

PCR1: PotatoMASH core primers

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>C12_6_R
GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGTAACTAGCACTCATTGGCCCTTTTT
>C12_7_F
TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGATTTGGTTGTTTACTCAGGGTCCCA
>C12_7_R
GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGATATGCTCAAATGACTTTGCAGCCA
>C12_8_F
TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGTCAAATGAAGAGAGCAAACCTTGTGC
>C12_8_R
GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGGGTCCACATCCCGAGATTTTCCTAT
>C12_9_F
TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGCCGCATCAGTGTGAGTCAATGTAAA
>C12_9_R
GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGATATGTTTCGCGCCCTGAGGTTATT
>C12_10_F
TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGTTTTCGCCCCGGATGTGTCATTC
>C12_10_R
GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGAGAGCTTATTAGAACGAGGAGTCCA
>C12_11_F
TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGTGCCGAGTCAAACCTAAGACAAACAT
>C12_11_R
GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGTGTACATTTGCTTCTTGCTGGATT
>C12_12_F
TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGTGATTTCTGTATCCCTGGATTGGAGA

>C12_12_R
 GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGACCAAAGCTATTAGTTGACACCATGG
 >C12_13_F
 TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGGCAATGAAGAAGGAGTTCCGCC
 >C12_13_R
 GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGCTGGCACTATAAGATCATAACGTGTTTAGG
 >C12_14_F
 TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGAGTGTTCTTCGGTAGATTGTTCACT
 >C12_14_R
 GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGGTGACAATGGTGAGAGTTGAAAGGG
 >C12_15_F
 TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGGCTACTATCATTCTATCTGAAACCTGGTAG
 >C12_15_R
 GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGCTTCAAATCATAGGCAAGCTCAGCT
 >C12_16_F
 TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGTGGAATAATCACTACTTGGTTCCTCC
 >C12_16_R
 GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGTACCAACTAGTTTGCTCTGAGGCAT
 >C12_17_F
 TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGCCCATTCACTTGTTTCCTAAATTCATCCC
 >C12_17_R
 GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGAACCTGACAAGTGAAGCGTGGG
 >C12_18_1_F
 TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGAAAGTGGACCACCGAATACTTTGTCC
 >C12_18_1_R
 GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGACTGGTCGCAGTTGTGAAAATTGTG
 >C12_19_F
 TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGATGTAATCGCCCTGATCCAACGTGT
 >C12_19_R
 GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGGTACATGCACAAAGACGAGCTTTCT
 >C12_20_F
 TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGGTCTTTTTGTTGCAGAGGGAAAGAT
 >C12_20_R
 GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGTTGGAGGCCTAATCACATGACTGAA
 >C12_21_F
 TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGCTCCAGCTCCTCTTGAACCTTTCTT
 >C12_21_R
 GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGGCACTGATTCATGAGCATAAGGTATG
 >C12_22_F
 TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGTGGTGCTGAAGATGATGCAACTTTT
 >C12_22_R
 GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGGAGGAGCCAAAGCGTCCTATCAAA
 >C12_23_F
 TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGCAGCGAAACTGCTATCACACTGTT
 >C12_23_R
 GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGTCCTTCACTGTTCTCATTCCAT

PCR2: i5-Primers

>A1_ATCACG
 AATGATACGGCGACCACCGAGATCTACACATCACGTCTCGTCGGCAGCGTC
 >B1_CGATGT
 AATGATACGGCGACCACCGAGATCTACACCGATGTTCTCGTCGGCAGCGTC
 >C1_TTAGGC
 AATGATACGGCGACCACCGAGATCTACACTTAGGCTCGTCGGCAGCGTC
 >D1_TGACCA
 AATGATACGGCGACCACCGAGATCTACACTGACCATCGTCGGCAGCGTC
 >E1_ACAGTG

