

T0302, Chromosome XI, 89 cM

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Introduction: E. Graham and P. Hanson (pers. Com.) have found that the *Ty-2* locus is associated with the markers, TG105 A and T0302. H24 from P. Hanson has the *Ty-2* locus.

Primers:

Table 1: PCR Primers on Chr. 11

Primer name	Sequence (5' to 3')
TG0302F	TGGCTCATCCTGAAGCTGATAGCGC (SGN primers)
TG0302R	AGTGATACATCCTTGCCATTGACT (SGN primers)

PCR at 55 C, (TGEN55), 850-bp fragment.

SEQ M82, 792 bp

ORIGIN

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1      TGGCTCATCC TGAAGCTGAT AGCGCGCTAA ACTGTGACTC AGGTATTATG TGATTTTTTC
61     GGAGGCTGTG TTTTCTTTGA TTTGATGATT GCGGATGCAT CCATTTTCAT TCTGAGCTCT
121    TTGGTCCTCC CTTTGACAAT TTCTTGTTAA TATTCAAGAA AATGAGAACA TTAGCACAAT
181    CTAGGCATCT AGAAACTTGT ATTAGAGATT TAAACCATAT TTGCGAAGAC TTTGGTCCCA
241    CTAGAGGGGG TGTGCATCAT ACAGTAATCT GACCCAAAAG ATTGAGAGAG CAAGTGTCTAG
301    CAAGGGAGAG AGAAGTGCAA ATATGAGTGA GAAAGAAAAC TTAATCCTAC AGTCAGGAGA
361    ATAAAGTTAA GAAGTAAATT TGGTGTGGC AAAATTTGTT GCGGATGTTT CCTATTGTTT
421    ACAGGCGAGA GAAGAGAACA TCAAATCAAG TCAATACCAG TAAAAAGAGG TGCTTCTAAC
481    TAATTCTGTT TAAGCCTTGA GTGAACTACA TTCTCTTCGA TCCCTTTCCA GAACCAGTCC
541    TAGAACTCTT TTGAAAATGT TTTCCGGGGG CTAAAAGATA TTAAGGACGA GGCAGAAAACA
601    AGGTGTGGGG GTGGGAAAGG TTTTGTATGT GCTCGACTTG TTTAGATTCA AGGTAGATGA
661    TATTTTTCAT CCTCGTCTCC CTTTTGAGA TCGTCAAATA GACTAATTAC ATCGATTTTC
721    TTCAATCACA CAGGCAATCT TCTTCGATCC GGTGATATCA GAGGTTACCA GTCAATGGCA
781    AGGATGTACA CT
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SEQ Gc143-2, 792 bp

ORIGIN

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1      TGGCTCATCC TGAAGCTGAT AGCGCGCTAA ACTGTGACTC AGGTATTATG TGATTTTTTC
61     GGAGGCTGTG TTTTCTTTGA TTTGATGATT GCGGATGCAT CCATTTTCAT TCTGAGCTCT
121    TTGGTCCTCC CTTTGACAAT TTCTTGTTAA TATTCAAGAA AATGAGAACA TTAGCACAAT
181    CTAGGCATCT AGAAACTTGT ATTAGAGATT TAAACCATAT TTGCGAAGAC TTTGGTCCCA
241    CTAGAGGGGG TGTGCATCAT ACAGTAATCT GACCCAAAAG ATTGAGAGAG CAAGTGTCTAG
301    CAAGGGAGAG AGAAGTGCAA ATATGAGTGA GAAAGAAAAC TTAATCCTAC AGTCAGGAGA
361    ATAAAGTTAA GAAGTAAATT TGGTGTGGC AAAATTTGTT GCGGATGTTT CCTATTGTTT
421    ACAGGCGAGA GAAGAGAACA TCAAATCAAG TCAATACCAG TAAAAAGAGG TGCTTCTAAC
481    TAATTCTGTT TAAGCCTTGA GTGAACTACA TTCTCTTCGA TCCCTTTCCA GAACCAGTCC
541    TAGAACTCTT TTGAAAATGT TTTCCGGGGG CTAAAAGATA TTAAGGACGA GGCAGAAAACA
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601 AGGTGTGGGG GTGGGAAAGG TTTTTGATGT GCTCGACTTG TTTAGATTCA AGGTAGATGA
661 TATTTTTTCAT CCTCGTCTCC CCTTTTGAGA TCGTCAAATA GACTAATTAC ATCGATTTTC
721 TTCAATCACA CAGGCAATCT TCTTCGATCC GGTGATATCA GAGGTTACCA GTCAATGGCA
781 AGGATGTACA CT

