

```

BIS1.1.SEQ ATGGCGCCTTGGTTAAGAATCATGTAGAGCCTCACATGCCAAAATCCTAGCCATTGGCACTGCAAATCCACCAAAGTCTACTACCAABAGACTATCCTGATTTCTTTTCGAGTC 120
BIS1.2.SEQ -----
BIS1.3.SEQ ATGGCGCCTTTTGGTTAAGCATCAAGTAGAGCCTCACATGCCAAAATCCTAGCCATTGGCACTGCAAATCCACCAAAGTCTACTACCAABAGACTATCCTGATTTCTTTTCGAGTC 120
BIS2.1.SEQ ATGGCGCCCTTGGTTAAGCATCAAGTAGAGCCTCACATGCCAAAATCCTAGCCATTGGCACTGCAAATCCACCAAATGTCTACTACCAAGAGGACTATCCTGATTTCTTTTCGAGTC 120
BIS2.2.SEQ ATGGCGCCTTTGGTTAAGCATCAAGTAGAGCCTCACATGCCAAAATCCTAGCCATTGGCACTGCAAATCCACCAAATGTCTACTACCAAGAGGACTATCCTGATTTCTTTTCGAGTC 120
BIS2.3.SEQ ATG-----
BIS2.4.SEQ ATGGCGCCCTTGGTTAAGCATCAAGTAGAGCCTCACATGCCAAAATCCTAGCCATTGGCACTGCAAATCCACCAAATGTCTACTACCAAGAGGACTATCCTGATTTCTTTTCGAGTC 120
BIS3.SEQ ATGGCGCCTTTGGTTAAGAAT-----GAGCCTCAACATGCCAAAATCCTAGCCATTGGCACTGCAAATCCACCAAAGTCTACTACCAAGAGGACTATCCTGATTTCTTTTCGAGTC 114
BIS4.SEQ ATGGCGCCTTTGGTTAAGAATCAAGTAGAGCCTCACATGCCAAAATCCTAGCCATTGGCACTGCAAATCCACCAAATGTCTACTACCAAGAGACTATCCTGATTTCTTTTCGAGTC 120

BIS1.1.SEQ ACCAAAAAGAGCACAGAACAAATTTAAGAGAGAAGTTCGATCGCATTTGTGAGAAATCAAAATAAGAAAGCGYTACTTGTATCTAACAGAAGAGATTCTAAATGCTAACCCGAGCATA 240
BIS1.2.SEQ -----GAGAAATCAAAATAAGGAAGCGTTACTTGTATCTAACAGAAGAGATTCTAAATGCTAACCCGAGCATA 69
BIS1.3.SEQ ACCAAAAAGAGCACAAACATATTTAAGAGAGAAGTTCGATCGCATTTGTGAGAAATCAAAATAAGAAAGCGYTACTTGTATCTAACAGAAGAGATTCTAAATGCTAACCCGAGCATA 240
BIS2.1.SEQ ACTAAAAACGAGCACAGAACGGATTTAAGAGAGAAGTTCGATCGCATATGTGAGAAATCAAGAACAAAGGAAGCGTTACTTGTACTAACAGAAGAGATTCTAAAGCTAACCCAAGCATA 240
BIS2.2.SEQ ACTAAAAACGAGCACAGAACGGATTTAAGAGAGAAGTTGATCGCATATGTGAGAAATCAAGAACAAAGGAAGCGTTACTTGTACTAACAGAAGAGATTCTAAAGCTAACCCAAGCATA 240
BIS2.3.SEQ -----
BIS2.4.SEQ ACTAAAAACGAGCACAGAACGGATTTAAGAGAGAAGTTCGATCGCATAT----- 169
BIS3.SEQ ACCAAAAAGAGCACAGAACGATTTAAGAGAGAAGTTCGATCGCATTTGTGAGAAATCAAGAACAAAGGAAGCGYTACTTGTACTAACAGAAGAGATTCTAAAGCTAACCCAAGCATA 234
BIS4.SEQ ACTAAAAACGAGCACAGAACGGATTTAAGAGAGAAGTTCGATCGCATATGTGAGAAATCAAGAACAAAGGAAGCGTTACTTGTACTAACAGAAGAGATTCTAAAGCTAACCCAAGCATA 240

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BIS1.2.SEQ TATACCTATGGAGCCCCATCACTCGATGTGCGCCAAGACATGTTGAACCTGAGGTCCCAAAGCTAGGGCAACAAGCACTGAAAGCCATCAAAGAGTGGGGCCAGCCCATCTCAAAG 189
BIS1.3.SEQ TATACCTATGGAGCCCCATCACTGATGTGCGCCAAGACATGTTGAACCTGAGGTCCCAAAGCTAGGGCAACAAGCACTGAAAGCCATCAAAGAGTGGGGCCAGCCCATCTCAAAG 360
BIS2.1.SEQ TATACCTATGGAGCCCCATCACTGATGTGCGCCAAGACATGTTGAACCTGAGGTCCCAAAGCTAGGGCAACAAGCAGCATTGAAAGCCATCAAAGAGTGGGGCCAGCCCATCTCAAAG 360
BIS2.2.SEQ TATACCTATGGAGCCCCATCACTGATGTGCGCCAAGACATGTTGAACCTGAGGTCCCAAAGCTAGGGCAACAAGCAGCATTGAAAGCCATCAAAGAGTGGGGCCAGCCCATCTCAAAG 360
BIS2.3.SEQ -----
BIS2.4.SEQ ----- 169
