g	Transcription	Aux/IAA		2.65943
SCJFST1009G05.g	Protein kinases	Putative RLCK caneRLCK-A3		2.13741
SCBFLR1039B05.g	Carbohydrate Metabolism	Xyloglucan endotransglycosylase		11.4992
SCSBHR1052C05.g	Inositol	Others Phospholipase C		1.7622
SCCCLR2C03D05.g	Stress	Superoxide dismutases Cu/Zn		3.71548
SCCCL4004C06.g	Unknown protein			5.53096
SCCCL3120C09.g	Receptors	Receptor Ser/Thr kinase cane RLK with LysM-1		4.75777
SCCCT1001E12.g	Small GTPases	Rab		3.51448
SCEQRT1028H06.g	Hormone biosynthesis	Auxin Nitrilase		2.22559
SCCCT2001H11.g	Small GTPases	Arf		3.62744
SCSGLR1045E07.g	Receptors	Receptor Ser/Thr kinase caneLTK1-15 (leucine-rich transmembrane kinase)		4.26249
SCCCRZ1001C12.g	Stress	Cytochrome P450 CYP51		1.63378
SCCCLB1023E12.g	Receptors	Receptor Ser/Thr kinase caneRLK-DXIV1 (with LRR)		1.75209
SCUTAM2115C12.g	Unknown protein			4.03376
SCCCRZ1001G10.g	Transcription	Aux/IAA		4.81226
SCCCLR1024E11.g	Stress	Superoxide dismutases Cu/Zn		2.64644
SCCCLR1072E03.g	Receptors	Receptor Ser/Thr kinase caneRLK-AX3		3.18447
SCCCRZ2C04A07.g	Stress	Cytochrome P450 CYP71E		7.26294
SCVPRT2074D04.g	Unknown protein			17.1483
SCCCL5002B10.g	Protein kinases	Undefined-unclassified caneUPK-87		2.6046
SCRURT2010A10.g	Transcription	Putative transcription factor (myb)		3.35245
SCRUSB1062E12.g	Lipid metabolism	Putative triacylglycerol lipase		2.38531
SCBGLR1096C08.g	Protein kinases	Cell cycle-related caneCDK-18		3.2602
SCUTST3086B02.g	Transcription	AP2/EREBP Tiny		2.12353
SCSBLB1035F03.g	Receptors	Receptor Ser/Thr kinase-unclassified caneURLK-119 (with LRR)		5.9116
SCEPRZ1009C10.g	Protein kinases	SNF-like kinases cane osmotic stress-activated protein kinase-1		3.54108
SCJLRZ1026F03.g	Protein kinases	Putative RLCK caneRLCK-AII2		2.347
SCEQRT1031D02.g	Adapters	14-3-3 proteins		3.968
SCSGFL5C08F04.g	Unknown protein			16.0517
SCUTRZ2024G05.g	Transport	Putative vesicle transport v-SNARE protein		1.9247
SCQGLR1085G10.g	Transcription	MADS	1.7433	
SCRUAD1063C06.g	Pathogenicity	Polygalacturonase-inhibiting	1.66301	
SCEPCL6019E04.g	Carbohydrate metabolism	Malic enzyme	1.89688	
SCCAD1004H02.g	Stress	Catalases	2.66819	
SCRLST3166F11.g	No matches (non-coding)		1.95495	
SCSFAD1124E07.g	Transcription	Myb	4.31601	
SCCCL5004D02.g	No matches		1.51467	
SCQGSB1140F12.g	Pathogenicity	R-genes NBS-LRR	2.44294	
SCCCRZ1003A03.g	Calcium	Calmodulin-binding proteins HSP7s (heat shock)	1.78283	



TABLE XVII

Genes differentially expressed between Internode 9 (mature rich in sugar)  
Internode 1 (immature, poor in sugar) from a pool of seven low brix plants.  
The individuals were selected from an F1 progeny of a cross between two commercial varieties, SP80-180 and SP80-4966. RNA samples from internode 9 (mature, rich in sugar) and internode 1 (immature, poor in sugar) were collected in March from the seven lowest brix individuals and used to generate probes for cDNA microarray hybridizations. The column High indicates the average ratios (fold induction) of genes more expressed in internode 9 than in internode 1. The column Low indicates the average ratios (fold induction) of genes more expressed in internode 1 than in internode 9. The average brix in the highest sugar internodes was 13.66.

SAS	Category	Description of homologue	High	Low
SCUTFL3073E12.g	Unknown protein			2.0326
SCBGLR1096E06.g	Nucleotide metabolism	Putative inosine monophosphate dehydrogen		2.58395
SCBFLR1039B05.g	Carbohydrate Metabolis	Xyloglucan endotransglycosylase		5.33996
SCSBAD1084C01.g	Others	Tubulin alpha-1 chain		2.90392
SCUTLR1037F12.g	Protein metabolism	60S Ribosomal protein L5		2.60981
SCCCST1004C05.g	Protein kinases	Others caneIre1-1 (Similar to ER-located transmembranereceptor protein kinase/ribonuclease)		2.12312
SCCCLB1001D03.g	Protein Phosphatases	Serine/Threonine - PPP Family PP2A/Catalytic Subunit		1.55983
SCCCCL5002B10.g	Protein kinases	Undefined-unclassified caneUPK-87		1.91338
SCRLFL1012B10.g	Protein kinases	Cell cycle-related caneCDK-6		1.8469
SCJFRZ2010A09.g	Ubiquitination	E1		2.19142
SCVPAM1055A12.g	Protein kinases	Casein kinases caneCKI-11		2.3001
SCRLSD1012E03.g	Ubiquitination	Ubiquitin		1.97292
SCCCLR2002D04.g	DNA metabolism	Histone H4		2.17368
SCJFRZ2032G01.g	Protein kinases	SNF-like kinases caneSnRK1-2		2.89539
SCSBHR1050B11.g	Development	Putative senescence-associated protein		7.68477
SCCCLR2002G09.g	DNA metabolism	Histone H4		4.16496
SCVPCL6042B07.g	Protein kinases	Others cane cyclin G-associated kinase-like protein-1		1.98527
SCJLLR1108H07.g	Calcium	Calmodulin-binding proteins ACA		1.94396
SCVPFL3045B09.g	Stress	Metallothionein		2.75676
SCCCLR2C03D05.g	Stress	Superoxide dismutases Cu/Zn		2.09879
SCJLRT1023G09.g	Protein kinases	SNF-like kinases caneCIPK-19		1.95006
SCVPLR1049C09.g	Calcium	Calmodulin-binding proteins ATPase		2.32277
SCCART1001E12.g	Small GTPases	Rab		1.78307
SCVPLR2019B03.g	Pathogenicity	Polygalacturonase inhibitor		4.69134
SCVPRZ3029G09.g	Receptors	Receptor Ser/Thr kinase caneLTK1-16 (leucine-rich transmembrane kinase)		1.72477
SCCCLB1023E12.g	Receptors	Receptor Ser/Thr kinase caneRLK-DXIV1 (with LRR)		1.94444
SCEZLR1052D02.g	Unknown protein			1.9867
SCCCRZ1001G10.g	Transcription	Aux/IAA		2.01005
SCEZLR1052F07.g	Protein Phosphatases	Serine/Threonine - PPP Family PP2A/Subunit A		1.69977
SCCCRZ1004H12.g	Transcription	EIL (ethylene-insensitive3-like)		2.6871
SCACLR1130H08.g	Transcription	Zinc finger proteins C2C2/YABBY		2.10948
SCCCLR1024F10.g	Transcription	Other Auxin-response factors With B3 domain		3.03055
SCQGRZ3011D06.g	Transcription	Alfin-like		2.17274
SCCCLR1048F03.g	Unknown protein	Chloroplast hypothetical protein		3.39922
SCCCLR1068G11.g	DNA metabolism	Histone H2B		3.37772
SCQSHR1023F08.g	Stress	Cytochrome P450 CYP71		4.45371
SCUTAM2088G02.g	Unknown protein	Putative GTP-binding protein		1.80345
SCRFLR2037F09.g	Calcium	Calreticulin		2.87788
SCCCLR1C03G01.g	Hormone biosynthesis	Jasmonic Acid Linoleic acid desaturase		3.49276
SCUTST3129E01.g	Unknown protein			1.93583
SCQGHR1012B09.g	Stress	Probable cytochrome P450 monooxygenase		5.67878
SCVPCL6041F12.g	Ubiquitination	Ubiquitin-specific protease		1.8455
SCJLHR1028C12.g	Stress	Infected libraries Histone H4		3.76242
SCVPLR2005H03.g	Transcription	Aux/IAA		3.15361
SCEQRT1031D02.g	Adapters	14-3-3 proteins		2.23343
SCCCCL3120C09.g	Receptors	Receptor Ser/Thr kinase cane RLK with LysM-1		1.97526
SCCCLR2C02A05.g	Development	Expansin		2.39903
SCCCCL4003D08.g	Transcription	Zinc finger proteins C3H		1.90193
SCSBSD2058D04.g	Ubiquitination	Ubiquitin		1.88495
SCVPRT2074D04.g	Unknown protein			6.8061
SCCCRZ1001D02.g	Adapters	14-3-3 proteins		2.70281
SCMST1053A06.g	Receptors	Receptor Ser/Thr kinase canePERK1-3		2.4114
SCCCLB2004C08.g	Ubiquitination	Ubiquitin		1.92442
SCCCRZ1002F06.g	Stress	Drought and cold response Enolase		2.80387
SCCCLR1022H07.g	Protein kinases	Cell cycle-related caneCDK-11		2.39455
SCCCRZ1001A09.g	Unknown protein			1.97585
SCSGAM1094D05.g	Hormone biosynthesis	Salicylic Acid		2.47418
SCCCLR1024E11.g	Stress	Superoxide dismutases Cu/Zn		2.62077

TABLE XVII-continued

Genes differentially expressed between Internode 9 (mature rich in sugar) Internode 1 (immature, poor in sugar) from a pool of seven low brix plants.

The individuals were selected from an F1 progeny of a cross between two commercial varieties, SP80-180 and SP80-4966. RNA samples from internode 9 (mature, rich in sugar) and internode 1 (immature, poor in sugar) were collected in March from the seven lowest brix individuals and used to generate probes for cDNA microarray hybridizations. The column High indicates the average ratios (fold induction) of genes more expressed in internode 9 than in internode 1. The column Low indicates the average ratios (fold induction) of genes more expressed in internode 1 than in internode 9. The average brix in the highest sugar internodes was 13.66.

SAS	Category	Description of homologue	High	Low
SCCCRZ1C01H06.g	Calcium	Calmodulin-binding proteins Apyrase		3.09699
SCQGLR2032G10.g	Ubiquitination	Polyubiquitin		1.63756
SCACLR1057C07.g	Two component	Response regulators (ARR-like)		2.18371
SCCCRZ2002C09.g	Others	Alpha tubulin		2.66313
SCQGST1034G10.g	Protein kinases	Putative RLCK caneRLCK-AIV3		2.34207
SCBGFL4052C11.g	Transcription	EIL (ethylene-insensitive3-like)		1.73335

TABLE XVIII

Genes differentially expressed between Internode 9 (mature, rich in sugar) and Internode 1 (immature, poor in sugar) from a pool of seven low brix plants.