SEQ Glh902, 792 bp

ORIGIN

1 TGGCTCATCC TGAAGCTGAT AGCGCGCTAA ACTGTGACTC AGGTATTATG TGATTTTTTC
61 GGAGGCTGTG TTTTCTTTGA TTTGATGATT GCGGATGCAT CCATTTTCAT TCTGAGCTCT
121 TTGGTCCTCC CTTTGACAAT TTCTTGTTAA TATTCAAGAA AATGAGAACA TTAGCACAAT
181 CTAGGCATCT AGAAACTTGT ATTAGAGATT TAAACCATAT TTGCGAAGAC TTTGGTCCCA
241 CTAGAGGGGG TGTGCATCAT ACAGTAATCT GACCCAAAAG ATTGAGAGAG CAAGTGTGAG
301 CAAGGGAGAG AGAAGTGCAA ATATGAGTGA GAAAGAAAAC TTAATCCTAC AGTCAGGAGA
361 ATAAAGTTAA GAAGTAAATT TGGTGTTGGC AAAATTTGTT GCGGATGTTT CCTATTGTTT
421 ACAGGCGAGA GAAGAGAACA TCAAATCAAG TCAATACCAG TAAAAAGAGG TGCTTCTAAC
481 TAATTCTGTT TAAGCCTTGA GTGAACTACA TTCTCTTCGA TCCCTTTCCA GAACCAGTCC
541 TAGAACTCTT TTGAAAATGT TTTCCGGGGG CTAAGAGATA TTAAGGACGA GGCGAAAACA
601 AGGTGTGGGG GTGGGAAAGG TTTTTGATGT GCTCGACTTG TTTAGATTCA AGGTAGATGA
661 TATTTTTTCAT CCTCGTCTCC CCTTTTGAGA TCGTCAAATA GACTAATTAC ATCGATTTTC
721 TTCAATCACA CAGGCAATCT TCTTCGATCC GGTGATATCA GAGGTTACCA GTCAATGGCA
781 AGGATGTACA CT

SEQ *S. chilense* LA2779, 789 bp

ORIGIN

1 TGGCTCATCC TGAAGCTGAT AGCGCGCTAA ACTGTGACTC AGGTATTATG TGATTTTTTC
61 GGAGGCTGTG TTTTCTTTGA TTTGATGATT GCGGATGCAT TCATTTTCAT TCTGAGCTCT
121 TAGGTCCTCC CTTTGACAAT TTCTTGTTAA TATTCAAGAA AATATGAGAA CATTAGCACA
181 ATCTAGGCAT CTAGAACTT GTATTAGAGA TTTAAACCAT ATTTGCGAAG ACTTTGGTCC
241 CACTAGAGGG GGTGTGCAGC ATACAGTAAT CTGACCCAAA GATTGAGAGA GCAAGTGTCA
301 GCAAGGGAGA GAGAAGTGCA AATATGAGTG AGAAAGAAAA CTTAATCCTA CAGTCAGGAG
361 ATAAAGTTAA GAAGTAAATT TGGTGTTGGC AAAATCTGTT GCGGATGTTT CCTATGGTTT
421 ACAGGCGAGA GAAGAGAACA TCAAATCAAG TCAATACCAG TAAAAAGAGG TGCTTCTAAC
481 TAATTCTGTT TAAGCCTTGA ATGAACTACA TTCTCTTCGA TCCCTTTCCA GAACCAGTCT
541 TAGAACTCTT TTAATGTTTT CCGGGGGCTA AAAGATACAA AGGACGAGGC GAAAACAAGG
601 TGTGGGGGTC GTATAGGTTT TTGATGTGCT CGACTTGTTT AGATTCAAGG TAGATGATAT
661 TATTTATCCT CGTCTCCCT TTTGAGATCG TCAAATAGAC TAATTACATC GATTTTCTTA
721 AATCACACAG GCAATCTTCT TCGATCCGGT GATATCAGAG GTTACCAGTC AATGGCAAGG
781 ATGTACTACT