BIS3.SEQ TATACCTATGGAGCCCCATCACTCGATGTGCGCCAAGACATTTGTAACATGAGGTCCCAAAGCTAGGGCAACAAGCAGCATTGAAAGCCATCAAAGAGTGGGGCCAGCCCATCTCAAAA 354
BIS4.SEQ TATACCTATGGAGCCCCATCACTCGATGTGCGCCAAGACATGTTGAACCTGAGGTCCCAAAGCTAGGGCAACAAGCAGCACTGAAAGCCATCAAAGAGTGGGGCCAGCCCATCTCAAAG 360

BIS1.1.SEQ ATCACCCACCTCATCTTTTGCACAGCTTTTTCGCTTGACATGCCAGGTGCCGACTTCCAATTGGTCAAGCTCCTCGGCCTTAACCCATCTGTCACCAGAACCATGATCTATGAAGCTGGT 480
BIS1.2.SEQ ATCACCCACCTCATCTTTTGCACAGCTTCTTTCGCTTGACATGCCAGGTGCCGACTTCCAATTGGTCAAGCTCCTCGGCCTTAACCCATCTGTCACCAGAACCATGATCTATGAAGCTGGT 309
BIS1.3.SEQ ATCACCCACCTCATCTTTTGCACAGCTTCTTTCGCTTGACATGCCAG-----CCTCGGCCTTAACCCATCTGTCACCAGAACCATGATCTATGAAGCTGGT 456
BIS2.1.SEQ ATCACCCACCTCATCTTTTGCACAGCTTCTTTCGCTTGACATGCCAGGTGCCGACTTCCAATTGGTCAAGCTTCTCGGCCTTAACCCATCTGTCACCAGAACCATGATCTATGAAGCTGGC 480
BIS2.2.SEQ ATCACCCACCTCATCTTTTGCACAGCTTCTTTCGCTTGACATGCCAGGTGCCGACTTCCAATTGGTCAAGCTTCTCGGCCTTAACCCATCTGTCACCAGAACCATGATCTATGAAGCTGGC 480
BIS2.3.SEQ -----
BIS2.4.SEQ ----- 169
BIS3.SEQ ATCACCCACCTCATCTTTTGCACAGCTTCTTTCGCTTGACATGCCAGGTGTTGACTTCCAATTAATCAAGCTCCTCGGCCTTGATCCATCTGTCACCAGAACCATGATCTATGAAGCTGGC 474
BIS4.SEQ ATCACCCACCTCATCTTTTGCACAGCTTCTTTCGCTTGACATGCCAGGTGCCGACTTCCAATTGGTCAAGCTCCTTGGCCTTAACCCATCTGTCACCAGAACCATGATCTATGAAGCTGGC 480

BIS1.1.SEQ TGCTATGCTGGTGGCAGCTGCCTCCGCCTGGCCAAGGACTTCCAGAGAAACAATGAGGGTGCACGCGTCTCTTGTGGTGTGCCCGGAGATCACGACCGTGTTTTTCCACGGACTCACTGAC 600
BIS1.2.SEQ TGCTATGCTGGTGGCAGCTGCCTCCGCCTGGCCAAGGACTTCCAGAGAGAAACAATGAGGGTGCACGCGTCTCTTGTGGTGTGCCCGGAGATCACGACCGTGTTTTTCCACGGACTCACTGAC 429
BIS1.3.SEQ TGCTATGCTGGTGGCAGCTGCCTCCGCCTGGCCAAGGACTTCCAGAGAGAAACAATGAGGGTGCACGCGTCTCTTGTGGTGTGCCCGGAGATCACGACCGTGTTTTTCCACGGACTCACTGAC 576
BIS2.1.SEQ TGCTATGCTGGTGGCAGCTGCCTCCGCCTGGCCAAGGACTTCCAGAGAGAAACAATGAGGGTGCACGCGTCTCTTGTGGTGTGCCCGGAGATCACGACCGTGTTTTTCCACGGACTCACTGAC 600
BIS2.2.SEQ TGCTATGCTGGTGGCAGCTGCCTCCGCCTGGCCAAGGACTTCCAGAGAGAAACAATGAGGGTGCACGCGTCTCTTGTGGTGTGCCCGGAGATCACGACCGTGTTTTTCCACGGACTCACTGAC 600
BIS2.3.SEQ -----CTGGTGCAATGTCCTCCGCCTGGCCAAGGA-TTCGAGAGAAACAATGAGGGTGCACGCGTCTCTTGTGGTGTGCCCGGAGATCACGACCGTGTTTTTCCACGGACTCACTGAC 114
BIS2.4.SEQ ----- 169
BIS3.SEQ TGCTATGCTGGTGGCAGCTGCCTCCGCCTGGCCAAGGACTTCCAGAGAGAAACAATGAGGGTGCACGCGTCTCTTGTGGTGTGCCCGGAGATCACGACCGTGTTTTTCCACGGACTCACTGAC 594
BIS4.SEQ TGCTATGCTGGTGGCAGCTGCCTCCGCCTGGCCAAGGACTTCCAGAGAGAAACAATGAGGGTGCACGCGTCTCTTGTGGTGTGCCCGGAGATCACGACCGTGTTTTTCCACGGACTCACTGAC 600

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Figure S1. Alignment of the nine predicted BIS coding sequences of 'Golden Delicious'. Shading indicates nucleotide identity, dashes mark gaps.

