

The *ben1-1* brassinosteroid-catabolism mutation is unstable due to epigenetic modifications of the intronic T-DNA insertion

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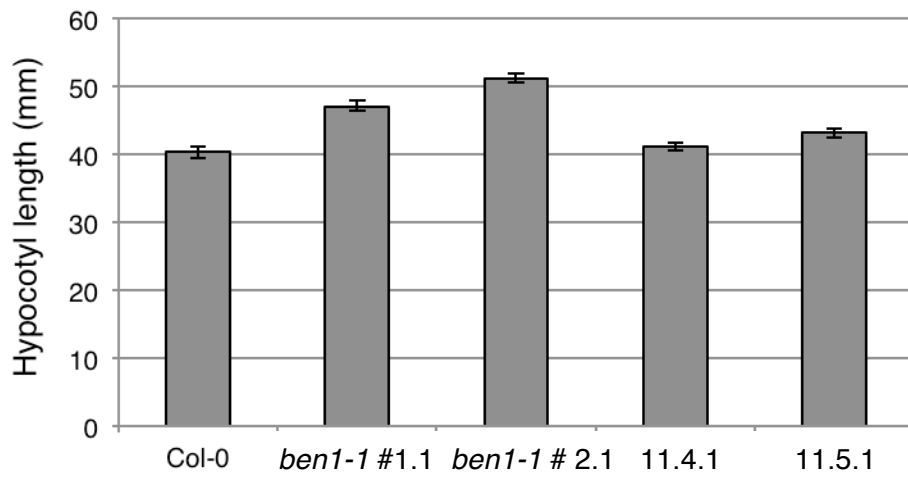


Figure S1 The attenuated hypocotyl-elongation phenotype of the re-isolated *ben1-1* lines is stably inherited to the next generation. The hypocotyl-elongation phenotype of progeny from the re-isolated *ben1-1* lines is significantly different from the original *ben1-1* lines ($p < 0.05$). Seedlings were grown in darkness or $9 \mu\text{mol m}^{-2} \text{sec}^{-1}$ of white-light for five days before being digitized and measured. Hypocotyl lengths were then normalized to seedlings grown in the dark and expressed as a percentage change. Error bars represent standard error (SE). To calculate SE, each seedling value in light was normalized to the average of the genotype in dark. The resulting group of values was used to calculate standard error (SE).

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ben1_O_NPTII-F1 NNNNNNNACNTNNNNGAGCCACTCAGCCGCGGGTTTCTGGAGTTTAATGAGCTAAGCACA
ben1_R_NPTII-F1 NNNNNNNACNTNNNANGANCCNCTCAGCCGCGGGTTTCTGGAGTTTAATGAGCTAAGCACA
*****

ben1_O_NPTII-F1 TACGTCAGAAACCATTTATTGCGCGTTCAAAGTCGCCTAAGGTCACCTATCAGCTAGCAAA
ben1_R_NPTII-F1 TACGTCAGAAACCATTTATTGCGCGTTCAAAGTCGCCTAAGGTCACCTATCAGCTAGCAAA
*****

ben1_O_NPTII-F1 TATTTCTTGTCAAAAATGCTCCACTGACGTTCCATAAATCCCCTCGGTATCCAATTAGA
ben1_R_NPTII-F1 TATTTCTTGTCAAAAATGCTCCACTGACGTTCCATAAATCCCCTCGGTATCCAATTAGA
*****

ben1_O_NPTII-F1 GTCTCATATTCACTCTCAATCCAAATAATCTGCACCGGATCTGGATCGTTTCGCATGATT
ben1_R_NPTII-F1 GTCTCATATTCACTCTCAATCCAAATAATCTGCACCGGATCTGGATCGTTTCGCATGATT
*****

ben1_O_NPTII-F1 GAACAAGATGGATTGCACGCAGGTTCTCCGCGCGCTTGGGTGGAGAGGCTATTCGGCTAT
ben1_R_NPTII-F1 GAACAAGATGGATTGCACGCAGGTTCTCCGCGCGCTTGGGTGGAGAGGCTATTCGGCTAT
*****

