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BnaA.FAD2.a (Yang)    ATGGGTGCAGGTGGAAGAATGCAAGTGTCTCCTCCCTCCAAAAAGTCTGAAACCGACAACATCAAGCGCGTACCCTGCGAGACACCGCCCTTCACTGTCG 100
BraA.FAD2.a (Yang)    ATGGGTGCAGGTGGAAGAATGCAAGTGTCTCCTCCCTCCAAAAAGTCTGAAACCGACAACATCAAGCGCGTACCCTGCGAGACACCGCCCTTCACTGTCG 100
BnaA.FAD2.a (Zhang)   ATGGGTGCAGGTGGAAGAATGCAAGTGTCTCCTCCCTCCAAAAAGTCTGAAACCGACAACATCAAGTGCGTACCCTGCGAGACACCGCCCTTCACTGTCG 100
H3H4CON1 primer                               5'-AGTGTCTCCTCCCTCCAAAAA-3'


BnaA.FAD2.a (Yang)    GAGAACTCAAGAAAGCAATCCCACCGCACTGTTTCAAACGCTCGATCCCTCGCTCTTTCTCCTACCTCATCTGGGACATCATCATAGC--CTCCTGCTTC 198
BraA.FAD2.a (Yang)    GAGAACTCAAGAAAGCAATCCCACCGCACTGTTTCAAACGCTCGATCCCTCGCTCTTTCTCCTACCTCATCTGGGACATCATCATAGC--CTCCTGCTTC 198
BnaA.FAD2.a (Zhang)   GAGAACTCAAGAAAGCAATCCCACCGCACTGTTTCAAACGCTCGATCCCTCGCTCTTTCTCCTACCTCATCTGGGACATCATCATAGC--CTCCTGCTTC 198


BnaA.FAD2.a (Yang)    TACTACGTCGCCACCACTTACTTCCCTCTCCTCCCTCACCCTCTCTCCTACTTCGCCTGGCCTCTCTACTGGGCCTGCCAGGGCTGCGTCCTAACCGGCG 298
BraA.FAD2.a (Yang)    TACTACGTCGCCACCACTTACTTCCCTCTCCTCCCTCACCCTCTCTCCTACTTCGCCTGGCCTCTCTACTGGGCCTGCCAGGGCTGCGTCCTAACCGGCG 298
BnaA.FAD2.a (Zhang)   TACTACGTCGCCACCACTTACTTCCCTCTCCTCCCTCACCCTCTCTCCTACTTCGCCTGGCCTCTCTACTGGGCCTGCCAGGGCTGCGTCCTAACCGGCG 298
HOR4 type mutation [8] (G→A at position 269)                                               CTAG


BnaA.FAD2.a (Yang)    TCTGGGTCATAGCCCACGAGTGCGGCCACCACGCCTTCAGCGACTACCAGTGGCTGGACGACACCGTCGGCCTCATCTTCCACTCCTTCCTCCTCGTCCC 398
BraA.FAD2.a (Yang)    TCTGGGTCATAGCCCACGAGTGCGGCCACCACGCCTTCAGCGACTACCAGTGGCTGGACGACACCGTCGGCCTCATCTTCCACTCCTTCCTCCTCGTCCC 398
BnaA.FAD2.a (Zhang)   TCTGGGTCATAGCCCACGAGTGCGGCCACCACGCCTTCAGCGACTACCAGTGGCTGGACGACACCGTCGGCCTCATCTTCCACTCCTTCCTCCTCGTCCC 398
HOR3 type mutation [8] (C→T at position 346)                      CTAG


BnaA.FAD2.a (Yang)    TTACTTCTCCTGGAAGTACAGTCATCGACGCCACCATTCCAACACTGGCTCCCTCGAGAGAGACGAAGTGTTTGTCCCCAAGAAGAAGTCAGACATCAAG 498
BraA.FAD2.a (Yang)    TTACTTCTCCTGGAAGTACAGTCATCGACGCCACCATTCCAACACTGGCTCCCTCGAGAGAGACGAAGTGTTTGTCCCCAAGAAGAAGTCAGACATCAAG 498
BnaA.FAD2.a (Zhang)   TTACTTCTCCTGGAAGTACAGTCATCGACGCCACCATTCCAACACTGGCTCCCTCGAGAGAGACGAAGTGTTTGTCCCCAAGAAGAAGTCAGACATCAAG 498


BnaA.FAD2.a (Yang)    TGGTACGGCAAGTACCTCAACAACCCTTTGGGACGCACCGTGATGTTAACGGTTCAGTTCACTCTCGGC----TGGCCTTTGTACTTAGCCTTCAACGTC 594
BraA.FAD2.a (Yang)    TGGTACGGCAAGTACCTCAACAACCCTTTGGGACGCACCGTGATGTTAACGGTTCAGTTCACTCTCGGC----TGGCCTTTGTACTTAGCCTTCAACGTC 594
BnaA.FAD2.a (Zhang)   TGGTACGGCAAGTACCTCAACAACCCTTTGGGACGCACCGTGATGTTAACGGTTCAGTTCACTCTCGGC----TGGCCTTTGTACTTAGCCTTCAACGTC 594
DMS100 type mutation [15] (C→T at position 553)                  CGGTTTAGTTC
SW Hickory type mutation [28] (AGCC insertion at position 567-568)              TCGGCAGCCTGGCC
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BnaA.FAD2.a (Yang)     TCGGGGAGACCTTACGACGGCGGCTTCGCTTGCCATTTCCACCCCAACGCTCCCATCTACAACGACCGTGAGCGTCTCCAGATATACATCTCCGACGCTG 694
BraA.FAD2.a (Yang)     TCGGGAAGACCTTACGACGGCGGCTTCGCTTGCCATTTCCACCCTAACGCTCCCATCTACAACGACCGTGAGCGTCTCCAGATATACATCTCCGACGCTG 694
BnaA.FAD2.a (Zhang)    TCGGGGAGACCTTACGACGGCGGGTTCGCTTGCCATTTCCACCCCAACGCTCCCATCTACAACGACCGTGAGCGTCTCCAGATATACATCTCCGACGCTG 694


