

## TG590: RFLP Probe, SGN, Chr. 6, 22.00 cM

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**Table 1:** PCR Primers from RFLP probe TG590 on Chr. 6.

Primer Name	Sequence (5' to 3')
TG590F2	GAGTGAGATCCATACAAACTAAAGC
TG590R2	GGATATATCGATAGGCTACAGACAAAG

### SEQ Heinz\_TG590F2-R2: 817 bp;

ORIGIN

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1 GAGTGAGATC CATACTTTGA TACTTTCTAC CATTCTCAT
61 GCTAATTGGT AACTCCGATC CGATCCAAAC CGAAGCCAAT AACACAGTA GTAATAATCA
121 AACACGGTAT CTCACAAGAG GATCCTTAAG AATAAGACGT TCGTGATAAA CTCTCCATGC
181 ATAATCCTCG AAAGAAAATG AATTGAACAT TTGACTTTCC TCCTCTACCG CTATAGTTTT
241 TGAATCATTG TTGCCAAGGC CATCATCATC TTCGCTAAGT GATAGCGATT TGATACGAAG
301 CAAGGGAGAG ACAGTGTTTT CATGAGCTAG TGTAACAAAC AATGTCATTG ATAGACAGTG
361 TGAGTTACTA CTACCGCTGT TGATTTTACC ATTAGTTATA GGTACTGGTC TTCCTCTCAC
421 TTGTTTACC TTTCCATTAC TCCATACCTG TCCATTATCA AAAAAATTA TAGTTAATCT
481 CAATTTGACA AACTTAAAA TAGGAGCAA TAACATCATT TTTACTGA TATAATAAGT
541 TCAATCAATC TATAGTTTTA CCAACGCTGC AAATTTTCTGTT CATTTTTATT TGACAGCTCC
601 GTATATTTTT ACTAACTAA CTTTGCAAAA ATTATAAGCT AGGGGTACCC AATATTATTC
661 CTTTCAATTG ACGTTGAACA ACCAACTACA AAATTCATAC TTAATTAAC GTCCAAAATC
721 TTTTAATTCT ATTACTTGTG CTTTTAAGT TAAGCAAAT AATGCAAATT ATGTCACAAT
781 CATTAAAAAT ACTTTGCTGT AGCCTATCGA TATATCC
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### SEQ Gh13\_TG590F2-R2: 813 bp; Gh13 was selected from begomovirus resistant hybrid provided by Favi Vidavski, Hebrew University of Jerusalem. Selections were made in Guatemala.

ORIGIN

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1 GAGTGAGATC CATACTTTGA TACTCTCTAC CATTCTCAT
61 GCTAATTGGT AACTCTGATC CAATCCAAAC CGAAGCCAAT AACACAGTA GTAATAATCA
121 AACACGGTAT CTCACAAGAG GATCCTTAAG AATAAGACGT TCGTGATAAA CTCTCCATGC
181 ATAATCCTCG AAAGAAAATG AATTGAACAT TTGACTTTCC TCATCTACCG CTATAGTTTT
241 TGAATCATTG TCGCCAAGGC CATCATCATC TTCGCTAAGT GATGGCGATT TGATAGGAAG
301 CAAGGGAGAG ACAGTGTTTT CATGAGCTAG CGTAACAAAC AATGTCATTG ATAGACAGTG
361 TGAGTTACTA CTACCGCTGT TGATTTTACC ATTAGTTATA GGTACTGGTC TTCCTCTCAC
421 TTTTTTACC TTTCCATTAC TCCATACCTG TCCATTATCA AAAAAATTA TAGTTATCTC
481 AATTTGACAA CACTAAATAG GAGCAAATA CATCATTTTT AACTGTTAT AATAAGTTCA
541 ATCAATCTAT AGTTTTACCA AACTGCAAA TTTCGTTTAT TTTTATTTGA CGGCTCCATA
601 TATTTTACTA AACTAACTT CAAAAATTA TAAGCTAGGG GTACCCAATA TTATTCCTTT
661 CAATTGACGT CGAACAACCA ACTACAAAAT TCATACTTAA TTAAACGTCC AAAATCTTTA
721 ATTCTATTAT TTGTGCCTTT TAAGTTAAGC AAAATAATGC AAATTATGTC ACAATCATT
781 ACAATACTTT GTCTGTAGCC TATCGATATA TCC
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SEQ LA1777\_TG590F2-R2: 799 bp; *S. habrochaites*, DNA from a single plant.

