## *New Phytologist* Supporting Information

Article title: **Mapping Quantitative Trait Loci for straw digestibility in *Brachypodium distachyon* implicates a gene encoding a glycosyl transferase family 43 protein involved in xylan biosynthesis.**

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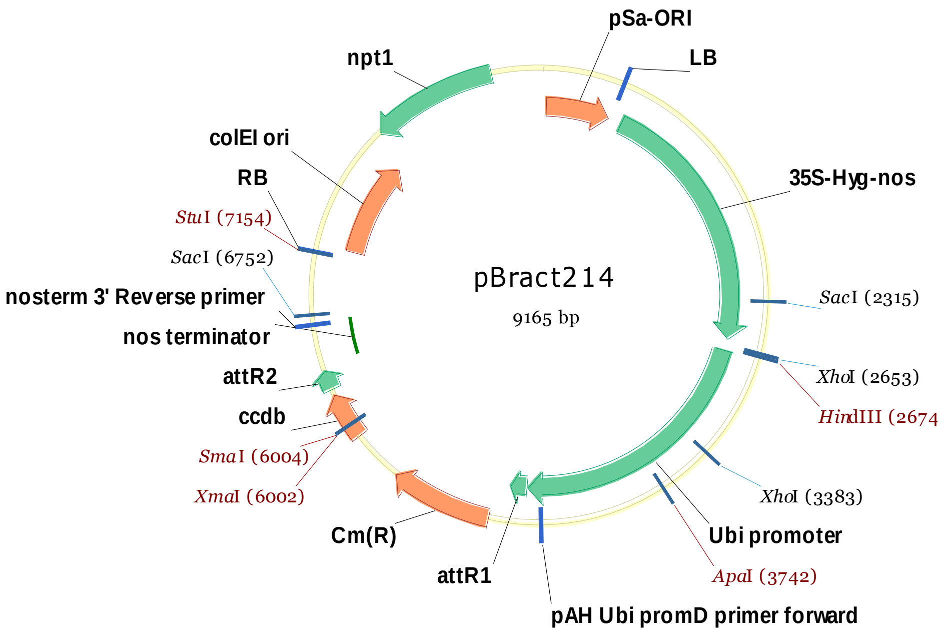
Article acceptance date: 5 February 2018

The following Supporting Information is available for this article:

**Fig. S1** Sequence and map of the silencing construct.



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121   CTAATCAGGG TACGTGAAAT CGCTAATCGG AGTACGTGAA ATCGCTAATA AGGTCACGTG

181   AAATCGCTAA TCAAAAAGGC ACGTGAGAAC GCTAATAGCC CTTTCAGATC AACAGCTTGC

241   AAACACCCCT CGCTCCGGCA AGTAGTTACA GCAAGTAGTA TGTTCAATTA GCTTTTCAAT

301   TATGAATATA TATATCAATT ATTGGTCGCC CTTGGCTTGT GGACAATGCG CTACGCGCAC

361   CGGCTCCGCC CGTGGACAAC CGCAAGCGGT TGCCCACCGT CGAGCGCCAG CGCCTTTGCC
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 421  CACAACCCGG CGGCCGGCCG CAACAGATCG TTTTATAAAT TTTTTTTTTT GAAAAAGAAA

                                                                      LB

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 481  AAGCCCGAAA GGCGGCAACC TCTCGGGCTT CTGGATTTCC GATCCCCGGA ATTAGATCTT

                LB

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 541  GGCAGGATAT ATTGTGGTGT AACGTATCAC AAGTTTGTAC AAAAAAGCAG GCTCCGCGGC