ben1_O_NPTII-F1 GACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCGGTGTTCCGGCTGTCAGCGCAG
ben1_R_NPTII-F1 GACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCGGTGTTCCGGCTGTCAGCGCAG
*****

ben1_O_NPTII-F1 GGGCGCCCGGTTCTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTGCAGGAC
ben1_R_NPTII-F1 GGGCGCCCGGTTCTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTGCAGGAC
*****

ben1_O_NPTII-F1 GAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTGCTCGAC
ben1_R_NPTII-F1 GAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTGCTCGAC
*****

ben1_O_NPTII-F1 GTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAGGATCTC
ben1_R_NPTII-F1 GTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAGGATCTC
*****

ben1_O_NPTII-F1 CTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATGCGGCGG
ben1_R_NPTII-F1 CTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATGCGGCGG
*****

ben1_O_NPTII-F1 CTGCATACGCTTGATCCGGCTACCTGCCATTTCGACCACCAAGCGAAACATCGCATCGAG
ben1_R_NPTII-F1 CTGCATACGCTTGATCCGGCTACCTGCCATTTCGACCACCAAGCGAAACATCGCATCGAG
*****

ben1_O_NPTII-F1 CGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAAGAGCAT
ben1_R_NPTII-F1 CGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAAGAGCAT
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ben1_O_NPTII-F2 ACCAAGCGAAACATCGCATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTG-TCGAT
ben1_R_NPTII-F2 ACCAAGCGAAACATCGCATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTNNGTCGAT
*****

ben1_O_NPTII-F2 CAGGATGATCTGGACGAAGAGCATCAGGGGCTCGCGCCAGCCGAACGTTCGCCAGGCTC
ben1_R_NPTII-F2 CAGGATGATCTGGACGAAGAGCATCAGGGGCTCGCGCCAGCCGAACGTTCGCCAGGCTC
*****

ben1_O_NPTII-F2 AAGGCGCGCATGCCGACGGCGATGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCG
ben1_R_NPTII-F2 AAGGCGCGCATGCCGACGGCGATGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCG
*****

ben1_O_NPTII-F2 AATATCATGGTGGAAAATGGCCGCTTTTCTGGATTTCATCGACTGTGGCCGGCTGGGTGTG
ben1_R_NPTII-F2 AATATCATGGTGGAAAATGGCCGCTTTTCTGGATTTCATCGACTGTGGCCGGCTGGGTGTG
*****

ben1_O_NPTII-F2 GCGGACCGCTATCAGGACATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGCGCGC
ben1_R_NPTII-F2 GCGGACCGCTATCAGGACATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGCGCGC
*****

ben1_O_NPTII-F2 GAATGGGCTGACCGCTTCCTCGTGCTTTACGGTATCGCCGCTCCCGATTTCGCAGCGCATC
ben1_R_NPTII-F2 GAATGGGCTGACCGCTTCCTCGTGCTTTACGGTATCGCCGCTCCCGATTTCGCAGCGCATC
*****

ben1_O_NPTII-F2 GCCTTCTATCGCCTTCTTGACGAGTTCTTCTGAGCGGGACTCTGGGGNN-GAAATGAAAG
ben1_R_NPTII-F2 GCCTTCTATCGCCTTCTTGACGAGTTCTTCTGAGCGGGACTCTGGGGNNCNAATGAANN
*****

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Figure S2 *NPTII* gene sequence did not change in the pre-triple and post-triple *ben1-1* mutants. The *NPTII* gene was amplified using NPT-Fv1, NPT-Fv2 and NPT-Rv from the pre-triple and post-triple *ben1-1* lines. Primers NPT-Fv1 and NPT-Fv2 were used for sequencing *NPTII* gene (Table S1). The color coded yellow nucleotides show the complete *NPTII* coding region in the sequence.