SEQ H24, 909 bp (*Ty-2* locus)

ORIGIN

1 TGGCTCATCC TGAAGCTGAT AGCGCTCTGA ACTGTGACTC AGGTATTATG TGATGTTTTTC
61 GGGGGCTGTA ATGTCTTTGA TTTGATGATT GCTGATGCAT TCATTTTCAT TCTGAGCTCT
121 TAGGTCCTCC CTTGAAAAT TCCTTGTTAA TATTCAAGAA AATATGATAA CATTACTACA
181 ATCTAGGCAT CTCGAACTT GTATTAGAGA TTTAAACCAT ATTTGCGAAG ACTTTGGTCC
241 CACTAGGGGG GGAGGGGCAT ACAGTAGATC CGACCCAAAG ATATATGAGA ACATTAGCAC
301 AATCTAGGCA TCTCAAACT TGTATTAGAG ATTTAAACAA TATTTGCGAA GCTTTGGTCC
361 CACTAGAGGG GGTGTGCAGC ATACAGTAGA TCCGACCCAA AGATTGAGAG AGCAAGTGTG
421 AGCATGGGAG AGAGAAGTGC AAATATGAGT GAGAAAGAAA ACTTAATCCT ACAGTCGGGA
481 GAATAAAGTT AAGTAAATTT GGTGTTGCAA AATCTGTTGC GGCTGTTTCC TATGGTTTAC
541 AGGCTAGAGA TGAGAACATC ACATCAAGTG ACTGCCAGGA AAAATTGGTG TTTCTAACTA

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601   ATTCTGTTTA AGCCTTGAAC GAACTACATT CTCTTCGATC CCTTTCCAGA ACCATTCTTA
661   GAACTCTTTT GAAAATGTTT TCCGGGGGCT AAAGATATAA AGGACGAGGT GAAAACAAGG
721   TGTGGGGGTG GTATAGGTTT TTGATGTGCT CGACTTGTTT AGATTCAAGG TAGATGATAT
781   TTTTCATCCT CGTCTCCCCT TTTGAGATCG TCAAATAGAC TAATTACATC GATTTTCTTA
841   AATCACACAG GCAATCTTCT TCGATCCGGT GATATCAGAG GTTACCAGTC AATGGCAAGG
901   ATGTACTACT

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SEQ *S. habrochatis* LA0386, 909 bp (may have the *Ty-2* gene)

ORIGIN

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1     TGGCTCATCC TGAAGCTGAT AGCGCTCTGA ACTGTGACTC AGGTATTATG TGATGTTTTC
61    GGGGGCTGTA ATGTCTTTGA TTTGATGATT GCTGATGCAT TCATTTTCAT TCTGAGCTCT
121   TAGGTCCTCC CTTTGAAAAT TCCTTGGTAA TATTCAAGAA AATATGATAA CATTACTACA
181   ATCTAGGCAT CTCGAAACTT GTATTAGAGA TTTAAACCAT ATTTGCGAAG ACTTTGGTCC
241   CACTAGGGGG GGAGGGGCAT ACAGTAGATC CGACCCAAAG ATATATGAGA ACATTAGCAC
301   AATCTAGGCA TCTCAAAACT TGTATTAGAG ATTTAAACAA TATTTGCGAA GCTTTGGTCC
361   CACTAGAGGG GGTGTGCAGC ATACAGTAGA TCCGACCCAA AGATTGAGAG AGCAAGTGTC
421   AGCATGGGAG AGAGAAGTGC AAATATGAGT GAGAAAAGAAA ACTTAATCCT ACAGTCGGGA
481   GAATAAAGTT AAGTAAATTT GGTGTTGCAA AATCTGTTGC GGCTGTTTCC TATGGTTTAC
541   AGGCTAGAGA TGAGAACATC ACATCAAGTG ACTGCCAGGA AAAATTGGTG TTTCTAACTA
601   ATTCTGTTTA AGCCTTGAAC GAACTACATT CTCTTCGATC CCTTTCCAGA ACCATTCTTA
661   GAACTCTTTT GAAAATGTTT TCCGGGGGCT AAAGATATAA AGGACGAGGT GAAAACAAGG
721   TGTGGGGGTG GTATAGGTTT TTGATGTGCT CGACTTGTTT AGATTCAAGG TAGATGATAT
781   TTTTCATCCT CGTCTCCCCT TTTGAGATCG TCAAATAGAC TAATTACATC GATTTTCTTA
841   AATCACACAG GCAATCTTCT TCGATCCGGT GATATCAGAG GTTACCAGTC AATGGCAAGG
901   ATGTACTACT