AATGATACGGCGACCACCGAGATCTACACACAGTGTCTCGTCGGCAGCGTC
>F1_GCCAAT
AATGATACGGCGACCACCGAGATCTACACGCCAATTCGTCTCGGCAGCGTC
>G1_CAGATC
AATGATACGGCGACCACCGAGATCTACACCAGATCTCGTCGGCAGCGTC
>H1_ACTTGA
AATGATACGGCGACCACCGAGATCTACACACTTGATCGTCGGCAGCGTC
>A2_GATCAG
AATGATACGGCGACCACCGAGATCTACACGATCAGTCGTCTCGGCAGCGTC
>B2_TAGCTT
AATGATACGGCGACCACCGAGATCTACACTAGCTTTCGTCTCGGCAGCGTC
>C2_GGCTAC
AATGATACGGCGACCACCGAGATCTACACGGCTACTCGTCGGCAGCGTC
>D2_CTTGTA
AATGATACGGCGACCACCGAGATCTACACCTTGTATCGTCGGCAGCGTC
>E2_AGTCAA
AATGATACGGCGACCACCGAGATCTACACAGTCAATCGTCGGCAGCGTC
>F2_AGTTCC
AATGATACGGCGACCACCGAGATCTACACAGTTCCTCGTCGGCAGCGTC
>G2_ATGTCA
AATGATACGGCGACCACCGAGATCTACACATGTCATCGTCGGCAGCGTC
>H2_CCGTCC
AATGATACGGCGACCACCGAGATCTACACCCGTCCTCGTCGGCAGCGTC
>A3_GTAGAG
AATGATACGGCGACCACCGAGATCTACACGTAGAGTCGTCTCGGCAGCGTC
>B3_GTCCGC
AATGATACGGCGACCACCGAGATCTACACGTCCGCTCGTCGGCAGCGTC
>C3_GTGAAA
AATGATACGGCGACCACCGAGATCTACACGTGAAATCGTCGGCAGCGTC
>D3_GTGGCC
AATGATACGGCGACCACCGAGATCTACACGTGGCCTCGTCGGCAGCGTC
>E3_GTTTCG
AATGATACGGCGACCACCGAGATCTACACGTTTCGTCTCGTCGGCAGCGTC
>F3_CGTACG
AATGATACGGCGACCACCGAGATCTACACCGTACGTCTCGTCGGCAGCGTC
>G3_GAGTGG
AATGATACGGCGACCACCGAGATCTACACGAGTGGTCGTCTCGGCAGCGTC
>H3_GGTAGC
AATGATACGGCGACCACCGAGATCTACACGGTAGCTCGTCGGCAGCGTC
>A4_ACTGAT
AATGATACGGCGACCACCGAGATCTACACACTGATTCGTCTCGGCAGCGTC
>B4_ATGAGC
AATGATACGGCGACCACCGAGATCTACACATGAGCTCGTCGGCAGCGTC
>C4_ATTCTT
AATGATACGGCGACCACCGAGATCTACACATTCTTCGTCTCGGCAGCGTC
>D4_CAAAAG
AATGATACGGCGACCACCGAGATCTACACCAAAGTCGTCTCGGCAGCGTC
>E4_CAACTA
AATGATACGGCGACCACCGAGATCTACACCAACTATCGTCGGCAGCGTC
>F4_CACCGG
AATGATACGGCGACCACCGAGATCTACACACCGGTCGTCTCGGCAGCGTC
>G4_CACGAT
AATGATACGGCGACCACCGAGATCTACACACGATTCGTCTCGGCAGCGTC
>H4_CACTCA
AATGATACGGCGACCACCGAGATCTACACCACTCATCGTCGGCAGCGTC
>A5_CAGGCG
AATGATACGGCGACCACCGAGATCTACACCAGGCGTCGTCTCGGCAGCGTC