Figure S1 continued

BIS1.1.SEQ ACCCACCTTGACATACTGGTGGGTCAGGCTCTTTTTGCTGATGGAGCATCTGCTGTGATAGTTGGGGCTAATCCAGAGCCTGAAATTGAGAGGCCCTGTGTTGAAAMCGTGGCATGCAGG 720
 BIS1.2.SEQ ACCCACCTTGACATACTGGTGGGTCAGGCTCTTTTTGCTGATGGAGCATCTGCTGTGATAGTTGGGGCTAATCCAGAGCCTGAAATTGAGAGGCCCTGTGTTGAAATCGTGGCATGCAGG 549
 BIS1.3.SEQ ACCCACCTTGACATACTGGTGGGTCAGGCTCTTTTTGCTGATGGAGCATCTGCTGTGATAGTTGGGGCTAATCCAGAGCCTGAAATTGAGAGGCCCTGTGTTGAAATCA----- 685
 BIS2.1.SEQ ACCCACCTTGACATACTAGTGGGGCAAGCTCTTTTTGCTGATGGAGCATCTGCTGTGATAGTTGGGGCCAATCCAGAGCCTGAAATTGAGAGGCCACTGTTTGAATCGTGGCATGCAGA 720
 BIS2.2.SEQ ACCCACCTTGACATACTAGTGGGGCAAGCTCTTTTTGCTGATGGAGCATCTGCTGTGATAGTTGGGGCCAATCCAGAGCCTGAAATTGAGAGGCCACTGTTTGAATCGTGGCATGCAGA 720
 BIS2.3.SEQ ACCCACCTTGACATACTAGTGGGGCAAGCTCTTTTTGCTGATGGAGCATCTGCTGTGATAGTTGGGGCCAATCCAGAGCCTGAAATTGAGAGGCCACTGTTTGAATCGTGGCATGCAGA 234
 BIS2.4.SEQ -----TGGGGCAAGCTCTTTTTGCTGATGGAGCATCTGCTGTGATAGTTGGGGCCAATCCAGAGCCTGAAATTGAGAGGCCACTGTTTGAATCGTGGCATGCAGA 270
 BIS3.SEQ ACCCACCTTGACATACTGGTGGGTCAGGCTCTTTTTGCTGATGGAGCATCTGCTGTGATAGTTGGGGCCAATCCAGAGCCTGAAATTGAGAGGCCACTGTTTGAATCGTGGCATGCAGG 714
 BIS4.SEQ ACCCACCTTGACATACTGGTGGGTCAGGCTCTTTTTGCTGATGGAGCATCTGCTGTGATAGTTGGGGCTAATCCAGAGCCTGAAATTGAGAGGCCACTGTTTGAATCGTGGCATGCAGG 720

 BIS1.1.SEQ CAGACGATCATACCTAACTCAGAGCATGGTGTAGTGGCCAACATTCGTGAAATGGGGTTAATTATTATTTATCAGGAGAAGTCCCAAAATTTGTTGGTGGAAATGTTGTGGATTTTCTG 840
 BIS1.2.SEQ CAGACGATCATACCTAACTCAGAGCATGGTGTAGTGGCCAACATTCGTGAAATGGGGTTAATTATTATTTATCAGGAGAAGTCCCAAAATTTGTTGGTGGAAATGTTGTGGATTTTCTG 669
 BIS1.3.SEQ ----- 685
 BIS2.1.SEQ CAGACGATCATACCTAAATTCAGAGCATGGTGTCTGTTGGCCAACATTCGTGAAATGGGGTTAATTATTATTTATCAGGAGAAGTCCCAAAATTTGTTGGTGGAAATGTTGTGGATTTTCTG 840
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 BIS2.3.SEQ CAGACGATCATACCTAAATTCAGAGCATGGTGTCTGTTGGCCAACATTCGTGAAATGGGGTTAATTATTATTTATCAGGAGAAGTCCCAAAATTTGTTGGTGGAAATGTTGTGGATTTTCTG 354
