

GD1	GAAGAATTCAAGTTCAAATTTACAGAGCA	GAGAGAGAGAGAGAGCGGGTTTGGT	TCGGGTACGAAAAGTCTTGAGAGGACCGGGGAATTCGGTGGGCCCACTGCACGGTGGCTGCAGAGGAATTTGGG	140
GD_haplotype2	GAAGAATTCAAGTTCAAATTTACAGAGCA	GAGAGAGAGAGAGAGCGGGTTTGGT	TCGGGTACGAAAAGTCTTGAGAGGACCGGGGAATTCGGTGGGCCCACTGCACGGTGGCTGCAGAGGAATTTGGG	131
Jonathan_haplotype1	GAAGAATTCAAGTTCAAATTTACAGAGCA	GAGAGAGAGAGAGAGCGGGTTTGGT	TCGGGTACGAAAAGTCTTGAGAGGACCGGGGAATTCGGTGGGCCCACTGCACGGTGGCTGCAGAGGAATTTGGG	140
Jonathan_haplotype2	GAAGAATTCAAGTTCAAATTTACAGAGCA	GAGAGAGAGAGAGAGCGGGTTTGGT	TCGGGTACGAAAAGTCTTGAGAGGACCGGGGAATTCGGTGGGCCCACTGCACGGTGGCTGCAGAGGAATTTGGG	131
GD1	ACTGCCAAGCGGCCCACTGCGTACACGACGACGGTACTTCCCTTTTAAACCAAAAGATCAAAGCGGATTTTCGCGGTTTTCAAAATTGTCGAGGTCGAGGCGCTC	CTGGTACGAGTCAAGTAGTGGG		280
GD_haplotype2	ACTGCCAAGCGGCCCACTGCGTACACGACGACGGTACTTCCCTTTTAAACCAAAAGATCAAAGCGGATTTTCGCGGTTTTCAAAATTGTCGAGGTCGAGGCGCTC	CTGGTACGAGTCAAGTAGTGGG		271
Jonathan_haplotype1	ACTGCCAAGCGGCCCACTGCGTACACGACGACGGTACTTCCCTTTTAAACCAAAAGATCAAAGCGGATTTTCGCGGTTTTCAAAATTGTCGAGGTCGAGGCGCTC	CTGGTACGAGTCAAGTAGTGGG		280
Jonathan_haplotype2	ACTGCCAAGCGGCCCACTGCGTACACGACGACGGTACTTCCCTTTTAAACCAAAAGATCAAAGCGGATTTTCGCGGTTTTCAAAATTGTCGAGGTCGAGGCGCTC	CTGGTACGAGTCAAGTAGTGGG		271
GD1	TGAGGCCCAAGTGAAATAGTTTGTGGGCT	TTGGGGCAATTGGGCA	TTTATGAGTCGGGATACGATTCCTATATGTCATAACAAAAGCGAAGGAATGACTCTTTTATGTGTCCTCCACTCTTGTAGATAGTACCTG	420
GD_haplotype2	TGAGGCCCAAGTGAAATAGTTTGTGGGCT	TTGGGGCA	TTTATGAGTCGGGATACGATTCCTATATGTCATAACAAAAGCGAAGGAATGACTCTTTTATGTGTCCTCCACTCTTGTGTAGATAGTACCTG	402
Jonathan_haplotype1	TGAGGCCCAAGTGAAATAGTTTGTGGGCT	TTGGGGCAATTGGGCA	TTTATGAGTCGGGATACGATTCCTATATGTCATAACAAAAGCGAAGGAATGACTCTTTTATGTGTCCTCCACTCTTGTAGATAGTACCTG	420
Jonathan_haplotype2	TGAGGCCCAAGTGAAATAGTTTGTGGGCT	TTGGGGCA	TTTATGAGTCGGGATACGATTCCTATATGTCATAACAAAAGCGAAGGAATGACTCTTTTATGTGTCCTCCACTCTTGTAGATAGTACCTG	402
GD1	TTCAATACGGGGCAATTGAAAAAATATCCTGAGTTAGGTTGGTGCATTGTGTTTTATTTTTTAATACGAATGGGAGGGGAGAAAGAGGAAACTGAGAC	TTGCATCTAGTTTTATTGATCTGTCTAAACTA		560
GD_haplotype2	TTCAATACGGGGCAATTGAAAAAATATCCTGAGTTAGGTTGGTGCATTGTGTTTTATTTTTTAATACGAATGGGAGGGGAGAAAGAGGAAACTGAGAC	TTGCATCTAGTTTTATTGATCTGTCTAAACTA		542
Jonathan_haplotype1	TTCAATACGGGGCAATTGAAAAAATATCCTGAGTTAGGTTGGTGCATTGTGTTTTATTTTTTAATACGAATGGGAGGGGAGAAAGAGGAAACTGAGAC	TTGCATCTAGTTTTATTGATCTGTCTAAACTA		560