The individuals were selected from an F1 progeny of a cross between two commercial varieties, SP80-180 and SP80-4966. RNA samples from internode 9 (mature, rich in sugar) and internode 1 (immature, poor in sugar) were collected in July from the seven lowest brix individuals and used to generate probes for cDNA microarray hybridizations. The column High indicates the average ratios (fold induction) of genes more expressed in internode 9 than in internode 1. The column Low indicates the average ratios (fold induction) of genes more expressed in internode 1 than in internode 9. The average brix in the highest sugar internodes was 18.96.

SAS	Category	Description of homologue	High	Low
SCCCRZ2C04A07.g	Stress	Cytochrome P450 CYP71E		9.59342
SCCCST1004A07.g	Protein kinases	SNF-like kinases cane osmotic stress-activated protein kinase-7		2.37339
SCCCLR1024E11.g	Stress	Superoxide dismutases Cu/Zn		2.21539
SCCCCL5002B10.g	Protein kinases	Undefined-unclassified caneUPK-87		2.15162
SCCCRZ2C03D11.g	Transcription	Scarecrow		3.38429
SCBFAD1046D01.g	Transcription	HLH (helix-loop-helix)		2.74633
SCBFRL1039B05.g	Carbohydrate Metabolism	Xyloglucan endotransglycosylase		13.7587
SCBGFL4053F12.g	Receptors	Receptor Ser/Thr kinase caneRLK-DV2		4.08493
SCEQRT1028H06.g	Hormone biosynthesis	Auxin Nitrilase		2.39496
SCCART2001H11.g	Small GTPases	Arf		2.33013
SCCCCL4004C06.g	Unknown protein			4.61263
SCCCRZ1C01H06.g	Calcium	Calmodulin-binding proteins Apyrase		8.66427
SCCCRZ2C03B08.g	Unknown protein			2.92174
SCCCLR1001E04.g	Carbohydrate Metabolism	Photosynthesis RUBISCO - small subunit		4.99165
SCSGFL5C08F04.g	Unknown protein			17.9899
SCUTAM2115C12.g	Unknown protein			3.94798
SCJLRZ1023H04.g	Protein kinases	SNF-like kinases caneCIPK-9		4.18557
SCMCF15005A02.g	Stress	Glutathione peroxidases		2.65839
SCVPRT2074D04.g	Unknown protein			15.4127
SCAGLR1021G10.g	Transcription	Homeobox knotted homeobox		2.46187
SCJLLR1054C09.g	Transcription	Aux/LAA		2.43353
SCEPRZ1009C10.g	Protein kinases	SNF-like kinases cane osmotic stress-activated protein kinase-1		2.41081
SCCCLR2C03D05.g	Stress	Superoxide dismutases Cu/Zn		3.06534
SCRLAM1010D08.g	Transcription	Homeobox knotted homeobox		2.66789
SCBFST1336A06.g	No matches			1.73546
SCRLFL3007C04.g	Receptors	Receptor Ser/Thr kinase caneRLK-D5		3.92386
SCCCHR1004H09.g	Others	Putative cholinephosphate cytidyltransferase		1.67693
SCCCRZ1001D02.g	Adapters	14-3-3 proteins		2.07764
SCEZRZ1012A02.g	Stress	Cytochrome P450 CYP9		4.02698
SCCCRZ1001G10.g	Transcription	Aux/LAA		4.19655
SCCCCL3120C09.g	Receptors	Receptor Ser/Thr kinase cane RLK with LysM-1		4.50352
SCCCRZ2002C09.g	Others	Alpha tubulin		2.30687
SCRUAD1063C06.g	Pathogenicity	Polygalacturonase-inhibiting		1.85181
SCCCST2004D11.g	Receptors	Receptor Ser/Thr kinase cane RLK with lectin domain-2		6.70096
SCCCLR2002F08.g	Hormone related	Auxin auxin repressed		1.67626
SCJFRZ2007F10.g	Development	ARC1 (am repeat protein)		2.00974

TABLE XIX

Genes differentially expressed between Internode 5 (intermediately mature, rich in sugar) and Internode 1 (immature, poor in sugar) from a pool of seven high brix plants. The individuals were selected from a F1 progeny of a cross between two commercial varieties, SP80-180 and SP80-4966. RNA samples from internode 5 (Intermediate sugar) and internode 1 (Low sugar) were collected in July from the seven highest brix individuals and used to generate probes for cDNA microarray hybridizations. The column High indicates the average ratios (fold induction) of genes more expressed in internode 5 than in internode 1. The column Low indicates the average ratios (fold induction) of genes more expressed in internode 1 than in internode 5. The average brix in the highest sugar internodes was 22.63.

SAS	Category	Description of homologue	High	Low
SCCCCL2001B01.b	Calcium	Calmodulin-binding proteins Apyrase		3.83704
SCRLAM1010D08.g	Transcription	Homeobox knotted homeobox		2.47858
SCEPLB1043H04.g	No matches			2.03771
SCRLFL3007C04.g	Receptors	Receptor Ser/Thr kinase caneRLK-D5		2.19385
SCJFRZ2032G01.g	Protein kinases	SNF-like kinases caneSnRK1-2		2.49118
SCRLSD1012E03.g	Ubiquitination	Ubiquitin		2.12917
SCEQRT1033F01.g	Pathogenicity	Zinc finger proteins C2C2/Dof		7.73845
SCVPLR1049E12.g	Small GTPases	Rab		2.20693
SCCCCL4003D08.g	Transcription	Zinc finger proteins C3H		3.08079
SCSBHR1050B11.g	Development	Putative senescence-associated protein		3.39882
SCCART2001H11.g	Small GTPases	Arf		1.91729
SCVPR2074D04.g	Unknown protein			9.59628
SCJLLR1108H07.g	Calcium	Calmodulin-binding proteins ACA		2.13521
SCEQRT1028H06.g	Hormone biosynthesis	Auxin Nitrilase		1.72814
SCCCRZ1001G10.g	Transcription	Aux/IAA		2.77082
SCRURT2010A10.g	Transcription	Putative transcription factor (myb)		2.08173
SCSBS2058D04.g	Ubiquitination	Ubiquitin		1.77273
SCAGLR1021G10.g	Transcription	Homeobox knotted homeobox		2.61934
SCCCLR1024F10.g	Transcription	Other Auxin-response factors With B3 domain		2.32277
SCSFHR1043G09.g	Stress	Infected libraries S-adenosylmethionine synthase		2.3562
SCCCLR1048F03.g	Unknown protein	Chloroplast hypothetical protein		20.3768
SCEZLR1052E07.g	No matches			1.59145
SCCCRZ2C03D11.g	Transcription	Scarecrow		3.57548
SCSGRT2066D05.g	Stress	Cytochrome P450		3.17506
SCCCRZ3002D03.g	Transcription	LIM (protein-protein interaction)		5.10403
SCVPRZ2038F04.g	Hormone biosynthesis	Jasmonic Acid Linoleic acid desaturase		2.7837
SCCCLR1C03G01.g	Hormone biosynthesis	Jasmonic Acid Linoleic acid desaturase		2.1299
SCUTLR1037F04.g	Others	Ankyrin repeat family protein Xa21 binding		2.00053
SCCCCL5002B10.g	Protein kinases	Undefined-unclassified caseUPK-87		2.09228
SCCCLR1C05B07.g	Protein kinases	SNF-like kinases caneCIPK-3		2.30631
SCJFRZ2007F10.g	Development	ARCI (arm repeat protein)		16.2237
SCEPLR1030B03.g	Pathogenicity	Tomato LRP protein		1.77057
SCQGHR1012B09.g	Stress	Probable cytochrome P450 monooxygenase		2.2378
SCCCCL3120C09.g	Receptors	Receptor Ser/Thr kinase case RLK with LysM-1		1.69331
SCEPRZ1009C10.g	Protein kinases	SNF-like kinases cane osmotic stress-activated protein kinase-1		2.15245
SCRUFL1112F04.b	Others	RNA stability UDP-GlcNAc		2.7596
SCVPLR2027A05.g	Transcription	Other Auxin-response factors With B3 domain		2.55167
SCCCRZ1001D02.g	Adapters	14-3-3 proteins		2.02234
SCVPRZ3025A12.g	Protein kinases	RLCK canePBS1-6		2.16888
SCJLRZ1023H04.g	Protein kinases	SNF-like kinases caneCIPK-9		3.53497
SCEQRT2099H01.g	Protein kinases	Calcium-related caneCDPK-27		1.84964
SCCCRZ1001H05.g	Transcription	HLH (helix-loop-helix)		4.52862
SCMCL6055H06.g	Pathogenicity	Tomato LRP protein		1.96121
SCCCRZ1002F06.g	Stress	Drought and cold response Enolase		2.22871
SCCCLR1048D07.g	Hormone biosynthesis	Salicylic Acid		14.2767
SCCCRZ1C01H06.g	Calcium	Calmodulin-binding proteins Apyrase		4.7337
SCSGAM1094D05.g	Hormone biosynthesis	Salicylic Acid		5.14944
SCCCLR1072E03.g	Receptors	Receptor Ser/Thr kinase caneRLK-AX3		2.08456
SCSGFL5C08F04.g	Unknown protein			10.083
SCCCRZ2C04A07.g	Stress	Cytochrome P450 CYP71E		4.14116
SCUTAM2088G02.g	Unknown protein	Putative GTP-binding protein		1.82251
SCCCLR1C04G08.g	Protein kinases	Casein kinases caneCKI-3		4.08444
SCUTLR2008E01.g	No matches		1.84352	
SCQSRT1036D03.g	Pathogenicity	R-genes transduction PR		2.02071
SCRLST3166F11.g	No matches (non-coding)			1.63126
SCEQLB1065H07.g	No matches			2.42131
SCRLAD1100E08.g	No matches			2.36751
SCRUAD1133D10.b	Receptors	Photoreceptors Blue light receptor cry1		2.95879
SCCCLR1001D10.g	Transcription	Putative AP2-domain transcription factor		2.30605
SCSBHR1056H08.g	Receptors	EIN2 (ethylene)		4.24768
SCCCLR1C07B07.g	Others	Glycine-rich RNA-binding protein		1.84253
SCCCRZ2C03B03.g	Receptors	Receptor Ser/Thr kinase cane RLK wish LysM-2		1.76512
SCCCLR2001H09.g	Stress	Thioredoxin		2.00805
SCRLFL1008C11.g	No matches			2.48511

TABLE XX

Genes differentially expressed between Internode 5 (intermediately mature, rich in sugar) and Internode 1 (immature, poor in sugar) from a pool of seven low brix plants. The individuals were selected from a F1 progeny of a cross between two commercial varieties, SP80-180 and SP80-4966. RNA samples from internode 5 (Intermediate sugar) and internode 1 (Low sugar) were collected in July from the seven lowest brix individuals and used to generate probes for cDNA microarray hybridizations. The column High indicates the average ratios (fold induction) of genes more expressed in internode 5 than in internode 1. The column Low indicates the average ratios (fold induction) of genes more expressed in internode 1 than in internode 5. The average brix in the highest sugar internodes was 18.96.

