

Table S5. Lists of oligonucleotides used for the analysis of the splicing profiles of wild-type and mutant plants by RT-qPCR experiments.

Gene	Forward primer	genome position	Reverse primer	genome position
<i>rpl2</i>	CCGAAGACGGATCAAGGTAA	155542..155561	CGCAATTCATCACCATTTTG	(157249..157268)
<i>rpl2</i> intron exon2	TTAGGAAGAGCCGTACGAGG	157142..157161	CGCAATTCATCACCATTTTG	(157249..157268)
<i>rps3</i>	AGCCGAAGGTGAGTCTCGTA	26990..27009	CCGATTTCCGTAAGACTTGG	(28696..28715)
<i>rps3</i> intron1 exon2	AGCCGAAGGTGAGTCTCGTA	26990..27009	TCTACGGCGGGGTCACTAT	(27088..27106)
<i>cox2</i>	TGGGGGATTAATTGATTGGA	40518..40537	TGATGCTGTACCTGGTCGTT	(42016..42035)
<i>cox2</i> intron1 exon2	TGGGGGATTAATTGATTGGA	40518..40537	AGCAGTACGAGCTGAAAGGC	(40640..40659)
<i>ccmFc</i>	GTGGGTCCATGTAAATGATCG	51765..51785	CACATGGAGGAGTGTGCATC	(52856..52875)
<i>ccmFc</i> intron1 exon1	CCCGGATCGAATCAGAGTT	52747..52765	CACATGGAGGAGTGTGCATC	(52856..52875)
<i>nad1</i> exon1-2	GACCAATAGATACTTCATAAGAGACCA	289014..289040	TTGCCATATCTTCGCTAGGTG	(318039..318059)
<i>nad1</i> intron1 exon2	GACCAATAGATACTTCATAAGAGACCA	289014..289040	CGTGCTCGTACGGTTCATAG	(289133..289152)
<i>nad1</i> exon2-3	ATTCAGCTTCCGCTTCTGG	287943..287961	TCTGCAGCTCAAATGGTCTC	(289034..289053)
<i>nad1</i> intron2 exon2	GGTTGGGTTAGGGGAACATC	288936..288955	TCTGCAGCTCAAATGGTCTC	(289034..289053)
<i>nad1</i> exon3-4	AAAAGAGCAGACCCCATTTGA	147026..147045	TCCGTTTGATCTCCCAGAAG	(287955..287974)
<i>nad1</i> intron3 exon4	AAAAGAGCAGACCCCATTTGA	147026..147045	GGGAGCTGTATGAGCGGTAA	(147113..147132)
<i>nad1</i> exon4-5	AGCCCGGGATCTTCTTGA	143401..143418	TCTTCAATGGGGTCTGCTC	(147030..147048)
<i>nad1</i> intron4 exon5	AGCCCGGGATCTTCTTGA	143401..143418	ACGGAGCTGCATCCCTACT	(143482..143500)
<i>nad2</i> exon1-2	GCGAGCAGAAGCAAGGTTAT	80109..80128	GGATCCTCCCACACATGTTT	(81259..81278)
<i>nad2</i> intron1 exon2	GCGAGCAGAAGCAAGGTTAT	80109..80128	CCCATTCTAACCAGTGGAG	(80272..80291)
<i>nad2</i> exon2-3	AAAGGAACTGCAGTGATCTTGA	332947..332968	AATATTTGATCTTAGGTGCATT TTC	(79761..79785)
<i>nad2</i> intron2 exon2	CCCGATCCGATAGTTTACAA	79641..79660	AATATTTGATCTTAGGTGCATT TTC	(79761..79785)
<i>nad2</i> exon3-4	GCGCAATAGAAAAGGAATGCT	330240..330259	CTATGGGTCTACTGGAGCTAC CC	(333071..333093)
<i>nad2</i> intron3 exon4	GCGCAATAGAAAAGGAATGCT	330240..330259	GGCGAATTTCAAACCTTGTGG	(330377..330396)
<i>nad2</i> exon4-5	CAAAGGAGAGGGGTATAGCAA	327932..327952	TATTTGTTCTTCGCCGCTTT	(329793..329812)
<i>nad2</i> intron4exon4	CTTATTCGTGGCAACCTTCC	329705..329724	TATTTGTTCTTCGCCGCTTT	(329793..329812)
<i>nad4</i> exon1-2	ATTCTATGTTTTTCCCGAAAGC	162115..162136	GAAAAACTGATATGCTGCCTT G	(163664..163685)
<i>nad4</i> intron1 exon2	CCGTATGATGCGGAAGTCTC	163512..163531	GAAAAACTGATATGCTGCCTT G	(163664..163685)
<i>nad4</i> exon2-3	AATACCCATGTTTCCCGAAG	163967..163986	TGCTACCTCCAATTCCTGT	(167228..167247)
<i>nad4</i> intron2 exon3	GCGGAACGACCAGAAAAATA	167110..167129	TGCTACCTCCAATTCCTGT	(167228..167247)
<i>nad4</i> exon3-4	TTCTCCATAAATTCCTCGATT	167577..167598	TGAAATTTGCCATGTTGCAC	(169651..169670)
<i>nad4</i> intron3 exon4	TCTAGCTTGGTTCGGAGAGC	169498..169517	TGAAATTTGCCATGTTGCAC	complement(169651..169670)
<i>nad5</i> exon1-2	TGGACCAAGCTACTTATGGATG	141880..141901	CCATGGATCTCATCGGAAAT	complement(142793..142812)
<i>nad5</i> intron1 exon2	TGGACCAAGCTACTTATGGATG	141880..141901	TTCGCAAATAGGTCCGACT	(141962..141980)
<i>nad5</i> exon2-3	TACCTAAACCAATCATCATATC	190740..1907610	CTGGCTCTCGGGAGTCTCTT	(140743..140762)
<i>nad5</i> intron2-exon2	GTACGATCGTGTCGGGTGA	140656..140674	CTGGCTCTCGGGAGTCTCTT	(140743..140762)
<i>nad5</i> exon3-4	AACTCGGATTCGGCAAGAA	22023..22041	GATATGATGATTGGTTAGGT A	(190740..1907610)
<i>nad5</i> intron3-exon4	AACTCGGATTCGGCAAGAA	22023..22041	GCCGTGTAATAGGCGACCA	(22150..22168)
<i>nad5</i> exon4-5	AACATTGCAAAGGCATAATGA	20695..20715	GTTCTGCGTTTCGGATATG	(21808..21827)
<i>nad5</i> intron4 exon5	AACATTGCAAAGGCATAATGA	20695..20715	CCTGTAAACCCCATGATGT	(20827..20846)
<i>nad7</i> exon1-2	ACCTCAACATCCTGCTGCTC	132118..132137	AAGGTAAAGCTTGAAGATAAG TTTTGT	(133203..133229)