(A)

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ben1_O_pBEN1_BST GGAATTTAATAATAATGTTTGTAAATAAATGGATAAAGAATGTGAATTATTTATATAAAATG
ben1_T_pBEN1_BST GGAATTTAATAATAATGTTTGTAAATAAATGGATAAAGAATGTGAATTATTTATATAAAATG
Col-0_BST GGAATTTAATAATAATGTTTGTAAATAAATGGATAAAGAATGTGAATTATTTATATAAAATG
Col-0_no_BST GGAATCCAATAACAATGTTTGTAAATAAACGGACAAAGAATGTGAATTATTCACATAAAATG
*****

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ben1_O_pBEN1_BST ATTTGTAAAATGTGAGTATTTGATTATAATGGATATAATAAAAATAAAAATTGTAATAAAG
ben1_T_pBEN1_BST ATTTGTAAAATGTGAGTATTTGATTATAATGGATATAATAAAAATAAAAATTGTAATAAAG
Col-0_BST ATTTGTAAAATGTGAGTATTTGATTATAATGGATATAATAAAAATAAAAATTGTAATAAAG
Col-0_no_BST ATCTGTAAAATGTGAGCATTGATTATAACGGATATAATAAAAACAAAATTGTAATAAAG
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ben1_O_pBEN1_BST AGAGAAGAGGGTAAAATGGGGAATATGTTATGTGGATAGGTGTGAGAGAGTAAATGATGT
ben1_T_pBEN1_BST AGAGAAGAGGGTAAAATGGGGAATATGTTATGTGGATAGGTGTGAGAGAGTAAATGATGT
Col-0_BST AGAGAAGAGGGTAAAATGGGGAATATGTTATGTGGATAGGTGTGAGAGAGTAAATGATGT
Col-0_no_BST AGAGAAGAGGGCAAAACGGGGAACATGTCACGCGGATAGGTGTGAGAGAGTAAATGACGT
*****

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ben1_O_pBEN1_BST AGGTTTTGTTATTTAAGAATTTTTTTAGAGAGGTTTTTATATAT-AGNNG-----
ben1_T_pBEN1_BST AGGTTTTGTTATTTAAGAATTTTTTTAGAGAGGTTTTTATATATTAGAAGAGAGAGAAAG
Col-0_BST AGGTTTTGTTATTTAAGAATTTTTTTAGAGAGGTTTTTATATATTAGAAGAGAGAGAAAG
Col-0_no_BST AGGTTCCGTTATTTAAGAACCCTTCTAGAGAGGTCCC-ACACACCAGAAGAG-----
*****

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ben1_O_pBEN1_BST -----
ben1_T_pBEN1_BST AGATAGAGAGAAAATGGTG
Col-0_BST AGATAGAGAGAAAATGGTG
Col-0_no_BST -----

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(B)

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ben1_O_Ex2_BST GGTGGTGTGTTGAGTTTGGTGGGAAGAATGGGTTAGAGGTTGTGATGTTTGTATTTTTTTT
ben1_T_Ex2_BST GGTGGTGTGTTGAGTTTGGTGGGAAGAATGGGTTAGAGGTTGTGATGTTTGTATTTTTTTT
Col-0_BST GGTGGTGTGTTGAGTTTGGTGGGAAGAATGGGTTAGAGGTTGTGATGTTTGTATTTTTTTT
Col-0_no_BST GCGGCGCTTGAGTTCGCTGGGAAGAATGGGTTAGAGGTTGTGACGCTCGTTATTCCCTCT
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ben1_O_Ex2_BST TGTTGTTGGATTTTTTATATTTTTTGTGTTGTTTTTTTTTGTTTTTTATATTTTTTGTAT
ben1_T_Ex2_BST TGTTGTTGGATTTTTTATATTTTTTGTGTTGTTTTTTTTTGTTTTTTATATTTTTTGTAT
Col-0_BST TGTTGTTGGATTTTTTATATTTTTTGTGTTGTTTTTTTTTGTTTTTTATATTTTTTGTAT
Col-0_no_BST CGTCGTCGGACCTTTTATATCTTCGTCGTTGCCTTCCCTCCGTCCTTCATATCTCTGCCAT
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ben1_O_Ex2_BST GTTTTTTG/GTATTTAA
ben1_T_Ex2_BST GTTTTTTG/GTATTTAA
Col-0_BST GTTTTTTG/GTATTTAA
Col-0_no_BST GCTCTTTG/GTACTTAA
*