SAS	Category	Description of homologue	High	Low
SCCST1004A07.g	Protein kinases	SNF-like kinases cane osmotic stress-activated protein kinase-7		2.24911
SCVPLR2027A05.g	Transcription	Other Auxin-response factors With B3 domain		1.92017
SCEZRZ1012A02.g	Stress	Cytochrome P450 CYP9		2.66254
SCBFLR1039B05.g	Carbohydrate Metabolism	Xyloglucan endotransglycosylase		6.00106
SCCCRZ1001G10.g	Transcription	Aux/IAA		1.58291
SCEQRT1033F01.g	Pathogenicity	Zinc finger proteins C2C2/Dof		2.69468
SCCCRZ1C01H06.g	Calcium	Calmodulin-binding proteins Apyrase		4.50294
SCSBAM1084F08.g	Unknown protein	Similar to cyclin		4.00643
SCCCLR1001E04.g	Carbohydrate Metabolism	Photosynthesis RUBISCO - small subunit		2.99228
SCSGAM1094D05.g	Hormone biosynthesis	Salicylic Acid		3.03142
SCCCLR1048D07.g	Hormone biosynthesis	Salicylic Acid		3.86262
SCSGFL5C08F04.g	Unknown protein			7.37235
SCCCRZ3002D03.g	Transcription	LIM (protein-protein interaction)		3.27664
SCVPRT2074D04.g	Unknown protein			9.96472
SCRURT2010A10.g	Transcription	Putative transcription factor (myb)		1.75219
SCCCRZ2C03D11.g	Transcription	Scarecrow		2.57578
SCRFL13007C04.g	Receptors	Receptor Ser/Thr kinase caneRLK-D5		2.6318
SCCCL4004C06.g	Unknown protein			2.12353
SCJFRZ2007F10.g	Development	ARC1 (am repeat protein)		4.00615
SCCCLR1048F03.g	Unknown protein	Chloroplast hypothetical protein		3.74571
SCCCRZ2C04A07.g	Stress	Cytochrome P450 CYP71E		7.42158
SCSGRT2066D05.g	Stress	Cytochrome P450		2.16937
SCBGLR1117A05.g	Small GTPases	Ran	1.86344	
SCCCLR1C04E03.g	Ubiquitination	E2	1.56768	
SCSBAD1084C01.g	Others	Tubulin alpha-1 chain	1.72259	
SCMCLR1123E10.g	Others	T-complex protein (chaperonin)	2.39987	
SCVPLR2012B07.g	Two component	Phosphorelay intermediate Similar to ATHP1 ATHP2 ATHP3	2.91613	
SCQGLR1019A10.g	Small GTPases	Ran	2.08538	
SCQSRT1036D03.g	Pathogenicity	R-genes transduction PR	1.86776	
SCCCLR2001H09.g	Stress	Thioredoxin	2.43049	
SCRFFL5034G07.g	No matches		2.21962	
SCCCLR2002F08.g	Hormone related	Auxin auxin repressed	1.78828	
SCCCLR1C07B07.g	Others	Glycine-rich RNA-binding protein	2.24474	
SCJFAM1066B05.g	Transcription	HIT (histidine triad) PKC inhibitor	1.85085	
SCCART2002B03.g	Protein metabolism	Putative ribosomal protein S14	2.48804	
SCRLLR1111D02.g	No matches (non-coding)		1.70582	
SCCCL4007H07.g	No matches		1.9409	
SCJFHR1C03E01.b	Protein kinases	Undefined canePK-BII3	1.60982	
SCCCFL4091A07.g	Hormone related	Giberellin Giberellin responsive	1.79817	
SCJFRT1062G05.g	Transcription	CCAAT	1.68245	
SCCCRZ2001F06.g	Protein metabolism	Putative 6S ribosomal protein L11	2.1963	
SCSBSD2029F05.g	Unknown protein		5.22372	
SCJFRZ2028F11.g	Receptors	Receptor Ser/Thr kinase caneSERK-5	2.07098	
SCCCRZ2003E12.g	Transcription	bZIP	1.7904	
SCUTLR2008E01.g	No matches		2.06397	
SCCCST3C01D11.g	Receptors	Receptor Ser/Thr kinase-unclassified caneURLK-84 (with LRR)	1.97063	
SCSBSD2029D11.g	No matches		1.77589	
SCEQLR1091A10.g	Protein metabolism	60S Ribosomal protein L23	2.04218	
SCCCLR2001E10.g	No matches		1.96151	
SCQSSB1077D06.g	Receptors	Receptor Ser/Thr kinase caneRLK-DXII4	2.11245	
SCEZHR1087F06.g	Stress	Cytochrome P450 CYP84	1.72424	
SCRFL11008C11.g	No matches		2.58471	
SCEZLR1009F06.g	Carbohydrate metabolism	Pyruvate dehydrogenase	2.60268	
SCCCL4004A10.g	Others	Putative polypeptide	1.97711	
SCJFLR1013A09.g	Stress	Drought and cold response Cysteine proteinase RD19A precursor	2.11721	
SCSBHR1056H08.g	Receptors	EIN2 (ethylene)	3.47771	
SCCCLR1001D10.g	Transcription	Putative AP2-domain transcription factor	1.884	
SCCCRZ2002C09.g	Others	Alpha tubulin	1.84438	

TABLE XXI

An example of genes that are differentially expressed both when High and Low Brix plants are compared and when Mature (Internode 9) and Immature (Internode 1) internodes are compared. Data indicated with an asterisk has been published by Felix J. M. (2006).

SAS	category	sub category 1	sub category 2	High vs Low brix	Internode 9 vs Internode 1
SCRFLR2037F09.g	Calcium	Calreticulin		Down High Brix	Down Mature Internode
SCCCRT1001E01.g	Hormone biosynthesis	Jasmonic Acid	Lipoxygenase	Down High Brix	Down Mature Internode*
SCCCLR2002F08.g	Hormone related	Auxin	auxin repressed	Down High Brix	Down Mature Internode
SCRFLR1012F12.g	Others	caffeic acid 3-O-methyltransferase		Up High Brix	Up Mature Internode*
SCSFAD1125C08.g	Pathogenicity	Polygalacturonase-inhibiting		Down High Brix	Down Mature Internode*
SCCCLR2C01G07.g	Protein kinases	SNF-like kinases	caneCIPK-20	Up High Brix	Up Mature Internode*
SCMCRT2103B04.g	Protein kinases	SNF-like kinases	caneCIPK-21	Up High Brix	Up Mature Internode*
SCEPRZ1010E06.g	Protein Phosphatases	Serine/Threonine - PPM Family	PP2C-like	Down High Brix	Down Internode*
SCCCLR2C01F06.g	Stress	Wound-induced		Up High Brix	Up Mature Internode*
SCJLRT1021D12.g	Stress	Wound-induced	Chalcone synthase	Down High Brix	Down Internode*
SCJFRT1005C11.g	Hormone biosynthesis	Ethylene	ACC oxidase	Up High Brix	Down Mature Internode*
SCVPLR2012A10.g	Hormone biosynthesis	Ethylene	ACC oxidase	Up High Brix	Down Mature Internode*
SCCCLR1048D07.g	Hormone biosynthesis	Salicylic Acid		Up High Brix	Down Mature Internode
SCEQRT1024E12.g	Hormone biosynthesis	Salicylic Acid		Up High Brix	Down Mature Internode*
SCCCLR1C02F07.g	Inositol	Others	myo-Inositol-1-phosphate synthase	Up High Brix	Down Mature Internode*
SCEZHR1087F06.g	Stress	Cytochrome P450	CYP84	Down High Brix	Up Mature Internode
SCAGFL1089C03.g	Stress	Glutathione S-transferases		Up High Brix	Down Mature Internode*
SCCCCL3002C09.b	Stress	Glutathione S-transferases		Up High Brix	Down Mature Internode*

### Genes of this Invention

The invention provides polynucleotides described above and their variants.

#### Variants

“Variants” is intended to include substantially similar polynucleotide sequences, as long as they still have a same or substantially similar function as polynucleotides of this invention, e.g., marker for plants with different sugar content, ability to modulate sugar content. Common sources for variants include sequence identity variants, fragments, hybridizing sequences, complements, or mutated sequences. A fragment of the sequence is defined as a portion or region of the sequence that can be used to alter the expression levels of one of the genes encoding SEQ ID Nos. 1-203 or 229 to 373 in transgenic plants.

#### Sequence Identity

Naturally and non-naturally occurring “variants” of differentially expressed sequences within the invention include nucleic acid molecules having at least about 65%, 70%, 75%, 80%, 85%, 90%, or 95% sequence identity with the native sugarcane sequences disclosed herein, i.e., SEQ ID Nos. 1-203 or 229 to 373, or complements of these sequences. More preferably, the variants have 97%, 98%, 99%, or at least about 99.5% sequence identity to the whole sequence or a fragment of the sequence. Comparisons for determination of sequence identity can be made using methods known to those of skill in the art.

#### Hybridization

“Variants” also include nucleic acids molecules that hybridize under high stringency conditions, as defined herein, to the sugarcane nucleic acid sequences of SEQ ID Nos. 1-203 or 229 to 373 or the complement of the sequences of SEQ ID Nos. 1-203 or 229 to 373. For example, such “variants” may be nucleic acid molecules that hybridize to the sequence of SEQ ID Nos. 1-203 or 229 to 373 or the complement of the sequences of SEQ ID Nos. 1-203 or 229 to 373 under low stringency conditions, moderate stringency conditions, or high stringency conditions. (See Sambrook et al.

(Most recent edition) *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y.).

As used herein, the phrase “low stringency hybridization conditions” refers to the following conditions and equivalents thereto: hybridization at 5×SSC, 2% SDS, and 100 μg/ml single stranded DNA at 40° C. for 8 hours, followed by at least one wash in 2×SSC, 0.2% SDS, at 40° C. for thirty minutes. As used herein, the phrase “moderate stringency hybridization conditions” refers to the following conditions and equivalents thereto: hybridization at 5×SSC, 2% SDS, and 100 μg/ml single stranded DNA at 50° C. for 8 hours, followed by at least one wash in 0.1×SSC, 0.1% SDS, at 50° C. for thirty minutes. As used herein, the phrase “high stringency hybridization conditions” refers to the following conditions and equivalents thereto: hybridization at 5×SSC, 2% SDS, and 100 μg/ml single stranded DNA at 65° C. for 8 hours, followed by at least one wash in 0.1×SSC, 0.1% SDS, at 65° C. for thirty minutes.

#### Complements

Alternatively, nucleic acids of this invention are those having a nucleotide sequence that is the complement of the full-length or portions of the sequences of SEQ ID Nos. 1-203 or 229 to 373.

Polynucleotides can be as short as 14 nucleotides, but they are not restricted to this length.

#### Mutants

The genes can also be mutated by radiation or chemical mutagenesis using EMS (ethylmethane sulfonate) and mutated alleles identified by Tilling or RFLP generating plants with increased sucrose content through non-transgenic methodologies.