 601  CGCCCCCTTC ACCTAGACTC GACGCGTCCT AGAGATCCGT CAACATGGTG GAGCACGACA

 661  CTCTCGTCTA CTCCAAGAAT ATCAAAGATA CAGTCTCAGA AGACCAAAGG GCTATTGAGA

 721  CTTTTCAACA AAGGGTAATA TCGGGAAACC TCCTCGGATT CCATTGCCCA GCTATCTGTC

 781  ACTTCATCAA AAGGACAGTA GAAAAGGAAG GTGGCACCTA CAAATGCCAT CATTGCGATA

 841  AAGGAAAGGC TATCGTTCAA GATGCCTCTG CCGACAGTGG TCCCAAAGAT GGACCCCCAC

 901  CCACGAGGAG CATCGTGGAA AAAGAAGACG TTCCAACCAC GTCTTCAAAG CAAGTGGATT

 961  GATGTGATAT CTCCACTGAC GTAAGGGATG ACGCACAATC CCACTATCCT TCGCAAGACC

1021  CTTCCTCTAT ATAAGGAAGT TCATTTCATT TGGAGAGGAC GACCCCGATA TGAAAAAGCC

1081  TGAACTCACC GCGACGTCTG TCGAGAAGTT TCTGATCGAA AAGTTCGACA GCGTCTCCGA

1141  CCTGATGCAG CTCTCGGAGG GCGAAGAATC TCGTGCTTTC AGCTTCGATG TAGGAGGGCG

1201  TGGATATGTC CTGCGGGTAA ATAGCTGCGC CGATGGTTTC TACAAAGATC GTTATGTTTA

1261  TCGGCACTTT GCATCGGCCG CGCTCCCGAT TCCGGAAGTG CTTGACATTG GGGAATTCAG

1321  CGAGAGCCTG ACCTATTGCA TCTCCCGCCG TGCACAGGGT GTCACGTTGC AAGACCTGCC

1381  TGAAACCGAA CTGCCCGCTG TTCTGCAGGT AAATTTCTAG TTTTTCTCCT TCATTTTCTT

1441  GGTTAGGACC CTTTTCTCTT TTTATTTTTT TGAGCTTTGA TCTTTCTTTA AACTGATCTA

1501  TTTTTTAATT GATTGGTTAT GGTGTAAATA TTACATAGCT TTAACTGATA ATCTGATTAC

1561  TTTATTTCGT GTGTCTATGA TGATGATGAT AACTGCAGCC GGTCGCGGAG GCCATGGATG

1621  CGATCGCTGC GGCCGATCTT AGCCAGACGA GCGGGTTCGG CCCATTCGGA CCGCAAGGAA

1681  TCGGTCAATA CACTACATGG CGTGATTTCA TATGCGCGAT TGCTGATCCC CATGTGTATC

1741  ACTGGCAAAC TGTGATGGAC GACACCGTCA GTGCGTCCGT CGCGCAGGCT CTCGATGAGC

1801  TGATGCTTTG GGCCGAGGAC TGCCCCGAAG TCCGGCACCT CGTGCACGCG GATTTCGGCT

1861  CCAACAATGT CCTGACGGAC AATGGCCGCA TAACAGCGGT CATTGACTGG AGCGAGGCGA

1921  TGTTCGGGGA TTCCCAATAC GAGGTCGCCA ACATCTTCTT CTGGAGGCCG TGGTTGGCTT

1981  GTATGGAGCA GCAGACGCGC TACTTCGAGC GGAGGCATCC GGAGCTTGCA GGATCGCCGC

2041  GGCTCCGGGC GTATATGCTC CGCATTGGTC TTGACCAACT CTATCAGAGC TTGGTTGACG
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2101  GCAATTTCGA TGATGCAGCT TGGGCGCAGG GTCGATGCGA CGCAATCGTC CGATCCGGAG
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2221  GTGTAGAAGT ACTCGCCGAT AGTGGAAACC GACGCCCCAG CACTCGTCCG AGGGCAAAGG
                                      SacI
                                     ~~~~~~~
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2341  TGGCAATAAA GTTTCTTAAG ATTGAATCCT GTTGCCGGTC TTGCGATGAT TATCATATAA
2401  TTTCTGTTGA ATTACGTTAA GCATGTAATA ATTAACATGT AATGCATGAC GTTATTTATG
2461  AGATGGGTTT TTATGATTAG AGTCCCGCAA TTATACATTT AATACGCGAT AGAAAACAAA
2521  ATATAGCGCG CAAACTAGGA TAAATTATCG CGCGCGGTGT CATCTATGTT ACTAGATCGG
2581  GAATTCATCG ATGATATCAG ATCAAGGGTG GGCGCGCCGA ACCAGCTTTC TTGTACAAAG
                   XhoI                  HindIII
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2701  GACCCGGTCG TGCCCCTCTC TAGAGATAAT GAGCATTGCA TGTCTAAGTT ATAAAAAATT
2761  ACCACATATT TTTTTTGTCA CACTTGTTTG AAGTGCAGTT TATCTATCTT TATACATATA
2821  TTTAAACTTT ACTCTACGAA TAATATAATC TATAGTACTA CAATAATATC AGTGTTTTAG
2881  AGAATCATAT AAATGAACAG TTAGACATGG TCTAAAGGAC AATTGAGTAT TTTGACAACA
2941  GGACTCTACA GTTTTATCTT TTTAGTGTGC ATGTGTTCTC CTTTTTTTTT GCAAATAGCT
3001  TCACCTATAT AATACTTCAT CCATTTTATT AGTACATCCA TTTAGGGTTT AGGGTTAATG
3061  GTTTTTATAG ACTAATTTTT TTAGTACATC TATTTTATTC TATTTTAGCC TCTAAATTAA
3121  GAAAACTAAA ACTCTATTTT AGTTTTTTTA TTTAATAATT TAGATATAAA ATAGAATAAA
3181  ATAAAGTGAC TAAAAATTAA ACAAATACCC TTTAAGAAAT TAAAAAAACT AAGGAAACAT
3241  TTTTCTTGTT TCGAGTAGAT AATGCCAGCC TGTTAAACGC CGTCGACGAG TCTAACGGAC