ORIGIN

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1 GAGTGAGATC CATACAAAC AAAGCATCAA CATACTTTGA TACTTTCTAC CATTCTCAT
61 GCTAATTGGT AACCGAAGCC AATAACAACA GTAGTAATAA TCAAACACGG TATCTCACAA
121 GAGGATCCTT AAGAATAAGA CGTTCGTGAT AAACCTCTCCA TGCATAATCC TCGAAAGAAA
181 ATGAATTGAA CTTTTGACTT TCCTCCTCTA CCGCTATAGT TTTTGAATCA TTGTCGCCAA
241 GGCCATCATC ATCTTCGCTA AGTGATAGCG ATTTGATAGG AAGCAAGGGA GAGACAGTGT
301 TTTTCATGAGC TAGTGTAAC AACAATGTCA TTGATAGACA GTGTGAGTTA CTACTACCGC
361 TGTTGATTTT ACCATTAGTT ATAGGTACTG GTCTTCCTCT CACTTGTTTC ACCTTTCCAT
421 TACTCCATAC CTGTCCATTA TCAACAAAAA TTATAGTTAA TCTCAATTTG ACAACCCTTA
481 AAATAGGAGC AAATAACATC ATTTTTAAAC TGTTATAATA AGTTCAATCA ATCTATAGTT
541 TTACCAACAC TGCAAAATTT GTTTCATCTTT ATTTACAGC TCCGTATATT TTAATAAACT
601 AACTTCGCAA AAATTATAAG CTAGGGGTAT CCAATATTAT TCCTTTCAAT TGATGTCGAA
661 CAACCAACTA CAAAATTCAT ACTTAATTAA ACGTCCAAAA TCTTTAATTC TACTACTTGT
721 ACCTTTTAAAG TTAAGCAAAA TAATGCTAAT TATGTCACAA TCATTAACAA TACTTTGTCT
781 GTAGCCTATC GATATATCC
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SEQ LA2779\_TG590F2-R2: 815 bp; *S. chilense*, DNA from a single plant

ORIGIN

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1 GAGTGAGATC CATACAAAC AAAGCATCAA CATACTTTGA TACTCTCTAC CATTCTCAT
61 GCTAATTGGT AACTCCGATC CAATCCAAAC CGAAGCCAAT AACAACAGTA GTAATAATCA
121 AACACGGTAT CTCACAAGAG GATCCTTAAG AATAAGACGT TCATGATAAA CTCTCCATGC
181 ATAATCATCA AAAGAAAATG AATTGAACAT TCGACTTTCC TCCTCTACCG CTATAGTTTT
241 TGAATCATTG TCGCCAAGGC CATCATCATC TTCACTAAGT GATGGCGATT TGATAGGAAG
301 CAAGGGAGAG ACAGTGTTTT CATGAGCTAG TGTAACCTAAC AATGTCATTG ATAGACAGTG
361 TGAGTTACTA CTACCGCTGT TGATTTTACC ATTAGTTATA GGTACTGGTC TTCCTCTCAC
421 TTTTTTACC TTTCCATTAC TCCATACCTA TCCATTATCA AAAAAATTA TAATTATCTC
481 AATTTGACAA CACTTAAAAAT AGGAGCAAAT AACATCATTT TTACTACTGTT ATAATAAGTT
541 CAATCAATCT ATAGTTTTTAC CAACACTGCA AATTTCTGTT ATTTTTATTT GACGGCTCCA
601 TATATTTTAC TAAACTAACT TCGCAAAAAA TATAAGCTAG GGGTACCCAA TATTATTCCT
661 TTCAATTGAC GTCGAACAAC CAACTACAAA ATTCATACTT AATTAAACGT CCGAAATCTT
721 TAATTCTATT ACTTGTGCCT TTTAAGTTGA GCAAATAAAT GCAAATTATG TCACAATCAT
781 TAACAATACT TTGTCTGTAG CCTATCGATA TATCC
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Blast Search:

April 16, 2009, match with AK323824, cDNA, added to GenBank, 3 March 09, match nt 1 to 459 of Heinz sequence with 1319 to 861 of cDNA. The remainder of Heinz (nt 500-800) does not match anything in GenBank. So unlikely this marker (TG590) is associated with this cDNA.

SGN BAC Clone Search:

No matches

Comparison With Germplasm From Guatemala:

Heinz ≠ Gh13 (18 SNP and 5 INDEL)

Heinz ≠ LA1777 (17 SNP and 4 INDEL)

Heinz ≠ LA2779 (22 SNP and 4 INDEL)

Gc9 did not sequence

FILE: Multiple\_Sequence\_Alignment  
PROJECT:

NAMES: HEINZ\_TG590F2-R2 (Susceptible) Gh13\_TG590F2-R2 (Resistant)  
*S. habrochaites*, LA1777\_TG590F2-R; *S. chilense* LA2779\_TG590F2-R

ORIGIN

HEINZ_TG590F2-R2	GAGTGAGATCCATACAAACTAAAGCATCAA.CATACTTTGATACTTCTACCATTCTCA	59
GH13_TG590F2-R2	GAGTGAGATCCATACAAACTAAAGCATCAA.CATACaTTGATACTcTCTACCATTCTCA	59
LA1777_TG590F2-R	GAGTGAGATCCATACAAACTAAAGCATCAAaCATACTTTGATACTTCTACCATTCTCA	60
LA2779_TG590F2-R	GAGTGAGATCCATACAAACTAAAGCATCAA.CATACaTTGATACTcTCTACCATTCTCA	59
Consensus	gagtgagatccatacaaaactaaagcatcaa catac ttgatact tctaccatttctca	
HEINZ_TG590F2-R2	TGCTAATTGGTAACTCCGATCCGATCCAAACCGAAGCCAATAACAACAGTAGTAATAATC	119
GH13_TG590F2-R2	TGCTAATTGGTAACTcTGATCCaATCCAAACCGAAGCCAATAACAACAGTAGTAATAATC	119
LA1777_TG590F2-R	TGCTAATTGGTAACT.....CGAAGCCAATAACAACAGTAGTAATAATC	103
LA2779_TG590F2-R	TGCTAATTGGTAACTCCGATCCaATCCAAACCGAAGCCAATAACAACAGTAGTAATAATC	119
Consensus	tgctaattggtaac cgaagccaataacaacagtagtaataatc	
HEINZ_TG590F2-R2	AAACACGGTATCTCACAAGAGGATCCTTAAGAATAAGACGTTTCGTGATAAACTCTCCATG	179
GH13_TG590F2-R2	AAACACGGTATCTCACAAGAGGATCCTTAAGAATAAGACGTTTCGTGATAAACTCTCCATG	179
LA1777_TG590F2-R	AAACACGGTATCTCACAAGAGGATCCTTAAGAATAAGACGTTTCGTGATAAACTCTCCATG	163
LA2779_TG590F2-R	AAACACGGTATCTCACAAGAGGATCCTTAAGAATAAGACGTTCaTGATAAACTCTCCATG	179
Consensus	aaacacggatctcacaagaggatccttaagaataagacgttc tgataaactctccatg	
HEINZ_TG590F2-R2	CATAATCCTCGAAAGAAAATGAATTGAACATTTGACTTTCCTCCTTACCCTATAGTTT	239
GH13_TG590F2-R2	CATAATCCTCGAAAGAAAATGAATTGAACATTTGACTTTCCTCCTaTCTACCCTATAGTTT	239
LA1777_TG590F2-R	CATAATCCTCGAAAGAAAATGAATTGAACATTTGACTTTCCTCCTTACCCTATAGTTT	223
LA2779_TG590F2-R	CATAATCaTcaAAAGAAAATGAATTGAACATTCGACTTTCCTCCTTACCCTATAGTTT	239
Consensus	cataatc tc aaagaaaatgaattgaac tt gactttcctc tctaccgctatagttt	
HEINZ_TG590F2-R2	TTGAATCATTGTTGCCAAGGCCATCATCATCTTCGCTAAGTGATAGCGATTGATACGAA	299
GH13_TG590F2-R2	TTGAATCATTGTTGCCAAGGCCATCATCATCTTCGCTAAGTGATgGCGATTGATAgGAA	299
LA1777_TG590F2-R	TTGAATCATTGTTGCCAAGGCCATCATCATCTTCGCTAAGTGATAGCGATTGATAgGAA	283