Jonathan_haplotype2	TTCAATACGGGGCAATTGAAAAAATATCCTGAGTTAGGTTGGTGCATTGTGTTTTATTTTTTAATACGAATGGGAGGGGAGAAAGAGGAAACTGAGAC	TTGCATCTAGTTTTATTGATCTGTCTAAACTA		542
GD1	GCATATGGCACACACGCAATCGCTGCGAAACAAAATTTGTTTTAAATGTGAACTTTAAATTTGTTTTGTTTTTTCATTTATTTGTAAGTTTTTATTTTATGTAAATTAACATATAG	AGTAAAGCCCGCTTTTCAGGGA		700
GD_haplotype2	GCATATGGCACACACGCAATCGCTGCGAAACAAAATTTGTTTTAAATGTGAACTTTAAATTTGTTTTGTTTTTTCATTTATTTGTAAGTTTTTATTTTATGTAAATTAACATATAG	AGTAAAGCCCGCTTTTCAGGGA		682
Jonathan_haplotype1	GCATATGGCACACACGCAATCGCTGCGAAACAAAATTTGTTTTAAATGTGAACTTTAAATTTGTTTTGTTTTTTCATTTATTTGTAAGTTTTTATTTTATGTAAATTAACATATAG	AGTAAAGCCCGCTTTTCAGGGA		700
Jonathan_haplotype2	GCATATGGCACACACGCAATCGCTGCGAAACAAAATTTGTTTTAAATGTGAACTTTAAATTTGTTTTGTTTTTTCATTTATTTGTAAGTTTTTATTTTATGTAAATTAACATATAG	AGTAAAGCCCGCTTTTCAGGGA		682
GD1	TGATGTGAAA	AAATAAACTTCAG	AAAGCACAACAACAGCGCTGCATGTTTGTTCCTCCCAAAATCCCAAGGGTTTAC	810
GD_haplotype2	TGATGTGAAA	AAATAAACTTCAG	AAAGCACAACAACAGCGCTGCATGTTTGTTCCTCCCAAAATCCCAAGGGTTTAC	807
Jonathan_haplotype1	TGATGTGAAA	AAATAAACTTCAG	AAAGCACAACAACAGCGCTGCATGTTTGTTCCTCCCAAAATCCCAAGGGTTTAC	825
Jonathan_haplotype2	TGATGTGAAA	AAATAAACTTCAG	AAAGCACAACAACAGCGCTGCATGTTTGTTCCTCCCAAAATCCCAAGGGTTTAC	822
GD1	GGTTAGGGGTTTGTGCTGCAATTTATGGCGTACATGTATATAAGCCCATTAARAACATCCCACTACTCCACATGAATATTAGGCGAATATTTATTCACATCCTAAB	ACAAGCACAACAAAATTTGCTAAATAGCCT		950
GD_haplotype2	GGTTAGGGGTTTGTGCTGCAATTTATGGCGTACATGTATATAAGCCCATTAARAACATCCCACTACTCCACATGAATATTAGGCGAATATTTATTCACATCCTAAB	ACAAGCACAACAAAATTTGCTAAATAGCCT		947
Jonathan_haplotype1	GGTTAGGGGTTTGTGCTGCAATTTATGGCGTACATGTATATAAGCCCATTAARAACATCCCACTACTCCACATGAATATTAGGCGAATATTTATTCACATCCTAAB	ACAAGCACAACAAAATTTGCTAAATAGCCT		965
Jonathan_haplotype2	GGTTAGGGGTTTGTGCTGCAATTTATGGCGTACATGTATATAAGCCCATTAARAACATCCCACTACTCCACATGAATATTAGGCGAATATTTATTCACATCCTAAB	ACAAGCACAACAAAATTTGCTAAATAGCCT		962
GD1	AGAAGATGGTGGACATGGTTCAACTTTAATAGGAGTATTC	GTTTTACATTC		1004
GD_haplotype2	AGAAGATGGTGGACATGGTTCAACTTTAATAGGAGTATTC	GTTTTACATTC		1001
Jonathan_haplotype1	AGAAGATGGTGGACATGGTTCAACTTTAATAGGAGTATTC	GTTTTACATTC		1019
Jonathan_haplotype2	AGAAGATGGTGGACATGGTTCAACTTTAATAGGAGTATTC	GTTTTACATTC		1016

