```
agactcaatcctcccgtaccactttccacgttgcttccctcaccaacaaaagacatacggagcgagtccatgagcccattcaggacggaa
atccagtttcgccgccggacagcagagaaccttgggcgctactctgcttcgacgcctacttatccatccctgaccaacagagcaaacaga
                  M  D  S  T  G  K  S  V  M  A  T  S  E  G  P  S  I  L  F  L  P  F  P  G
acacccaagaactgaatcatggacagcacaggcaaatcggtgatggcgaccagcgaggggccgagcatcctcttcctcccgttcccgggg
 A  Q  G  H  A  N  P  M  L  Q  F  G  H  R  L  A  Y  Q  Y  G  F  R  P  T  L  V  V  T  R  Y
gcgcagggccacgcgaacccgatgctccagttcggccaccgcctggcttaccagtacggcttccgccccacgctcgtcgtcacccgctac
 V  L  S  T  A  L  P  P  D  A  P  F  R  V  A  A  I  S  D  G  F  D  A  G  G  I  R  S  C  L
gtgctctccacggccctgccccccgacgcgcccttccgcgtggccgccatctccgacggcttcgacgccggcggcattcggtcgtgcctc
 D  M  A  E  Y  W  R  R  L  E  A  V  G  S  E  T  L  S  R  L  I  S  D  E  A  R  E  G  R  P
gacatggcggagtactggcgccggctggaggcggtcgggtcggagactttgtcgcggctcatctccgacgaggcgcgcgaggggcggccc
 V  R  V  L  V  Y  D  P  H  V  A  W  A  R  R  V  A  R  E  A  G  V  P  A  A  A  F  F  S  Q
gtcagggtgctcgtgtacgacccgcacgtggcgtgggcgcggcgggtggcacgggaggccggcgtgcccgcggcggccttcttttcgcag
 P  C  A  V  D  I  F  Y  G  E  L  H  A  G  R  M  A  M  P  V  T  E  A  D  A  R  A  L  L  V
ccgtgcgcggtggacatcttctacggggagctgcacgcggggcggatggcgatgcccgtcacggaggcggacgcgcgagcgctgctggtg
 R  G  A  I  G  V  E  L  A  L  D  D  V  P  P  F  V  V  V  P  E  S  Q  P  V  F  T  K  A  S
cgcggagcgataggggtggagcttgcgctggatgatgtgccgcccttcgtggtcgtgccggagtcgcagccggtgttcaccaaggcgtcg
 I  G  Q  F  E  G  L  E  D  A  D  D  V  L  V  N  S  F  R  D  I  E  P  M
attgggcagttcgaagggctggaggatgccgacgacgtgctcgtcaattccttccgcgacatcgagccaatggtgagtcatcgttatttg
tttggtcaaggaatggctatttaattcagagcccctcattttcgcttgccactcactcgaatcattatacaatctgtgctctggttggta
gttcatgtcatcatgcaatcagctaaaaacttcggaaatcacactcaatttttcgaaaattcagttacaaaaaaaggcacaactaaaaaa
tacaatcgaattacacaaagtgcaaatgggtctagggatggggaattaagctacagagcgacgaatcatggggttgaatccctgtgtctg
cacgcacataattttccctttcctttttccaaaatacgtaaactgcacggatctttgagcagatctgacagccggcaaatcccgacaaa
tcgactgtgctctaacaaaatttcagtcgcagtgaaatagcacatccattaatcttacacattttggatttcagtcgcagtgaaatagca
catccattaatcttacacattttggaactaactagagttagaaatttcgcagcaatagtcctccgctgtcactaccaccaaatatttggg UGT33N1F2
ttacccctcgatctttttcaacagatccctcaagggcagaaatgaacgaatttgctccatcactttttaaaaaggtacttggttgttgat 3300_N2Ft1
                      E  V  E  Y  M  E  S  T  W  R  A  K  T  I  G  P  T  L  P  S  F  Y
agttatgctttccaatcgagcaggaggtagaatatatggagtcaacgtggcgagccaagacgataggcccaaccttgccgtcattctac
 L  D  D  D  R  L  P  S  N  K  S  Y  G  F  N  L  F  N  G  G  D  A  V  C  M  K  W  L  D  Q
cttgatgacgaccgtctgccatccaacaagtcttatggtttcaatctcttcaacggtggtgatgcagtttgcatgaaatggttggatcaa
 Q  S  M  S  S  V  V  L  V  S  Y  G  T  V  S  N  Y  D  E  S  Q  L  E  E  L  G  N  G  L  C
cagagcatgtcatctgttgtgcttgtgtcctatgggactgtctccaactacgacgaatcccagctagaggagctaggaaatggactatgc
 S  S  G  K  P  F  I  W  V  V  R  S  N  E  A  H  K  L  S  G  E  L  K  A  K  C  E  K  K  G
agttctggcaagccttttatttgggttgtgagatccaacgaggcacacaaattgtcaggcgaactcaaggcgaaatgcgagaagaagga
   L  I  V  S  W  C  P  Q  L  E  V  L  A  H  K  A  T
ctaattgtttcttggtgcccccaactcgaggttctggcacacaaggccacgggtaagacaccacaaattcgattaattttctcttctact
                                                                                G  C  F  L  T  H  C
tgatacgaggatttgaaaatgaaaaaactagttaagtgtttaaattttaattcttaaaacattcatccaggttgtttcttaacacattgt
 G  W  N  S  T  L  E  A  I  V  N  G  V  P  V  V  G  I  P  H  W  A  D  Q  P  T  I  A  K  Y
ggatggaactccacattagaggcgatcgttaacggtgtacctgtagtgggaattccacattgggcagaccagccaaccatcgcgaagtat
 V  E  S  A  W  D  M  G  V  R  V  K  K  S  L  N  G  Q  L  R  R  E  E  I  E  R  C  I  K  E
gtggagagcgcatgggacatgggcgtgcgagtgaagaaaagcttgaatggacaactaaggagggaggagatcgagagatgcatcaaggag
 V  M  D  S  E  R  K  D  E  Y  T  R  N  A  A  K  W  M  Q  K  A  K  E  T  M  H  A  G  G  S
gtgatggatagtgagaggaaggatgagtatacaaggaatgccgcgaagtggatgcaaaaggccaaggagacaatgcacgcgggaggaagc
 S  N  K  H  I  A  E  F  A  A  K  Y  S  S  S  *
tcaaacaaacatattgctgaattcgctgctaagtattcgtcaagttaaaagttatagctatgcaatcttttacttcatgataaataatta
cgcaatgatttgttattcacaaaatgtttagggccgaaggagcacacatttgccctacatattttggataacctaatcatacctcctaca 3300_N2Rt1
tcatttctggtctttgtcactttttactttggatgtttcgaaagtgggagttttcactgtttttt                         UGT33N1R1
```

Supplementary Figure S1. Nucleotide and deduced amino acid sequences of the *Bradi5g03300* gene. *Bradi5g03300* nucleotide sequence is presented as small-case letters and the corresponding protein sequence is indicated above in upper-case letters. Start and Stop codons as well as the initial Methionin residue are indicated in white letters with a black bottom. Introns are shaded in gray. The amino acid residues of the PSPG domain are shown by a black box. The primers used to amplify the region submitted to the TILLING screen are indicated by bold and underlined letters:

Primers UGT33N1F2 and 3300_N2Ft1 are in the forward orientation whereas primers 3300_N2Rt1 and UGT33N1R1 are in the reverse orientation.