One or more point mutations can be introduced into a nucleic acid molecule to yield a modified nucleic acid molecule using, for example, site-directed mutagenesis (see Wu (Ed.), *Meth. In Enzymol.* Vol. 217, San Diego: Academic Press (1993); Higuchi, “Recombinant PCR” in Innis et al. (Ed.), *PCR Protocols*, San Diego: Academic Press, Inc. (1990), each of which is incorporated herein by reference). Such mutagenesis can be used to introduce a specific, desired

amino acid insertion, deletion or substitution; alternatively, a nucleic acid sequence can be synthesized having random nucleotides at one or more predetermined positions to generate random amino acid substitutions. Scanning mutagenesis also can be useful in generating a modified nucleic acid molecule encoding substantially the amino acid sequence as polypeptides of this invention.

#### Polypeptides of this Invention

In certain embodiments, this invention provides polypeptides partially or fully encoded by the polynucleotides of this invention or by variants of a polynucleotide of this invention.

In other embodiments, the polypeptide has an amino acid sequence substantially similar to that encoded by polynucleotides of this invention. As used herein, the term "substantially the same amino acid sequence," is intended to mean a polypeptide or polypeptide segment having an identical amino acid sequence, or a polypeptide or polypeptide segment having a similar, non-identical sequence that is considered by those skilled in the art to be a functionally equivalent amino acid sequence. In particular, polypeptide with "substantially the amino acid sequence" can have one or more modifications such as amino acid additions, deletions or substitutions, including conservative or non-conservation substitutions.

Comparison of sequences for substantial similarity can be performed between two sequences of any length and usually is performed with sequences between about 6 and 1200 residues, preferably between about 10 and 100 residues and more preferably between about 25 and 35 residues. Such comparisons for substantial similarity are performed using methodology routine in the art.

The preferred percentage of sequence similarity for polypeptides includes polypeptides having at least about 65% similarity, 70% similarity, 75% similarity, 80% similarity, 85% similarity, 90% similarity, 95% similarity, 97% similarity, 98% similarity, 99% similarity, or more preferably at least about 99.5% similarity.

Sequence similarity is preferably calculated as the number of similar amino acids in a pairwise alignment expressed as a percentage of the shorter of the two sequences in the alignment. The pairwise alignment is preferably constructed using the Clustal W program, using the following parameter settings: fixed gap penalty=10, floating gap penalty=-0, protein weight matrix=BLOSUM62. Similar amino acids in a pairwise alignment are those pairs of amino acids which have positive alignment scores defined in the preferred protein weight matrix (BLOSUM62). The protein weight matrix BLOSUM62 is considered appropriate for the comparisons described here by those skilled in the art of bioinformatics. (The reference for the clustal w program (algorithm) is Thompson, J. D., Higgins, D. G. and Gibson, T. J. (1994) CLUSTAL W: improving the sensitivity of progressive multiple sequence alignment through sequence weighting, positions-specific gap penalties and weight matrix choice. *Nucleic Acids Research*, 22:4673-4680; and the reference for BLOSUM62 scoring matrix is Henikoff, S, and Henikoff, J. G. (1993) Performance evaluation of amino acid substitution matrices. *Proteins*, 7:49-61.)

It is understood that minor modifications of primary amino acid sequence can result in a polypeptide that has substantially equivalent or enhanced function polypeptides of this invention. Further, various molecules can be attached to polypeptide thereof, for example, other polypeptides, antigenic or other peptide tags, carbohydrates, lipids, or chemical moieties.

Sugarcane Plants for Identification of Genes of this Invention

#### A—Crossings

##### 1—An Example of Characterization of a Progeny Derived from Wild-Type Ancestors:

Two initial intra-specific polycrosses could be performed, one among *Saccharum officinarum* genotypes and the other combining *Saccharum spontaneum* genotypes. The crossing and selection process that could follow is illustrated in FIG. 1. For each generation 500 individuals could be sampled for brix content and gene expression and the extreme segregants selected. The hybrid individuals selected for molecular studies could be planted in the field in one row of 5 meters using standard sugarcane cultivation practices. Brix readings and tissue samples could be collected very early in the season, in March of the following year, when plants were 10 months. For brix content determination plants could be sampled by using a hand held juice sample collector. Juice could be collected by punching a hole in the middle of the 5<sup>th</sup> visible internode counted from the top after removal of the lowest dry leaf sheath still attached to the culm. A few drops of the juice could be placed in a handheld refractometer (N1, ATAGO, Japan) and a direct brix reading obtained. Individuals or pools of individuals (for example, seven or eight individuals) can have their tissues collected and RNA extracted.

##### 2—Examples of a Progeny Derived from Commercial Varieties:

Five hundred sugarcane F1 plants from a cross between two commercial varieties (SP80-180×SP80-4966, or SP80-144×SP85-7215) could be kept in a green house or field-grown. They could segregate for stem sugar content in a normal manner and the seven plants presenting extreme values for gene expression associated to high sugar and low sugar could be selected. Mature leaves (Leaf+1, Van Dillewijn, 1952), immature leaf, mature internode, immature and intermediate internode, root, lateral bud and a mix of flowers in different developmental stages could be collected from the selected plants 6, 7, 9, 11 and 13 months after planting (but not restricted to). Tissues collected at each time point could be pooled from seven individuals of each group or characterized for each individual sample. For RNA blot analysis all time points could be evaluated, or only one time point could be evaluated. Gene expression profiles could be analyzed independently, using three individuals from each group (for example), or be determined for a group of plants.

#### B—Commercial Varieties or Cultivars

Varieties can be field-grown for a year (for example, since September) and samples collected throughout the year (for example in March, May, July or September, but not restricted to). Tissue samples can be collected from 2 to 4 individuals of each variety which are pooled or analyzed independently. Examples of varieties that have been shown to have altered expression for the genes are the high sucrose and precocious accumulating cultivars SP91-1049 and SP89-1115 in comparison to the low sucrose and late accumulating cultivars SP83-2847 and SP94-3116. Samples can be collected as described above.

#### Methods for Determining the Ability of a Plant to Accumulate Sugar

In certain embodiments, this invention uses genes that are differentially expressed in plants having different sugar levels, such as SEQ ID NO:s 1 to 203 and SEQ ID NO:s 229 to 373, to determine the ability of the plant to accumulate sugar. In some embodiments, the expression level of genes is measured using various methods known in the art, such as those

described below. In other embodiments, the expression level of the polypeptide expressed by polynucleotides of this invention is detected.

#### Measurement of Gene Expression

Gene expression can be determined using any technique that will measure the product of the gene's activity, for example transcript or mRNA levels or protein levels, including cDNA microarrays, oligonucleotide arrays or gene chips, quantitative PCR, northern blots, western blots/ELISA/mass spectrometry, according to the methods described in this work.

Gene expression can be measured by various methods, including:

- quantitative PCR
- real-time PCR
- cDNA microarrays
- oligonucleotide arrays or gene chips
- northern blots
- any technique that will measure transcript levels for genes such as NASBA or TMA
- any technique that will use hybridization of genes or of a product of the gene as a measure of gene expression

any technique that will measure a product of gene expression such as the protein encoded by the genes such as with the aid of an antibody (as in western blots and ELISA) or mass spectrometry.

#### cDNA Microarrays

##### Tissue Sampling and RNA Extraction from Sugarcane Plants

The first leaf with a visible dewlap (leaf+1) and internodes 1, 2, 5 and 9 (counted from top to bottom where number 1 was the smallest visible internode after all leaves were removed) can be collected from 6 to 18 month old plants. The internodal tissue can be separated from the node, cut in small pieces, frozen in liquid nitrogen, and stored at  $-80^{\circ}\text{C}$ . Internodes 1 and 2 can be pooled prior to RNA extraction and are referred as internode 1. Frozen tissues can be grinded using a homogenizer. 2-2.5 g were weighted and grinded to a fine powder, in liquid nitrogen, using pre-cooled mortar and pestle. The pulverized tissue will be transferred to a 50 ml tube and homogenized with 5 ml Trizol® (Invitrogen) per gram of tissue. The manufacturer's recommendations for high polysaccharide content tissues will be followed for the mature internode samples. Samples can be incubated for 5 min at room temperature (RT), with occasional vortexing. The homogenate will be centrifuged at 3,000 rpm;  $4^{\circ}\text{C}$ . for 10 min and the supernatant transferred to a new 50 ml tube. 0.2 ml of chloroform (RT) will be added for each ml of Trizol® solution. The solution will be mixed vigorously for 15 s and incubated for 3 min at RT. After centrifugation (3,000 rpm,  $4^{\circ}\text{C}$ ., 15 min), the aqueous phase will be transferred to tubes containing 0.6 volumes of isopropanol. The solution will be mixed several times by gentle inversion and incubated at RT for 10 min. Tubes will be centrifuged at 10,000 rpm,  $4^{\circ}\text{C}$ . for 10 min and the supernatant was carefully discarded. Pellets will be washed with cold 75% ethanol. Samples will be briefly vortexed and centrifuged at 6,000 rpm for 5 min. The supernatant can be again discarded and pellets washed with cold 100% ethanol. After centrifugation, the supernatant will be discarded and pellets were allowed to dry at RT for at least 10 min. Pellets will be resuspended in 20  $\mu\text{l}$  of warm diethyl pyrocarbonate-treated water, vortexing gently for about 15 min. RNA samples can be quantified in a spectrophotometer and loaded on 1.0% agarose/formaldehyde gels for quality inspection.

#### PCR Amplification and Array Printing

Sugarcane cDNA plasmid clones of 6438 ESTs obtained from the SUCEST collection can be re-arranged and amplified in 100  $\mu\text{l}$  PCR reactions (40 cycles, annealing at  $51^{\circ}\text{C}$ .), directly from bacterial clones in culture, using T7 and SP6 primers. For this work, clones had their identity validated by re-sequencing. PCR products can be purified by filtration using 96 well filter plates (Millipore Multiscreen® MAFBN0B50). Samples can be visualized on 1% agarose gels to inspect PCR-amplification quality and quantity. Purified PCR products (in 10 mM Tris-HCl pH 8.0 solution) can be mixed with an equal volume of DMSO in 384 well V-bottom plates. Microarrays can be constructed by arraying cDNA fragments on DMSO optimized, metal coated glass slides (type 7, Amersham Biosciences) using the Generation III Microarray Spotter (Molecular Dynamics/Amersham Pharmacia Biotech). Each cDNA fragment was spotted for this work on the slides at least four times (i.e., technical replicates). Following printing, the slides will be allowed to dry and the spotted DNA was bound to the slides by UV-cross linking (50 mJ).

#### Probe Preparation and Hybridization

Ten micrograms of total RNA can be reverse transcribed, labeled, and hybridized using the reagents provided with the CyScribe Post-Labeling kit (Amersham Biosciences), according to the manufacturer's instructions. The products of the labeling reactions can be purified in Millipore Multiscreen® filtering plates to remove unincorporated labeled nucleotides. Microarrays can be co-hybridized with the fluorescently labeled probes. Hybridizations were performed overnight at  $42^{\circ}\text{C}$ . in humid chambers. The slides can be then washed in  $1\times\text{SSC}$  and 0.2% SDS (10 min,  $55^{\circ}\text{C}$ .), twice in  $0.1\times\text{SSC}$  and 0.2% SDS (10 min,  $55^{\circ}\text{C}$ .), and in  $0.1\times\text{SSC}$  (1 min, RT). Slides will then be rinsed briefly in filtered milli-Q water and dried with a nitrogen stream.