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Figure S3 Genomic DNA in the *BEN1* Promoter and *BEN1* 2nd Exon-Intron junction does not show any methylation in both the pre-triple *ben1-1* and the *bas1-2 sob7-1 ben1-1* triple-mutant lines. (A) *BEN1* promoter DNA was amplified using primers pBEN1-BS-F and pBEN1-BS-R from the bisulfite converted genomic DNA from the Col-0, pre-triple *ben1-1* and the triple-mutant lines. (B) *BEN1* DNA from the 2nd Exon-Intron junction was amplified using primers BEN1-E2-BS-F and BEN1-E2-BS-R from the bisulfite converted genomic DNA from the Col-0, pre-triple *ben1-1* and the triple-mutant lines. BST= bisulfite treatment. ben1_O= pre-triple *ben1-1*, and ben1_T= *bas1-2 sob7-1 ben1-1* triple-mutant.

Bisulfite *BEN1* 2nd exon raw sequences

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 GCAAGGGGATTTCTTTAAATTTATGAGGATTTTGTGTTAAATTTGTATATGAATTGAAAATATGTTTTTCTTTATTGGCCATTTCC
 GTTTTGTAACATGTTCTAGTACTTGTGACGAAAAAAAAAAGAAAGTGTGTTTATTGATTGAG

BLUE=Exons; Black=Introns

Primers:

BEN1-E2-BS-F: TTAGGAATTAAGGAGAAGAG

BEN1-E2-BS-R: AATTAATACCAAAAAACATAAC

Replicate 1

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Col-0_BST GGTGGTGTGGTTGAGTTTGGTGGGAAGAATGGGTAGAGGTTGTGATGTTGTTATTTTTT
Col-0_no_BST GGCGGCGCTTGAGTTCGGTGGGAAGAATGGGTAGAGGTTGTGACGCTCGTTATTCTCT
* * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *

ben1_O_Ex2_BST TGTTGTTGGATTTTTTATATTTTTGTTGTTGTTTTTTTTTTGTTTTTATATTTTTTTGTTAT
ben1_T_Ex2_BST TGTTGTTGGATTTTTTATATTTTTGTTGTTGTTTTTTTTTTGTTTTTATATTTTTTTGTTAT
Col-0_BST TGTTGTTGGATTTTTTATATTTTTGTTGTTGTTTTTTTTTTGTTTTTATATTTTTTTGTTAT
Col-0_no_BST CGTCGTCGGACCTTTTTATATCTTCGTCGTTGCCTTCCCTCCGTCTTCATATCTCTCGCCAT
* * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *

ben1_O_Ex2_BST GTTTTTTG/GTATTTAA
ben1_T_Ex2_BST GTTTTTTG/GTATTTAA
Col-0_BST GTTTTTTG/GTATTTAA
Col-0_no_BST GCTCTTTG/GTACTTAA
* * * * * * * * * * * * * * * *

Replicate 2

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GGGGCTAANNNTGGANTNNCCTACNACAGCCACAANNCTATATCCTGTTTCNATTCNNTGAAGAACAGCANCNCNGTGAA
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>PK_329142-525_17_BS4_C07.ab1/>ben1_O_Ex2_BST

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GGACCCACNGTGTGTGAAATNGCTGGTGCATAGNGCCGGCTAAATGCACTNCTCGTTGGNNGACNACTCCCATGTTGGGC
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>PK_329142-527_19_BS4_E07.ab1/>ben1_T_Ex2_BST

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>PK_329142-528_20_BS4_F07.ab1/>ben1_T_Ex2_BST

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ANGCTGNNGGTGNAGNCNACACCNANGCANNNTNGCTGNCCGNTGTACTTGNNGNCACTCNANCGNNN

