

Hba78A16T7, Chromosome XI, 89.7 cM

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February 7, 2007

Primers:

Table 1: PCR Primers on Chr. 11

Primer name	Sequence (5' to 3')
BAC-11-89F	CCTCTCAGGAAGTCTGAGATTGA (SGN primers)
BAC-11-89R	TTGAAGGATATTCAACCAGCAGT (SGN primers)

PCR at 53 C, (TGEN53), 750-bp fragment.

SEQ M82, 765 bp, partial sequence

ORIGIN

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1      CCTCTCAGGA AGTCTGAGAT TGAGTATTAT GCTATGTTGG CAAAGGTTGG AGTCCACCAC
61     TACAACGGAA GTAAGTGAAT ATCTTTGTGT GTATAGACAG TAATATAGAT GTTTGAACTT
121    CTTTTTGGTG CTTTTGAAAT GTTTTTAAAT ATTGTTTGCT GTTTTGACTG CTTGCGAATG
181    AAAATATATA TATCTTCCTT TCGTTTGGTT CGGACATGAA TTATGTAAct TTGCTAGGAG
241    TGCTGAAGTT CCTTCTGATG ACTGCTTGTT TTAAAAACCA AATGCCTCGT AATGTCATTG
301    ATTATATTAG ATTTTTAGGA AGCTTAGTTC CTAAGTTTTA GTGTAGTTGG ATCAATTGTA
361    TGGAACTATT AACAGAGCCG TGAATCTTTG GTATCTATCG TGTGAAGAAT TAGTTGTCAA
421    CTGCCCTAGG TCTTTTCGTT CAGTAGCAAG GACACGTCAA ATAATCTGTG TTAAGGCACG
481    TCAAAATGTT TGAActCTAT ATACAAActC CTTTTCTGGT TGCTGATGTA TTTTCTACCC
541    ACGGCCTATC AGTATACCTC TTATTCAACG TACGTGATGA TCTTTAGATT GGTAGTATCA
601    TACAAGTCTC TGAAATTATA TTCTGACATA TATACGTCTT GTTTCAGACA ATGTAGACTT
661    GGGGACGGCT TGTGGTAAAT ACTACAGGGT CTGTTGCCTC AGCATCATTG ATCCAGGTGA
721    ATTTCTCGCC CCGACTCGAT TTACTGCTGG TTGAATATCC TTCAA
  
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SEQ Gc143-2, 765 bp, partial sequence

ORIGIN

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1      CCTCTCAGGA AGTCTGAGAT TGAGTATTAT GCTATGTTGG CAAAGGTTGG AGTCCACCAC
61     TACAACGGAA GTAAGTGAAT ATCTTTGTGT GTATAGACAG TAATATAGAT GTTTGAACTT
121    CTTTTTGGTG CTTTTGAAAT GTTTTTAAAT ATTGTTTGCT GTTTTGACTG CTTGCGAGTG
181    AAAATATATA TATCTTCCTT TCGTTTGGTT CGGACATGAA TTATGTAAct TTGCTAGGAG
241    TGCTGAAGTT CCTTCTGATG ACTGCTTGTT TTAAAAACCA AATGCCTCGT AATGTCATTG
301    ATTATATTAG ATTTTTAGGA AGCTTAGTTC CTAAGTTTTA GTGTAGTTGG ATCAATTGTA
361    TGGGACTATT AACAGAGCCG TGAATCTTTG GTATCTATCG TGTGAAGAAT TAGTTGTCAA
421    CTGCCCTAGG TCTTTTCGTT CAGTAGCAAG GACACGTCAA ATAATCTGTG TTAAGGCACG
481    TCAAAATGTT TGAActCTAT ATACAAActC CTTTTCTGGT TGCTGATGTA TTTTCTACCC
541    ACGGCCTATC AGTATACCTC TTATTCAACG TACGTGATGA TCTTTAGATT GGTAGTATCA
601    TACAAGTCTC TGAAATTATA TTCTGACATA TATACGTCTT GTTTCAGACA ATGTAGACTT
661    GGGGACGGCT TGTGGTAAAT ACTACAGGGT CTGTTGCCTC AGCATCATTG ATCCAGGTGA
721    ATTTCTCGCC CCGACTCGAT TTACTGCTGG TTGAATATCC TTCAA
  
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SEQ Glh902b, 711 bp, partial sequence

