

## Appendix A. Primers used in the study

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Primer	Sequence
<i>NRT2L12A-F</i>	TCTTCAGTCCGCGGTGCAG
<i>NRT2L12A-R</i>	ATTGCTCATTCGCATAACAT
<i>NRT2L12B-F</i>	CGAGCCTCAACAAAAAAGGATAT
<i>NRT2L12B-R</i>	CCCAGATATTATTGACTAAGGCA
<i>NRT2L12D-F</i>	AACTGAAGTAAGGTCCGTGCATG
<i>NRT2L12D-R</i>	GCCCCAGGTAATGACTAAGG
<i>NRT2L12-A-ZC</i>	ATCTGCGACCTTCTTGGCC
<i>NRT2L12-B-ZC</i>	ACACGTTTCACCGCGTGG
<i>NRT2L12-D-ZC-R</i>	ATGGAGGTGGAAGGGTGG
T7 Forward Sequencing Primer	TAATACGACTCACTATAGGG
RSP Reverse Sequencing Primer	AAGAACATCGATTTTCCATGGCAG
<i>NRT2L12B-RT-F</i>	TAGCAGCATCCACCAACTTCTC
<i>NRT2L12B-RT-R</i>	AGCACCAGACACAGAGGCAAC
P-Tubulin-F	TGAGGACTGGTGCTTACCGC
P-Tubulin-R	GCACCATCAAACCTCAGGGA
B-CSNP1-F	GCCATAGCAGCATCCACCAAC
B-CSNP1-R	ACCAGACACAGAGGCCACACC
B-CSNP2-F	TCTGCCTTTGTCTTGGTCGTGC
B-CSNP2-R	CTTTGCTGGTGGTGTATGTCGA
A-CSNP1-F	ATCATGCTTTCTGCACCTGC
A-CSNP1-R	CTTGATGGCATCGAAGACGA
A-CSNP2-F	TGGTGACATGAACAAGGACGA
A-CSNP2-R	GCACCAAGGTCGGAGAGGTAC

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Appendix B. Nucleotide variations in *TaNRT2L12-A* coding region

No.	Site (bp)	Nucleotide variation (x/y) <sup>1)</sup>	Variation type <sup>2)</sup>
1	12	C/T	S
2	78	A/G	S
3	100	A/G	N(Ser/Gly)
4	120	A/G	S
5	132	A/G	S
6	144	C/T	S
7	174	C/T	S
8	177	A/G	S
9	195	C/T	S
10	237	C/T	S
11	240	A/G	S
12	258	C/T	S
13	351	A/G	S
14	372	C/T	S
15	384	C/T	S
16	395	C/T	N(Thr/Ile)
17	396	C/T	N(Thr/Ile)
18	411	C/T	S
19	447	C/T	S
20	480	C/T	S
21	501	A/G	S
22	583	A/G	S
23	591	A/G	S
24	606	A/C	S
25	681	C/T	S
26	692	A/G	N(Arg/Lys)

27	729	A/G	S
28	753	C/T	S
29	807	C/T	S
30	834	C/T	S
31	837	C/T	S
32	849	C/T	S
33	933	C/T	S
34	1087	A/G	N(Ile/Val)
35	1113	C/T	S
36	1134	C/T	S
37	1280	C/T	N(Ala/Val)
38	1399	A/G	N(Ser/Gly)

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- 1) x/y, nucleotide variation from x to y.
  - 2) S, synonymous; N, nonsynonymous.
- The same below.

Appendix C. Nucleotide variations in *TaNRT2L12-B* coding region

No.	Site (bp)	Nucleotide variation (x/y)	Variation type
1	237	C/T	S
2	492	C/T	S
3	576	C/T	S
4	615	C/T	S
5	642	A/G	N(Ile/Met)
6	678	C/T	S
7	730	C/T	N(Phe/Ala)
8	951	C/T	S
9	1227	A/G	S
10	1345	C/G	N(Pro/Ala)
11	1458	C/G	S