#### Data Acquisition, Processing and Statistical Analysis

Slides can be scanned using the Generation III Scanner™ (Molecular Dynamics) adjusting the photomultiplier tube (PMT) to 700 for both channels. Images can be processed and data collected using the ArrayVision (Imaging Research Inc.) software. For this work, local median background was subtracted from the MTM (median-based trimmed mean) density for each spot. Data from clones that generated poor-quality PCR fragments (no amplification or unspecific bands) or poor-quality spots (visually inspected) were excluded. The data were stored and managed by the BioArray Software environment<sup>14</sup> free web-based database.

A set of custom programs based on R language were developed for data processing based on methods described previously (Papini-Terzi et al., 2005). Pearson correlation values among the samples were calculated using normalized expression ratios obtained from high sugar samples against low sugar samples or test samples versus pool of samples hybridizations for 6438 genes. We used homotypic or 'self-self' hybridizations of the reference pool sample to define intensity-dependent cutoff levels that would indicate differentially expressed genes. The identification of differentially expressed genes was performed using a local implementation of the HTself method (Vencio and Koide, 2005; available at [blasto.iq.usp.br/~rvencio/HTself](http://blasto.iq.usp.br/~rvencio/HTself)), that uses "self-self" hybridizations to derive an intensity-dependent cut-off for significant fold-changes integrating the probability density function to 98% for different signal intensity levels. The SAS (Sugarcane Assembled Sequences) presenting more than 70% of its replicates outside fold-change cut-off curves were defined as differentially expressed. The fluorescence ratios

were normalized to account for systematic errors using the LOWESS fitting (Yang et al. 2002) and used to calculate the expression ratios for all genes between the tissue sample and the reference sample. For every gene, the percentage of replicates within or outside the cutoff limits was calculated in each tissue sample. Further details on the method are available on the World Wide Web at [succest-fun.org/pub/SUCAST](http://succest-fun.org/pub/SUCAST).

Other methods that compare an expression pattern to another or score a change from expressed to non-expressed, or the reverse are useful. Changes in intensity of expression may be scored, either increases or decreases. Any statistically significant change can be used. Typically changes in one of SEQ ID NO. 1-203 are suitable. However, more genes may be usefully analyzed. SEQ ID NO. 1-203 gene expression data can be used as molecular classifiers or used to train methods to distinguish between high and low sucrose plants or popu-

lations of plants using a variety of established techniques such as the Fisher's linear discriminant analysis (Meireles et al., 2004), the Prediction Analysis of Microarrays software PAM (Tibshirani et al., 2002) or commonly used methods as SVM (Support Vector Machines) or LVQ (Learning Vector Quantization) (Mattfeldt et al., 2004). By doing so, SEQ ID NO. 1-203 expression profile can be used to predict between high brix and low brix plants and can be used to classify the individuals of a progeny or cultivars. Genes whose expression were found to be unaltered in the microarray experiments can aid in defining classes and be used to train the algorithms, together with the differentially expressed SEQ ID NO. 1-203. Table XI lists as an example 25 SAS (SEQ ID NO. 204 to 228) and the corresponding ESTs that are consistently expressed in similar levels in all samples analyzed (high and low brix).

TABLE XI

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Twenty-five genes not differentially expressed between all the high and all the low brix populations and varieties.

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The SAS (Sugarcane Assembled Sequences) and corresponding ESTs presenting more than 70% of its replicates inside fold-change cut-off curves were defined as not differentially expressed and can be used as controls in real-time PCR reactions or to train classification algorithms.

SEQ ID NO. 204: SCAGLR1043C02.g  
(CA291199, CA126773, CA103634, CA278537, CA291283, CA105620, CA129564, CA135982, CA154949, CA137234, CA131175, CA131096, CA136766, CA079897, CA112911, CA202743, CA212218, CA130074, CA116962, CA300529, CA233427, CA275519, CA215010, CA190793, CA264955, CA275590, CA148445, CA276733, CA197411, CA285562, CA143450, CA158699, CA148266, CA276787, CA223611, CA131410, CA129260, CA282689, CA143509, CA127374, CA223701, CA107631, CA102547, CA200880, CA126777, CA168082, CA143088, CA139235)

SEQ ID NO. 205: SCAGRT3046D01.g  
(CA300723, CA294382, CA264769, CA294452)

SEQ ID NO. 206: SCBGLR1002006.g  
(CA278315, CA117650, CA127739, CA212804, CA073244, CA138816, CA152521, CA152509, CA153113, CA283276, CA259474, CA289253, CA101319, CA126194, CA187565, CA093995, CA150472, CA252354, CA226461, CA286965, CA142703, CA298971, CA286850, CA111071, CA128235, CA130953, CA283578, CA181244, CA190282, CA241875, CA076812)

SEQ ID NO. 207: SCCCL3005D01.b  
(CA271043, CA272368, CA215896, CA098903, CA093456, CA150890, CA266868, CA263152, CA093454, CA284141, CA270967, CA070480, CA223204, CA261258)

SEQ ID NO. 208: SCCCL3080C09.g  
(CA259330, CA152240, CA289512, CA124276, CA269953, CA282554, CA150365, CA076742, CA124252, CA125409, CA189780, CA150360, CA067168, CA185260, CA268877, CA287161, CA079640, CA180418, CA284801, CA268954, CA296365, CA118827, CA184393, CA289786, CA111364, CA150081, CA229568, CA200556, CA120906, CA286941, CA225985, CA285992, CA255183, CA262927, CA277963, CA103076, CA118794, CA118790, CA103799, CA129390, CA286405, CA100864, CA129384, CA074893, CA093506, CA214051, CA129364, CA111366, CA152568, CA076728, CA074983, CA124214, CA093579, CA122181, CA071338, CA249655, CA152647, CA128317, CA131033, CA071425, CA077256, CA117737, CA078093, CA199165, CA168557, CA125328, CA084326, CA150876, CA082480, CA254028, CA189858, CA276734, CA118424, CA268830, CA231681, CA276788, CA117438, CA225602, CA277928, CA114620, CA247257, CA185669, CA076943, CA075590, CA202758)

SEQ ID NO. 209: SCCCL7001A04.g  
(CA100620, CA223268, CA100961, CA199955, CA223191, CA279575, CA103970, CA110326)

SEQ ID NO. 210: SCCCLB1C03B04.g  
(CA086997, CA198468, CA164949, CA299431, CA189172, CA279831, CA175292, CA190805, CA155239, CA074671, CA131422, CA172088, CA237966, CA113643, CA099312, CA097078, CA168581)

SEQ ID NO. 211: SCCCLR1022H01.g  
(CA119702, CA189837, CA274251, CA124160, CA152830, CA202385, CA214786, CA223178, CA094030, CA092004, CA283613, CA277116, CA146444, CA297712, CA223255, CA067746, CA116394, CA067839, CA297889)

SEQ ID NO. 212: SCCCLR1070B11.g  
(CA194863, CA069696, CA120150, CA067031, CA087323, CA292894, CA165329, CA185869, CA168662, CA064663, CA256320, CA079508, CA064662, CA209676)



TABLE XI-continued

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Twenty-five genes not differentially expressed between all the high and all the low  
brix populations and varieties.

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SEQ ID NO. 213: SCCCLR1072A03.g  
(CA257676, CA241502, CA103767, CA119541, CA212813, CA072979, CA076246, CA260516,  
CA173103, CA092491, CA279357, CA076330, CA298956, CA235977, CA283443, CA067187,  
CA172026, CA102965, CA243748, CA157421, CA254836, CA086831, CA067267, CA254991,  
CA165072, CA254121, CA281218, CA194801, CA107489, CA241226, CA183169, CA259059,  
CA110302, CA074064, CA211578, CA259058, CA241304, CA222499, CA167440, CA166656,  
CA103379, CA092495, CA251886, CA198331, CA197814, CA095062, CA089849, CA181078,  
CA238993, CA080070, CA160829, CA257963, CA077196, CA244970, CA085039, CA170461,  
CA159351, CA272807, CA245352, CA107493, CA159440)

SEQ ID NO. 214: SCCCLR1075G05.g  
(CA064776, CA104174, CA262368, CA073013, CA168309, CA121412, CA226304, CA230815,  
CA129021, CA299276, CA123604, CA267396, CA263329, CA120286, CA177583, CA147731,  
CA264721, CA123599, CA263403, CA194813, CA241253)

SEQ ID NO. 215: SCCCLR1078F05.g  
(CA124384, CA112238, CA228635, CA253815, CA228634, CA120519, CA228633, CA088403,  
CA284381, CA153412, CA257810, CA243271, CA089170)

SEQ ID NO. 216: SCCNR1001B12.g  
(CA282544)

SEQ ID NO. 217: SCCCRZ2002E06.g  
(CA079679, CA231568, CA121168, CA149726, CA278060, CA136300)

SEQ ID NO. 218: SCCCRZ2C04B04.g  
(CA246886, CA220871, CA154329, CA280029, CA268704, CA150217, CA219829, CA268689,  
CA068008, CA068007, CA117830, CA087866, CA261807, CA268749, CA156666, CA205929,  
CA158955, CA167141, CA239715)

SEQ ID NO. 219: SCEPAM1020E03.g  
(CA072822, CA072801, CA188039, CA072796)

SEQ ID NO. 220: SCEQRT1024H10.g  
(CA139099, CA281552, CA281378, CA132555, CA287054, CA251801, CA132401, CA143578,  
CA284175, CA143345, CA143889, CA284251, CA143429, CA143390, CA284886, CA296940,  
CA143494, CA139010, CA138862, CA300775, CA143467, CA134226, CA277302, CA141676,  
CA285542, CA142420, CA258267, CA267581, CA130719, CA274036, CA267666, CA144676,  
CA278111)

SEQ ID NO. 221: SCEQRT1030A03.g  
(CA228274, CA133004, CA230581, CA230389, CA230510, CA235035, CA197298, CA088047)

SEQ ID NO. 222: SCJFRT1009A08.g  
(CA133624, CA190354)

SEQ ID NO. 223: SCJFRZ2009G01.g  
(CA088829, CA075098, CA139326, CA272034, CA075189, CA151398, CA276729, CA223035,  
CA237807, CA111462, CA106723, CA213636, CA123369, CA135723, CA244358, CA246251,  
CA226436, CA190274, CA123851, CA244439, CA132084, CA178674, CA113343)

SEQ ID NO. 224: SCJLFL3014C10.g  
(CA227690, CA227772)

SEQ ID NO. 225: SCMCL6055H06.g  
(CA183309, CA272155, CA071587, CA154790, CA236184, CA111608, CA231710, CA288208,  
CA098251, CA238333, CA187031, CA071503, CA293423)

SEQ ID NO. 226: SCQGLR1019C05.g  
(CA239321, CA259641, CA170537, CA094369, CA124046, CA147545, CA082777, CA187852,  
CA199413, CA154540, CA169696, CA099319, CA204586, CA196716, CA199496, CA171670,  
CA200284, CA234725, CA068506)

SEQ ID NO. 227: SCQSST1037B07.g  
(CA261004, CA241250, CA183198, CA296123, CA067033, CA177822, CA241340, CA217804,  
CA266141, CA126550, CA217886, CA183583, CA285691, CA266216)