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Alignment: M82, Glh902b, Gc143-2, LA2779, H24,LA0386

NAMES: M82-302FR 902-302FR Gc143_302F-R 2779_302F-R H24_302F-R 386_302F-R

ORIGIN

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M82-302FR   TGGCTCATCCTGAAGCTGATAGCGCGCTAAACTGTGACTCAGGTATTATGTGATTTTTTC   60
902-302FR   TGGCTCATCCTGAAGCTGATAGCGCGCTAAACTGTGACTCAGGTATTATGTGATTTTTTC   60
Gc143_302F-R TGGCTCATCCTGAAGCTGATAGCGCGCTAAACTGTGACTCAGGTATTATGTGATTTTTTC   60
2779_302F-R TGGCTCATCCTGAAGCTGATAGCGCGCTAAACTGTGACTCAGGTATTATGTGATTTTTTC   60
H24_302F-R   TGGCTCATCCTGAAGCTGATAGCGCTGCTGAAGTGTGACTCAGGTATTATGTGATGTTTTTC   60
386_302F-R   TGGCTCATCCTGAAGCTGATAGCGCTGCTGAAGTGTGACTCAGGTATTATGTGATGTTTTTC   60
Consensus   tggctcatcctgaagctgatagcgc ct aactgtgactcaggtattatgtgat ttttc

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M82-302FR   GGAGGCTGTGTTTTCTTTGATTTGATGATTGCGGATGCATCCATTTTCATTCTGAGCTCT   120
902-302FR   GGAGGCTGTGTTTTCTTTGATTTGATGATTGCGGATGCATCCATTTTCATTCTGAGCTCT   120
Gc143_302F-R GGAGGCTGTGTTTTCTTTGATTTGATGATTGCGGATGCATCCATTTTCATTCTGAGCTCT   120
2779_302F-R GGAGGCTGTGTTTTCTTTGATTTGATGATTGCGGATGCATcCATTTTTCATTCTGAGCTCT   120
H24_302F-R   GGGGGCTGTAATGTCCTTTGATTTGATGATTGCTGATGCATTCATTTTCATTCTGAGCTCT   120
386_302F-R   GGGGGCTGTAATGTCCTTTGATTTGATGATTGCTGATGCATTCATTTTCATTCTGAGCTCT   120
Consensus   gg ggctgt t tctttgatttgatgattgc gatgcat cattttcattctgagctct

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M82-302FR   TTGGTCCTCCCCTTGACAATTTCTTGTTAATATTCAAGAAAAAT..GAGAACATTAGCACA   178
902-302FR   TTGGTCCTCCCCTTGACAATTTCTTGTTAATATTCAAGAAAAAT..GAGAACATTAGCACA   178
Gc143_302F-R TTGGTCCTCCCCTTGACAATTTCTTGTTAATATTCAAGAAAAAT..GAGAACATTAGCACA   178
2779_302F-R TAGGTCCTCCCCTTGACAATTTCTTGTTAATATTCAAGAAAAATATGAGAACATTAGCACA   180
H24_302F-R   TAGGTCCTCCCCTTGAAAATTCCTTGTTAATATTCAAGAAAAATATGATAACATTACTACA   180
386_302F-R   TAGGTCCTCCCCTTGAAAATTCCTTGTTAATATTCAAGAAAAATATGATAACATTACTACA   180
Consensus   t ggtcctccccttga aatt cttg taatattcaagaaaat ga aacatta aca

