

# **Transcriptome analysis highlights key differentially expressed genes involved in cellulose and lignin biosynthesis of sugarcane genotypes varying in fiber content**

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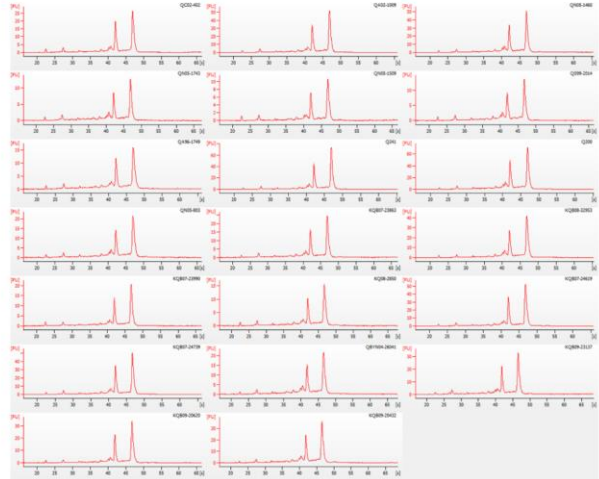
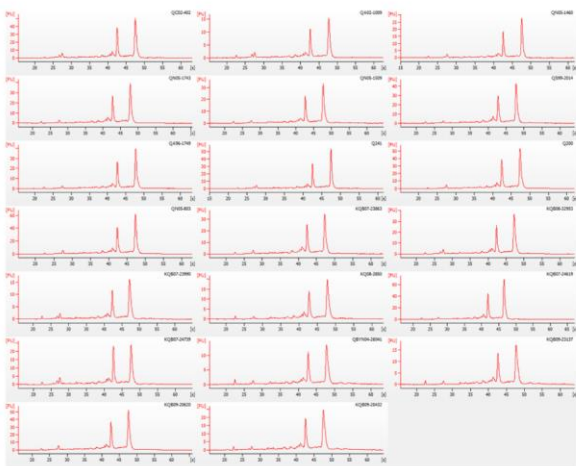
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# ADDITIONAL METHODS

**Bioanalyser profiles of 40 internodal RNA samples used in this study.** Left panel: top internodal samples, right panel: bottom internodal samples (adapted from<sup>1</sup>).

TOP INTERNODAL SAMPLES						
Sample	CODE	RIN	RNA Con. (ng/μl)	rRNA Ratio [25e / 18s]	Total (μg) in 50 μl	
1	QC02-402	T1	8.0	1776.3	1.8	88.8
2	QA02-1009	T2	8.1	505.4	1.9	25.3
3	QN05-1460	T3	8.2	1788.0	2.0	39.4
4	QN05-1743	T4	8.0	678.5	1.9	33.9
5	QN05-1509	T5	8.1	575.2	1.8	28.8
6	QS09-2014	T6	8.0	1011.2	1.9	50.6
7	QA06-1740	T7	6.1	637.3	1.9	31.9
8	Q241	T8	8.2	1404.2	1.9	70.2
9	Q200	T9	8.0	1792.9	1.8	89.6
10	QN05-803	T10	8.0	2063.2	1.9	103.2
11	KQB07-23863	T11	7.8	1257.0	1.7	62.9
12	KQB08-32953	T12	8.2	1290.7	2.1	64.5
13	KQB07-23990	T13	8.1	618.6	2.0	30.9
14	KQB8-2850	T14	8.1	399.3	1.9	20.0
15	KQB07-24619	T15	8.5	963.7	1.9	48.2
16	KQB07-24739	T16	7.5	529.4	1.5	26.5
17	QBY104-26041	T17	7.8	301.4	1.7	15.1
18	KQB09-23137	T18	7.8	392.1	1.8	19.6
19	KQB09-20620	T19	8.0	1008.9	1.9	50.4
20	KQB09-20432	T20	8.0	581.3	1.8	28.1