<i>nad7</i> intron1 exon2	ACGGTTTTTAGGGGGATCTG	133128..133147	AAGGTAAAGCTTGAAGATAAG TTTTGT	(133203..133229)
<i>nad7</i> exon2-3	GAGGGACTGAGAAATTAATAGAGTACA	133179..133205	TGGTACCTCGCAATTCAAAA	(134362..134381)
<i>nad7</i> intron2 exon3	AGTGGGAGAGCCGTGTTATG	134182..134201	TGGTACCTCGCAATTCAAAA	(134362..134381)
<i>nad7</i> exon3-4	ACTGTCACTGCACAGCAAGC	134718..134737	CATTGCACAATGATCCGAAG	(135963..135982)
<i>nad7</i> intron3 exon4	TAAAGTGAAGTGGTGGGCCT	135797..135816	CATTGCACAATGATCCGAAG	(135963..135982)
<i>nad7</i> exon4-5	GATCAAAGCCGATGATCGTAA	136007..136027	AGGTGCTTCAACTGCGGTAT	(137951..137970)
<i>nad7</i> intron4 exon5	CGGCCAAATGACTACAGGAT	137856..137875	AGGTGCTTCAACTGCGGTAT	(137951..137970)
<i>rpl5B</i>	CAGAAGACCTTTCCGTGCTC	chr5 15904477..15904496	CACTGGAACCGTGTGTTTG	(15904525..15904544)
<i>actin2</i>	GGTAACATTGTGCTCAGTGGTGG	chr3 6476501..6476523	AACGACCTTAATCTTCATGCTG C	(6476608..6476586)
<i>matR</i>	AATTTTTGCGAGAGCTGGAA	231141.. 231160	TTGAACCCCGTCCTGTAGAC	(231313 .. 231294)
18S nuclear rRNA	AAACGGCTACCACATCCAAG	chr3 14198079..14198098	ACTCGAAAGAGCCCGGTATT	(14198179..14198160)
26S rRNA	GACGAGACTTTCGCCTTTTG	38542 ... 38523	CTTGGAGCGAATTGGATGAT	(38387... 38406)