Figure S15 Sequence alignment of candidate genes for resistance/susceptibility to *Botryosphaeria dothidea* serine/threonine-protein kinase (MD03G1259600) of ‘Jonathan’, ‘Golden Delicious’ (GD), and the apple reference genome (DH).

reference	TGGAAGGACGAGGGGTTTATGTA	AGAGGGGAGGGGAAGGGGAAGGG	AAAGG	GGTGGGCACTCCAAAGAGCTCTATTTTTTCTTGGAAAAGTGACAGAGATGTT	113
GD_haplotype1	TGGAAGGACGAGGGGTTTATGTA	AGAGGGGAGGGGAAGGGGAAGGG	AAAGG	GGTGGGCACTCCAAAGAGCTCTATTTTTTCTTGGAAAAGTGACAGAGATGTT	113
GD_haplotype1	TGGAAGGACGAGGGGTTTATGTA	AGAGGGGAGGGGAAGGGGAAGGG	AAAGG	GGTGGGCACTCCAAAGAGCTCTATTTTTTCTTGGAAAAGTGACAGAGATGTT	113
Jonathan_haplotype1	TGGAAGGACGAGGGGTTTATGTA	AGAGGGGAGGGGAAGGGGAAGGG	AAAGG	GGTGGGCACTCCAAAGAGCTCTATTTTTTCTTGGAAAAGTGACAGAGATGTT	123
Jonathan_haplotype2	TGGAAGGACGAGGGGTTTATGTA	AGAGGGGAGGGGAAGGGGAAGGG	AAAGG	GGTGGGCACTCCAAAGAGCTCTATTTTTTCTTGGAAAAGTGACAGAGATGTT	130
reference	GACTACAGTGATCTCCAGTCTAAATGTAGAGGGGCGCTTTATTTGATTTCACTCCGCTACTGTTAAATTATCTAC	TTGGATTGGAGCATAAAGTTTTAA	TTTGGCGGGTTAACTCTGTAATTG	CTAAAT	253
GD_haplotype1	GACTACAGTGATCTCCAGTCTAAATGTAGAGGGGCGCTTTATTTGATTTCACTCCGCTACTGTTAAATTATCTAC	TTGGATTGGAGCATAAAGTTTTAA	TTTGGCGGGTTAACTCTGTAATTG	CTAAAT	253
GD_haplotype1	GACTACAGTGATCTCCAGTCTAAATGTAGAGGGGCGCTTTATTTGATTTCACTCCGCTACTGTTAAATTATCTAC	TTGGATTGGAGCATAAAGTTTTAA	TTTGGCGGGTTAACTCTGTAATTG	CTAAAT	253
Jonathan_haplotype1	GACTACAGTGATCTCCAGTCTAAATGTAGAGGGGCGCTTTATTTGATTTCACTCCGCTACTGTTAAATTATCTAC	TTGGATTGGAGCATAAAGTTTTAA	TTTGGCGGGTTAACTCTGTAATTG	CTAAAT	263
Jonathan_haplotype2	GACTACAGTGATCTCCAGTCTAAATGTAGAGGGGCGCTTTATTTGATTTCACTCCGCTACTGTTAAATTATCTAC	TTGGATTGGAGCATAAAGTTTTAA	TTTGGCGGGTTAACTCTGTAATTG	CTAAAT	270
reference	TTTTGAGGTTTTATCACTCCCTCTTCCACATTTATTTTGGTCTCATATGATCTGGACTACTACAG	TAGTTTTGGGAGTGAGGTGCTTAAAAAAAAGCA	CCATGAAAAAAGCTGTGAGGTTTTAGGTGTTTG		393
GD_haplotype1	TTTTGAGGTTTTATCACTCCCTCTTCCACATTTATTTTGGTCTCATATGATCTGGACTACTACAG	TAGTTTTGGGAGTGAGGTGCTTAAAAAAAAGCA	CCATGAAAAAAGCTGTGAGGTTTTAGGTGTTTG		393