BOTTOM INTERNODAL SAMPLES						
Sample	CODE	RIN	RNA Con. (ng/μl)	rRNA Ratio [25e / 18s]	Total (μg) in 50 μl	
1	QC02-402	B1	8.3	478.1	1.8	24.0
2	QA02-1009	B2	8.5	833.6	1.8	41.7
3	QN05-1460	B3	8.3	864.4	1.9	43.2
4	QN05-1743	B4	7.7	380.0	1.9	19.0
5	QN05-1509	B5	8.3	282.6	2.3	13.1
6	QS09-2014	B6	7.8	413.8	1.9	20.7
7	QA06-1740	B7	7.8	534.3	1.9	26.7
8	Q241	B8	8.6	1050.4	2.0	52.5
9	Q200	B9	8.2	1283.8	1.7	64.2
10	QN05-803	B10	8.1	684.6	2.2	34.2
11	KQB07-23863	B11	8.1	632.5	2.2	31.6
12	KQB08-32953	B12	8.2	770.7	2.0	38.5
13	KQB07-23990	B13	8.1	269.1	2.1	18.5
14	KQB8-2850	B14	8.0	442.8	2.0	22.1
15	KQB07-24619	B15	8.5	856.3	1.9	42.8
16	KQB07-24739	B16	8.4	865.5	1.9	43.3
17	QBY104-26041	B17	7.9	714.0	2.2	35.7
18	KQB09-23137	B18	8.2	902.7	2.0	45.1
19	KQB09-20620	B19	8.6	539.2	2.1	27.0
20	KQB09-20432	B20	8.1	1021.9	2.0	51.1



**Summary statistics of *Saccharum officinarum* gene index (SoGI) database**

([ftp://occamsdfciharvardedu/pub/bio/tgi/data/Saccharum\\_officinarum](ftp://occamsdfciharvardedu/pub/bio/tgi/data/Saccharum_officinarum))

<b>Statistics</b>	<b>SoGI</b>
Number of sequences ( $\geq 0$ bp)	121,342
Number of sequences ( $\geq 1000$ bp)	13,279
Number of sequences ( $\geq 5000$ bp)	0
Total length ( $\geq 0$ bp)	88,397,709
Total length ( $\geq 1000$ bp)	16,570,859
Total sequences	121,342
Largest sequence	4,854
Total length	88,397,709
GC (%)	52
N50	729
N75	641
L50	46,463
L75	78,851
# N's	125,596
# N's per 100 kbp	142

## qPCR primers and amplicon length from SoGI and SUGIT database

### 1. SoGI - TC113051 UniRef100\_O82056 Cluster: Cinnamyl alcohol dehydrogenase; n=1; *Saccharum officinarum*

N5_CAD_Forward	GTTCTTGCCGTTCTGTTCTGG
N5_CAD_R	CCACATCCTGGCGTACTTCG

CGGCACGAGAGGCGCACTAGTTGTCGCGCTGCTTGCTTTCTTTCCGAAGGCTAAGCCACCCGGCCGGCTCGCTCGTCT  
CCATCGCCCGCTCCCTCCGGGCTCCGCCCGCTCCGTGAGTCGTCTTCCCCGCGCCGCCCGCCGTAGCAGTCGATCGC  
GGCCGGTCCCAACTCCAGGAAGAGAATGGGGAGCCTGGCGTCCGAGAGGAAGGTGGTCGGGTGGGCCCGCCAGGG  
ACGCCACCGGACACCTCGCCCCCTACACCTACACCCTCAGGAGCACAGGCCCTGAAGATGTGGTGGTGAAGGTGCTCT  
ACTGTGGGATCTGCCACACAGACATCCACCAGGCCAAGAACCACCTCGGGGCTTCAAAGTACCCCATGGTCCCTGGGC  
ACGAGGTGGTCGGTGAGGTGGTGGAGTCCGGGCCGAGGTGACCAAGTACGGCGTCGGCGACGTGGTAGGCGTCG  
GGGTGATCGTCGGGTGCTGCCGCGAGTGCAACCCTGCAAGGCCAACGTTGAGCAGTACTGCAACAAGAAGATCTGG  
TCCTACAACGATGTCTACACTGACGGCCGGCCACGCAGGGCGGCTTCGCTCCACCATGGTCGTCGACCAGAAGTTT  
GTGATGAAGATCCCGCGGGTCTGGCGCCGAGCAAGCGGCGCCGCTGCTGTGCGCGGGCGTGACGGTGTACAGCC  
CGCTGAAAGCCTTTGGGCTGACGACCCCGGGCTCCGTGGCGGATCCTGGGCCTCGGCGGCGTGGGCCACATGGGC  
GTGAAGGTGGCCAAGGCCATGGGCCACCACGTGACGGTGTACAGCTCGTCGTCCAAGAAGCGCGCGGAGGCGATGG  
ACCACCTGGGCGCGGACGCGTACCTGGTGAGCTCGGACGCGGCGGCCATGGCGGCGGCCCCCGACTCGCTGGACTA  
CATCATCGACACGGTGCCCGTGACCACCCGCTGGAGCCCTACCTGGCGCTGCTGAAGCTGGACGGCAAGCACGTTCT  
GCTGGGCGTCATCGGCGAGCCCTCAGCTTCGTGTCCCAATGGTGTGCTGGGGCGGAAGGCCATCACGGGGAGCT  
TCATCGGCAGCATCGACGAGACCGCCGAGGTGCTCCAGTTCTGCGTCGACAAGGGGCTCACCTCCAGATCGAGGTG  
GTCAAGATGGGGTACGTGAACGAGGCGCTGGATCGGCTGGAGCGCAACGACGTCCGCTACCGCTTCGTCGTCGACGT  
CGCCGGCAGCAACGTCGAGGAGGTGGCGGCCGATGCGCCGAGCAACTGACGTGCGGCTGCGTCGTCGAACCGTGA  
GGGGAGGTTGTGCCCCGCTGCAACGTTGTTGTCGTCGAGGCTGCGTGCCTTCTGCTTCTTTAGTAGTTGTGGGC  
TTGTCGCG**GTTCTTGCCGTTCTGTTCTGG**GCTTTCAGATGAGCTGATGGATGGTCTGTTAAATGTCATCAGACTAAATA  
ACTATGTTAGTACTGTAGTACGTTTAACT**CGAAGTACGCCAGGATGTGG**TGTGGTGTACCAGCAATCTGGATTT  
GCCAAGTGTGAAGTGTCTCTTTTTCTTC