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M82-302FR	ATCTAGGCATCTAGAACTTGTATTAGAGATTAAACCATATTTGCGAAGACTTTGGTCC	238
902-302FR	ATCTAGGCATCTAGAACTTGTATTAGAGATTAAACCATATTTGCGAAGACTTTGGTCC	238
Gc143_302F-R	ATCTAGGCATCTAGAACTTGTATTAGAGATTAAACCATATTTGCGAAGACTTTGGTCC	238
2779_302F-R	ATCTAGGCATCTAGAACTTGTATTAGAGATTAAACCATATTTGCGAAGACTTTGGTCC	240
H24_302F-R	ATCTAGGCATCTCGAACTTGTATTAGAGATTAAACCATATTTGCGAAGACTTTGGTCC	240
386_302F-R	ATCTAGGCATCTCGAACTTGTATTAGAGATTAAACCATATTTGCGAAGACTTTGGTCC	240
Consensus	atctagggcatct gaaacttgtattagagatttaaaccatatttgccaagactttgggtcc	
M82-302FR	CACTAG.....	244
902-302FR	CACTAG.....	244
Gc143_302F-R	CACTAG.....	244
2779_302F-R	CACTAG.....	246
H24_302F-R	CACTAGGGGGGGAGGGGCATACAGTAGATCCGACCCAAAGATATATGAGAACATTAGCAC	300
386_302F-R	CACTAGGGGGGGAGGGGCATACAGTAGATCCGACCCAAAGATATATGAGAACATTAGCAC	300
Consensus	cactag	
M82-302FR	244
902-302FR	244
Gc143_302F-R	244
2779_302F-R	246
H24_302F-R	AATCTAGGCATCTCAAACTTGTATTAGAGATTAAACAATATTTGCGAAGCTTTGGTCC	360
386_302F-R	AATCTAGGCATCTCAAACTTGTATTAGAGATTAAACAATATTTGCGAAGCTTTGGTCC	360
Consensus		
M82-302FRAGGGGGTGTGCATCATAACAGTA . ATCTGACCCAAAAGATTGAGAGAGCAAGTGT	297
902-302FRAGGGGGTGTGCATCATAACAGTA . ATCTGACCCAAAAGATTGAGAGAGCAAGTGT	297
Gc143_302F-RAGGGGGTGTGCATCATAACAGTA . ATCTGACCCAAAAGATTGAGAGAGCAAGTGT	297
2779_302F-RAGGGGGTGTGCAGCATAACAGTA . ATCTGACCCAAA . GATTGAGAGAGCAAGTGT	298
H24_302F-R	CACTAGAGGGGGTGTGCAGCATAACAGTAGATCCGACCCAAA . GATTGAGAGAGCAAGTGT	419
386_302F-R	CACTAGAGGGGGTGTGCAGCATAACAGTAGATCCGACCCAAA . GATTGAGAGAGCAAGTGT	419
Consensus	agggggtgtgca catacagta atc gacccaaa gattgagagagcaagtgt	
M82-302FR	CAGCAAGGGGAGAGAGAAGTGCAAAATATGAGTGAGAAAAGAAAACCTTAATCCTACAGTCAGG	357
902-302FR	CAGCAAGGGGAGAGAGAAGTGCAAAATATGAGTGAGAAAAGAAAACCTTAATCCTACAGTCAGG	357
Gc143_302F-R	CAGCAAGGGGAGAGAGAAGTGCAAAATATGAGTGAGAAAAGAAAACCTTAATCCTACAGTCAGG	357
2779_302F-R	CAGCAAGGGGAGAGAGAAGTGCAAAATATGAGTGAGAAAAGAAAACCTTAATCCTACAGTCAGG	358