GD_haplotype1	TTTTGAGGTTTTATCACTCCCTCTTCCACATTTATTTTGGTCTCATATGATCTGGACTACTACAG	TAGTTTTGGGAGTGAGGTGCTTAAAAAAAAGCA	CCATGAAAAAAGCTGTGAGGTTTTAGGTGTTTG		393
Jonathan_haplotype1	TTTTGAGGTTTTATCACTCCCTCTTCCACATTTATTTTGGTCTCATATGATCTGGACTACTACAG	TAGTTTTGGGAGTGAGGTGCTTAAAAAAAAGCA	CCATGAAAAAAGCTGTGAGGTTTTAGGTGTTTG		403
Jonathan_haplotype2	TTTTGAGGTTTTATCACTCCCTCTTCCACATTTATTTTGGTCTCATATGATCTGGACTACTACAG	TAGTTTTGGGAGTGAGGTGCTTAAAAAAAAGCA	CCATGAAAAAAGCTGTGAGGTTTTAGGTGTTTG		410
reference	TAACTGAAAAAATAA	TTATTTTGGAGCTGATGTGAGAATAAGCTGAAATCAAGGAAAAAATCAAGCTGCTATTTCGACCTTTGGAAACTGGTTTTTTTCAAGACACAGGAGCTACAGTCTCTTTAA			533
GD_haplotype1	TAACTGAAAAAATAA	TTATTTTGGAGCTGATGTGAGAATAAGCTGAAATCAAGGAAAAAATCAAGCTGCTATTTCGACCTTTGGAAACTGGTTTTTTTCAAGACACAGGAGCTACAGTCTCTTTAA			532
GD_haplotype1	TAACTGAAAAAATAA	TTATTTTGGAGCTGATGTGAGAATAAGCTGAAATCAAGGAAAAAATCAAGCTGCTATTTCGACCTTTGGAAACTGGTTTTTTTCAAGACACAGGAGCTACAGTCTCTTTAA			533
Jonathan_haplotype1	TAACTGAAAAAATAA	TTATTTTGGAGCTGATGTGAGAATAAGCTGAAATCAAGGAAAAAATCAAGCTGCTATTTCGACCTTTGGAAACTGGTTTTTTTCAAGACACAGGAGCTACAGTCTCTTTAA			543
Jonathan_haplotype2	TAACTGAAAAAATAA	TTATTTTGGAGCTGATGTGAGAATAAGCTGAAATCAAGGAAAAAATCAAGCTGCTATTTCGACCTTTGGAAACTGGTTTTTTTCAAGACACAGGAGCTACAGTCTCTTTAA			550
reference	GAAAAGGCCACATATTATATCTG	TTTTTTTTCCAAAAGCACTTTTACAAAAAAGTTTACCAACACTCTGCTGATTATTTACAGACCGCTTATTCTCACAGCACAG	TCATTATCTCACAGCAC	TTTTTCAAG	673
GD_haplotype1	GAAAAGGCCACATATTATATCTG	TTTTTTTTCCAAAAGCACTTTTACAAAAAAGTTTACCAACACTCTGCTGATTATTTACAGACCGCTTATTCTCACAGCACAG	TCATTATCTCACAGCAC	TTTTTCAAG	671
GD_haplotype1	GAAAAGGCCACATATTATATCTG	TTTTTTTTCCAAAAGCACTTTTACAAAAAAGTTTACCAACACTCTGCTGATTATTTACAGACCGCTTATTCTCACAGCACAG	TCATTATCTCACAGCAC	TTTTTCAAG	673
Jonathan_haplotype1	GAAAAGGCCACATATTATATCTG	TTTTTTTTCCAAAAGCACTTTTACAAAAAAGTTTACCAACACTCTGCTGATTATTTACAGACCGCTTATTCTCACAGCACAG	TCATTATCTCACAGCAC	TTTTTCAAG	683
Jonathan_haplotype2	GAAAAGGCCACATATTATATCTG	TTTTTTTTCCAAAAGCACTTTTACAAAAAAGTTTACCAACACTCTGCTGATTATTTACAGACCGCTTATTCTCACAGCACAG	TCATTATCTCACAGCAC	TTTTTCAAG	689