ORIGIN

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1      CACCACTACA ACGGAAGTAA GTGAATATCT TTGTGTGTAT AGACAGTAAT ATAGATGTTT
61     GAACTTCTTT TTGGTGCTTT TGAAATGTTT TTAATATTG TTTGCTGTTT TGACTGCTTG
121    CGAGTGAAAA TATATATATC TTCCTTTCGT TTGGTTCGGA CATGAATTAT GTAACCTTGC
181    TAGGAGTGCT GAAGTTCCTT CTGATGACTG CTTGTTTTAA AAACCAAATG CCTCGTAATG
241    TCATTGATTA TATTAGATTT TTAGGAAGCT TAGTTCCTAA GTTTTAGTGT AGTTGGATCA
301    ATTGTATGGG ACTATTAACA GAGCCGTGAA TCTTTGGTAT CTATCGTGTG AAGAATTAGT
361    TGTCAACTGC CCTAGGTCTT TTCGTTTCAGT AGCAAGGACA CGTCAAATAA TCTGTGTTAA
421    GGCACGTCAA AATGTTTTGAA CTCTATATAC AAACCTCTTT TCTGGTTGCT GATGTATTTT
481    CTACCCACGG CCTATCAGTA TACCTCTTAT TCAACGTACG TGATGATCTT TAGATTGGTA
541    GTATCATACA AGTCTCTGAA ATTATATTCT GACATATATA CGTCTTGTTT CAGACAATGT
601    AGACTTGGGG ACGGCTTGTG GTAAATACTA CAGGGTCTGT TGCCTCAGCA TCATTGATCC
661    AGGTGAATTT CTCGCCCGA CTCGATTTAC TGCTGGTTGA ATATCCTTCA A
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SEQ H24, 759 bp, partial sequence

ORIGIN

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1      CCTCTCAGGA AGTCTGAGAT TGAGTATTAT GCTATGTTGG CAAAGGTTGG AGTCCACCAC
61     TACAACGGAA GTAAGTGAAT ATCTTTGTGT GTATAGACAG TAATATAGAT GTTTGAACTT
121    CTTTTTGGTG CTTTTGAAAT GTTTTTAAAT ATTGTTTGCT GTTTTGACTG CTTGCGAGTG
181    AAAATATATA TATCTTCCTT TCGTTTGGTT CGGACATGAA TTATGTAACT TTGCTAGGAG
241    TACTGAAGTT CTTTCTGATG ACTGCTTGTT TTA AAAACCA AATGCCTCGT AATGTCATTG
301    ATTATATTAG ATTTTTAGGA AGCTTAGTTT CTAAGTTTTA GTGTAGTTGG ATCAATTGTA
361    TGGAACTATT AACAAAGCCG TGAATCTTTG GTATCTATCG TGTGAAGAAT TAGTTGACAA
421    CTGCCCTAGG TCTTTTGTTT AGTAGTAAGG ACACGTCAA TAATCTGTGT TAAGGCACGT
481    CAAAATGTTC GAACTCTATA TTCAAACCTC TTTTCTGGTT GCTGATGTAT TTTCTACCCA
541    CGGCCTATCA GTATACCTCT TATTCAACGT ACGTGATGAT CTTTAGATTG GTAGTACAAG
601    TCTCTGAAAT TATATGCTGA CATATATACG TCTTGTTTCA GACAATGTAG ACTTGGGGAC
661    GGCTTGTGGT AAATACTACA GGGTCTGTTG CCTCAGCATC ATCGATCCAG GTGAATTTCT
721    CGCCCCGACT CAATTTACTG CTGGTTGAAT ATCCTTCAA
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SEQ M82, Gc143-2, Glh 902b,H24.