**Amplicon = 124 bp**

### SUGIT Cinnamyl alcohol dehydrogenase

ACCCTACTACCCAAAAAGACAGGCGCACTAATTGTCGCGCTGCTTGCTTTCTTTCCGAAGGCTAAGCCACCCGGCCG  
GCTCGCTCGTCTCCATCGCCCGCTCCCTCCGGGCTCCGCCCGCTCCGTGCGTCTTCCCCGCGCCGCCCGCCGTA  
GCAGTCGATCGCGGCCGGTCCCAACTCCAGGAAGAGAATGGGGAGCCTGGCGTCCGAGAGGAAGGTGGTCGGGT  
GGGCCCGCCAGGGACGCCACCGGACACCTCGCCCCCTACACCTACACCCTCAGGAGCACAGGCCCTGAAGATGTGGT  
GTGAAGGTGCTCTACTGTGGGATCTGCCACACAGACATCCACCAGGCCAAGAACCACCTCGGGGCTTCAAAGTACCC  
ATGGTCCCTGGGCACGAGGTGGTCGGTGAGGTGGTGGAGGTCGGGCCGAGGTGACCAAGTACGGCGTCGGCGAC  
GTGGTAGGCGTCGGGGTGTGTCGGGTGCTGCCGCGAGTGCAACCCTGCAAGGCCAACGTTGAGCAGTACTGCA  
ACAAGAAGATCTGGTCTACAACGATGTCTACACTGACGGCCGGCCACGCAGGGCGGCTTCGCTCCACCATGGTCG  
TCGACCAGAAGTTTGTGATGAAGATCCCGGCGGGTCTGGCGCCGAGCAAGCGGCGCCGCTGCTGTGCGCGGGCGT  
GACGGTGTACAGCCGCTGAAAGCCTTTGGGCTGACGACCCCGGCCCTCCGTGGCGGATCCTGGGCCTCGGCGGCG  
TGGGCCACATGGGCGTGAAGGTGGCCAAGGCCATGGGCCACCACGTGACGGTGTACAGCTCGTCGTCCAAGAAGCG  
CGCGGAGGCGATGGACCACCTGGGCGCGGACGCGTACCTGGTGAGCTCGGACGCGGCGGCCATGGCGGCGGCCG

CGACTCGCTGGACTACATCATCGACACGGTGCCCGTGCACCACCCGCTGGAGCCCTACCTGGCGCTGCTGAAGCTGGA  
 CGGCAAGCACGTTCTGCTGGGCGTCATCGGCGAGCCCCTCAGCTTCGTGTCCCAATGGTGATGCTGGGGCGGAAGG  
 CCATCACGGGGAGCTTCATCGGCAGCATCGACGAGACCGCCGAGGTGCTCCAGTTCTGCGTCGACAAGGGGCTCACC  
 TCCAGATCGAGGTGGTCAAGATGGGGTACGTGAACGAGGCGCTGGATCGGCTGGAGCGCAACGACGTCCGCTACC  
 GCTTCGTGTCGACGTCGCCGCGAGCAACGTCGAGGAGGTGGCGGCCGATGCGCCGAGCAACTGACGTGCGCGCTG  
 CGTCGTGAACCGTGAGGGGAGGTTGTGCCCCGCGTGCAACGTTCTGTTCTGTCGAGGCTGCGTGCCTTCTGTTCC  
 TTTAGTAGTTGTGGCTTGTGCGC**GTTCTTGCCGTTCTGTTCTGG**GCTTTCAGATGAGCTGATGGATGGTCTGTTAAAT  
**GTCATCAGACTGAATAACTATGTGTAGTACTGTAGTACGTTTTATACTCGAAGTACGCCAGGATGTGG**TGTGGTGTCA  
 CCAGCAATCTGGATTTTTTTTTATAGAACATACTGCATTATAGTTAAGG