 BIS2.4.SEQ CAGACGATCATACCTAAATTCAGAGCATGGTGTCTGTTGGCCAACATTCGTGAAATGGGGTTAATTATTATTTATCAGGAGAAGTCCCAAAATTTGTTGGTGGAAATGTTGTGGATTTTCTG 390
 BIS3.SEQ CAGACGATCATACCTAACTCAGAGCATGGTGTAGTGGCCAACATTCGTGAAATGGGGTTAATTATTATTTATCAGGAGAAGTCCCAAAATTTGTTGGTGGAAATGTTGTGGATTTTCTG 834
 BIS4.SEQ CAGACGATCATACCTAACTCAGAGCATGGTGTAGTGGCCACATTCGTGATAGTGGGATTTTGAATATTATTTATCAGGAGAAGTCCCAAAATTTGTTGGTGGAAATGTTGTGGATTTTCTG 840

 BIS1.1.SEQ ACTAAAACCTTTTGAAGGTTGACGGAAAGAATAAGGATGGAACCTCTGTTTTTTCAGTGTGCACCCTGGTGGGCCCTGCATTTAGTAGACCAGGTGGAGGAGCAATGGGTTTGAAGGAA 960
 BIS1.2.SEQ ACTAAAACCTTTTGAAGGTTGACGGAAAGAATAAGGATGGAACCTCTGTTTTTTCAGTGTGCACCCTGGTGGGCCCTGCATTTAGTAGACCAGGTGGAGGAGCAATGGGTTTGAAGGAA 789
 BIS1.3.SEQ -----GAAAGAAATA-----TGCTTTCA----- 704
 BIS2.1.SEQ ACTAAACTTTTGAAGGTTGACGGAAAGAATAAGGATGGAACCTCTGTTTTTTCAGTGTGCACCCTGGTGGGCCCGCTATTGTAGACCAGGTGGAGGAGCAATGGGTTTGAAGGAA 960
 BIS2.2.SEQ ACTAAACTTTTGAAGGTTGACGGAAAGAATAAGGATGGAACCTCTGTTTTTTCAGTGTGCACCCTGGTGGGCCCGCTATTGTAGACCAGGTGGAGGAGCAATGGGTTTGAAGGAA 960
 BIS2.3.SEQ ACTAAAACCTTTTGAAGGTTGACGGAAAGAATAAGGATGGAACCTCTGTTTTTTCAGTGTGCACCCTGGTGGGCCCGCTATTGTAGACCAGGTGGAGGAGCAATGGGTTTGAAGGAA 474
 BIS2.4.SEQ ACTAAACTTTTGAAGGTTGACGGAAAGAATAAGGATGGAACCTCTGTTTTTTCAGTGTGCACCCTGGTGGGCCCGCTATTGTAGACCAGGTGGAGGAGCAATGGGTTTGAAGGAA 510
 BIS3.SEQ ACTAAAACCTTTTGAAGGTTGACGGAAAGAATAAGGATGGAACCTCTGTTTTTTCAGTGTGCACCCTGGTGGGCCCGCTATTGTAGACCAGGTGGAGGAGCAATGGGTTTGAAGGAA 954
 BIS4.SEQ ACTAAAACCTTTTGAAGGTTGACGGAAAGAATAAGGATGGAACCTCTGTTTTTTCAGTGTGCACCCTGGTGGGCCCGCTATTGTAGACCAGGTGGAGGAGCAATGGGTTTGAAGGAA 960

 BIS1.1.SEQ GGGAACTTAGGGCTACAAGGCATGTGTTGAGTGAGTATGGCAACATGGGAGCTCCATCTGTGCACCTTATTTTGGATGAGATGAGAAATAAGTCGATTGGGAAGGCCAAAGCCACAAC 1080
 BIS1.2.SEQ GGGAACTTAGGGCTACAAGGCATGTGTTGAGTGAGTATGGCAACATGGGAGCTCCATCTGTGCACCTTATTTTGGATGAGATGAGAAATAAGTCGATTGGGAAGGCCAAAGCCACAAC 909
 BIS1.3.SEQ ----- 704
 BIS2.1.SEQ GGGAACTTAGGGCAACAAGGCATGTGTTGAGTGAGTATGGCAACATGGGAGCTCCATCTGTGCACCTTATTTTGGATGAGATGAGAAAGAAGTCGATTGGGAAGGCCAAAGCCACAAC 1080