reference	CACAGCAATACCAAAACGAGCCACATCTCTTTTCTTTGG	TTTTTTTTTCTTTTTTTATGGAAGAGAGGCTCTAGACTTTGAAATGTGTTAATACATTGTAACTGTATCTTAACCATTTTATTCTTCAACG			813
GD_haplotype1	CACAGCAATACCAAAACGAGCCACATCTCTTTTCTTTGG	TTTTTTTTTCTTTTTTTATGGAAGAGAGGCTCTAGACTTTGAAATGTGTTAATACATTGTAACTGTATCTTAACCATTTTATTCTTCAACG			811
GD_haplotype1	CACAGCAATACCAAAACGAGCCACATCTCTTTTCTTTGG	TTTTTTTTTCTTTTTTTATGGAAGAGAGGCTCTAGACTTTGAAATGTGTTAATACATTGTAACTGTATCTTAACCATTTTATTCTTCAACG			813
Jonathan_haplotype1	CACAGCAATACCAAAACGAGCCACATCTCTTTTCTTTGG	TTTTTTTTTCTTTTTTTATGGAAGAGAGGCTCTAGACTTTGAAATGTGTTAATACATTGTAACTGTATCTTAACCATTTTATTCTTCAACG			823
Jonathan_haplotype2	CACAGCAATACCAAAACGAGCCACATCTCTTTTCTTTGG	TTTTTTTTTCTTTTTTTATGGAAGAGAGGCTCTAGACTTTGAAATGTGTTAATACATTGTAACTGTATCTTAACCATTTTATTCTTCAACG			829
reference	ATAAAGTCTAAGAGAGCTCTCTTAAAGTTG	TATTGTGTGGTTTAGCGGAATCTCCGACCTCTTAGTGTAATAATATATTTTACTGAAGAAAAA	ATGCTAAGGAGCTCTCAAAATGAGAGCTCTCAATAAATCT		953
GD_haplotype1	ATAAAGTCTAAGAGAGCTCTCTTAAAGTTG	TATTGTGTGGTTTAGCGGAATCTCCGACCTCTTAGTGTAATAATATATTTTACTGAAGAAAAA	ATGCTAAGGAGCTCTCAAAATGAGAGCTCTCAATAAATCT		951
GD_haplotype1	ATAAAGTCTAAGAGAGCTCTCTTAAAGTTG	TATTGTGTGGTTTAGCGGAATCTCCGACCTCTTAGTGTAATAATATATTTTACTGAAGAAAAA	ATGCTAAGGAGCTCTCAAAATGAGAGCTCTCAATAAATCT		953
Jonathan_haplotype1	ATAAAGTCTAAGAGAGCTCTCTTAAAGTTG	TATTGTGTGGTTTAGCGGAATCTCCGACCTCTTAGTGTAATAATATATTTTACTGAAGAAAAA	ATGCTAAGGAGCTCTCAAAATGAGAGCTCTCAATAAATCT		963
Jonathan_haplotype2	ATAAAGTCTAAGAGAGCTCTCTTAAAGTTG	TATTGTGTGGTTTAGCGGAATCTCCGACCTCTTAGTGTAATAATATATTTTACTGAAGAAAAA	ATGCTAAGGAGCTCTCAAAATGAGAGCTCTCAATAAATCT		969
reference	TTTATCATCTTACAGTTTAAAGTCAATTCATGGCCAACTATTATAA				1000
GD_haplotype1	TTTATCATCTTACAGTTTAAAGTCAATTCATGGCCAACTATTATAA				998
GD_haplotype1	TTTATCATCTTACAGTTTAAAGTCAATTCATGGCCAACTATTATAA				1000
Jonathan_haplotype1	TTTATCATCTTACAGTTTAAAGTCAATTCATGGCCAACTATTATAA				1010
Jonathan_haplotype2	TTTATCATCTTACAGTTTAAAGTCAATTCATGGCCAACTATTATAA				1016