>B5_CATGGC
AATGATACGGCGACCACCGAGATCTACACCATGGCTCGTCGGCAGCGTC
>C5_CATTTT
AATGATACGGCGACCACCGAGATCTACACCATTTTTTCGTCGGCAGCGTC
>D5_CCAACA
AATGATACGGCGACCACCGAGATCTACACCCAACATCGTCGGCAGCGTC
>E5_CGGAAT
AATGATACGGCGACCACCGAGATCTACACCGGAATTCGTCGGCAGCGTC
>F5_CTAGCT
AATGATACGGCGACCACCGAGATCTACACCTAGCTTCGTCGGCAGCGTC
>G5_CTATAC
AATGATACGGCGACCACCGAGATCTACACCTATACTCGTCGGCAGCGTC
>H5_CTCAGA
AATGATACGGCGACCACCGAGATCTACACCTCAGATCGTCGGCAGCGTC
>A6_GACGAC
AATGATACGGCGACCACCGAGATCTACACGACGACTCGTCGGCAGCGTC
>B6_TAATCG
AATGATACGGCGACCACCGAGATCTACACTAATCGTCGTCGGCAGCGTC
>C6_TACAGC
AATGATACGGCGACCACCGAGATCTACACTACAGCTCGTCGGCAGCGTC
>D6_TATAAT
AATGATACGGCGACCACCGAGATCTACACTATAATTCGTCGGCAGCGTC
>E6_TCATT
AATGATACGGCGACCACCGAGATCTACACTCATTCTCGTCGGCAGCGTC
>F6_TCCCGA
AATGATACGGCGACCACCGAGATCTACACTCCCGATCGTCGGCAGCGTC
>G6_TCGAAG
AATGATACGGCGACCACCGAGATCTACACTCGAAGTCGTCGGCAGCGTC
>H6_TCGGCA
AATGATACGGCGACCACCGAGATCTACACTCGGCATCGTCGGCAGCGTC
>A7_AAGTAC
AATGATACGGCGACCACCGAGATCTACACAAGTACTCGTCGGCAGCGTC
>B7_TGCCAT
AATGATACGGCGACCACCGAGATCTACACTGCCATTCTCGTCGGCAGCGTC
>C7_CTCCTT
AATGATACGGCGACCACCGAGATCTACACCTCCTTTTCGTCGGCAGCGTC
>D7_AGATAG
AATGATACGGCGACCACCGAGATCTACACAGATAGTCGTCGGCAGCGTC
>E7_GATATA
AATGATACGGCGACCACCGAGATCTACACGATATATCGTCGGCAGCGTC
>F7_ATAATA
AATGATACGGCGACCACCGAGATCTACACATAATATCGTCGGCAGCGTC
>G7_GGTGCT
AATGATACGGCGACCACCGAGATCTACACGGTGCTTCGTCGGCAGCGTC
>H7_TGTGGA
AATGATACGGCGACCACCGAGATCTACACTGTGGATCGTCGGCAGCGTC
>A8_CGAGAA
AATGATACGGCGACCACCGAGATCTACACCGAGAATCGTCGGCAGCGTC
>B8_GCAGGA
AATGATACGGCGACCACCGAGATCTACACGCAGGATCGTCGGCAGCGTC
>C8_GCCGCG
AATGATACGGCGACCACCGAGATCTACACGCCGCGTCGTCGGCAGCGTC
>D8_AGCGCA
AATGATACGGCGACCACCGAGATCTACACAGCGCATCGTCGGCAGCGTC
>E8_TCCGTT
AATGATACGGCGACCACCGAGATCTACACTCCGTTTCGTCGGCAGCGTC
>F8_ATCGTC