LA2779_TG590F2-R	TTGAATCATTGTTGCCAAGGCCATCATCATCTTCaCTAAGTGATgGCGATTGATAgGAA	299
Consensus	ttgaatcattgt gccaaggccatcatcatcttc ctaagtgat gcgatttgata gaa	
HEINZ_TG590F2-R2	GCAAGGGAGAGACAGTGTTTTCATGAGCTAGTGTAACATAACAATGTCATTGATAGACAGT	359
GH13_TG590F2-R2	GCAAGGGAGAGACAGTGTTTTCATGAGCTAGcGTAACATAACAATGTCATTGATAGACAGT	359
LA1777_TG590F2-R	GCAAGGGAGAGACAGTGTTTTCATGAGCTAGTGTAACATAACAATGTCATTGATAGACAGT	343
LA2779_TG590F2-R	GCAAGGGAGAGACAGTGTTTTCATGAGCTAGTGTAACATAACAATGTCATTGATAGACAGT	359
Consensus	gcaagggagagacagtgttttcatgagctag gtaactaacaatgtcattgatagacagt	
HEINZ_TG590F2-R2	GTGAGTTACTACTACCGCTGTTGATTTACCATTAGTTATAGGTACTGGTCTTCCTCTCA	419
GH13_TG590F2-R2	GTGAGTTACTACTACCGCTGTTGATTTACCATTAGTTATAGGTACTGGTCTTCCTCTCA	419
LA1777_TG590F2-R	GTGAGTTACTACTACCGCTGTTGATTTACCATTAGTTATAGGTACTGGTCTTCCTCTCA	403
LA2779_TG590F2-R	GTGAGTTACTACTACCGCTGTTGATTTACCATTAGTTATAGGTACTGGTCTTCCTCTCA	419
Consensus	gtgagttactactaccgctgttgatttcaccattagttataggtactggcttctcctctca	
HEINZ_TG590F2-R2	CTTGTTCACCTTTCCATTACTCCATACCTGTCCATTATCAACAAAAATTATAGTTAATC	479
GH13_TG590F2-R2	CTTtTTTCACCTTTCCATTACTCCATACCTGTCCATTATCAACAAAAATTATAGTTA.TC	478
LA1777_TG590F2-R	CTTGTTCACCTTTCCATTACTCCATACCTGTCCATTATCAACAAAAATTATAGTTAATC	463
LA2779_TG590F2-R	CTTtTTTCACCTTTCCATTACTCCATACCTaTCCATTATCAACAAAAATTATAaTTA.TC	478
Consensus	ctt tttcacctttccattactccatacct tccattatcaacaaaaattata tta tc	
HEINZ_TG590F2-R2	TCAATTTGACAACACTTAAATAGGAGCAAATAACATCATTTTTTACACTGATATAATAAG	539
GH13_TG590F2-R2	TCAATTTGACAACACT..AAATAGGAGCAAATAACATCATTTTTTACACTGtTATAATAAG	536
LA1777_TG590F2-R	TCAATTTGACAACcCTTAAATAGGAGCAAATAACATCATTTTTTaaACTGtTATAATAAG	523
LA2779_TG590F2-R	TCAATTTGACAACACTTAAATAGGAGCAAATAACATCATTTTTTACACTGtTATAATAAG	538
Consensus	tcaatttgacaac ct aaataggagcaataacatcattttta actg tataataag	
HEINZ_TG590F2-R2	TTCAATCAATCTATAGTTTTACCAACCGCTGCAAAATTCGTTTATTATTGACAGCTC	599
GH13_TG590F2-R2	TTCAATCAATCTATAGTTTTACCAACaCTGCAAAATTCGTTTATTATTGACgGCTC	596
LA1777_TG590F2-R	TTCAATCAATCTATAGTTTTACCAACaCTGCAAAATTCGTTTATTATTcACAGCTC	583
LA2779_TG590F2-R	TTCAATCAATCTATAGTTTTACCAACaCTGCAAAATTCGTTTATTATTGACgGCTC	598
Consensus	ttcaatcaatctatagttttaccaac ctgcaaaatctgttcatttttattttgacgctc	
HEINZ_TG590F2-R2	CGTATATTTTTACTAACTAACTTTGCAAAAATTATAAGCTAGGGGTACCCAATATTATT	659
GH13_TG590F2-R2	CaTATATTTTT.ACTAACTAACTTcGCAAAAATTATAAGCTAGGGGTACCCAATATTATT	655
LA1777_TG590F2-R	CGTATATTTTT.ACTAACTAACTTcGCAAAAATTATAAGCTAGGGGTaTCCAATATTATT	642
LA2779_TG590F2-R	CaTATATTTTT.ACTAACTAACTTcGCAAAAATTATAAGCTAGGGGTACCCAATATTATT	657
Consensus	c tatatttt actaaactaactt gcaaaaattataagctaggggta ccaatattatt	