**Amplicon = 124 bp**

**2. SoGI - CA165461 homologue to UniRef100\_O82055 Cluster: Cinnamoyl-CoA reductase; n=1; Saccharum officinarum**

N7_CCR_Forward	GTAGTAGTGCCGAAGCAGAAAG
N7_CCR_Reverse	CCTAGCTACCAACTCGGTCATC

CGATCGCAAGAGAGAATCCTGCCAAA**CCTAGCTACCAACTCGGTCATC**ACATCACTCGACCGCACACAAAGGGGA  
**ACCTAAAACTAACTCTCTTCAACTTCTCTGCTTTCTGCTTCTGCTTCTTATCATCATCGCCGCGCCAAGATGACCGTCGTC**  
 GCTTTCGTGACGAACTAGCTAAAGAGGAACAGCTGGTCGGTCTCTTATCATCATCGCCGCGCCAAGATGACCGTCGTC  
 GACGCCGTGTCCACTGATGCCGCCGCGCCCTGCAGCCGCCGCGGCACCGGTGCAGCAGCCCGGGAACGGGCAGA  
 CCGTGTGCGTACCGGCGCGGCCGGGTACATCGCCTCGTGGCTGGTCAAGCTGCTGCTCGAGAAGGGATACTACTGTC  
 AAGGGAACCGTCAGGAACCCAGATGACCCGAAGAACGCGCACCTCAAGGCGCTGGACGGCGCCCGGAGCGGCTGA  
 TCCTCTGCAACGCCGACCTCCTGCACTACGACGCCATCTGGCGCCCCGTGCAGGCGTGCCATGGCGTTCTTCCACACCG  
 CCCCCCGTACCGACGACCCCCGATCAAAATGGTTGAACCCTGCCGGTGCAGCGGGGCTACGACATAACTCTATCCA  
 CCCGCGAGGCGGAAGCCCGGAACCCGTGCAGCGAGGTGGTGTTCACCTCCTCCC

**Amplicon = 106 bp**

**SUGIT Cinnamoyl-CoA reductase**

TTTTTTTTTTTTTTTTTTTTTTTTCTAGAAATAAATGAACATTAGCCATTTTTATTCACTCATCACTATAGTCCACAAGAACGA  
 ACATGACGTTACAACAAGCTTAGGGTAGGGTATCAGCCACCGAACAAACTAGTTTGTTTACACAGCTGGGGCAG  
 GGCTGTATGAACATTGCTTTTCTGTTTCATGTGTACGTGGCATCTCTCTCTCACGCACGGATGGCGATTCTCCCTGCTGC  
 AGCTCGGCGGGCGGGGGCCGCTCCTTGTGTCGCGCCTCCGTGCTGCTCTCCGAGCACCAGGAGGTGGCCCTTC  
 TCCTGAAGTTTCTCACCGTGTGTCGACAGCGACTGGCTCACCGGCCGGAACCTCAGCCCCAGGTCCCGGAGCTTCTGG  
 TTCGAGAAGTTGTACGGCTGCTTCCGCGGGTTCACCTCGTCCGAGCACCTGGTGGGGACGGGGTACTCGGGGAAGAG  
 CTTGGCGAGGATGCGGACGACGTCTCGCGGTGGAGGACGCGCTCGGCGCAGAGGTATCGGCCGACGCGCGCGG  
 GCTCTCGAAGACGCGGAGGTGCGCGTCCGCGACGTGCGGACGTCCACGTACGCCTGCACGGCGTTGGCGAAGGTG  
 CGCGCGGAGCCGTCCAGTACTTGGCCACGTGCGCGATGCTGGCGTTCACCGTCCGCTGCAGCAGTGGGCCACAC  
 CAGCACCAGGTTACCACCACCAGTCCACGCCGCGCTGCCGGCCGCGTCCACGCCGCTGCTCCGCCACCGCCTT  
 GCCGTAGCAGTACCAGTTCCTGGTTTTCTGCAAGAACTCGAGTTCGCTCCAGCACGACTCGTCGACCACGACGTCCGG  
 CCCGCGGCTGGGGTCCATGGTACCAGCGCCGATGGAGGACGTGAACACCACCCGCCGACCGTCCCGGCTCCGCCG  
 CCGGTTGATCACGTAATCCGTGCCGCGCACCGCCGGTCCACATTTGCTCCGGGTCGTGCGGTGACCGGGGAGGCG  
 GTGTGGAAGACGCCATGGCAGCCCTGCACGGCGCGGCAGATGGCGTGTAGTCAAGGAGGTCGGCCTTGCAGAGGA