3301  ACCAACCAGC GAACCAGCAG CGTCGCGTCG GGCCAAGCGA AGCAGACGGC ACGGCATCTC
                              XhoI
                             ~~~~~~
3361  TGTCGCTGCC TCTGGACCCC TCTCGAGAGT TCCGCTCCAC CGTTGGACTT GCTCCGCTGT
3421  CGGCATCCAG AAATTGCGTG TCGGACGGCA GACGTGAGCC GGCACGGCAG GCGGCCTCCT
3481  CCTCCTCTCA CGGCACCGGC AGCTACGGGG GATTCCTTTC CCACCGCTCC TTCGCTTTCC
3541  CTTCCTCGCC CGCCGTAATA AATAGACACC CCCTCCACAC CCTCTTTCCC CAACCTCGTG
3601  TTGTTCGGAG CGCACACACA CACAACCAGA TCTCCCCCAA ATCCACCCGT CGGCACCTCC
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3661  GCTTCAAGGT ACGCCGCTCG TCCTCCCCCC CCCCCCCTCT CTACCTTCTC TAGATCGGCG
                        ApaI
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3781  GTTTGTGTTA GATCCGTGCT GCTAGCGTTC GTACACGGAT GCGACCTGTA CGTCAGACAC
3841  GTTCTGATTG CTAACTTGCC AGTGTTTCTC TTTGGGGAAT CCTGGGATGG CTCTAGCCGT
3901  TCCGCAGACG GGATCGATTT CATGATTTTT TTTTGTTTCG TTGCATAGGG TTTGGTTTGC
3961  CCTTTTCCTT TATTTCAATA TATGCCGTGC ACTTGTTTGT CGGGTCATCT TTTCATGCTT
4021  TTTTTTGTCT TGGTTGTGAT GATGTGGTCT GGTTGGGCGG TCGTTCTAGA TCGGAGTAGA
4081  ATTAATTCTG TTTCAAACTA CCTGGTGGAT TTATTAATTT TGGATCTGTA TGTGTGTGCC
4141  ATACATATTC ATAGTTACGA ATTGAAGATG ATGGATGGAA ATATCGATCT AGGATAGGTA
4201  TACATGTTGA TGCGGGTTTT ACTGATGCAT ATACAGAGAT GCTTTTTGTT CGCTTGGTTG
4261  TGATGATGTG GTGTGGTTGG GCGGTCGTTC ATTCGTTCTA GATCGGAGTA GAATACTGTT
4321  TCAAACTACC TGGTGTATTT ATTAATTTTG GAACTGTATG TGTGTGTCAT ACATCTTCAT
4381  AGTTACGAGT TTAAGATGGA TGGAAATATC GATCTAGGAT AGGTATACAT GTTGATGTGG
4441  GTTTTACTGA TGCATATACA TGATGGCATA TGCAGCATCT ATTCATATGC TCTAACCTTG
4501  AGTACCTATC TATTATAATA AACAAGTATG TTTTATAATT ATTTTGATCT TGATATACTT
              pAH Ubi_promD primer forward
              ~~~~~~~~~~~~~~~~~~~~~~~~~
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4681  CCATCACAAG TTTGTACAAA AAAGCTGAAC GAGAAACGTA AAATGATATA AATATCAATA
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5101  CATTCTTGCC CGCCTGATGA ATGCTCATCC GGAATTCCGT ATGGCAATGA AAGACGGTGA
5161  GCTGGTGATA TGGGATAGTG TTCACCCTTG TTACACCGTT TTCCATGAGC AAACTGAAAC
5221  GTTTTCATCG CTCTGGAGTG AATACCACGA CGATTTCCGG CAGTTTCTAC ACATATATTC
5281  GCAAGATGTG GCGTGTTACG GTGAAAACCT GGCCTATTTC CCTAAAGGGT TTATTGAGAA
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5821  CCGAACGCTG GAAAGCGGAA AATCAGGAAG GGATGGCTGA GGTCGCCCGG TTTATTGAAA
5881  TGAACGGCTC TTTTGCTGAC GAGAACAGGG GCTGGTGAAA TGCAGTTTAA GGTTTACACC
5941  TATAAAAGAG AGAGCCGTTA TCGTCTGTTT GTGGATGTAC AGAGTGATAT TATTGACACG
       XmaI
      ~~~~~~
       SmaI
      ~~~~~~
6001  CCCGGGCGAC GGATGGTGAT CCCCCTGGCC AGTGCACGTC TGCTGTCAGA TAAAGTCTCC
6061  CGTGAACTTT ACCCGGTGGT GCATATCGGG GATGAAAGCT GGCGCATGAT GACCACCGAT
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6181  AATGACATCA AAAACGCCAT TAACCTGATG TTCTGGGGAA TATAAATGTC AGGCTCCCTT
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6301  TGTAGTCTGT TTTTTATGCA AAATCTAATT TAATATATTG ATATTTATAT CATTTTACGT
6361  TTCTCGTTCA GCTTTCTTGT ACAAAGTGGT GATGGGGGAT CCACTAGTTC TAGAATTCGA
6421  TTGAGTCAAG CAGGATCGTT CAAACATTTG GCAATAAAGT TTCTTAAGAT TGAATCCTGT
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6601  ATACATTTAA TACGCGATAG AAAACAAAAT ATAGCGCGCA AACTAGGATA AATTATCGCG
                                  nosterm_3' Reverse primer
                                  ~~~~~~~~~~~~~~~~~~~~~~~~
6661  CGCGGTGTCA TCTATGTTAC TAGATCGACC GGCATGCAAG CTGATATCAA TCACTAGTGA