SEQ ID NO. 228: SCSBSD1029F09.g  
(CA281292, CA275363, CA285616, CA286914, CA273656, CA286500, CA296413, CA283987,  
CA291253, CA274747)

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## Quantitative or Real-Time PCR (RT-PCR)

Any method to measure mRNA levels for the genes can be used. For this work, five micrograms of total RNA were treated with DNase I (Amplification grade, Invitrogen) according to the manufacturer's instructions and an aliquot of 7.5  $\mu$ l of the treated RNA was reverse-transcribed using the SuperScript First-Strand Synthesis System for RT-PCR (Invitrogen). The 20  $\mu$ l reverse transcription reactions contained the RNA template, 2  $\mu$ l 10 $\times$ RT buffer, 0.5 mM each dATP, dGTP, dCTP and dTTP, 50 ng random hexamers, 0.25  $\mu$ g oligo(dT), 5 mM MgCl<sub>2</sub>, 10 mM DTT (dithiothreitol), 40 U Rnase OUT and 50 U SuperScript II Reverse Transcriptase. RNA, random hexamers, dNTPs, and oligo(dT) were mixed first, incubated at 70° C. for 5 min and placed on ice. Subsequently, the remaining components, except the SuperScript II Reverse Transcriptase, were added to the reaction and the mixture was heated to 25° C. for 10 min and then incubated at 42° C. for 2 min. The SuperScript II Reverse Transcriptase was added to each tube and the reaction was incubated at 42° C. for 1.5 h, 72° C. for 10 min, and chilled on ice. An identical reaction without the reverse transcriptase was performed as a control, to confirm the absence of genomic DNA. The cDNA product was treated with 2 U of RNaseH (Invitrogen) for 30 min at 37° C. and for 10 min at 72° C. Real-time PCR reactions were performed using SYBR Green PCR Master Mix (Applied Biosystems) in a GeneAmp 5700 Sequence

Detection System (Applied Biosystems). Primers were designed using the Primer Express 2.0 Software (Applied Biosystems). BLAST searches against the SUCEST database were conducted to ensure the specificity of the selected primers. The primer sequences designed are listed in Table XII. Each reaction was performed in duplicates and contained 2  $\mu$ l of a 1:10 dilution of the synthesized cDNA, primers to a final concentration of 600 nM each, 12.5  $\mu$ l of the SYBR Green PCR Master Mix and PCR-grade water to a total volume of 25  $\mu$ l. The parameters for the PCR reaction were 50° C. for 2 min, 95° C. for 10 min, 40 cycles of 95° C. for 15 s and 60° C. for 1 min. The specificity of the amplified products was evaluated by the analysis of the dissociation curves generated by the equipment. Negative controls were also prepared in order to confirm the absence of any contamination. The ratio between the relative amounts of the target gene and the endogenous control gene in the RT-PCR reactions was determined based on the  $2^{-\Delta\Delta C_t}$  method<sup>18</sup> with modifications. The normalized expression level was calculated as  $L=2^{-\Delta C_t}$  and  $\Delta C_t = C_{T, target} - C_{T, reference}$  for each sample. A polyubiquitin gene (SCCST2001G02.g) and a GAPDH gene (SCQGAM2027G09.g) was used as an endogenous reference in the RT-PCR reactions after verification that its mRNA levels were similar in the populations and individuals tissues (not shown).

TABLE XII

Oligonucleotide sequences used in real-time PCR reactions. Primers were designed using the Primer Express 2.0 Software (Applied Biosystems) and BLAST searches were conducted to ensure the specificity of the selected primers. The polyubiquitin gene (SCCST2001G02.g) or the GAPDH gene (SCQGAM2027G09.g) were used as the endogenous reference in the RT-PCR reactions.

SAS	Category	Subcategory	Oligonucleotide sequences	
SCEQRT1024E12.g	Hormone biosynthesis	Salicylic Acid	CTTCCAGGGCACTCCCATT (SEQ ID No. 381)	GAGAACTGCGCGAACATGAG (SEQ ID No. 396)
SCRFLR1012F12.g	Others	Caffeic acid 3-O-methyltransferase	CGGGTTCAAGGCCACCTA (SEQ ID No. 382)	AGGTGTGCGTATTTACTTGATGAACT (SEQ ID No. 397)
SCEQRT1028C03.g	Pathogenicity	R-genes transduction - PR protein	GAAATCGAGCCTCTCCTTCGT (SEQ ID No. 383)	GCAGCATCAGGCAGTTC AAC (SEQ ID No. 398)
SCAGLR1043E04.g	Stress	Cytochrome P450 - CYP74A	TGAAGCGGACGAATTTGAGTAG (SEQ ID No. 384)	AGCTCGCCATAGAGACTTGGAT (SEQ ID No. 399)
SCEQRT1026H08.g	Stress	Cytochrome P450 - CYP75	GAACACCAGGTCTCTGGTAGTTGT (SEQ ID No. 385)	AGCAACCGCCCTCCAAA (SEQ ID No. 400)
SCACCL6008H06.g	Stress	Low temperature induced (LTI)	AATCCCATCCATCCAAGCTAAG (SEQ ID No. 386)	CGGCGGCCGATCCT (SEQ ID No. 401)
SCCCRZ1002E08.g	Stress	Putative aquaporin (TIP)	AGGCATTGGAAACAACCATGA (SEQ ID No. 387)	GCTTTCAGATGCCGATTCAAG (SEQ ID No. 402)
SCJLRT1016G06.g	Stress	Ribonuclease	TACTACACGCTGAGCCAGATCAA (SEQ ID No. 388)	CACTCCACGTAGGGCTCGAA (SEQ ID No. 403)
SCCCLR2003E10.g	Transcription	NAM - NAC	CATCTTCTCCACTCGTTCTTCTT (SEQ ID No. 389)	AGGGATCGCTCAGCTGGAT (SEQ ID No. 404)
SCCST2001G02.g	Ubiquitination	Polyubiquitin	CCGGTCTTTAAACCAACTCAGT (SEQ ID No. 390)	CCCTCTGGTGTACCTCCATTG (SEQ ID No. 405)
SCEQLB2019B08.g	Protein Kinase	CIPK-8	TCCGCATATACGAGGTGATG (SEQ ID No. 391)	AAAGAGCTGCCACCAGTAG (SEQ ID No. 406)
SCSGHR1070F12.g	Protein Kinase	CIPK-29	GGAAATCTCGACGATGAAGTTGA (SEQ ID No. 392)	TTGTTTACTTCCCATCACCTCGTA (SEQ ID No. 407)
SCCCL5001D11.g	Protein Kinase	CIPK-1	GGACCTCTGGTGCAACGTAGTT (SEQ ID No. 393)	CGCTATCTCAGCAAATCAAGGA (SEQ ID No. 408)
SCQGAM2027G09.g	GAPDH*	COMT	CACGGCCACTGGAAGCA (SEQ ID No. 394)	TCCTCAGGGTCTCTGATGCC (SEQ ID No. 409)
SCRFLR1012F12.g	Others		CGGGTTCAAGGCCACCTA (SEQ ID No. 395)	AGGTGTGCGTATTTACTTGATGAACT (SEQ ID No. 410)

\*The GAPDH primer sequences were retrieved from Iskandar et al., (2004).

## Northern Blot

Electrophoresis of total RNA samples (10 µg) can be carried out on 1.5% formaldehyde-containing agarose gels by standard procedures (Sambrook et al., 1989) and transferred to nylon filter (Hybond-N<sup>+</sup>, Amersham Biosciences). For this work, for each gene tested, the longest EST clone of each SUCEST SAS was selected as probe for RNA blot hybridization. Inserts were labeled with the Read-To-Go kit (Amersham Biosciences) according to the protocol recommended by the manufacturer. Hybridized filters were exposed to imaging plates for 24 h and the digitized images of RNA blot hybridization signals were detected with the FLA3000-G screen system (Fuji Photo Film, Japan) and quantified with the Image Gauge software v. 3.12 (Fuji Photo Film, Japan).

## Methods for Detecting Protein Expression Levels

To measure or evaluate the proteins encoded by polynucleotide SEQ ID NO. 1-203 or SEQ ID Nos. 229 to 373 a number of well established techniques can be used (Cell Biology—A Laboratory Handbook, Academic Press). Antibodies can be raised against a purified recombinant protein expressed, for example in bacterial strains, after the coding sequence is cloned in a bacterial expression vector such as the pET vector series from Invitrogen. Plant tissue samples can be collected, protein extracts can be prepared and separated by gel electrophoresis or applied in multi-well plates, and protein levels can be measured by western blot or ELISA (enzyme-linked immunosorbent assay) using the antibody and a secondary antibody conjugated to horseradish peroxidase, alkaline phosphatase or fluoresceine isothiocyanate. Alternatively, whole proteome analysis can analyze the proteins encoded by SEQ ID NO. 1-203 or SEQ ID Nos. 229 to 373 in large scale with the aid of mass-spectrometry technology (MALDI-TOF and related techniques) after protein separation. Techniques that can analyze (for a review see Newton et al., 2004) and evaluate protein levels in large scale have also been described (Kirpatrick et al., 2005).

## Transgenic Plants of this Invention

Transgenic plants can be generated using SEQ ID NO. 1 to 203 or SEQ ID Nos. 229 to 373. Alternatively, transgenic plants can be generated by a variety of techniques using additional genes and characterized using SEQ ID NO.1 to 203 or SEQ ID Nos. 229 to 373. Techniques for transforming a wide variety of higher plant species are well known and described (Weising et al., 1988). A DNA sequence coding for the desired polypeptide, for example a cDNA sequence encoding a full length protein, will preferably be combined with transcriptional and translational initiation regulatory sequences which will direct the transcription of the sequence from the gene in the intended tissues of the transformed plant. For example, for overexpression, a plant promoter fragment may be employed which will direct expression of the gene in all tissues of a regenerated plant.

Such promoters are referred to herein as “constitutive” promoters and are active under most environmental conditions and states of development or cell differentiation. Examples of constitutive promoters include the cauliflower mosaic virus (CaMV) 35S transcription initiation region, the 1'- or 2'-promoter derived from T-DNA of *Agrobacterium tumefaciens*, the maize ubi1 promoter derived from the ubiquitin gene, and other transcription initiation regions from various plant genes known to those of skill in the art.

Genes can be introduced into plants in expression cassettes that will increase the expression of the genes or silence the genes by anti-sense expression or RNA interference and lead to a higher sucrose content plant according to the methods described in this work.

## Methods for Generating Plants with Increased Sugar Content

In certain embodiments, this invention provides methods for generating plants with increased sugar content by either increasing the expression of or interfering with the expression of or decreasing the expression of the polynucleotides of this invention. In some embodiments, the plant is transgenic and generated by expression of a gene expressing or interfering with the expression of a polynucleotide or polypeptide of this invention. Transgenic plants can be generated using SEQ ID NO. 1 to 203 or SEQ ID Nos. 229 to 373. In other embodiments, the plant is one generated by standard breeding techniques or mutagenesis.