 BIS2.2.SEQ GGGAACTTAGGGCAACAAGGCATGTGTTGAGTGAGTATGGCAACATGGGAGCTCCATCTGTGCACCTTATTTTGGATGAGATGAGAAAGAAGTCGATTGGGAAGGCCAAAGCCACAAC 1080
 BIS2.3.SEQ GGGAACTTAGGGCAACAAGGCATGTGTTGAGTGAGTATGGCAACATGGGAGCTCCATCTGTGCACCTTATTTTGGATGAGATGAGAAAGAAGTCGATTGGGAAGGCCAAAGCCACAAC 594
 BIS2.4.SEQ GGGAACTTAGGGCAACAAGGCATGTGTTGAGTGAGTATGGCAACATGGGAGCTCCATCTGTGCACCTTATTTTGGATGAGATGAGAAAGAAGTCGATTGGGAAGGCCAAAGCCACAAC 630
 BIS3.SEQ GGGAACTTAGGGCAACAAGGCATGTGTTGAGTGAGTATGGCAACATGGGAGCTCCATCTGTGCACCTTATTTTGGATGAGATGAGAAATAAGTCGATTGGGAAGGCCAAAGCCACAAC 1074
 BIS4.SEQ GGGAACTTAGGGCAACAAGGCATGTGTTGAGTGAGTATGGCAACATGGGAGCTCCATCTGTGCACCTTATTTTGGATGAGATGAGAAATAAGTCGATTGGGAAGGCCAAAGCCACAAC 1080

 BIS1.1.SEQ GGTGAAGGTTTGAATGGGGTGTGCTGATTGGAATCGGACCGGGACTCACTGTCGAGACAGCCGTCGCTAGTGAATCTATTACATAC-----TAA 1173
 BIS1.2.SEQ GGTGAAGGTTTGAATGGGGTGTGCTGATTGGAATCGGACCGGGACTCACTGTCGAGACAGCCGTCGCTAGTGAATCTATTACATAC-----TAA 1002
 BIS1.3.SEQ -----ATCA----- 708
 BIS2.1.SEQ GGTGAAGGTTTGAATGGGGTGTGCTGATTGGAATCGGACCGGGACTTACGTCGAGACAGCCGTCGCTAGTGAATCTATTACATGC-----TAA 1173
 BIS2.2.SEQ GGTGAAGGTTTGAATGGGGTGTGCTGATTGGAATCGGACCGGGACTTACGTCGAGACAGCCGTCGCTAGTGAATCTATTACATGC-----TAA 1173
 BIS2.3.SEQ GGTGAAGGTTTGAATGGGGTGTGCTGATTGGAATCGGACCGGGACTTACGTCGAGACAGCCGTCGCTAGTGAATCTATTACATGC-----TAA 687
 BIS2.4.SEQ GGTGAAGGTTTGAATGGGGTGTGCTGATTGGAATCGGACCGGGACTTACGTCGAGACAGCCGTCGCTAGTGAATCTATTACATGC-----TAA 723
 BIS3.SEQ GGTGAAGGTTTGAATGGGGTGTGCTGATTGGAATCGGACCGGGACTCACTGTCGAGACAGCCGTCGCTAGTGAATCTATTACATGC-----TAA 1167
 BIS4.SEQ GGTGAAGGTTTGAATGGGGTGTGCTGATTGGAATCGGACCGGGACTCACTGTCGAGACAGCCGTCGCTAGTGAATCTATTACATGC-----TAA 1185

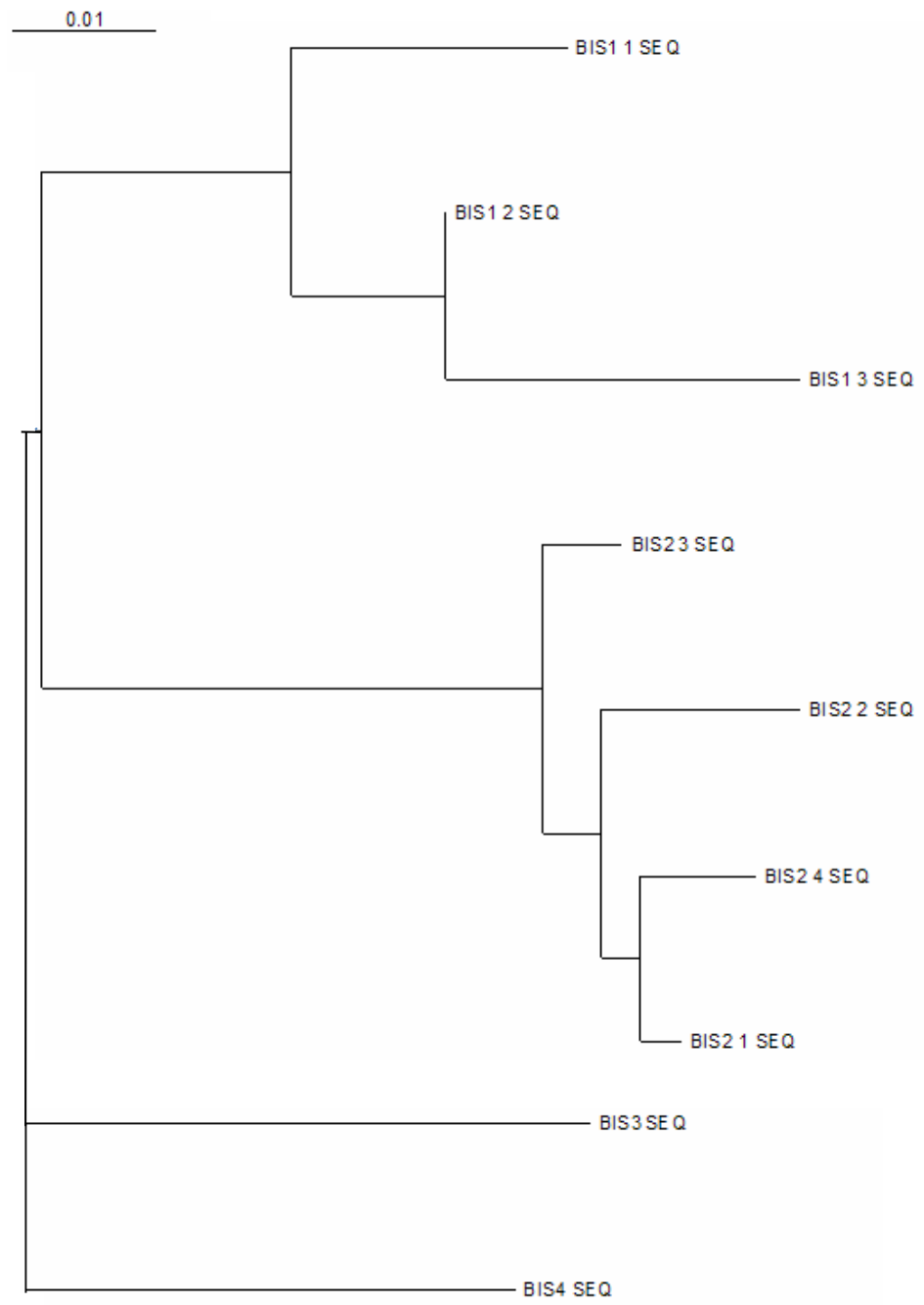


Figure S2. Phylogenetic tree of nine BIS coding sequences of 'Golden Delicious'.

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pred. gene.SEQ ATGGCGCCTTCGGTTAAGAATCATGTAGAGCCTCCACATGCCAAAATCCTAGCCATTGGCACTGCAAATCCACCCAACGTCTACTACCAAAAAGACTATCCTGATTTCTTA 111