Figure S16 Sequence alignment of candidate genes for resistance/susceptibility to *Botryosphaeria dothidea* kinase-like protein TMKL1 (MD10G1169200) of ‘Jonathan’, ‘Golden Delicious’ (GD), and the apple reference genome (DH).

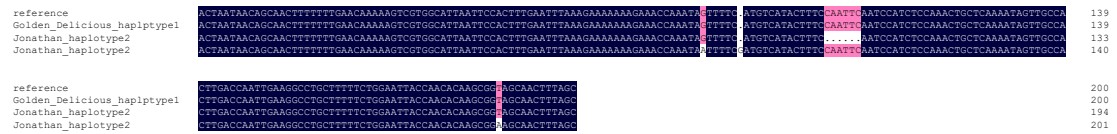


Figure S17 Sequence alignment of candidate genes for resistance/susceptibility to *Botryosphaeria dothidea* serine/threonine-protein kinase-like protein (MD10G1288400) of ‘Jonathan’, ‘Golden Delicious’ (GD), and the apple reference genome (DH).

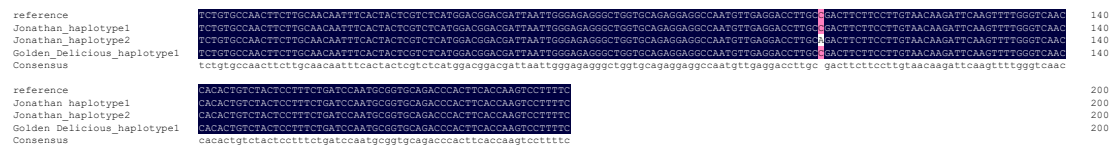


Figure S18 Sequence alignment of candidate genes for resistance/susceptibility to *Botryosphaeria dothidea* receptor-like protein kinase HSL1 (MD10G1288500) of ‘Jonathan’, ‘Golden Delicious’ (GD), and the apple reference genome (DH).

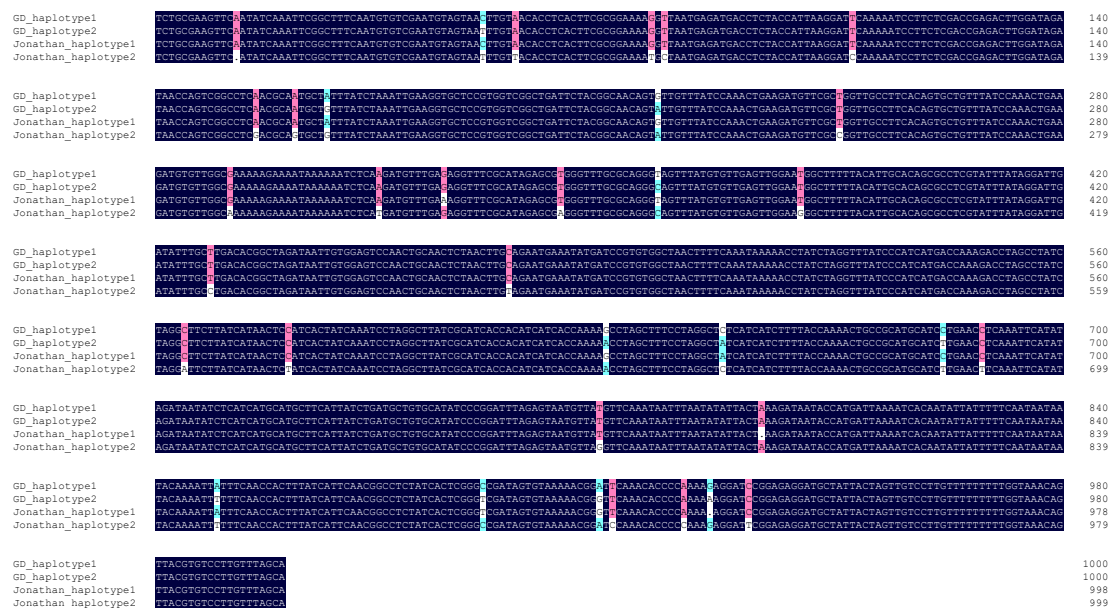


Figure S19 Sequence alignment of candidate genes for resistance/susceptibility to *Botryosphaeria dothidea* NDR1/HIN1-like 8 (MD06G1037600) of ‘Jonathan’, ‘Golden Delicious’ (GD), and the apple reference genome (DH).



Figure S20 Sequence alignment of candidate genes for resistance/susceptibility to *Botryosphaeria dothidea* pentatricopeptide repeat-containing protein (MD02G1213800) of ‘Jonathan’, ‘Golden Delicious’ (GD), and the apple reference genome (DH).