## Preparation of Recombinant Vectors for Plant Transformation

SEQ ID NO. 1-203 or SEQ ID Nos 229 to 373 can be used to generate transgenic plants with higher sucrose content. For this, recombinant DNA vectors suitable for transformation of plant cells are prepared. Transgenic plants can be obtained that express a recombinant expression cassette containing a promoter linked to one of polynucleotides 1 to 203 or SEQ ID NO. 229 to 373 that causes an increase in sucrose content in the transgenic plant when compared to control untransformed plants or plants transformed with vector alone.

Depending on whether increased sugar content is correlated with increased or decreased expression of a particular polynucleotide, DNA constructs can be designed to either increase or interfere with/decrease the expression of specific genes.

Gene expression can be increased using recombinant DNA constructs with a polynucleotide of interest in the sense orientation relative to the promoter to achieve gene overexpression.

Gene expression can be decreased using recombinant DNA constructs with a polynucleotide of interest in the antisense orientation relative to the promoter to achieve gene silencing. For example, a fragment of a gene of interest can be cloned in the pAHC17 vector (Christensen and Quail, 1996). Transgenic plants obtained through this method include sugarcane transgenic plants T1a, T1f, T2a, T2c and T3d originated from cultivar SP83-2847. Embryogenic calli originated from this cultivar were transformed by biolistic as described below with the COMT-AS/pAHC17 construct containing a 535 bp fragment of SEQ NO. 161 cloned into the BamHI site for the antisense orientation. Plants were co-transformed with pHA9 vector (Wei and Albert, U.S. Pat. No. 6,706,948).

Gene expression can be decreased or interfered with by suppressing transcription of a gene or the accumulation of the mRNA corresponding to that gene thereby preventing translation of the transcript into protein. Posttranscriptional gene suppression is mediated by transcription of integrated recombinant DNA to form double-stranded RNA (dsRNA) having homology to a gene targeted for suppression. This formation of dsRNA most commonly results from transcription of an integrated inverted repeat of the target gene, and is a common feature of gene suppression methods known as anti-sense suppression, co-suppression and RNA interference (RNAi). Transcriptional suppression can be mediated by a transcribed dsRNA having homology to a promoter DNA sequence to effect what is called promoter trans suppression.

More particularly, posttranscriptional gene suppression by inserting a recombinant DNA construct with anti-sense oriented DNA to regulate gene expression in plant cells is disclosed in U.S. Pat. No. 5,107,065 (Shewmaker et al.) and U.S. Pat. No. 5,759,829 (Shewmaker et al.). Transgenic plants transformed using such anti-sense oriented DNA constructs for gene suppression can comprise integrated DNA arranged

as an inverted repeats that result from insertion of the DNA construct into plants by *Agrobacterium*-mediated transformation, as disclosed by Redenbaugh et al., in "Safety Assessment of Genetically Engineered Flavr Savr™ Tomato, CRC Press, Inc. (1992). Inverted repeat insertions can comprise a part or all of the T-DNA construct, e.g., an inverted repeat of a complete transcription unit or an inverted repeat of transcription terminator sequence. Screening for inserted DNA comprising inverted repeat elements can improve the efficiency of identifying transformation events effective for gene silencing whether the transformation construct is a simple anti-sense DNA construct which must be inserted in multiple copies or a complex inverted repeat DNA construct (e.g., an RNAi construct) which can be inserted as a single copy.

Posttranscriptional gene suppression by inserting a recombinant DNA construct with sense-oriented DNA to regulate gene expression in plants is disclosed in U.S. Pat. No. 5,283,184 (Jorgensen et al.) and U.S. Pat. No. 5,231,020 (Jorgensen et al.). Inserted T-DNA providing gene suppression in plants transformed with such sense constructs by *Agrobacterium* is organized predominately in inverted repeat structures, as disclosed by Jorgensen et al., *Mol. Gen. Genet.*, 207:471-477 (1987). See also Stam et al. *The Plant Journal*, 12(1), 63-82 (1997) who used segregation studies to support Jorgensen's finding that gene silencing is mediated by multimeric transgene T-DNA loci in which the T-DNAs are arranged in inverted repeats. Screening for inserted DNA comprising inverted repeat elements can improve the gene silencing efficiency when transforming with simple sense-orientated DNA constructs. Gene silencing efficiency can also be improved by screening for single insertion events when transforming with an RNAi construct containing inverted repeat elements

As disclosed by Redenbaugh et al., gene suppression can be achieved by inserting into a plant genome recombinant DNA that transcribes dsRNA. Such a DNA insert can be transcribed to an RNA element having the 3' region as a double stranded RNA. RNAi constructs are also disclosed in EP 0426195 A1 (Goldbach et al., 1991) where recombinant DNA constructs for transcription into hairpin dsRNA for providing transgenic plants with resistance to tobacco spotted wilt virus. Double-stranded RNAs were also disclosed in WO 94/01550 (Agrawal et al.) where anti-sense RNA was stabilized with a self-complementary 3' segment. Agrawal et al., referred to U.S. Pat. No. 5,107,065 for using such self-stabilized anti-sense RNAs for regulating gene expression in plant cells; see International Publication No. 94/01550. Other double-stranded hairpin-forming elements in transcribed RNA are disclosed in International Publication No. 98/05770 (Werner et al.) where the anti-sense RNA is stabilized by hairpin forming repeats of poly(CG) nucleotides. See also U.S. Patent Application Publication No. 2003/0175965 A1 (Lowe et al.) which discloses gene suppression using and RNAi construct comprising a gene, coding sequence preceded by inverted repeats of 5'UTR. See also U.S. Patent Application Publication No. 2002/0048814 A1 (Oeller) where RNAi constructs are transcribed to sense or anti-sense RNA which is stabilized by a poly(T)-poly(A) tail. See also U.S. Patent Application Publication No. 2003/0018993 A1 (Gutterson et al.) where sense or anti-sense RNA is stabilized by an inverted repeat of a of the 3' untranslated region of the NOS gene. See also U.S. Patent Application Publication No. 2003/0036197 A1 (Glassman et al.) where RNA having homology to a target is stabilized by two complementary RNA regions.

Gene silencing can also be effected by transcribing RNA from both a sense and an anti-sense oriented DNA, e.g., as disclosed by Shewmaker et al., in U.S. Pat. No. 5,107,065

where in Example 1a binary vector was prepared with both sense and anti-sense aroA genes. See also U.S. Pat. No. 6,326,193 where gene targeted DNA is operably linked to opposing promoters.

Gene silencing can also be affected by transcribing from contiguous sense and anti-sense DNA. In this regard see Sijen et al. *The Plant Cell*, Vol. 8, 2277-2294 (1996) discloses the use of constructs carrying inverted repeats of a cowpea mosaic virus gene in transgenic plants to mediate virus resistance. Such constructs for posttranscriptional gene suppression in plants by double-stranded RNA are also disclosed in International Publication No. WO 99/53050 (Waterhouse et al.), International Publication No. WO 99/49029 (Graham et al.), U.S. patent application Ser. No. 10/465,800 (Fillatti), U.S. Pat. No. 6,506,559 (Fire et al.). See also U.S. application Ser. No. 10/393,347 (Shewmaker et al.) that discloses constructs and methods for simultaneously expressing one or more recombinant genes while simultaneously suppressing one or more native genes in a transgenic plant. See also U.S. Pat. No. 6,448,473 (Mitsky et al.) that discloses multi-gene suppression vectors for use in plants. All of the above-described patents, applications and international publications disclosing materials and methods for posttranscriptional gene suppression in plants are incorporated herein by reference.

Transcriptional suppression such as promoter trans suppression can be affected by a expressing a DNA construct comprising a promoter operably linked to inverted repeats of promoter DNA for a target gene. Constructs useful for such gene suppression mediated by promoter trans suppression are disclosed by Mette et al. *The EMBO Journal*, Vol. 18, No. 1, pp. 241-148, 1999 and by Mette et al. *The EMBO Journal*, Vol. 19, No. 19, pp. 5194-5201-148, 2000, both of which are incorporated herein by reference.

Suppression can also be achieved by insertion mutations created by transposable elements may also prevent gene function. For example, in many dicot plants, transformation with the T-DNA of *Agrobacterium* may be readily achieved and large numbers of transformants can be rapidly obtained. Also, some species have lines with active transposable elements that can efficiently be used for the generation of large numbers of insertion mutations, while some other species lack such options. Mutant plants produced by *Agrobacterium* or transposon mutagenesis and having altered expression of a polypeptide of interest can be identified using the polynucleotides of the present invention. For example, a large population of mutated plants may be screened with polynucleotides encoding the polypeptide of interest to detect mutated plants having an insertion in the gene encoding the polypeptide of interest.

In some embodiments, DNA constructs can be the full length cDNA cloned in the expression vector pAHC17 (Christensen and Quail, 1996) in a sense orientation for over-expression or in an antisense orientation for gene silencing. Full length cDNAs can be amplified by PCR using specific primers and cloned into the BamHI site of the vector pAHC17 that will drive the constitutive expression of genes under the control of the maize ubi1 promoter (Christensen et al. 1992) and has been shown to be effective in the transformation and expression of genes in sugarcane. Other examples of constitutive promoters include the cauliflower mosaic virus (CaMV) 35S transcription initiation region, the 1'- or 2'-promoter derived from T-DNA of *Agrobacterium tumefaciens*, the ubi4 and ubi9 promoters isolated from sugarcane polyubiquitin genes (Wei et al. 1999; Wei et al. 2003), the rice actin Act1 promoter (McElroy et al. 1990, McElroy et al. 1991), the pEmu promoter (Last et al. 1990, Chamberlain et

al. 1994) and other transcription initiation regions from various plant genes known to those of skill.

Alternatively, expression vectors can be constructed using sugarcane promoters. Constitutive promoters and regulatory elements can be isolated from genes that are expressed constitutively or at least expressed in most if not all tissues of the plant. Such genes include, for example, the 153 genes described by Papini-Terzi et al., 2005 as ubiquitously expressed in sugarcane tissues.

Alternatively, the sugarcane promoter may direct expression of a nucleic acid of the invention in a specific tissue, organ or cell type (i.e. tissue-specific promoters) such as the 217 genes described by Papini-Terzi et al., 2005 as being preferentially expressed in roots, internodes, leaves, lateral buds or inflorescences of sugarcane. For antisense constructs full length cDNA or cDNA fragments of around (but not restricted to) 500 bp in length can be used. If a full length coding sequence is not available it can be cloned for instance by RACE (Frohman et al., 1988). For RNA interference (RNAi) the vector pKannibal and pHannibal (Wesley et al., 2001) can be used. Primers can be designed that specifically amplify around (but not restricted to) 200 to 400 bp of the target gene. Two PCR fragments will be produced with oligonucleotide primers planned to allow for cloning in the sense and antisense orientation and for a self complementary hairpin to be formed when expressed in the plant cell. The PCR fragments will contain restriction sites at their end that will allow for their introduction on the sites of XhoI/EcoRI/KpnI (sense) and ClaI/HindIII/XbaI/BamHI (antisense) in the pKannibal or pHannibal vector for instance. If proper polypeptide expression is desired, a polyadenylation region at the 3'-end of the coding region should be included. The polyadenylation region can be derived from the natural gene, from a variety of other plant genes, or from T-DNA. Transgenic plants obtained through this method include sugarcane transgenic plants 12SNF8b, 12SNF7c, 8SNF2a and 8SNF2b originated from cultivar SP94-3116. Embryogenic calli originated from this cultivar were transformed by biolistic as described below using a 331 bp fragment of SEQ NO. 106 cloned into the XhoI/EcoRI sites for the sense and HindIII/XbaI sites for the antisense orientations.