pred. cDNA.SEQ ATGGCGCCTTCGGTTAAGAATCATGTAGAGCCTCCACATGCCAAAATCCTAGCCATTGGCACTGCAAATCCACCCAACGTCTACTACCAAAAAGACTATCCTGATTTCTTA 111
cloned cDNA.SEQ ATGGCGCCTTCGGTTAAGAATCATGTAGAGCCTCCACATGCCAAAATCCTAGCCATTGGCACTGCAAATCCACCCAATGTCTACTACCAAAAAGACTATCCTGATTTCTTA 111

pred. gene.SEQ TTTTCGAGTCACCAAAAATGAGCACAGAACAATTTAAGAGAGAAGTTTCGATCGCATTGTAAGTATAATTTTACAAACACTACTCCTGCACATTTATACTGCACATGCAC 222
pred. cDNA.SEQ TTTTCGAGTCACCAAAAATGAGCACAGAACAATTTAAGAGAGAAGTTTCGATCGCATT----- 169
cloned cDNA.SEQ TTTTCGAGTCACAAAAATGAGCACAGAACAATTTAAGAGAGAAGTTTCGATCGCATT----- 171

pred. gene.SEQ GAGATTACCTTATATTTATATGTAGGAAGAAAACATATCATGCATTAAATTGTATGAAAGATTTTGGACCTCTCAATGAATTGACTTTGATCTTGAGTTGTAAAAATCCAAC 333
pred. cDNA.SEQ ----- 169
cloned cDNA.SEQ ----- 171

pred. gene.SEQ TCTACCAAAATTATGAGCTAAAATGAATCACATCCCAGACTCAACACGCCACGCGACATGTTTCATTTCAAAAAGATACATTGTTATTAACGGAAGAAAATAGTCACTTTAGAC 444
pred. cDNA.SEQ ----- 169
cloned cDNA.SEQ ----- 171

pred. gene.SEQ ATGTTACACTAATTAATTTGTGGCATCTCGGTCCAATAGTACATTATCATATGTGAGTTTTTCTTCAAATTATATTGTATTAGTTGATGCACAAGGATATAAAAACATGTCC 555
pred. cDNA.SEQ ----- 169
cloned cDNA.SEQ ----- 171

pred. gene.SEQ TAACTTAATTACTAATTAAACAGGTGAGAAGTCAAAAAYAAGRAAGCGYACTTGTATCTAACATAAGAGATTCTAAATGCTAACCCGAGCATATATACCTATGGAGCCCCA 666
pred. cDNA.SEQ -----CCCCA 174
cloned cDNA.SEQ -----GTGAGAAGTCAAAAACAAGAAAGCGCTACTTGTATCTAACAGAAGAGATTCTAAATGCTAACCCGAGCATATATACCTATGGGCCCCA 258

pred. gene.SEQ TCACTCGATGTGCGCCAAGACATGTTGAACCCCTGAGGTCCCAAAGCTAGGGCAACAAGCAGCACTAAAAGCCATCAAAGAGTGGGGCCAGCCCATCTCAAAGATCACCCAC 777
pred. cDNA.SEQ TCACTCGATGTGCGCCAAGACATGTTGAACCCCTGAGGTCCCAAAGCTAGGGCAACAAGCAGCACTAAAAGCCATCAAAGAGTGGGGCCAGCCCATCTCAAAGATCACCCAC 285
cloned cDNA.SEQ TCACTCGATGTGCGCCAAGACATGTTGAACCCCTGAGGTCCCAAAGCTAGGGCAACAAGCAGCACTGAAAAGCCATCAAAGAGTGGGGCCAGCCCATCTCAAAGATCACCCAC 369

pred. gene.SEQ CTCATCTTTTGCACAGCTTTTTGCGTTGACATGCCAGGTGCCGACTTCCAATTGGTCAAGCTCCTCGGCCTTAACCCATCCGTCACCAGAACCATGATCTATGAAGCTGGT 888