                                   SacI
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6721  ATTCTAGAGC GGCCGCCACC GCGGTGGAGC TCCAGCTTTT GTTCCCTTTA GTGAGGGTTA
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6901  GTGAGCTAAC TCACATTAAT TGCGTTGCGC TCACTGCCCG CTTTCCAGTC GGGAAACCTG
6961  TCGTGCCAGC TGCATTAATG AATCGGCCAA CGCGCGGGGA GAGGCGGTTT GCGTATTGGG
7021  CGCTCTTCCG CTTCCTCGCT CACTGACTCG CTGCGCTCGG TCGTTCGGCT GCGGCGAGCG
7081  GTATCAGCTC ACTCAAAGGC GGTAATACGG TTATCCACAG AATCAGGGGA TAACGCAGGA
                                   RB
                       ~~~~~~~~~~~~~~~~~~~~~~~~~~~~
                  StuI
                 ~~~~~~
7141  AAGAACATGA AGGCCTTGAC AGGATATATT GGCGGGTAAA CTAAGTCGCT GTATGTGTTT
7201  GTTTGAGATC TCATGTGAGC AAAAGGCCAG CAAAAGGCCA GGAACCGTAA AAAGGCCGCG
7261  TTGCTGGCGT TTTTCCATAG GCTCCGCCCC CCTGACGAGC ATCACAAAAA TCGACGCTCA
7321  AGTCAGAGGT GGCGAAACCC GACAGGACTA TAAAGATACC AGGCGTTTCC CCCTGGAAGC
7381  TCCCTCGTGC GCTCTCCTGT TCCGACCCTG CCGCTTACCG GATACCTGTC CGCCTTTCTC
7441  CCTTCGGGAA GCGTGGCGCT TTCTCATAGC TCACGCTGTA GGTATCTCAG TTCGGTGTAG
7501  GTCGTTCGCT CCAAGCTGGG CTGTGTGCAC GAACCCCCCG TTCAGCCCGA CCGCTGCGCC
7561  TTATCCGGTA ACTATCGTCT TGAGTCCAAC CCGGTAAGAC ACGACTTATC GCCACTGGCA
7621  GCAGCCACTG GTAACAGGAT TAGCAGAGCG AGGTATGTAG GCGGTGCTAC AGAGTTCTTG
7681  AAGTGGTGGC CTAACTACGG CTACACTAGA AGAACAGTAT TTGGTATCTG CGCTCTGCTG
7741  AAGCCAGTTA CCTTCGGAAG AAGAGTTGGT AGCTCTTGAT CCGGCAAACA AACCACCGCT
7801  GGTAGCGGTG GTTTTTTTGT TTGCAAGCAG CAGATTACGC GCAGAAAAAA AGGATCTCAA
7861  GAAGATCCTT TGATCTTTTC TACGGGGTCT GACGCTCAGT GGAACGAAAA CTCACGTTAA
7921  GGGATTTTGG TCATGAGATT ATCAAAAAGG ATCTTCACCT AGATCCTTTT AAATTAAAAA
7981  TGAAGTTTTA AATCAATCTA AAGTATATAT GTGTAACATT GGTCTAGTGA TTAGAAAAAC
8041  TCATCGAGCA TCAAATGAAA CTGCAATTTA TTCATATCAG GATTATCAAT ACCATATTTT
8101  TGAAAAAGCC GTTTCTGTAA TGAAGGAGAA AACTCACCGA GGCAGTTCCA TAGGATGGCA
8161  AGATCCTGGT ATCGGTCTGC GATTCCGACT CGTCCAACAT CAATACAACC TATTAATTTC
8221  CCCTCGTCAA AAATAAGGTT ATCAAGTGAG AAATCACCAT GAGTGACGAC TGAATCCGGT
8281  GAGAATGGCA AAAGTTTATG CATTTCTTTC CAGACTTGTT CAACAGGCCA GCCATTACGC
8341  TCGTCATCAA AATCACTCGC ATCAACCAAA CCGTTATTCA TTCGTGATTG CGCCTGAGCG
8401  AGACGAAATA CGCGATCGCT GTTAAAAGGA CAATTACAAA CAGGAATCGA ATGCAACCGG
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8581  CGGATAAAAT GCTTGATGGT CGGAAGAGGC ATAAATTCCG TCAGCCAGTT TAGTCTGACC
8641  ATCTCATCTG TAACAACATT GGCAACGCTA CCTTTGCCAT GTTTCAGAAA CAACTCTGGC
8701  GCATCGGGCT TCCCATACAA TCGGTAGATT GTCGCACCTG ATTGCCCGAC ATTATCGCGA
8761  GCCCATTTAT ACCCATATAA ATCAGCATCC ATGTTGGAAT TTAATCGCGG CCTTGAGCAA
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8881  AGTTTTATTG TTCATGATGA TATATTTTTA TCTTGTGCAA TGTAACATCA GAGATTTTGA
8941  GACACAACGT GGCTTTGTTG AATAAATCGA ACTTTTGCTG AGTTGAAGGA TCAGATCACG
9001  CATCTTCCCG ACAACGCAGA CCGTTCCGTG GCAAAGCAAA AGTTCAAAAT CACCAACTGG
9061  TCCACCTACA ACAAAGCTCT CATCAACCGT GGCTCCCTCA CTTTCTGGCT GGATGATGGG
9121  GCGATTCAGG CGATCCCCAT CCAACAGCCC GCCGTCGAGC GGGCT
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**Fig. S2** Comparison of the Brachypodium parental lines Bd21 and Bd3-1 in terms of (A) germination frequency (B) height, excluding inflorescence (C) total biomass and (D) stem only biomass. The results indicate the mean and +/- SD and Anova indicates that those sharing the same letter are not significantly different.