TCAGCCGCTCGGGCGGCGCCGTCCAGCGCCTTGAGGTGCGGTTCTTCGGGTCATCTGGGTTCTGACGGTTCCCTTGA  
CAGTGTATCCCTTCTCGAGCAGCAGCTTGACGAGCCACGAGGCGATGTACCCGGCCGCGCCGGTGACACACACAGTC  
TGCCCGTTCCCGCGGGCTGCACAGGCGCCGCGGCGCAGCTGGGGCGCCGCGGCATCAGTGGACACGGCGTCGA  
CGATGGTCATCTTGGCGCGGCGATGATGATAAGAGACCGACCAGCTGTTCTCTTTAGCTAGTTTCGTACGAAAGCTA  
GCTAGCTCGCGGTGTGTCTCGTAGTA**GTAGTAGTGCCGAAGCAGAAAG**GCAGAGGAAGTTGAAGAGAGTTAGTTTT  
**TAGGTTAATTTCCCTTTGTGTGTGCGGTGCGAGTGATGAGATGACCGAGTTGGTAGCTAGG**TTTGGTAGGATTCTTTC  
TTGCGGTGATAATCCTCCCATGTACCTCATGCGTTGATACCACTTACGCCGCTATATCAGAAGTGAAGAGAGTGAG  
AGAGTAGAATCAGAGTCATATCACACAGGACGCAGATGTAGAGGAGAGTGTGTGTACGTCACCACCAGTATGCTATA  
GACAGGTATTACCGACAGATCAAACATTCGTCGAGCGAGGCTACCAATAGCTGATCGATAGAGGTAGATAACATCTC  
GTGCCTCACAAGAACGCGCCACGAGAGTCCCACAGGAGAATAGGCTTCTGTGAGTATGAGGACGCATAAAACGGATA  
TCAGATGTCACACCCGCGTCCGCCGGAGTAACGAGAAGCACTAGTCGATTGAGACTATTGAGGACGAACGAGACA  
CACCGCGAGCTAGCTAGCTTTCGTGACGAACTAGCTAAAGAGGAACAGCTGGTGGTCTCTTATCATCATCGCCGCGC  
CAAGATGACCATCGTCGACGCCGTGCCACTGATGCCGCCGCGCCCCAGCTGCCGCCGCGGCGCCGGTGCAGCCCG  
CGGGGAACGGGCAGACTGTGTGTGTACCCGGCGCGGCCGGGTACATCGCCTCGTGGCTCGTCAAGCTGCTGCTCGAG  
AAGGGATACACTGTCAAGGGAACCGTCAGGAACCCAGATGACCCGAAGAACGCGCACCTCAAGGCGCTGGACGGCG  
CCGCCGAGCGGCTGATCCTCTGCAAGGCCGACCTCCTGGACTACGACGCCATCTGCCGCGCCGTGCAGGGCTGCCAT  
GGCGTCTCCACACCGCCTCCCGGTACCCGACGACCCGGAGCAAATGGTGGAGCCGGCGGTGCGCGGCACGGAGT  
ACGTGATCAACGCGGCGGCGGAGGCCGGCACGGTGGCGGGTGGTGTTCACGTCCTCCATCGGCGCGGTGACCAT  
GGACCCAGCCGCGGGCCCGACGTCGTGGTGCAGAGTCGTGCTGGAGCGACCTCGAGTTCTGCAAGAAAACAGG  
AACTGGTACTGCTACGGCAAGGCGGTGGCGGAGCAGGCGGCGTGGGACGCGCCCCGGCAGCGCGGCGTGGACCTG  
GTGGTGGTGAACCCGGTGTGGTGGTGGGCCCGTGTGTCAGCCGACGGTGAACGCCAGCATCGCGCACGTGGCCA  
AGTACCTGGACGGCTCCGCGCGCACCTTCGCCAACGCCGTGCAGGCGTACGTGGACGTCCGCGACGTGCGCCGACGCG  
CACCTCCGCGTCTTCGAGAGCCCGCGCGTCCGGCCGATACCTCTGCGCCGAGCGCGTCTCCACCGCGAGGACGTC  
GTCCGCATCCTCGCCAAGCTCTTCCCGAGTACCCCGTCCCACCAGGTGCTCCGACGAGGTGAATCCGCGGAAGCAG  
CCGTACAAGTTCTCGAACCAGAAGCTCCGGGACCTGGGGCTGGAGTTCCGGCCGGTGAAGCCAGTCGCTGTACGACAC  
GGTGAAGAACCTTCAGGAGAAGGGCCACCTGCCGGTGTCTGGAGAGCAGACGACGGAGGCCGACGACAAGGAGGC  
GGCCCCCGCCCGCCGAGCTGCAGCAGGGAGGAATCGCCATCCGTGCGTGAGAGAGAGATGCCACGTACACATGA  
ACAGAAAAGCAATGTTACATACAGCCCTGCCCCAGCTGTGTAACAAACTAGTGTGTTGTTGGTGGCTGATACCCCTACC  
CTAAGCTTGTGTAACGTCATGTTCTGTGGACTATAGTGATGAGTGAATAAAAATGGCTAATGTTTCATTATTTT  
C