pred. cDNA.SEQ CTCATCTTTTGCACAGCTTTTTGCGTTGACATGCCAGGTGCCGACTTCCAATTGGTCAAGCTCCTCGGCCTTAACCCATCCGTCACCAGAACCATGATCTATGAAGCTGGT 396
cloned cDNA.SEQ CTCATCTTTTGCACAGCTTTTTCGTTGACATGCCAGGTGCCGACTTCCAATTGGTCAAGCTCCTCGGCCTTAACCCATCCGTCACCAGAACCATGATCTATGAAGCTGGT 480

pred. gene.SEQ TGCTATGCTGGTGCAGCTGTCTCCGCTGGCCAAGGACTTCACAGAGAACAATGAGGTTGCACGCGTCTTGTGGTGTGCACCGAGATCACGACCGGTTTTTTCCACGGA 998
pred. cDNA.SEQ TGCTATGCTGGTGCAGCTGTCTCCGCTGGCCAAGGACTTCACAGAGAACAATGAGG-----ATCACGACCGGTTTTTTCCACGGA 477
cloned cDNA.SEQ TGCTATGCTGGTGCAGCTGTCTCCGCTGGCCAAGGACTTTCAGAGAGAACAAGAGGTGCACGCGTCTTGTGGTGTGCACCGAGATCACGACCGTTTTTTCCACGGA 591

pred. gene.SEQ CTCACTGACACCCACCTTGACATACTGGTGGGCCAGGCTCTTTTTGCTGAYGGAGCATCTGCTGTGATAGTTGGGGCTAATCCAGAGCCTRAAATTGAGAGGCCGCTGTTT 1109
pred. cDNA.SEQ CTCACTGACACCCACCTTGACATACTGGTGGGCCAGGCTCTTTTTGCTGAYGGAGCATCTGCTGTGATAGTTGGGGCTAATCCAGAGCCTRAAATTGAGAGGCCGCTGTTT 588
cloned cDNA.SEQ CTCACTGACACCCACCTTGACATACTGGTGGGCCAGGCTCTTTTTGCTGAGGAGCATCTGCTGTGATAGTTGGGGCTAATCCAGAGCCTGAAATTGAGAGGCCGCTGTTT 702

pred. gene.SEQ GAAAWCGTGGCATGCAGGCAGACGATCATACTAACTCAGAGCATGGTGTAGTGGCCAACATTCGTGAAATGGGGTTTAATTATTATTTATCGGGAGAAGTCCCYAAATTT 1220
pred. cDNA.SEQ GAAAWCGTGGCATGCAGGCAGACGATCATACTAACTCAGAGCATGGTGTAGTGGCCAACATTCGTGAAATGGGGTTTAATTATTATTTATCGGGAGAAGTCCCYAAATTT 699
cloned cDNA.SEQ GAAAWCGTGGCATGCAGGCAGACGATCATACTAACTCAGAGCATGGTGTAGTGGCCAACATTCGTGAAATGGGGTTTAATTATTATTTATCGGGAGAAGTCCCAAAATTT 813

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Figure S3. Alignment of the predicted *BIS1.1* gene and cDNA sequences of 'Golden Delicious' (MDP0000641583) with the cloned cDNA sequence of 'Holsteiner Cox'. An intron is labeled in yellow, as well as some single nucleotide substitutions. Segments that were annotated as intron sequences but are coding sequences are marked in green. The red box indicates a nucleotide deletion in the sequence of the predicted gene.