AATGATACGGCGACCACCGAGATCTACACATCGTCTCGTCGGCAGCGTC
>G8_CCGCAA
AATGATACGGCGACCACCGAGATCTACACCCGCAATCGTCGGCAGCGTC
>H8_AACTTG
AATGATACGGCGACCACCGAGATCTACACAACTTGTCGTCTCGTCGGCAGCGTC
>A9_AAGGTA
AATGATACGGCGACCACCGAGATCTACACAAGGTATCGTCGGCAGCGTC
>B9_GCGCTC
AATGATACGGCGACCACCGAGATCTACACGCGCTCTCGTCGGCAGCGTC
>C9_CCTCGT
AATGATACGGCGACCACCGAGATCTACACCCTCGTTCGTCTCGTCGGCAGCGTC
>D9_ACGATT
AATGATACGGCGACCACCGAGATCTACACACGATTTCTCGTCGGCAGCGTC
>E9_AGACTC
AATGATACGGCGACCACCGAGATCTACACAGACTCTCGTCGGCAGCGTC
>F9_TGGTCT
AATGATACGGCGACCACCGAGATCTACACTGGTCTTCGTCTCGTCGGCAGCGTC
>G9_GGAATT
AATGATACGGCGACCACCGAGATCTACACGGAATTTCTCGTCGGCAGCGTC
>H9_ACATCT
AATGATACGGCGACCACCGAGATCTACACACATCTTCGTCTCGTCGGCAGCGTC
>A10_TTCTCC
AATGATACGGCGACCACCGAGATCTACACTTCTCCTCGTCGGCAGCGTC
>B10_ATCTAT
AATGATACGGCGACCACCGAGATCTACACATCTATTCGTCTCGTCGGCAGCGTC
>C10_TGCATA
AATGATACGGCGACCACCGAGATCTACACTGCATATCGTCGGCAGCGTC
>D10_AATAGG
AATGATACGGCGACCACCGAGATCTACACAATAGGTCGTCTCGTCGGCAGCGTC
>E10_CGGTTA
AATGATACGGCGACCACCGAGATCTACACCGGTTATCGTCGGCAGCGTC
>F10_GAGACT
AATGATACGGCGACCACCGAGATCTACACGAGACTTCGTCTCGTCGGCAGCGTC
>G10_GCTCCA
AATGATACGGCGACCACCGAGATCTACACGCTCCATCGTCGGCAGCGTC
>H10_ATGCAG
AATGATACGGCGACCACCGAGATCTACACATGCAGTCGTCTCGTCGGCAGCGTC
>A11_GGCCTG
AATGATACGGCGACCACCGAGATCTACACGGCCTGTCTCGTCGGCAGCGTC
>B11_TTACTG
AATGATACGGCGACCACCGAGATCTACACTTACTGTCTCGTCGGCAGCGTC
>C11_TCAAGT
AATGATACGGCGACCACCGAGATCTACACTCAAGTTCGTCTCGTCGGCAGCGTC
>D11_AGCAGT
AATGATACGGCGACCACCGAGATCTACACAGCAGTTCGTCTCGTCGGCAGCGTC
>E11_CCTTAG
AATGATACGGCGACCACCGAGATCTACACCCTTAGTCGTCTCGTCGGCAGCGTC
>F11_TTGGAT
AATGATACGGCGACCACCGAGATCTACACTTGGATTCTCGTCGGCAGCGTC
>G11_TCTCAC
AATGATACGGCGACCACCGAGATCTACACTCTCACTCGTCGGCAGCGTC
>H11_GTCTTA
AATGATACGGCGACCACCGAGATCTACACGTCTTATCGTCGGCAGCGTC
>A12_CTAACG
AATGATACGGCGACCACCGAGATCTACACCTAACGTCTCGTCGGCAGCGTC
>B12_ATACAC
AATGATACGGCGACCACCGAGATCTACACATACTCGTCGGCAGCGTC