**Amplicon = 111 bp**

**3. SoGI - TC134289 homologue to UniRef100\_Q9LLI3 Cluster: Cellulose synthase-7; n=1; Zea mays**

N8\_CesA\_Forward: CACCATCGGTAAGCTGGTG

N8\_CesA\_Reverse: AAGCCCAAATGCGAGACAG

CCGCTGACACCCTAATTCATATGGCCACAATGCTTTTGCCGTTCTTTCTTTAGCTGTCCAACGCTGCAACGATATGGTT  
TCTTGGCCCTTTCATGTCCATCATCTTGACGAGCGTGTGGAGCTGCGGTGGAGTGGCATCGGGATTGAGGACTGGT  
GGCGCAACGAGCAGTTCTGGGTCAATGGAGGTGTGTCGCGCACCTGTTCCGCGTGTTCAGGGTATTCTCAAGATGA  
TTGCCGGGCTGGACACCAACTTCACGGTCACGGCGAAGGCCACGGACGACACCGAGTTCGGGGAGCTGTACGTGTTT  
AAGTGGACAACGGTGTGATCCCGCCACCAGCATCCTGGTGTCAACCTGGTGGGCGTGGTGGCTGGCTTCTCGGC  
CGCGCTCAACAGCGGCTACGAGTCTGGGGCCCGCTTTTGCAAGGTGTTCTTCGCAATGTGGGTGATCATGCACCT  
GTACCCGTTCTCAAGGGTCTCATGGGCCGCGCAGAACCACGACGCCACCATCGTGGTGTCTGGTCCGTCCTCCTCGCC

TCCGCTTCTCCCTCCTCTGGGTCAAGATCGACCCATTCGTCCGAGGAACCGAGACCGTCAACACCAACAACACTGCAACA  
CAGTCATCTGCTGATT **CACCATCGGTAAGCTGGT**TCGGGCC

