

COSII Marker C2_At2g34470, 38.5 cM, Chr. 2

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Primer Name	Primer Sequence (5' to 3')
BG2-F4	TTGAGGGAAAATACAGTCTTGC
BG2-R4	AAGAACTCTCCATCTTCTTTCGTG

Cera BG2F4-R4: 611 bp;

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1      TTGAGGGAAA AATACAGTCT TGCAGCAGTA TGTACCACCA AATGATTTCT TTCTTTTGCC
61     ATTGTGACAT ACTTACTTCA TGAATAAGTT TAGTCTGCAC AATTTTTTGG AACTGGTGGA
121    TTCACTTTTG TGGTTTGGAA AATGGAACTC AAGTTTATTG GTGGTTTTCA TATCTTTCTC
181    TGCCTCATCA TTTGAAATTC TAGATGAAGA TGGGTGTTAC ATGCAATTTT CCGTTTGATT
241    GAGTCATTTT AAGTGGAATA ACAACATTCT TTATACACAA TTGCCTTTGG AGATTATCTC
301    AATAGGTCAT GTTCTTGTTT TTTAATCATT AAGGACTCCT TCCTAAACAT CACATATTGG
361    CATCTGCCAA AACTTCAAAC CGAGGTTTTG GGAGTTTACT TGACGTTTGT TAGTTTGACA
421    GGAAATACGT TATGTGCAAG CATGTATTTG GTGTTCTGGA ATTCCGACGC TCTTTCATCA
481    CTTTCCAAGT CTATGATCTT GAAATCTTCA CGTTTTTGTT CTAAGATGTA GAATGAATTA
541    ATGTCCATGT TAAGATGCAT TTCTTTGTAG GTAACAAATG ATATATTCAC GAAAGAAGAT
601    GGAGAGTTCT T
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902 BG2R4: 499 bp;

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1      TTGAGGGAAA AATACAGTCT TGCAGCAGTA TGTACCACCA AATGATTTCT TTCTTTTGCC
61     ATTGTGACAT ACTTACTTCA TGAATAAGTT TAGTCTGCAC AATTTTTTGG AACTGGTGGA
121    TTCACTTTTG TGGTTTGGAA AATGGAACTC AAGTTTATTG GTGGTTTTCA TATCTTCCTC
181    TGCCTCATCA TTTGAAATTC TAGATGAAGA TGGGGGTTAC ATGCAATTTT CCGTTTGATT
241    GAGTCATTTT AAGTGGAATA ACAACATTCT TTATACACAA TTGCCTTTGG AGATTATCTC
301    AATAGGTCAT GTTCTTGTTT TTTAATCATT AAGGACTCCT TCCTAAACAT CACATATTGG
361    CATCTGCCAA AACTTCAAAC CGAGGTTTTG GGAGTTTACT TGACGTTTGT TAGTTTGACA
421    GGAAATACGT TATGTGCAAG CATGTATTTG GTGTTCTGGA ATTCCGACGC TCTTTCATCA
481    CTTTCCAAGT CTATGATCT
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Blast Search

SGN BAC Clone Search

Comparison With Other Breeding Lines

Cerasiforme gave good sequence with both the forward and reverse primers. 902h gave sequence with only the reverse primer. Upon alignment Cerasiforme differed from 902h by 2 SNP in 499-bp of overlap.