

Supplementary Table S3. Sequences of primers and oligonucleotide standards for targeted deep sequencing, HRM analysis, and CAPS markers developed for the identification of the G to A mutation in exon 1 of *FAD3A*, C to T mutation in exon 2 of *FAD3B*, and C to T mutation in exon 5 of *FAD3A*.

Mutation	Primer name	Sequence
Targeted deep sequencing		
G to A in exon 1 of <i>FAD3A</i> and C to T in exon 2 of <i>FAD3B</i>	DeepSeq_FAD3_4_F	TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGTGGGTGAAGAACCCCTGGA
	DeepSeq_FAD3_4_R	GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGTCTTCTCCACATTGCCGTGA
C to T in exon 5 of <i>FAD3A4</i>	DeepSeq_FAD3_9_F	TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGCCACGGGTACGAGCAGAAG
	DeepSeq_FAD3_9_A_R	GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGAGGSTGATCAYGTGGGTGAA
High resolution melting (HRM) analysis		
G to A in exon 1 of <i>FAD3A</i>	HRM_FAD3A_E1_F	AAGCTGGACAGCTGGACTG
	HRM_FAD3A_E1_R	CAGAACATGGTTCCTTGAGCAAT
	HRM_FAD3A_E1_ref	AAGCTGGACAGCTGGACTGTCTGGCCTCTCTACTGGATTGCTCAAGGAACCATGTTCTG
	HRM_FAD3A_E1_alt	AAGCTGGACAGCTGGACTGTCTGACCTCTCTACTGGATTGCTCAAGGAACCATGTTCTG
C to T in exon 5 of <i>FAD3A</i>	HRM_FAD3A_E5_F	GAGGGCTGACGACCGTC
	HRM_FAD3A_E5_R	CATTTGAGGGAAGAGATGGTGAATA
	HRM_FAD3A_E5_ref	GAGGGCTGACGACCGTCGATCGAGATTACGGGGTCATCAACACCATCCACCATGACATTGGCACCCATGTTATTACCATTCTTCCCTCAAATG
	HRM_FAD3A_E5_alt	GAGGGCTGACGACCGTCGATTGAGATTACGGGGTCATCAACACCATCCACCATGACATTGGCACCCATGTTATTACCATTCTTCCCTCAAATG
C to T in exon 2 of <i>FAD3B</i>	HRM_FAD3B_E2_F	ATCTGGGTTGTTGCATGC
	HRM_FAD3B_E2_R	TGTCTGAGAAGCTCCCAT
	HRM_FAD3B_E2_ref	ATCTGGGCTGTTGCATGCAGTGGCCATGGGAGCTTCTCAGACA
	HRM_FAD3B_E2_alt	ATCTGGGCTGTTGCATGCAGTGGCTATGGGAGCTTCTCAGACA
Cleaved amplified polymorphic sequences (CAPS) markers		
G to A in exon 1 of <i>FAD3A</i>	CAPS_FAD3A_exon 1_F	TCAATGGGGCGAAGAAGCTA
	CAPS_FAD3A_exon 1_R	AGAAAAGAAAACCCACATTACCAGA
C to T in exon 5 of <i>FAD3A</i>	CAPS_FAD3A_exon 5_F	GGCTTCCTCCGGTCTTCAA
	CAPS_FAD3A_exon 5_R	GACCTCCTACCGCTTCGAC
C to T in exon 2 of <i>FAD3B</i>	CAPS_FAD3B_exon 2_F	TGTTCTTGACATGATTGGTAAACT
	CAPS_FAD3B_exon 2_R	AAATTAGGGTTTGGATTCTTCAGC

Note: The G to A mutation in exon 1 of *FAD3A* gene is located on CP027631.1: 16092348 (according to the assembly of cultivar CDC Bethune – GCA_000224295.2 ASM22429v2) and results in tryptophan with a stop codon substitution; the C to T mutation in exon 5 of *FAD3A* gene is located on CP027631.1: 16090340 and results in arginine with a stop codon substitution; the C to T mutation in exon 2 of *FAD3B* gene is located on CP027622.1: 1035655 and results in histidine with tyrosine substitution.