#### SUGIT Cellulose synthase

CGAGAGAAAAGACCAGGCTACCAACACCACAAGAAGGCAGGGGCTATGAATGCTCTGGTCCGAGTGTCCGCTGTTCT  
GACAAATGCACCTTACATTCTTAATCTTGACTGTGATCACTATGTTAAACAACAGCAAAGCCGTTTCGTGAAGCAATGTGC  
TTCATGATGGACCCTACTGTTGGCAGAGATGTTTGCTATGTGCAATCCCCAGAGGTTTCGATGGCATTGATCGCAGT  
GATCGATATGCCAATAGGAACGTTGTGTTCTTTGATGTTAATATGAAAGGACTTGATGGCATCCAAGGCCAGTTTAT  
GTGGGAACCTGGTTGTTGTTTCTATAGGCAGGCACCTTATGGTTATGGACCTCCATCTCTGCCTGCACTTCCAAAGTCTT  
CAATTTGTTTCGTGGTGTGCTGCTGTCCCAAGAAAAAGTTGAAAGAAGTGAGAGGGAAATCAACAGAGACTCC  
CGGCGAGAAGACCTTGAGTCTGCCATTTTAAATCTTCGTGAAATTGACAACTACGATGAGTATGAGAGGTCCATGCTG  
ATCTCTCAGATGAGCTTCGAGAAATCTTTGGGCTGTCCTCAGTCTTTATTGAATCAACTCTTATGGAGAATGGGGGCG  
TCCCTGAATCTGCAAACCCATCTACCCTAATTAAGAAGCCATTGATGTCATTAGCTGCGGATATGAAGAGAAAAGTGA  
ATGGGGAAAAGAGATTGGCTGGATCTATGGTTACAGAGGATATTCTGACTGGGTTAAGATGCAGTGCCGTG  
GCTGGAGATCCATCTACTGCATGCCGGTGAGACCTGCATTCAAGGGATCAGCCCCTATCAATCTTCCGATCGTCTTCA  
CCAGTTTCTCCGGTGGGCTCTTGGTTCTGTGAGATCTTCTCAGTCGGCACTGCCCGCTGTGGTACGGTTACGGTGG  
CGGCCGTCTGAAATGGCTCCAGAGGCTGTCCTACATCAACACCATCGTGTACCCGTTCACTTCTTCTCCTCTCGTTGCCT  
ACTGTTGCCTGCCTGCCATTTGCCTGCTCACAGGAAAGTTCATTATTCCTACGCTGTCCAACGCTGCAACGATATGGTT  
CTTGGCCTCTTCATGTCCATCATCTTGACGAGCGTGTGGAGCTGCGGTGGAGTGGCATCGGGATTGAGGACTGGTG  
GCGCAACGAGCAGTTCTGGGTCATTGGAGGTGTGTCCGCGCACCTGTTCCCGTGTTCAGGGTATTCTCAAGATGAT  
TGCCGGGCTGGACACCAACTTACGGTCACGGCGAAGGCCACGGACGACACCGATTTCCGGGAGCTGTACGTGTTCA  
AGTGGACGACGGTGTGATCCCGCCACCAGCATCCTGGTGTCAACCTGGTGGGCGTGGTGGCTGGCTTCTCGGCC  
GCGCTCAACAGCGGCTACGAGTCTGGGGCCGCTCTTGGCAAGGTGTTCTTCGCAATGTGGGTGATCATGCACCTG  
TACCCGTTCTCAAGGGTCTCATGGGCCGCCAGAACCACGACGCCACCATCGTGGTGTCTGGTCCGTCCTCCTCGCCT  
CCGCTTCTCCCTCCTCTGGGTCAAGATCGACCCATTCGTCCGAGGAACCGAGACCGTCAACACCAACAACACTGCAACA  
CAGTCATCTGCTGATT **CACCATCGGTAAGCTGGT**TCGGGCCGCGGCCGCGCTGTTTCTGGTGTTCAGCCTGATGCA  
GGCGGGTTACCTCTGTCTGTCTCGATTTGGGCTTTGCCCCAGGATCTGGGAGAGGTGGTATAGGTTAGCTCTGTTT  
TACATCCAAGTGTGATTGCTGTCTGTATTATGAAAAGTTTTGGTGTCTAAAGTGTCAAACCTCGCCTCAATTGTGAG  
AATGCACTGTTTAAAGTGTGTAAATCATAGGAACGTGGGAAAAAGGAAGTGAAGATACTTGCCTACCAAAAGGCA  
AGATCATTTACAT

#### 4. SoGI -TC130010 homologue to UniRef100\_A0EJ90 Cluster: Brittle stalk-2; n=1; Zea mays

N3_BC1I5_Forward	CCTTCCACCTCTCATCTGTGC
N3_BC1I5_Reverse	TATGCCCTGCCTACTCTGC

CCCACGCTCCGCAAGGACGCCAGGACCTTACCTTACGCCAGGGCTGGGCTTCCCGCGCAAGATCTACTTCAACGG  
CGACGAGTGAAGATGCCACCGCCGACTCCTACCCCTACCTGCCAACGCCGCGCCCGCTGCCTCGCAGCTGAT  
CGTGTCCGCCGCCCTCAGCGTTCCTACTGGCGCTGCTCCTGGTAGCATGACCATGACCGACCAGGGCCTCCATTTCT  
TCCTTTGTTTC **CCTTCCACCTCTCATCTGTGC**CCGTCTTCAATCCCATTTCCATGATCCCATCCCGTGGGAGGGGGCAG  
**CAGAGTAGGCAGGGCATA**TTGGTTGCCAAGACTTCAACACTTGGGTTTTGCTTCGCTTAATTGCTTCGTGAGAGGGAA  
ACTGTCATGCACTGTATGTAATGTAACCTCCAGTTGCAGGTCGTGATCCCAAGACAATCAGGCTGGCAGACTTTT  
GGGTCTGCAACTACTATTAGAGAGCCTGCCTGAGCGAGAGAGAGGGGGAAAAAAGCAGACATATAGAGCATAACAG  
GTTTTCTGTTATTTGTTCTGTAAACATAATGCAGATACTCTGTTCAAATGATATACGAATCAACTTACTGGACATTAGC  
ATGCT