Bisulfite sequences of the *BEN1* promoter

ccattccatctcattcacgcggttttattttctctcattcatattaattatatattaatcacacaatcctaataatatcccttaatctatgcct
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 aatgacgtaggttccggttatttaagaacccttctagagaggttcccacacaccagaagagagagaaagagacagagagaaaATGGTGAGAGA
[AGAACAAGAAGAAGATGACAACAACAACAAC](#)

Primers:

pBEN1-BS-Fv: 5'-GTATAGTAGTAAAAAAAAGAAGAAGAAG-3'

pBEN1-BS-Rv: 5'-CTTRTTCTTCTCTCACCATTTTCTCTCT-3'

(RC=reverse compliment)

Replicate 1

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 CACCTATCCGCGTGACATGTTCCCGTTTTGCCCTCTTCTCTCTTTATTACAATTTTTGTTTTATTATATCCGTTATAAT
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 CCACCTATCCACATAACCATTTTCCCCCTTTCACCCCTTCTCTCTTTATNCAAATCTTTTTTGCTCATCNCNNACNAAT
 CAAATACCCCATTTTTACATCNNTCTTCTAAATAAATCCATTCTTTATCCATTTTCCCTCACATTAGGCTAATTCCTC
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>PK_328409-530_6-R_Primer-D_C02.ab1/>Col-0_BST
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>PK_328409-535_9-F_Primer-C_H02.ab1/>ben1_T_pBEN1_BST
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Sequence alignment:

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ben1_O_pBEN1_BST  GGAATTTAATAATAATGTTTGTAAATAAATGGATAAAGAATGTGAATTATTTATATAAATG
ben1_T_pBEN1_BST  GGAATTTAATAATAATGTTTGTAAATAAATGGATAAAGAATGTGAATTATTTATATAAATG
Col-0_BST         GGAATTTAATAATAATGTTTGTAAATAAATGGATAAAGAATGTGAATTATTTATATAAATG
Col-0_no_BST      GGAATCCAATAACAATGTTTGTAAATAACGGACAAAGAATGTGAATTATTCACATAAATG
*****          ***** ***** * * ***** * *****
```

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ben1_O_pBEN1_BST  ATTTGTAAAATGTGAGTATTTGATTATAATGGATATAATAAAAATAAAAATTGTAATAAAG
ben1_T_pBEN1_BST  ATTTGTAAAATGTGAGTATTTGATTATAATGGATATAATAAAAATAAAAATTGTAATAAAG
Col-0_BST         ATTTGTAAAATGTGAGTATTTGATTATAATGGATATAATAAAAATAAAAATTGTAATAAAG
Col-0_no_BST      ATCTGTAAAATGTGAGCATTGATTATAACGGATATAATAAAAACAAAATTGTAATAAAG
** ***** ***** ***** ***** *****
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ben1_O_pBEN1_BST  AGAGAAGAGGGTAAAAATGGGGAATATGTTATGTGGATAGGTGTGAGAGAGTAAATGATGT
ben1_T_pBEN1_BST  AGAGAAGAGGGTAAAAATGGGGAATATGTTATGTGGATAGGTGTGAGAGAGTAAATGATGT
Col-0_BST         AGAGAAGAGGGTAAAAATGGGGAATATGTTATGTGGATAGGTGTGAGAGAGTAAATGATGT
Col-0_no_BST      AGAGAAGAGGGCAAAACGGGGAACATGTCACGCGGATAGGTGTGAGAGAGTAAATGACGT
*****          ***** ***** * * ***** *****
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ben1_O_pBEN1_BST AGGTTTTGTTATTTAAGAATTTTTTTAGAGAGGTTTTTATATAT-AGNNG-----
ben1_T_pBEN1_BST AGGTTTTGTTATTTAAGAATTTTTTTAGAGAGGTTTTTATATATTAGAAGAGAGAGAAAG
Col-0_BST AGGTTTTGTTATTTAAGAATTTTTTTAGAGAGGTTTTTATATATTAGAAGAGAGAGAAAG
Col-0_no_BST AGGTTCCGTTATTTAAGAACCCTTCTAGAGAGGTCCC-ACACACCAGAAGAG-----
***** ***** ** ***** * * * * *

ben1_O_pBEN1_BST -----
ben1_T_pBEN1_BST AGATAGAGAGAAAATGGTG
Col-0_BST AGATAGAGAGAAAATGGTG
Col-0_no_BST -----

Replicate 2

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GTCNNATCCCCTNGACAANNCCCCTCCCCNACGCCCTCCGGACCNNCCCTCCNNNNNCTCNCCTCANNANANCCATGCT
NCNCTCTNNNTGTCNCCNCCCCNCCGAGCCACCCTCCTCCACCNCGCCCCCCCGCCCCCCCCCTCTGCCNCTTT
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>PK_329142-504_8_pBEN1-Fv_D04.ab1/>ben1_R_pBEN1_BST
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Bisulfite pNOS raw sequences

GTTTACCCGCCAATATATCTGTCAAACTGATAGTTTAAACTGAAGGCGGGAAACGACAATCTGATCATGAGCGGAGAATTAAGGGAGTCACGT
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 GCTACCCGTGATATTGCTGAAGAGCTTGCGGCGAATGGGCTGACCGCTTCTCGTGCTTTACGGTATCGCCGCTCCCGATTGCGAGCGCATCGCCT
 TCTATCGCCTTCTTGACGAGTTCTTCTGA

Primers:

pNOS-BS-F (Primer A/_{pROK2-Fv}): 5'-GGGTTTTYTGGAGTTTAATGAGYTAAG-3'

pNOS-BS-R (Primer B/_{pROK2-Rv}): 5'-CACTTCRCCCAATARCARTCCCTTCC-3'

Replicate 1

>PK_328409-501_1-F_Primer-A_A01.ab1/>*ben1_o_pNOS_no_BST*

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>RC_328409-502_1-R_Primer-B_B01.ab1/>*ben1_o_pNOS_no-BST*

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>PK_328409-503_2-F_Primer-A_C01.ab1/>*ben1_o_pNOS_BST*

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AGATTGACCTGTCTGGNGCCTGAATGAAGTGCAGGATGAGGCANNGTGGCTATTGTGGCTGGNCATGATGGGTGTTCTT
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>PK_328409-504_2-R_Primer-B_D01.ab1

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ACATCAAAACAACCAATTATCTATTATGCCAATCATAACCAATAACCTCTCCACCCAAACAACCCAAAAAANTGCGNT
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>RC_328409-504_2-R_Primer-B_D01.ab1/>*ben1_o_pNOS-BST*