NAMES: Gc143-2, Glh902b, M82, H24

ORIGIN

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Gc143-2_BACF-R TACAACGGAAGTAAGTGAATATCTTTGTGTGTATAGACAGTAATATAGATGTTTGAACCTT 120
902_BACF      TACAACGGAAGTAAGTGAATATCTTTGTGTGTATAGACAGTAATATAGATGTTTGAACCTT 66
M82_BACF-R   TACAACGGAAGTAAGTGAATATCTTTGTGTGTATAGACAGTAATATAGATGTTTGAACCTT 120
H24_BACF-R   TACAACGGAAGTAAGTGAATATCTTTGTGTGTATAGACAGTAATATAGATGTTTGAACCTT 120
Consensus    tacaacggaagtaagtgaaatcttttggtgtgtatagacagtaatatagatgtttgaacctt
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Gc143-2_BACF-R CTTTTTGGTGCTTTTGAATGTTTTTAAATATTGTTTGCTGTTTTGACTGCTTGCGAGTG 180
902_BACF      CTTTTTGGTGCTTTTGAATGTTTTTAAATATTGTTTGCTGTTTTGACTGCTTGCGAGTG 126
M82_BACF-R   CTTTTTGGTGCTTTTGAATGTTTTTAAATATTGTTTGCTGTTTTGACTGCTTGCGAATG 180
H24_BACF-R   CTTTTTGGTGCTTTTGAATGTTTTTAAATATTGTTTGCTGTTTTGACTGCTTGCGAGTG 180
Consensus    ctttttggtgcttttgaaatgTTTTTAAATATTGTTTGCTGTTTTGACTGCTTGCGA tg
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Gc143-2_BACF-R AAAATATATATATCTTCCTTTCGTTTGGTTCGGACATGAATTATGTAACCTTGCTAGGAG 240
902_BACF      AAAATATATATATCTTCCTTTCGTTTGGTTCGGACATGAATTATGTAACCTTGCTAGGAG 186
M82_BACF-R   AAAATATATATATCTTCCTTTCGTTTGGTTCGGACATGAATTATGTAACCTTGCTAGGAG 240
H24_BACF-R   AAAATATATATATCTTCCTTTCGTTTGGTTCGGACATGAATTATGTAACCTTGCTAGGAG 240
Consensus    aaaatatatatatcttccttTCGTTTGGTTCGGACATGAATTATGTAACCTTGCTAGGAG
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Gc143-2_BACF-R	TGCTGAAGTTCCTTCTGATGACTGCTTGTTTTAAAAACCAAATGCCTCGTAATGTCATTG	300
902_BACF	TGCTGAAGTTCCTTCTGATGACTGCTTGTTTTAAAAACCAAATGCCTCGTAATGTCATTG	246
M82_BACF-R	TGCTGAAGTTCCTTCTGATGACTGCTTGTTTTAAAAACCAAATGCCTCGTAATGTCATTG	300
H24_BACF-R	TACTGAAGTTCCTTCTGATGACTGCTTGTTTTAAAAACCAAATGCCTCGTAATGTCATTG	300
Consensus	t ctgaagttccttctgatgactgcttgTTTTAAAAACCAAATGCCTCGTAATGTCATTG	
Gc143-2_BACF-R	ATTATATTAGATTTTTAGGAAGCTTAGTTCCTAAGTTTTAGTGTAGTTGGATCAATTGTA	360
902_BACF	ATTATATTAGATTTTTAGGAAGCTTAGTTCCTAAGTTTTAGTGTAGTTGGATCAATTGTA	306
M82_BACF-R	ATTATATTAGATTTTTAGGAAGCTTAGTTCCTAAGTTTTAGTGTAGTTGGATCAATTGTA	360
H24_BACF-R	ATTATATTAGATTTTTAGGAAGCTTAGTTCCTAAGTTTTAGTGTAGTTGGATCAATTGTA	360
Consensus	attatattagatTTTTAGGAAGCTTAGTTCCTAAGTTTTAGTGTAGTTGGATCAATTGTA	
Gc143-2_BACF-R	TGGGACTATTAACAGAGCCGTGAATCTTTGGTATCTATCGTGTGAAGAATTAGTTGTC	420
902_BACF	TGGGACTATTAACAGAGCCGTGAATCTTTGGTATCTATCGTGTGAAGAATTAGTTGTC	366
M82_BACF-R	TGGAACTATTAACAGAGCCGTGAATCTTTGGTATCTATCGTGTGAAGAATTAGTTGTC	420
H24_BACF-R	TGGAACTATTAACAAGCCGTGAATCTTTGGTATCTATCGTGTGAAGAATTAGTTGTC	420