Amplicon = 87 bp

SUGIT BC1I5

GGGTCGGAGCTTGTGCTACCAGCTAGCAGCAGCCGTGGTGGTGTACTTACGTTCTTGCAGAGGCCGCCGGCCGGCT  
CGCTCATCGATCGATGGGGCTCCGCGACTCCTCCGCGTCTGGCTCTGGCCCTCGCCCTCGCCTACTGCTCCGTCGCA  
GGTTCAATTCGTGTCACGCCATTCCATCATCTGAAAACCAACCTTGTTTCGTTCTATCTAATGTCGATCAACGGACGAT  
GCTCACCTCTTGTGTCGATCGTCGTTCTCCTCCCTGGCTGGCTGACGGCTTGTCTCCTTGCAGTGGTGGCTACGATCC  
CCTGGACCCGAGGGGCAACATCACCATCAAGTGGGACGTGATCTCGTGGACGCCGACGGGTACGTGGCGATGGTG  
ACGATGAGCAACTACCAGATGTACCGGCACATCATGGCGCCCGGGTGGACGGTGGGGTGGTCTGGGCCAAGAAGG  
AGGTGATCTGGTCCATCGTGGGCGCGCAGGCCACGGAGCAGGGCGACTGCTCCAAGTTCAAGGCCGGCATCCCGCA  
CTGCTGCAAGCGGACGCCCGCCGTGGTGGACCTGCTCCCGGGCGTGCCTACAACCAGCAGATCGCCAACCTGCTGCA  
AGGCCGGCGTGGTGTGCGCGTACGGGCAGGACCAGGCGGGGTCCGTCTCCGCGTTCAGGTCTCCGTCGGCCCTCGCC  
GGCACCACCAACAAGACGGTGAAGCTGCCAAGAACTTACCATCATGGGGCCCGGGCCAGGGTACACCTGCGGGCC  
GGCGACGATCGTGGTCCACCGTGTACTGGACGCTGACCACCGCGCGGACGCAGGGCGCTCATGACGTGGACC  
GTCACCTGCACCTATTCGACGAGCTGGCGTCCAAGTACCCGCTCTGCTGCGTCTCCTTCTCCTCTTCTACAACGACAC  
CATCGTGCCGTGCGCACGGTGCAGCGTGCAGGCTGCGGCCACGGCGGCCACGCCGGGCGGGAGGGTGCATCGAGGG  
GGACTCCAAGCGCGCGTGTGCCCCGGGTGAACACGCCGCGCAAGGACGGGCAGGGCGTCTGTCAGTGCACGCCG  
CACATGTGCCCCATCCGGGTGCACTGGCACGTCAAGCTCAACTACAAGGACTACTGGCGGCCAAGATCGCCATCACC  
AACTTCAACTACCGGATGAACTACACGCAGTGGACGCTCGTGGCGCAGCACCCCAACCTGGACAACGTACCCGAGGT  
CTTCAGCTTCCAGTACAAGCCGCTGCTACCATACGGCAGCATCAATGACACTGGCATGTTCTACGGGGCTCAAGTTCTAC  
AACGACCTGCTCATGGAGGCCGGCCCGTTCGGCAACGTGCAGTCCGAGGTGCTCATGCGCAAGGACGCCAGGACCTT  
CACCTCAGCCAGGGCTGGGCCTTCCCGCGCAAGATCTACTTCAACGGCGACGAGTGCAAGATGCCACCGCCGGACTC  
CTACCCCTACCTGCCAACGCCGCGCCCGCCGTCGCTCGCAGTGCATCGTGTCCGCCGCCGCTTCTACTGGCGCTG  
CTCCTGGTAGCATGACCATGACCGACCAGGGCCTCCATTTCTCCTTTGTTTCCTTCCACCTCTCATCTGTGCGCGTCTT  
CAATCCCATTCCCATGATCCCATCCCGTGGGCAGGGGGCAGCAGAGTAGGCAGGGCATAATTGGTTGCCAAGACTTCA  
AACTTGGGTTTTGCTTCGCTTAATTGCTTCGTGAGAGGGAAACTGTCATGCACTGTATGTAATGTAACCTCCAGTTG  
CAGGTCGTGAGATCCCAAGACAATCAGGCTGGCAGACTTTTTGGGTCTGCAACTACTATTAGAGAGCCTGCCTGAGCG  
AGAGAGAGGGGGAAAAAAGCAGACATATAGAGCATAACAGGTTTTCTGTTATTTGTTCTGTAAACATAATGCAGA  
TACTCTGTTCAAATGATATACGAATC

**Amplicon = 87 bp**

## References

- 1 Hoang, N. V. *Analysis of genes controlling biomass traits in the genome of sugarcane (Saccharum spp. hybrids)* PhD Degree thesis, The University of Queensland, (2017).