BnaA.FAD2.a (Yang)     GCATCCTCGCCGTCTGCTACGGTCTCTACCGCTACGCTGCTGTCCAAGGAGTTGCCTCGATGGTCTGCTTCTACGGAGTTCCTCTTCTGATTGTCAACGG 794
BraA.FAD2.a (Yang)     GCATCCTCGCCGTCTGCTACGGTCTCTACCGCTACGCTGCTGTCCAAGGAGTTGCCTCGATGGTCTGCTTCTACGGAGTCCCGCTTCTGATAGTCAACGG 794
BnaA.FAD2.a (Zhang)    GCATCCTCGCCGTCTGCTACGGTCTCTACCGCTACGCTGCTGTCCAAGGAGTTGCCTCGATGGTCTGCTTCTACGGAGTTCCTCTTCTGATTGTCAACGG 794
H3H4CON2 primer                                                3'-AGGTTCCTCAACGGAGCTA-5'


BnaA.FAD2.a (Yang)     GTTCTTAGTTTTGATCACTTACTTGCAGCACACGCATCCTTCCCTGCCTCACTATGACTCGTCTGAGTGGGATTGGTTGAGGGGAGCTTTGGCCACCGTT 894
BraA.FAD2.a (Yang)     GTTCTTAGTTTTGATCACTTACTTGCAGCACACGCATCCTTCCCTGCCTCACTACGATTCGTCTGAGTGGGATTGGTTGAGGGGAGCGTTGGCTACCGTT 894
BnaA.FAD2.a (Zhang)    GTTCTTAGTTTTGATCACTTACTTGCAGCACACGCATCCTTCCCTGCCTCACTATGACTCGTCTGAGTGGGATTGGTTGAGGGGAGCTTTGGCCACCGTT 894


BnaA.FAD2.a (Yang)     GACAGAGACTACGGAATCTTGAACAAGGTCTTCCACAATATCACGGACACGCACGTGGCGCATCACCTGTTCTCGACCATGCCGCATTATCATGCGATGG 994
BraA.FAD2.a (Yang)     GACAGAGACTACGGGATCTTGAACAAGGTCTTCCACAATATCACGGACACGCACGTGGCGCATCACCTGTTCTCGACCACGCCGCATTATCACGCGATGG 994
BnaA.FAD2.a (Zhang)    GACAGAGACTACGGAATCTTGAACAAGGTCTTCCACAATATCACGGACACGCACGTGGCGCATCACCTGTTCTCGACCATGCCGCATTATCATGCGATGG 994


BnaA.FAD2.a (Yang)     AAGCTACGAAGGCGATAAAGCCGATACTG-GGAGAGTATTATCAGTTCGATGGGACGCCGGTGGTTAAGGCGATGTGGAGGGAGGCGAAGGAGTGTATCT 1093
BraA.FAD2.a (Yang)     AAGCTACCAAGGCGATAAAGCCGATACTG-GGAGAGTATTATCAGTTCGATGGGACGCCGGTGGTTAAGGCGATGTGGAGGGAGGCGAAGGAGTGTATCT 1093
BnaA.FAD2.a (Zhang)    AAGCTACGAAGGTGATAAAGCCGATACTG-GGAGAGTATTATCAGTTCGATGGGACGCCGGTGGTTAAGGCGATGTGGAGGGAGGCGAAGGAGTGTATCT 1093


BnaA.FAD2.a (Yang)     ATGTGGAACCGGACAGGCAAGGTGAGAAGAAAGGTGTGTTCTGGTACAACAATAAGTTATGA 1155
BraA.FAD2.a (Yang)     ATGTGGAACCGGACAGGCAAGGTGAGAAGAAAGGTGTGTTCTGGTACAACAATAAGTTATGA 1155
BnaA.FAD2.a (Zhang)    ATGTGGAACCGGACAGGCAAGGTGAGAAGAAAGGTGTGTTCTGGTACAACAATAAGTTATGA 1155
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Fig. S1 The alignment of the sequences of the *BnaA.FAD2.a* (Yang) gene from *B.napus*, the *BraA.FAD2.a* (Yang) gene from *B.rapa* [28] and the *BnaA.FAD2.a* (Zhang) gene from *B.napus* [18] (GenBank accession AY577313). The differences are indicated with green color and the underlined nucleotides represent the codons in the coding sequence. The sequence of the *BnaA.FAD2.a* (Zhang) gene was used for amplification of the Δ12 oleate desaturase gene from genome A (located on the chromosome A5), and therefore, this sequence is the basis for design of described CAPS markers. The positions of HOR3 and HOR4 type mutations in the studied gene, and the allelic forms that are specific to the HO mutants [8], are indicated using the color scheme that corresponds to the colors used for the display of each mutation shown in Fig. 1. The sequences of the H3H4CON1 (forward) and the H3H4CON2 (reverse) primers used for the amplification of the specific fragment of the *BnaA.FAD2* gene are also shown and the corresponding sequences of the gene are indicated with yellow color. In addition, the positions of other mutations in this gene, discovered and described by other authors [15, 28] are also indicated for comparison

Cleaved amplified polymorphic sequences (CAPS) marker for identification of two mutant alleles of the rapeseed *BnaA.FAD2* gene

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