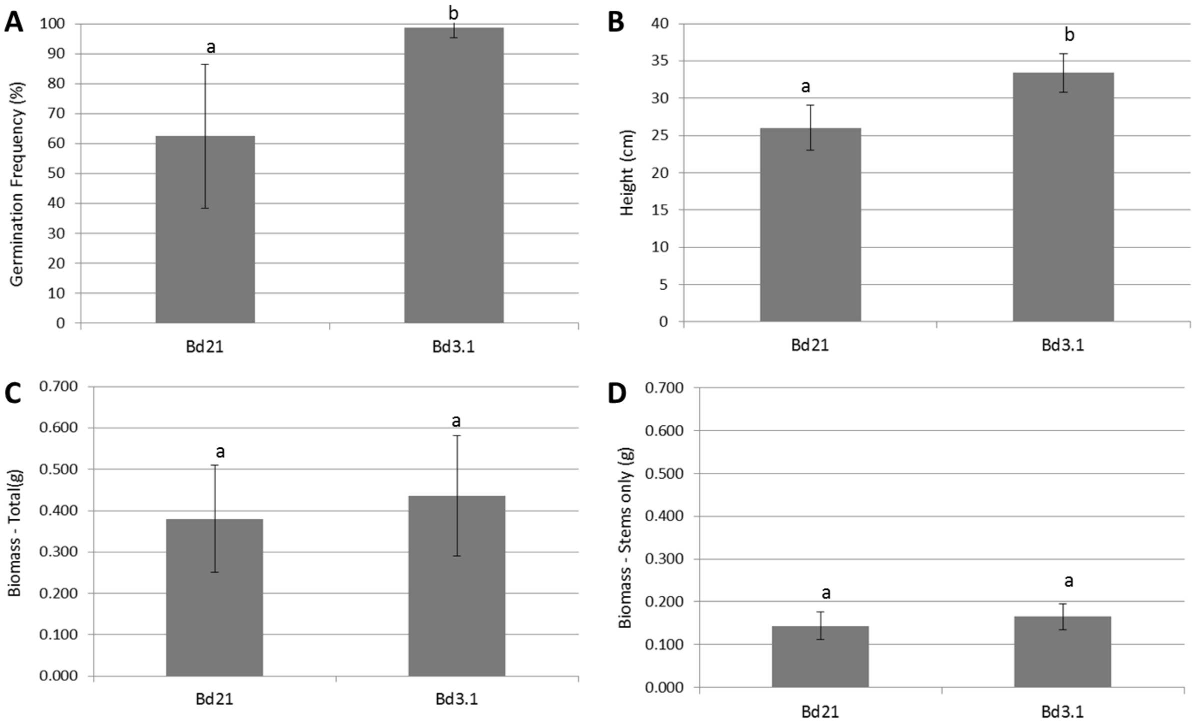


**Fig. S3** Saccharification analysis of Arabidopsis Col.0 and T-DNA line GT43. The results indicate the mean and +/- SD.