The expression vector comprising the sequences (e.g., promoters or coding regions) from genes of the invention will typically comprise a marker gene that confers a selectable phenotype on plant cells. For example, the marker may encode biocide resistance, particularly antibiotic resistance, such as resistance to kanamycin, G418, bleomycin, hygromycin, or herbicide resistance, such as resistance to chlorosulfuron or Basta.

Vector DNA preparation for transformation of sugarcane by bombardment uses a variation of the co-precipitation method of Klein et al. (1988a,b).

#### Plant Transformation and Propagation

Sugarcane transformation is as a well established technique (see Falco et al., 2000 for an example). Transgenic plants are recovered from embryogenic callus transformed using a modified biolistic protocol. Callus initiation and maintenance from sugarcane varieties is done on medium containing Murashige & Skoog salts, 3 mg/L 2,4-D, 5% coconut water, 150 mg/L citric acid, 250 mg/L Clavulin Beecham, and 7 g/L agar (CI-3 medium). Young leaf rolls of 6-12 month old plants are cultured for a month in the dark, at 27° C. and selected embryogenic callus is subcultured on the same medium every 3 weeks. Embryogenic calli can be bombarded with plasmid expression vectors containing one of the sequences 1 to 203 or SEQ ID Nos. 229 to 373. After bom-

bardment, calli are kept in the dark for 1 week on C<sub>1-3</sub> medium, without selection, for recovery. Transgenic calli are selected on the same medium containing 35 mg/L of geneticin for 6 weeks. Resistant calli are placed on the same medium without 2,4-D to regenerate plants. After approximately 3 months, plants are transferred to soil and kept in the greenhouse, where they are tested for vector genomic insertion and expression. Non-transgenic control plants are obtained by regeneration from the same callus type going through the same tissue culture steps without bombardment and selection. Generally, embryogenic calli of the Brazilian sugarcane (*Saccharum officinarum* L.) genotype SP80-180, SP80-185, SP94-3116, CTC1, SP83-2847, SP80-1842, SP91-1049. (but not restricted to) can be co-transformed with the plasmid pHA9 containing genes coding for neomycin phosphotransferase (neo) and a plasmid containing the gene of interest (one of SEQ ID NO. 1 to 203 or SEQ ID NO. 229 to 373 in plasmid pAHC17, pKannibal or pHannibal, for instance), by particle bombardment. Transformed plants will be initially selected on culture medium containing Geneticin, and resistance can be confirmed by localized application of a kanamycin solution to leaves of hardened plants at the nursery if desired. Southern analysis can confirm stable integration of both target and neo genes. Alternatively, plants can be submitted to analysis by PCR to confirm the insertion of the expression constructs in the sugarcane genome. Oligonucleotide primers specific to the expression constructs will be used in amplification reactions using genomic DNA extracted from a sample of the transformed plants. Confirmed plants are then allowed to regenerate to 4 cm high plants and then allowed to grow in green houses when the expression levels of the target gene will be verified by real-time PCR. Also, brix measures will be taken to verify sucrose content. Alternatively, genes can be introduced into sugarcane or other plants using techniques such as electroporation or microinjection of plant cell protoplasts.

Plant regeneration from cultured protoplasts is described in Evans et al., *Protoplasts Isolation and Culture, Handbook of Plant Cell Culture*, pp. 124-176, MacMillan Publishing Company, New York, 1983; and Binding, *Regeneration of Plants, Plant Protoplasts*, pp. 21-73, CRC Press, Boca Raton, 1985. Regeneration can also be obtained from plant callus, explants, organs, or parts thereof. Such regeneration techniques are described generally in Klee et al. *Ann. Rev. of Plant Phys.* 38:467-486 (1987). The introduction of DNA constructs using polyethylene glycol precipitation is described in Paszkowski et al. *EMBO. J.* 3:2717-2722 (1984). Electroporation techniques are described in Fromm et al. *Proc. Natl. Acad. Sci. USA* 82:5824 (1985). Additional details of ballistic transformation techniques are described in Klein et al. *Nature* 327:70-73 (1987). Transgenes can also be transferred to plant cells without the need of a vector DNA backbone, using linear transgene constructs (Fu et al., 2000, Loc et al., 2002).

Alternatively, the DNA constructs may be combined with suitable T-DNA flanking regions and introduced into a conventional *Agrobacterium tumefaciens* host vector. The virulence functions of the *Agrobacterium tumefaciens* host will direct the insertion of the construct and adjacent marker into the plant cell DNA when the cell is infected by the bacteria. *Agrobacterium tumefaciens*-mediated transformation techniques, including disarming and use of binary vectors, are well described in the scientific literature. See, for example Horsch et al. *Science* 233:496-498 (1984), and Fraley et al. *Proc. Natl. Acad. Sci. USA* 80:4803 (1983) and *Gene Transfer to Plants*, Potrykus, ed. (Springer-Verlag, Berlin 1995).

Alternatively, the DNA constructs may be combined with suitable T-DNA vectors, such as pCAMB1A vectors pC1105.1, pC1105.1r or modified versions of those, and introduced into alternative bacterial host vectors such as *Sinorhizobium meliloti*, *Rhizobium* sp. or *Mesorhizobium loti* (also known as Transbacter strains) as described (Broothaerts et al., 2005).

Sugar measurements can be done in six month old plants. Total and reductive sugars can be determined in leaves from control and transgenic plants collected, immediately frozen in liquid nitrogen and lyophilized. Twenty mg of the lyophilized material can be ground using a ball mill and subjected to extraction of soluble sugars with 1 mL of ethanol 80% for 20 minutes. This process is repeated six times (exhaustive extraction). The alcoholic extract is dried in a roto-evaporator and resuspended in 1 mL of milli-Q water. The levels of total and reductive sugars (Glc+Fru) are quantified by a colorimetric method using the phenol-sulphuric (Dubois et al., 1956) and the Somogy-Nelson (Somogy, 1945) procedures and glucose 1 mg/mL as standard. The sucrose content is estimated by subtracting the amount of reductive sugars from the amount of total sugars. Transgenic plants can also be characterized for brix content and considered to be improved for sucrose content if a brix difference of 3 degrees is observed. Differential expression of SEQ ID NO. 1-203 can be used in sucrose yield field-trials to select for the best events (transformants) or in a pre-test prior to field trials. Tissue samples can be obtained as described above.

#### Identification of Plants with Mutated Alleles

Variations in SEQ ID NO. 1-203 or SEQ ID NO. 229 to 373 locus can be generated by non-transgenic methods, can be found in progenies generated by traditional breeding, or can be found in naturally occurring genotypes.

The *Saccharum officinarum* and *Saccharum spontaneum* genotypes, the progenies of crosses between them and the crosses of commercial varieties described in this work can be screened for mutations in SEQ ID NO. 1-203 or SEQ ID NO. 229 to 373. Alternatively, sugarcane seeds can be mutagenized to increase the allelic variation for SEQ ID Nos. 1-203 or SEQ ID NO. 229 to 373. For example sugarcane can be chemically mutagenized with EMS (Ethylmethane sulfonate—EMS).

Mutations or natural variations in SEQ ID NO. 1-203 or SEQ ID NO. 229 to 373 can be identified by Tilling as was described for wheat (Slade et al., 2005). With Tilling a library of DNA samples from mutagenized or naturally occurring variants, or variants generated by traditional breeding can be identified. Mutations will be detected by amplifying regions of SEQ ID NO. 1-203 by Polymerase Chain Reaction (PCR). The PCR products will be heated and re-annealed to allow heteroduplexes to form between mutated and wild-type DNA. Heteroduplexes are identified through cleavage of mismatched sites by endonucleases such as Cell and cleaved products identified by gel-electrophoresis. The nature of the mutation will be identified by sequencing the PCR fragment.

#### Use as Molecular Markers: Generation of Molecular Markers Based on Restriction Fragment Length Polymorphisms

SEQ ID NO. 1-203 can be used to detect differences between individuals at the DNA sequence level. Genomic DNAs from any number of individuals can be digested with a restriction enzyme, preferably a six-base pair cutting enzyme, electrophoresed and can be probed with any of the SEQ ID NO. 1-203 DNA clones, labelled with radioisotopes. Polymorphisms in the hybridization patterns can be due to differences in the gene sequences between the individuals. The term “restriction fragment length polymorphism” has been

coined to describe this variation. For example, genomic DNA can be extracted from sugarcane individuals from any of the populations cited in this invention, digested with one restriction enzyme, such as (but not limited to) EcoRI, Hind III, DraI, BamHI. Restriction fragments can be separated on 0.8% (w/v) agarose gel, using TAE (40 mM Tris acetate, pH 8.0; 2 mM EDTA) as running buffer at 20 mA for 22 h and transferred to nylon membranes.

SEQ ID NO. 1-203 can be used to generated probes using <sup>32</sup>PdCTP using any commercial kit, such as the Rediprime II kit from Amersham (USA). Hybridizations can be performed in a hybridization solution containing for example 0.5 M Na<sub>2</sub>PO<sub>4</sub> pH 7.2, 1% BSA, 7% SDS, 100 µg/mL sheared herring sperm DNA), at 65° C. for up to 24 h. The membranes can be washed once during 20 min at 65° C. solution I (2×SSC; 5% SDS), then 20 min at 65° C. in solution II (1×SSC; 5% SDS 5%) and 20 min at 65° C. in solution III (0.5×SSC; 5% SDS).

Restriction fragment length polymorphism can be visualized by exposition to an imaging plate for 3-10 days at -80° C. and detected using a phosphorimager, such as the FLA3000 (Fuji, Japan). Those skilled in the art will easily use standard procedures to marker notation, analysis of each molecular marker segregation in the population individuals, and finally the linkage analysis to predict the usefulness of each of the SEQ ID Nos. 1-203 as molecular markers. An example of these steps has been described by Garcia et al., (2006).

Although the foregoing invention has been described in some detail by way of illustration and examples for purposes of clarity and understanding, it will be obvious that certain modifications and alternative embodiments of the invention are contemplated which do not depart from the spirit and scope of the invention as defined by the foregoing teachings and appended claims.

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- All references cited herein are incorporated by reference.

## SEQUENCE LISTING

The patent contains a lengthy "Sequence Listing" section. A copy of the "Sequence Listing" is available in electronic form from the USPTO web site (<http://seqdata.uspto.gov/?pageRequest=docDetail&DocID=US07732664B2>). An electronic copy of the "Sequence Listing" will also be available from the USPTO upon request and payment of the fee set forth in 37 CFR 1.19(b)(3).

What we claim:

1. A transgenic plant, wherein said plant comprises a vector expressing a recombinant polynucleotide, wherein the polynucleotide comprises the nucleotide sequence of SEQ ID NO: 106 or the complement thereof.

2. Seed, seed-cane, or setts of the transgenic plant of claim 1, wherein the seed, seed-cane, or setts comprise the vector.

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