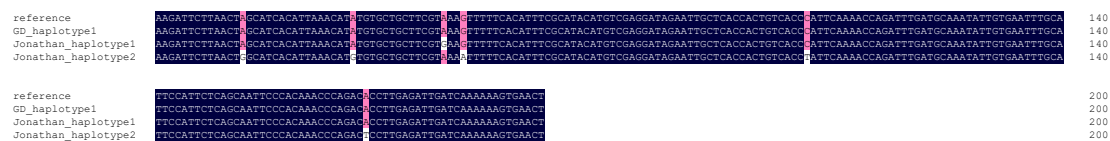


Figure S21 Sequence alignment of candidate genes for resistance/susceptibility to *Botryosphaeria dothidea* pentatricopeptide repeat-containing protein (MD08G1120500) of ‘Jonathan’, ‘Golden Delicious’ (GD), and the apple reference genome (DH).

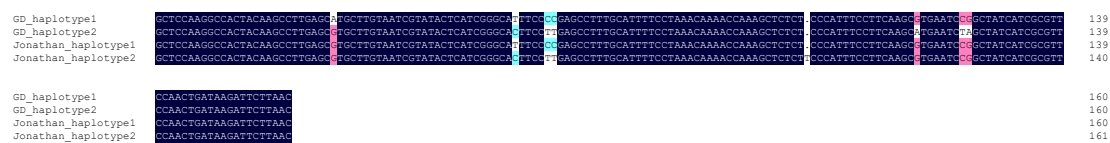


Figure S22 Sequence alignment of candidate genes for resistance/susceptibility to *Botryosphaeria dothidea* pentatricopeptide repeat-containing protein (MD08G1120700) of ‘Jonathan’, ‘Golden Delicious’ (GD), and the apple reference genome (DH).



Figure S23 Sequence alignment of candidate genes for resistance/susceptibility to *Botryosphaeria dothidea* disease resistance protein (MD15G1416500) of ‘Jonathan’, ‘Golden Delicious’ (GD), and the apple reference genome (DH).

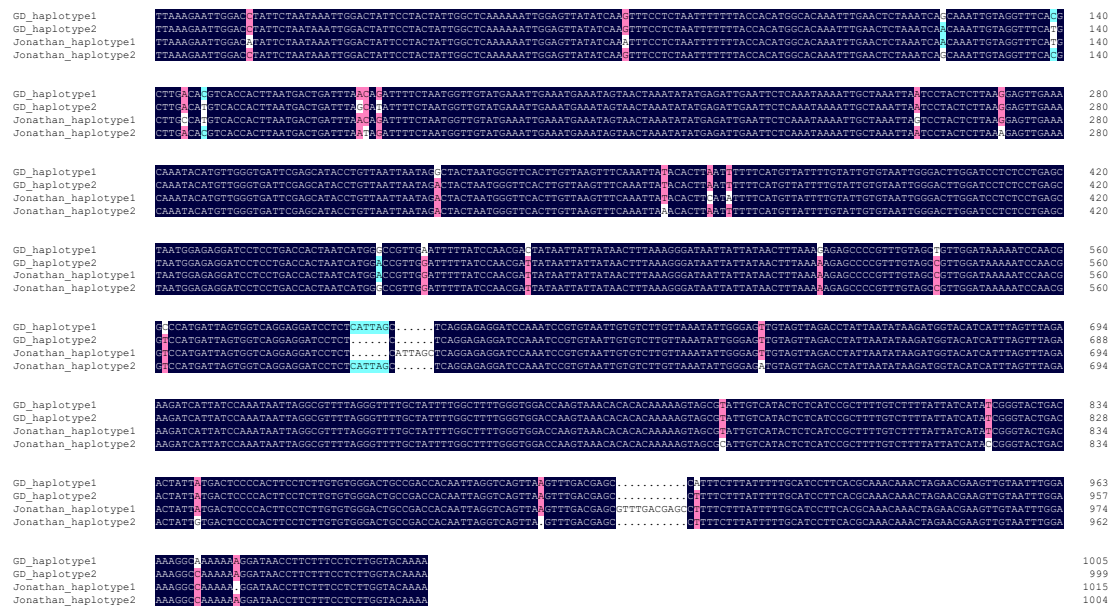


Figure S24 Sequence alignment of candidate genes for resistance/susceptibility to *Botryosphaeria dothidea* F-box/kelch-repeat protein (MD06G1017400) of ‘Jonathan’, ‘Golden Delicious’ (GD), and the apple reference genome (DH).



Figure S25 Sequence alignment of candidate genes for resistance/susceptibility to *Botryosphaeria dothidea* F-box/kelch-repeat protein (MD10G1255900) of ‘Jonathan’, ‘Golden Delicious’ (GD), and the apple reference genome (DH).