H24_302F-R	CAGCATGGGAGAGAGAAGTGCAAAATATGAGTGAGAAAAGAAAACCTTAATCCTACAGTCGGG	479
386_302F-R	CAGCATGGGAGAGAGAAGTGCAAAATATGAGTGAGAAAAGAAAACCTTAATCCTACAGTCGGG	479
Consensus	cagca ggggagagagaagtgc aaaat atg agt gaga aaaa act taat cct ac agtc gg	
M82-302FR	AGAATAAAGTTAAGAAGTAAATTTGGTGTGGCAAATTTGTTGCGGATGTTCCCTATTG	417
902-302FR	AGAATAAAGTTAAGAAGTAAATTTGGTGTGGCAAATTTGTTGCGGATGTTCCCTATTG	417
Gc143_302F-R	AGAATAAAGTTAAGAAGTAAATTTGGTGTGGCAAATTTGTTGCGGATGTTCCCTATTG	417
2779_302F-R	AGA . TAAAGTTAAGAAGTAAATTTGGTGTGGCAAATCTGTTGCGGATGTTCCCTATTG	417
H24_302F-R	AGAATAAAGTTAA . . . GTAAATTTGGTGTGG . CAAAATCTGTTGCGGCTGTTTCCATGG	535
386_302F-R	AGAATAAAGTTAA . . . GTAAATTTGGTGTGG . CAAAATCTGTTGCGGCTGTTTCCATGG	535
Consensus	aga taaagttaa gtaaatttgggtgttg caaaat tgttgagg tgtt cctat g	
M82-302FR	TTTACAGGCGAGAGAAGAGAACATCAAATCAAGTCAATACCAGTAAAAAGAGGTGCTTCT	477
902-302FR	TTTACAGGCGAGAGAAGAGAACATCAAATCAAGTCAATACCAGTAAAAAGAGGTGCTTCT	477
Gc143_302F-R	TTTACAGGCGAGAGAAGAGAACATCAAATCAAGTCAATACCAGTAAAAAGAGGTGCTTCT	477
2779_302F-R	TTTACAGGCGAGAGAAGAGAACATCAAATCAAGTCAATACCAGTAAAAAGAGGTGCTTCT	477
H24_302F-R	TTTACAGGCTAGAGATGAGAACATCAATCAAGTACTGCCAGGAAAAATTTGGTGTTTCT	595
386_302F-R	TTTACAGGCTAGAGATGAGAACATCAATCAAGTACTGCCAGGAAAAATTTGGTGTTTCT	595
Consensus	tttacaggc agaga gagaacatca atcaagt a t ccag aaaaa ggtg ttct	
M82-302FR	AACTAATTCGTTTAAGCCTTGAGTGAACACTACATTCTCTTCGATCCCTTTCCAGAACCAG	537
902-302FR	AACTAATTCGTTTAAGCCTTGAGTGAACACTACATTCTCTTCGATCCCTTTCCAGAACCAG	537
Gc143_302F-R	AACTAATTCGTTTAAGCCTTGAGTGAACACTACATTCTCTTCGATCCCTTTCCAGAACCAG	537
2779_302F-R	AACTAATTCGTTTAAGCCTTGAATGAACACTACATTCTCTTCGATCCCTTTCCAGAACCAG	537
H24_302F-R	AACTAATTCGTTTAAGCCTTGAACGAACACTACATTCTCTTCGATCCCTTTCCAGAACCAG	655
386_302F-R	AACTAATTCGTTTAAGCCTTGAACGAACACTACATTCTCTTCGATCCCTTTCCAGAACCAG	655
Consensus	aactaattctgtttaagccttga gaactacattctcttcgatccctttccagaacca	