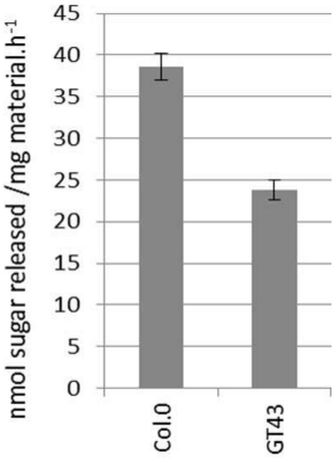


**Table S1** Primers used during construction of the RNAi lines.

| Oligo Name | Sequence 5' to 3' |
|---|---|
| miR-XS24290A-I | agTCTTCAGTATTTACTACGCTGcaggagattcagtttga |
| miR-XS24290A-II | tgCAGCGTAGTAAATACTGAAGActgctgctgctacagcc |
| miR*-XS24290A-III | ctCAGCGAAGTTAATACTGAAGAttcctgctgctaggctg |
| miR*-XS24290A-IV | aaTCTTCAGTATTAACTTCGCTGagagaggcaaaagtgaa |
| miR-XS24290B-I | agTTCAAATTTCCATACATGCGGcaggagattcagtttga |
| miR-XS24290B-II | tgCCGCATGTATGGAAATTTGAActgctgctgctacagcc |
| miR*-XS24290B-III | ctCCGCAAGTAAGGAAATTTGAAttcctgctgctaggctg |
| miR*-XS24290B-IV | aaTTCAAATTTCCTTACTTGCGGagagaggcaaaagtgaa |
| G-4368 | CTGCAAGGCGATTAAGTTGGGTAAC |
| G-4369 | GCGGATAACAATTTCACACAGGAAACAG |

**Table S2** Primers used during qPCR of the RNAi lines.

| Oligo Name | Direction | Size (bp) | Sequence 5’ to 3’ |
|---|---|---|---|
| SamDC | Forward | 190 | TGCTAATCTGCTCCAATGGC |
|  | Reverse |  | GACGCAGCTGACCACCTAGA |
| UBC18 | Forward | 193 | GGAGGCACCTCAGGTCATTT |
|  | Reverse |  | ATAGCGGTCATTGTCTTGCG |
| Ubi10 | Forward | 237 | TCCACACTCCACTTGGTGCT |
|  | Reverse |  | GAGGGTGGACTCCTTTTGGA |
| BraXS90-RT-1 | Forward | 167 | CACGCCCTCAGGGAGATACG |
|  | Reverse |  | AACGACTCCTTGGTGCCTTC |
| BraXS90-RT-2 | Forward | 163 | AGTCAAATTCCCGCATGAATGG |
|  | Reverse |  | TCGGTGGAGGCTTCACAAAG |

**Table S3** Genes identified on chromosome 5 around the QTL linked to marker BD1676_1.

| Gene Name | | Function | Pfam | Panther |
|---|---|---|---|---|
| Bradi5g | 24160.1 | Motor activity, ATPase activity, Rab GTPase binding | | GOLGIN-84 |
| | 24160.2 | Motor activity, ATPase activity, Rab GTPase binding | | GOLGIN-84 |
| | 24170.1 | Secondary active sulfate transmembrane transporter activity, chloride channel activity, anion exchanger activity | Sulfate transporter family | Sulfate transporter |
| | 24170.2 | Secondary active sulfate transmembrane transporter activity, chloride channel activity, anion exchanger activity | Sulfate transporter family | Sulfate transporter |
| | 24180.1 | WAK receptor-like protein kinase, expressed, subfamily WAKb | Protein kinase domain | |
| | 24190.1 | WAK receptor-like protein kinase, expressed, subfamily WAKb | Protein kinase domain | |
| | 24200.1 | Putative Gene | Peroxidase | |
| | 24207.1 | Putative Gene | Alpha-N-acetylglucosaminidase (NAGLU) | Alpha-N-acetylglucosaminidase |
| | 24220.1 | Transcription corepressor activity, phosphoglycerate dehydrogenase activity | | 2-Hydroxyacid dehydrogenase |
| | 24227.1 | Putative Gene | Asparaginase | Protease T2 asparaginase |
| | 24240.1 | Putative Gene | Sec1 family | Vesicle protein sorting-associated |
| | 24250.1 | Single-standed DNA specific 3'-5' exodeoxyribonuclease activity | Exonuclease | Exonuclease-related |
| | 24257.1 | Putative Gene | DUF2930 | |
| | | | | |
| | 24267.1 | Putative Gene | Dedicator of cytokinesis | dedicator of cytokinesis (DOCK) |
| | 24280.1 | UDP-galactosyltransferase activity | UDP-glucoronosyl and UDP-glucosyl transferase | UDP-glucuronosyltransferase related |