>C12_GCATTCT
 AATGATACGGCGACCACCGAGATCTACACGCATTCTCGTCGGCAGCGTC
 >D12_TACTCT
 AATGATACGGCGACCACCGAGATCTACACTACTCTTCGTCGGCAGCGTC
 >E12_TGGACT
 AATGATACGGCGACCACCGAGATCTACACTGGACTTCGTCGGCAGCGTC
 >F12_CCATAG
 AATGATACGGCGACCACCGAGATCTACACCCATAGTCGTCGGCAGCGTC
 >G12_TAAGGT
 AATGATACGGCGACCACCGAGATCTACACTAAGGTTCGTCGGCAGCGTC
 >H12_TTGCG
 AATGATACGGCGACCACCGAGATCTACACTTGGCGTCGTCGGCAGCGTC

PCR2: i7-Primers

>pl1_ATCACG
 CAAGCAGAAGACGGCATACGAGATCGTGATGTCTCGTGGGCTCGG
 >pl2_CGATGT
 CAAGCAGAAGACGGCATACGAGATACATCGGTCTCGTGGGCTCGG
 >pl3_TTAGGC
 CAAGCAGAAGACGGCATACGAGATGCCTAAGTCTCGTGGGCTCGG
 >pl4_TGACCA
 CAAGCAGAAGACGGCATACGAGATTGGTCAGTCTCGTGGGCTCGG
 >pl5_ACAGTG
 CAAGCAGAAGACGGCATACGAGATCACTGTGTCTCGTGGGCTCGG
 >pl6_GCCAAT
 CAAGCAGAAGACGGCATACGAGATATTGGCGTCTCGTGGGCTCGG
 >pl7_GACATC
 CAAGCAGAAGACGGCATACGAGATGATGTCTCGTGGGCTCGG
 >pl8_ACTTGA
 CAAGCAGAAGACGGCATACGAGATTCAAGTGTCTCGTGGGCTCGG
 >pl9_GATCAG
 CAAGCAGAAGACGGCATACGAGATCTGATCGTCTCGTGGGCTCGG
 >pl10_TAGCTT
 CAAGCAGAAGACGGCATACGAGATAAGCTAGTCTCGTGGGCTCGG

PCR1: PotatoMASH primers for selected pest resistance markers *(Note the first two pairs in chromosome IV are part of the core panel)*

>C2_B2_F
 TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGGAGGCAACAAAGAGTTATTATGGCTTG
 >C2_B2_R
 GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGGTGGTTTCAGCCCTTGTCTTAAGAA
 >C2_B3_F
 TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGAATGTGTGCAAGATCCTTGTCCTG
 >C2_B3_R
 GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGTCCTGGAAAAGCTTGTTATTGCTGA
 >C4_5_C4_B1_F
 TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGAGTAGTTTACTCATGGGTTCTCGTTC
 >C4_5_C4_B1_R
 GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGACTCAAATGGGTTGAAATCATCAGACC
 >C4_6_C4_B2_F
 TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGCTGATAAGCAGCCTATTGTGCCATG
 >C4_6_C4_B2_R
 GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGGCCAACTAAATTCAGCAAATGTAATTTACT
 >C5_B9_1_F
 TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGGCAGAGAAAAGAAGAGCTGCGAAA
 >C5_B9_1_R

GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGGCAATAAGCAGAATATACTATTGAATGAATAA
>C5_B10_F
TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGAATTACATACATCAGTGCATCAAT
>C5_B10_R
GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGCGCATGTTTGAAACTCAGTAAGT
>C6_B1_F
TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGTTCTCAGATTCTGTCCTGTTTTGCC
>C6_B1_R
GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGCTTCAAAGTGGGAAGGACTCGAAAG
>C11_B1_F
TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGGGTCAGGGTTCTTTGCTCTCTG
>C11_B1_R
GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGCCTCAAATTCTTTTCTATTGCTGATTGC
>C11_B3_F
TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGGATAGGGGATAGAGGAATTGAAGCAT
>C11_B3_R
GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGGTTGTTGTTGGAGCAATTGTTGTTG
>C12_B6_F
TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGGGTAGCCGTTGAAGCCTTAAAGAAG
>C12_B6_R
GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGTGGATTTAGCAACTTTTGATAGTTCA