BIS1.2 genome.seq	-----	0
pred. gene.SEQ	-----	0
pred. cDNA.SEQ	-----	0
cloned cDNA.SEQ	ATGGCGCCTTTGGTTAAGAATCATGTAGAGCCTCCACATGCCAAAATCCTAGCCATTGGCACTGCAAATCCACCCAATGTCTACTACCAAAAAGACTATCCTGATTTCTTA	111
BIS1.2 genome.seq	----- n×N TTGATCTTGAGTTGCAAACATAAATCTACCAAAATTATGAGCT	44
pred. gene.SEQ	-----	0
pred. cDNA.SEQ	-----	0
cloned cDNA.SEQ	TTTCGAGTCACTAAAAATGAGCACAGAACAGATTTAAGAGAGAAGTTCGATCGCATT	169
BIS1.2 genome.seq	AAAATGAATCACATCCCGGACTCAACGCGCCACACGACGTGTTTCATTTCAAAGATACATTGTTATTAACGGAAGAAAATAGTCACTTTAGACATGTTACACAAATTAAT	155
pred. gene.SEQ	-----	0
pred. cDNA.SEQ	-----	0
cloned cDNA.SEQ	-----	169
BIS1.2 genome.seq	TGTGGCATCTCGGTCCAATAGTACATTATCATATGTAAGTTTTTCTTCAAATTACATTGTATTAGTTGATGCACAAGGATATAAAAACATGTCCTAACTTAATTAATAATTA	266
pred. gene.SEQ	-----	0
pred. cDNA.SEQ	-----	0
cloned cDNA.SEQ	-----	169
BIS1.2 genome.seq	ACACGTGAGAAGTCAAAAATAAGGAAGCGTTACTTGTATCTAACAGAAGAGATTCTAAATGCTAACCAGCATATATACCTATGGAGCCCCATCACTCGATGTGCGCCAA	377
pred. gene.SEQ	-----	0
pred. cDNA.SEQ	-----	0
cloned cDNA.SEQ	GTGAGAAGTCAAAAACAAGAAAGCGCTACTTGTATCTAACAGAAGAGATTCTAAATGCTAACCAGCATATATACCTATGGGGCCCCATCACTCGATGTGCGCCAA	276
BIS1.2 genome.seq	GACATGTTGAACCCCAAGGTCCCAAAGCTAGGGCAACAAGCAACATTGAAAGCCATCAAAGAGTGGGGCCAGCCCATCTCAAAGATCACCCACCTCATCTTTTGCACAGCT	488
pred. gene.SEQ	-----	0
pred. cDNA.SEQ	-----	0
cloned cDNA.SEQ	GACATGTTGAACCCCTGAGGTCCCAAAGCTAGGGCAACAAGCAGCACTGAAAGCCATCAAAGAGTGGGGCCAGCCCATCTCAAAGATCACCCACCTCATCTTTTGCACAGCT	387
BIS1.2 genome.seq	TCCTACGTTGACATGCCAGGTGCCAACTTCCAACCTGGTCAAGC CCTCGGCCTTAACCCATCTGTCACTAGAACC ATCATCTATGAAGCTGGTTGCTATGCTGGTGCGACT	599
pred. gene.SEQ	-----	36
pred. cDNA.SEQ	-----	36
cloned cDNA.SEQ	TCTTGCCTTGACATGCCAGGTGCCAGACTTCCAATTGGTCAAGCTCCTCGGCCTTAACCCATCCGTCAACAGAACCATCATCTATGAAGCTGGTTGCTATGCTGGTGCGACT	498
BIS1.2 genome.seq	GTCCCTCCCCCTGGCCAAGGACTTCGCAGAGAACAACAAGGGTGCACGCATCCTTGTGGTGTGCGCCGAGATCACGACCGTGTTTTTTCCACGGACTCACTGACACCCACCTT	710
pred. gene.SEQ	GTCCCTCCCCCTGGCCAAGGACTTCGCAGAGAACAACAAGGGTGCACGCATCCTTGTGGTGTGCGCCGAGATCACGACCGTGTTTTTTCCACGGACTCACTGACACCCACCTT	147
pred. cDNA.SEQ	GTCCCTCCCCCTGGCCAAGGACTTCGCAGAGAACAACAAGGGTGCACGCATCCTTGTGGTGTGCGCCGAGATCACGACCGTGTTTTTTCCACGGACTCACTGACACCCACCTT	147
cloned cDNA.SEQ	GTCCCTCCGCTGGCCAAGGACTTCGCAGAGAACAACAAGGGTGCACGCCTCCTTGTGGTGTGCGCCGAGATCACGACCGTGTTTTTTCCACGGACTCACTGACACCCACCTT	609

Figure S4. Alignment of the predicted *BIS1.2* gene and cDNA (MDP0000257119) with the corresponding genome sequence of 'Golden Delicious' and the cloned cDNA of 'Holsteiner Cox'. Nucleotides of the cloned cDNA that are located upstream of the predicted start codon (pink box) are labeled in yellow, as well as some single nucleotide substitutions. The corresponding genome sequence, as far as is available, is marked in green. The upstream genome sequence that is an intron is marked in red. The label n×N against a blue background indicates an unknown number of missing nucleotides in the genome sequence. A deletion behind nucleotide 531 in the coding part of the genome sequence is indicated by a red box.