|  |  |  |  |  |
|---|---|---|---|---|
|  | 24290.1 | Putative xylosyltransferase, CAZy family GT43 | Glycosyltransferase family 43 | Beta-1,3-glucuronyltransferase-related |
|  | 24300.1 | Serine-type carboxypeptidase activity | Serine carboxypeptidase | Serine carbosypeptidase II (carboxypeptidase D) |
|  | 24310.1 | WAK receptor-like protein kinase, expressed, subfamily WAKb | Protein kinase domain |  |
|  | 24320.1 | Putative Gene |  |  |
|  | 24330.1 | Putative Gene |  |  |
|  | 34340.1 | Putative Gene |  |  |
|  | 34350.1 | Putative Gene |  |  |
|  | 24360.1 | Putative Gene | AP2 domain | Protein kinase |
|  | 24370.1 | NADPH-hemoprotein reductase activity, iron ion binding, FAD binding, nitric-oxide synthase activity |  | NADPH-cytochrome P450 reductase |
|  | 24380.1 | Putative Gene | AUX/IAA family |  |
|  | 24387.1 | Putative Gene | Sodium/calcium exchanger protein |  |
|  | 24397.1 | Putative Gene | Transmembrane proteins 14C |  |
|  | 24410.1 | Putative Gene | Tify domain |  |
|  | 24410.2 | Putative Gene | Tify domain |  |
|  | 24420.1 | Aminoacyl-tRNA hydrolase activity | Peptidyl-tRNA hydrolase PTH2 | Peptidyl-tRNA hydrolase 2 |
|  | 24430.1 | Endonuclease activity | S1/P1 nuclease |  |
|  | 24430.2 | Endonuclease activity | S1/P1 nuclease |  |
|  | 24440.1 | Putative Gene |  |  |
|  | 24450.1 | Protein kinase family protein, putative, expressed, subfamily RLCK-VI | Protein tyrosine kinase |  |
|  | 24460.1 | Putative Gene | Calmodulin binding protein-like |  |
|  | 24460.2 | Putative Gene | Calmodulin binding protein-like |  |

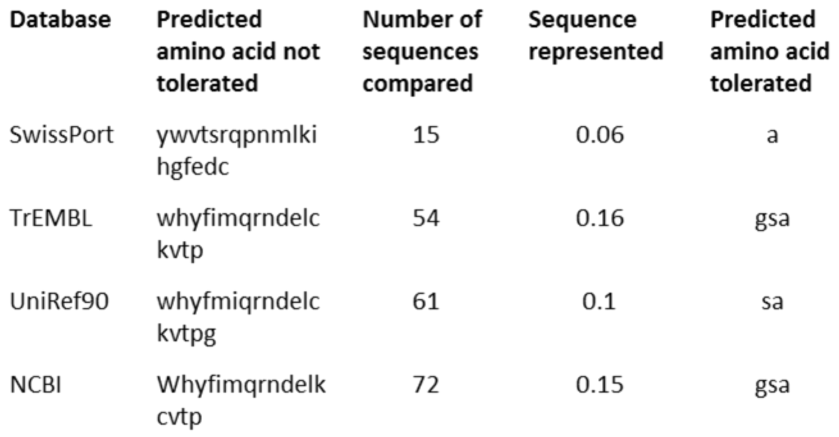
| | | | | |
|---|---|---|---|---|
| | 24460.3 | Putative Gene | Calmodulin binding protein-like | |
| | 24470.1 | Metalloendopeptidase activity | Mov34/MPN/PAD-1 family | JUN activation domain binding protein |
| | 24480.1 | Protein kinase family protein, putative, subfamily, SD-2a | Protein kinase domain | |
| | 24490.1 | F-Box | F-Box | |
| | 24490.2 | F-Box | F-Box | |
| | 24490.3 | F-Box | F-Box | |
| | 24500.1 | Serine-type endopeptidase activity | | Subtilinsin/Kexin-related serine protease |
| | 24510.1 | Putative Gene | | |
| | 24520.1 | Serine-type endopeptidase activity | Peptidase inhibitor I9 | Subtilinsin/Kexin-related serine protease |
| | 24530.1 | Protein serine/threonine phosphatase activity | Protein phosphatase 2C | Protein phosphatase 2c |
| | 24536.1 | Putative Gene | | |
| | 24542.1 | Putative Gene | Cupin superfamily protein | MINA53 (MYC induced nuclear antigen |
| | 24550.1 | Glutamate-ammonia ligase activity, ATP binding | Glutamine synthetase | Glutamine synthetase |
| | 24550.2 | Glutamate-ammonia ligase activity, ATP binding | Glutamine synthetase | Glutamine synthetase |
| | 24560.1 | Putative Gene | | |
| | 24570.1 | Protein kinase family protein, putative, subfamily, RLCK-OS1 | Protein kinase domain | |
| | 24580.1 | Putative Gene | Nucleolar protein, Nop52 | NNP-1 protein (novel nuclear protein 1, NOP52 |
| | 24590.1 | ATP binding | ATPase family associated with various cellular activities (AAA) | |
| | 24600.1 | Putative Gene | | |
| | 24610.2 | Glucose-6-phosphate 1-epimerase activity | Aldose 1-epimerase | Apospory-associated protein c-related |
| | 24610.3 | Glucose-6-phosphate 1-epimerase activity | Aldose 1-epimerase | Apospory-associated protein c-related |