M82-302FR	TCCTAGAACTCTTTTAAAAATGTTTTCCGGGGGCTAAAAGATA	TTAAGGACGAGGCGAAA	597
902-302FR	TCCTAGAACTCTTTTAAAAATGTTTTCCGGGGGCTAAAAGATA	TTAAGGACGAGGCGAAA	597
Gc143_302F-R	TCCTAGAACTCTTTTAAAAATGTTTTCCGGGGGCTAAAAGATA	TTAAGGACGAGGCGAAA	597
2779_302F-R	TCCTAGAACTCTTTT...AATGTTTTCCGGGGGCTAAAAGATA	CAAAGGACGAGGCGAAA	594
H24_302F-R	TCCTAGAACTCTTTTAAAAATGTTTTCCGGGGGCTAAA	.GATA	714
386_302F-R	TCCTAGAACTCTTTTAAAAATGTTTTCCGGGGGCTAAA	.GATA	714
Consensus	tc tagaactctttt	aatgttttccgggggctaaa gata	aaggacgagg gaaa
M82-302FR	ACAAGGTGTGGGGGTGGGAAAGGTTTTTGATGTGCTCGACTT	GTTT	657
902-302FR	ACAAGGTGTGGGGGTGGGAAAGGTTTTTGATGTGCTCGACTT	GTTT	657
Gc143_302F-R	ACAAGGTGTGGGGGTGGGAAAGGTTTTTGATGTGCTCGACTT	GTTT	657
2779_302F-R	ACAAGGTGTGGGGGTGGTATAGGTTTTTGATGTGCTCGACTT	GTTT	654
H24_302F-R	ACAAGGTGTGGGGGTGGTATAGGTTTTTGATGTGCTCGACTT	GTTT	774
386_302F-R	ACAAGGTGTGGGGGTGGTATAGGTTTTTGATGTGCTCGACTT	GTTT	774
Consensus	acaaggtgtgggggt	g a aggtttttgatgtgctcgactt	gtttagattcaaggtaga
M82-302FR	TGATATTTCATCCTCGTCTCCCCTTTTGAGATCGTCAAATAGACTA	AATTACATCGATT	717
902-302FR	TGATATTTCATCCTCGTCTCCCCTTTTGAGATCGTCAAATAGACTA	AATTACATCGATT	717
Gc143_302F-R	TGATATTTCATCCTCGTCTCCCCTTTTGAGATCGTCAAATAGACTA	AATTACATCGATT	717
2779_302F-R	TGATATTATTCATCCTCGTCTCCCCTTTTGAGATCGTCAAATAGACTA	AATTACATCGATT	714
H24_302F-R	TGATATTTCATCCTCGTCTCCCCTTTTGAGATCGTCAAATAGACTA	AATTACATCGATT	834
386_302F-R	TGATATTTCATCCTCGTCTCCCCTTTTGAGATCGTCAAATAGACTA	AATTACATCGATT	834
Consensus	tgatatt tt atcctcgtctccccttttgagatcgtcaaata	gactaattacatcgatt	
M82-302FR	TTCTTCAATCACACAGGCAATCTTCTTCGATCCGGTGATATCAGAGGT	TACCAGTCAATG	777
902-302FR	TTCTTCAATCACACAGGCAATCTTCTTCGATCCGGTGATATCAGAGGT	TACCAGTCAATG	777
Gc143_302F-R	TTCTTCAATCACACAGGCAATCTTCTTCGATCCGGTGATATCAGAGGT	TACCAGTCAATG	777
2779_302F-R	TTCTTAAATCACACAGGCAATCTTCTTCGATCCGGTGATATCAGAGGT	TACCAGTCAATG	774
H24_302F-R	TTCTTAAATCACACAGGCAATCTTCTTCGATCCGGTGATATCAGAGGT	TACCAGTCAATG	894
386_302F-R	TTCTTAAATCACACAGGCAATCTTCTTCGATCCGGTGATATCAGAGGT	TACCAGTCAATG	894
Consensus	ttctt aatcacacaggcaatcttcttcgatccggtgat	atcagaggttaccagtcaatg	
M82-302FR	GCAAGGATGTACT		792
902-302FR	GCAAGGATGTACT		792
Gc143_302F-R	GCAAGGATGTACT		792
2779_302F-R	GCAAGGATGTACT		789
H24_302F-R	GCAAGGATGTACT		909
386_302F-R	GCAAGGATGTACT		909
Consensus	gcaaggatgtact		

Comments: Sequence M82= Gc143-2=Glh902b#LA2779#H24=LA0386 (There is an introgression from wild species (*S. habrochaites*) found in begomovirus-resistant breeding lines.) H24 is nearly identical to *S. habrochaites* LA0386.

NOTE: These primers will give different size PCR fragments with the H24-introgression and the *S. lycopersicum* sequences, so they can be used directly to detect this H24 introgression (*Ty-2* locus).