Consensus	tgg actattaaca agccgtgaatctTTGGTATCTATCGTGTGAAGAATTAGTTGTC	
Gc143-2_BACF-R	CTGCCCTAGGTCTTTTCGTTTCAGTAGCAAGGACACGTCAAATAATCTGTGTTAAGGCACG	480
902_BACF	CTGCCCTAGGTCTTTTCGTTTCAGTAGCAAGGACACGTCAAATAATCTGTGTTAAGGCACG	426
M82_BACF-R	CTGCCCTAGGTCTTTTCGTTTCAGTAGCAAGGACACGTCAAATAATCTGTGTTAAGGCACG	480
H24_BACF-R	CTGCCCTAGGTCTTTTCGTTTCAGTAGCAAGGACACGTCAAATAATCTGTGTTAAGGCACG	479
Consensus	ctgccctaggtctTTTCGTTTCAGTAGCAAGGACACGTCAAATAATCTGTGTTAAGGCACG	
Gc143-2_BACF-R	TCAAATGTTTGAAGTCTATATACAACTCCTTTTCTGGTTGCTGATGTATTTTCTACCC	540
902_BACF	TCAAATGTTTGAAGTCTATATACAACTCCTTTTCTGGTTGCTGATGTATTTTCTACCC	486
M82_BACF-R	TCAAATGTTTGAAGTCTATATACAACTCCTTTTCTGGTTGCTGATGTATTTTCTACCC	540
H24_BACF-R	TCAAATGTTTGAAGTCTATATACAACTCCTTTTCTGGTTGCTGATGTATTTTCTACCC	539
Consensus	tcaaatgTTTGAAGTCTATATACAACTCCTTTTCTGGTTGCTGATGTATTTTCTACCC	
Gc143-2_BACF-R	ACGGCCTATCAGTATACCTCTTATTCAACGTACGTGATGATCTTTAGATTGGTAGTATCA	600
902_BACF	ACGGCCTATCAGTATACCTCTTATTCAACGTACGTGATGATCTTTAGATTGGTAGTATCA	546
M82_BACF-R	ACGGCCTATCAGTATACCTCTTATTCAACGTACGTGATGATCTTTAGATTGGTAGTATCA	600
H24_BACF-R	ACGGCCTATCAGTATACCTCTTATTCAACGTACGTGATGATCTTTAGATTGGTAGTATCA	596
Consensus	acggcctatcagTATACCTCTTATTCAACGTACGTGATGATCTTTAGATTGGTAGTATCA	
Gc143-2_BACF-R	TACAAGTCTCTGAAATTATATCTGACATATATACGTCTTGTTTCAGACAATGTAGACTT	660
902_BACF	TACAAGTCTCTGAAATTATATCTGACATATATACGTCTTGTTTCAGACAATGTAGACTT	606
M82_BACF-R	TACAAGTCTCTGAAATTATATCTGACATATATACGTCTTGTTTCAGACAATGTAGACTT	660
H24_BACF-R	. . CAAGTCTCTGAAATTATATCTGACATATATACGTCTTGTTTCAGACAATGTAGACTT	654
Consensus	caagtctctgaaattatATCTGACATATATACGTCTTGTTTCAGACAATGTAGACTT	
Gc143-2_BACF-R	GGGGACGGCTTGTGGTAAATACTACAGGGTCTGTTGCCTCAGCATCATGATCCAGGTGA	720
902_BACF	GGGGACGGCTTGTGGTAAATACTACAGGGTCTGTTGCCTCAGCATCATGATCCAGGTGA	666
M82_BACF-R	GGGGACGGCTTGTGGTAAATACTACAGGGTCTGTTGCCTCAGCATCATGATCCAGGTGA	720
H24_BACF-R	GGGGACGGCTTGTGGTAAATACTACAGGGTCTGTTGCCTCAGCATCATGATCCAGGTGA	714
Consensus	ggggacggctTGTGGTAAATACTACAGGGTCTGTTGCCTCAGCATCATGATCCAGGTGA	
Gc143-2_BACF-R	ATTTCTCGCCCCGACTCGATTTACTGCTGGTTGAATATCCTTCAA	765
902_BACF	ATTTCTCGCCCCGACTCGATTTACTGCTGGTTGAATATCCTTCAA	711
M82_BACF-R	ATTTCTCGCCCCGACTCGATTTACTGCTGGTTGAATATCCTTCAA	765
H24_BACF-R	ATTTCTCGCCCCGACTCAATTTACTGCTGGTTGAATATCCTTCAA	759
Consensus	atTTCTCGCCCCGACTC ATTTACTGCTGGTTGAATATCCTTCAA	

Comments: Sequence M82 = Gc143-2 = Glh902b ≠ H24 [There is an introgression from wild species (*S. habrochaites*) found in begomovirus-resistant breeding lines, H24 (*Ty-2* locus).]