| | | | | |
|---|---|---|---|---|
| | 24610.4 | Glucose-6-phosphate 1-epimerase activity | Aldose 1-epimerase | Apospory-associated protein c-related |
| | 24620.1 | Putative Gene | | |
| | 24630.1 | ATP binding | Lipase (class 3) | Alpha/beta hydrolase related |
| | 24640.1 | Protein farnesyltransferase activity | Polyprenyl synthetase | Farnesyl-prophosphate synthetase |
| | 24640.2 | Protein farnesyltransferase activity | Polyprenyl synthetase | Farnesyl-prophosphate synthetase |
| | 24650.1 | Putative Gene | Peroxidase | |
| | 24660.1 | Putative Gene | Universal stress protein family | |
| | 24670.1 | Putative Gene | SBP domain | |
| | 24680.1 | Putative Gene | Ribosomal protein L7Ae/L30e/S12e/Gadd45 family | 60S Ribosomal protein 10A-related |
| | 24690.1 | Autoinhibited H+ P-type ATPase subfamily P3 cluster 2 from PMID:12805592. Similar to AtAHA1 plasma membrane H+ transporter | | |
| | 24700.1 | Putative Gene | AP2 domain | |
| | 24710.1 | Putative Gene | AP2 domain | |
| | 24720.1 | Putative Gene | AP2 domain | |
| | 24730.1 | Protein kinase activity | | |
| | 24730.2 | Protein kinase activity | | |
| | 24737.1 | Putative Gene | Protein tyrosine kinase | |
| | 24750.1 | Protein kinase family protein, putative, expressed, subfamily RLCK-Os4 | Protein tyrosine kinase | |
| | 24760.1 | Protein kinase family protein, putative, expressed, subfamily RLCK-Os4 | Protein tyrosine kinase | |
| | 24770.1 | Putative Gene | | |
| | 24780.1 | Serine-type endopeptidase activity | | Subtilisin/Kexin-related Serine protease |
| | 24790.1 | BTB | BTB/POZ domain | |

| | | | | |
|---|---|---|---|---|
| | 24800.1 | Neutral amino acid transmembrane transporter activity, L-amino acid transmembrane transporter activity | Transmembrane amino acid transporter protein | Amino acid transporter |
| | 24810.1 | Neutral amino acid transmembrane transporter activity, L-amino acid transmembrane transporter activity | Transmembrane amino acid transporter protein | Amino acid transporter |
| | 24820.1 | Endoribonuclease activity | eRF1 domain | PELOTA |
| | 24830.1 | Putative Gene | | |
| | 24836.1 | Putative Gene | ABC1 family | ABC transporter-related |
| | 24842.1 | Putative Gene | | |
| | 24850.1 | Similar to UDP-arabinopyranose mutase. Reversibly glycosylated polypeptide. CAZy family GT75 | Reversibly glycosylated polypeptiede | |
| | 24860.1 | Putative Gene | | |
| | 24870.1 | STE_MEKK_ste11_MAP3K.24 - STE kinases include homologs to sterile 7, sterile 11 and sterile 20 from yeast, expressed, subfamily | Protein kinase domain | |
| | 24870.2 | STE_MEKK_ste11_MAP3K.24 - STE kinases include homologs to sterile 7, sterile 11 and sterile 20 from yeast, expressed, subfamily | Protein kinase domain | |
| | 24870.3 | STE_MEKK_ste11_MAP3K.24 - STE kinases include homologs to sterile 7, sterile 11 and sterile 20 from yeast, expressed, subfamily | Protein kinase domain | |
| | 24880.1 | Putative Gene | Heavy-metal-associated domain | Copper transport protein ATOX1-related |
| | 24890.1 | Inositol pentakisphosphate 2-kinase activity, ATP binding | Inositol-pentakisphosphate 2-kinase | Inositol polyphosphate kinase 1 |
| | 24900.1 | Putative Gene | | |
| | 24900.3 | Putative Gene | | |
| | 24910.1 | Putative Gene | | |
| | 24917.1 | Putative Gene | Eukaryotic DNA topoisomerase I | DNA topoisomerase Type 1 |

| | | | | |
|---|---|---|---|---|
| | 24930.1 | Putative Gene | | Molybdopterin biosynthesis protein |
| | 24930.3 | Putative Gene | | Molybdopterin biosynthesis protein |
| | 24930.4 | Putative Gene | | Molybdopterin biosynthesis protein |
| | 24937.1 | Putative Gene | | |
| | 24950.1 | Transcription coactivator activity | MED7 protein | |
| | 24950.3 | Transcription coactivator activity | MED7 protein | |
| | 24960.1 | 26S, subfamily 19S | Mov34/MPN/PAD-1 family | EIF3F-related |
| | 24967.1 | Putative Gene | BSD domain | |
| | 24980.1 | Putative Gene | | 40S Ribosomal protein S9 |

**Table S4** SIFT analysis of the changes produced by the SNP in *Bradi5g24290.1*.



| Database | Predicted amino acid not tolerated | Number of sequences compared | Sequence represented | Predicted amino acid tolerated |
|---|---|---|---|---|
| SwissPort | ywvtsrqpnmlkihgfedc | 15 | 0.06 | a |
| TrEMBL | whyfimqrndelckvtp | 54 | 0.16 | gsa |
| UniRef90 | whyfmiqrndelckvtpg | 61 | 0.1 | sa |
| NCBI | Whyfimqrndelkcvtp | 72 | 0.15 | gsa |