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>PK_328409-505_3-F_Primer-A_E01.ab1/>*ben1_R_pNOS_BST*

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>RC_328409-506_3-R_Primer-B_F01.ab1/>*ben1_R_pNOS-BST*

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>PK_328409-507_4-F_Primer-A_G01.ab1/>Triple_pNOS-BST

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>PK_328409-508_4-R_Primer-B_H01.ab1

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 GGCGGCATCAGAACAGCCGATTGTCTGTTGTACCCAGTCATAGCCGAATAGCCTCTCCACCAAGCGNNNGGANAACCTG
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 CTAATTGAATACCGAGANAATTTATGGAACGTCAGTGNAGCATTTTTGACAAAAAATATTTGCTAGCTGATAGTANCT
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>RC_328409-508_4-R_Primer-B_H01.ab1/>Triple_pNOS-BST

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 TAATCTGTACCGGATCTGGATCGTTTCGNATGATTGAACAAGATGGATNNNACGCAGGTTNTCCNNCGCTTGGGTGGAGAGGCTA
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Sequence alignment:

ben1_O_pNOS_no-BST AAATATTTCTTGTCAAAAATGCTCCACTGACGTTCCATAAATTCCTCGGTATCCAATT
 ben1_R_pNOS_BST AAATATTTTTGTCAAAAATGTTTTACTGACGTTCCATAAATTTTTCTCGGTATTCAATT
 ben1_O_pNOS_BST AAATATTTCTTGTCAAAAATGCTCCACTGATGTTCCATAAATTCCTCGGTATCCAATT
 ***** ***** * ***** ***** ** ***** *****

ben1_O_pNOS_no-BST AGAGTCTCATATTCACTCTCAATCAAATAATCTGCACCGGATCTGGATCGTTTCGATG
 ben1_R_pNOS_BST AGAGTCTCATATTTATCTCAATCAAATAATCTGTACCGGATCTGGATCGTTTCGTATG
 ben1_O_pNOS_BST AGAGTCTCATATTCACTCTCAATCAAATAATCTGCACCTGGATCTGGATTGTTTTGCATG
 ***** * ***** ***** ** ***** ***** * * *

ben1_O_pNOS_no-BST ATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTCCGGC
 ben1_R_pNOS_BST ATTGAACAAGATGGATTGTACGCANGTTTTCCGGTCGTTTGGGTGGAGAGGCTATTCCGGC
 ben1_O_pNOS_BST ATTGAACAAGATGGATTGCATGCAGGTTCTTTGGTTGTTTGGGTGGAGAGGTTATTTGGT
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ben1_O_pNOS_no-BST   TATGACTGGGACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTTC
ben1_R_pNOS_BST      TATGACTGGGTACAACAGACAATCGGCTGTTCTGATGCCGCCGTGTTTC
ben1_O_pNOS_BST      TATGANTGGGCACAACANATAAATTGGCTGCTCTGATGTCGTTGTGTTT
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Replicate 2

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CNNCTTTGGTCTTCCCTCNCNNCTGCTCTCTCCCTCCCN
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NPTII gene sequencing V2

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ben1_O_NPTII-F1 NNNNNNACNTNNNNGAGCCACTCAGCCGCGGGTTTTCTGGAGTTTAAATGAGCTAAGCACA
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ben1_O_NPTII-F1 TACGTCAGAAACCATTATTGCGCGTTCAAAGTTCGCTAAGGTCACTATCAGCTAGCAAA
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ben1_O_NPTII-F1 GAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTTCGGCTAT
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ben1_O_NPTII-F1 GACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCAGCGCAG
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ben1_O_NPTII-F1 GGGCGCCCGGTTCTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTGCAGGAC
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ben1_O_NPTII-F1 GAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTGCTCGAC
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*****

ben1_O_NPTII-F1 GATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAATGGCCGC
ben1_R_NPTII-F1 GATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAATGGCCGC
*****

ben1_O_NPTII-F1 TTTTCTGGATTTCATCGACTGTGGCCGGCTGGGTGTGGCGACCCTATCNNNCATAAGCGT
ben1_R_NPTII-F1 TTTTCTGGATTTCATCGACTGTGGCCGGCTGGGTGTGGCGACCCTATCNNGACATAAGCGT
*****

ben1_O_NPTII-F1 TGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTCCTCGTGC
ben1_R_NPTII-F1 TGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTCCTCGTGC
*****

ben1_O_NPTII-F1 TTTACGGTATCGCCGCTCCCGATTTCGACGCGCATCNCCTTCTATCGCCTNCTTGACNAGT
ben1_R_NPTII-F1 TTTACGGTATCGCCGCTCCCGATTTCGACGCGCATCNCCTTCTATCGCCTTCTTGACGANT
*****

ben1_O_NPTII-F1 TCTTCTGANCGGNNNNNNNNNNGGGNNNNNNNNNNNNNNNNNAAAAGNAN
ben1_R_NPTII-F1 TCTTCTGANCGGNNNNNNNNNNNNNNNNGGNNGNNNANNNNNAA-----
*****

ben1_O_NPTII-F2 -NNNNNNNGNGGCGGNNGCNNNNNNCNNNNNTCCGGCTNACCTNCCATT--CGACC
ben1_R_NPTII-F2 NNNNNNNNGCGGNNNNNNNNNNNNNNNNCNNNNNNCCGNNTNACNTNCCATTTNCGACC
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ben1_O_NPTII-F2 ACCAAGCGAAACATCGCATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTG-TCGAT
ben1_R_NPTII-F2 ACCAAGCGAAACATCGCATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTNNGTCGAT
*****
ben1_O_NPTII-F2 CAGGATGATCTGGACGAAGAGCATCAGGGGCTCGCGCCAGCCGAACTGTTTCGCCAGGCTC
ben1_R_NPTII-F2 CAGGATGATCTGGACGAAGAGCATCAGGGGCTCGCGCCAGCCGAACTGTTTCGCCAGGCTC
*****
ben1_O_NPTII-F2 AAGGCGCGCATGCCCGACGGCGATGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCG
ben1_R_NPTII-F2 AAGGCGCGCATGCCCGACGGCGATGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCG
*****
ben1_O_NPTII-F2 AATATCATGGTGGAAAATGGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTG
ben1_R_NPTII-F2 AATATCATGGTGGAAAATGGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTG
*****
ben1_O_NPTII-F2 GCGGACCGCTATCAGGACATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGC
ben1_R_NPTII-F2 GCGGACCGCTATCAGGACATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGC
*****
ben1_O_NPTII-F2 GAATGGGCTGACCGCTTCCCTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATC
ben1_R_NPTII-F2 GAATGGGCTGACCGCTTCCCTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATC
*****
ben1_O_NPTII-F2 GCCTTCTATCGCCTTCTTGACGAGTTCTTCTGAGCGGGACTCTGGGGNN-GAAATGAAAG
ben1_R_NPTII-F2 GCCTTCTATCGCCTTCTTGACGAGTTCTTCTGAGCGGGACTCTGGGGNNCNAATGAAANN
*****

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File S5

BEN1 BL-100 analysis

File S6

Fluence rate analysis

File S7

Next generation unstable *ben1-1* Hypocotyl data

File S8

Real time RT-PCR Expression data

Files S5-S8 are available for download at <http://www.g3journal.org/lookup/suppl/doi:10.1534/g3.113.006353/-/DC1>.

Table S1 Table of PCR primer sequences used in the study.

Primer Name	Primer Sequences
GSP1	5'-TTTATATCTTCGTCGTTGCCT-3'
GSP2	5'-ACCTTTTGCAACTGGCTTTT-3'
LBb1.3	5'-ATTTTGCCGATTTTCGGAAC-3'
PRT1	5'-ATGGTGAGAGAAGAACAAGA-3'
PRT2	5'-TTAAAGAAATCCCCTTGCTTG-3'
PQ1	5'-ATCTCTCGCCATGCTCTTTG-3'
PQ2	5'-CTTCATCTCCACCGACGAAC-3'
UBQ1	5'-GAAATGCATGGAGACGGATT-3'
UBQ2	5'-TTGGTCTCTGCTCCCACTCT-3'
ACTIN2 RT-F	5'-GGTCGTACAACCGGTATTGTGCTGG-3'
ACTIN2 RT-R	5'-CTGTGAACGATTCTGGACCTGCC-3'
PQ3	5'-TCTAAACAAGGAATTCGAGGTC-3'
PQ4	5'-AACCAGAAATGTAGCACCGT-3'
NPT-Fv1/MT1	5'-ACAAGCCGTTTTACGTTTGG-3'
NPT-Rv	5'-TCATTTCGAACCCAGAGTC-3'
MT2	5'-ATACTTTCTCGGCAGGAGCA-3'
MT3	5'-TTCGCAAGACCCTTCTCTA-3'
MT4	5'-GTTTTCCAGTCACGACGTT-3'
NPT-Fv2	5'-TGCTCCTGCCGAGAAAGTAT-3'
pNOS-BS-F	5'-GGGTTTTYTGAGTTTAATGAGYTAAG-3'
pNOS-BS-R	5'-CACTTCRCCAATARCARTCCCTTCC-3'
pBEN1-BS-F	5'-GTATAGTAGTAAAAAAGAAGAAGAAG-3'
pBEN1-BS-R	5'-CTTRTTCTTCTCTACCATTTTCTCTCT-3'
BEN1-E2-BS-F	5'-TTAGGAATTAAGGAGAAGAG-3'
BEN1-E2-BS-R	5'-AATTAATACCAAAAAACATAAC-3'