HEINZ_TG590F2-R2	CCTTTCAATTGACGTTGAACAACCAACTACAAAATTCATACTTAATTAACGTCCAAAAT	719
GH13_TG590F2-R2	CCTTTCAATTGACGTcGAACAACCAACTACAAAATTCATACTTAATTAACGTCCAAAAT	715
LA1777_TG590F2-R	CCTTTCAATTGAtGTcGAACAACCAACTACAAAATTCATACTTAATTAACGTCCAAAAT	702
LA2779_TG590F2-R	CCTTTCAATTGACGTcGAACAACCAACTACAAAATTCATACTTAATTAACGTCCgAAAT	717
Consensus	cctttcaattga gt gaacaaccaactacaaaattcatacttaattaaacgtcc aaat	
HEINZ_TG590F2-R2	CTTTTAATTCTATTACTTGTGCCTTTTAAGTTAAGCAAAAATAATGCAAATTATGTCACAA	779
GH13_TG590F2-R2	CTTT.AATTCTATTAtTTGTGCCTTTTAAGTTAAGCAAAAATAATGCAAATTATGTCACAA	774
LA1777_TG590F2-R	CTTT.AATTCTAcTACTTGTaCCTTTTAAGTTAAGCAAAAATAATGCTaATTATGTCACAA	761
LA2779_TG590F2-R	CTTT.AATTCTATTACTTGTGCCTTTTAAGTTgAGCAAAAATAATGCAAATTATGTCACAA	776
Consensus	cttt aattcta ta ttgt ccttttaagtt agcaaaaataatgc aattatgtcacaa	
HEINZ_TG590F2-R2	TCATTAAAAATACTTTG.CTGTAGCCTATCGATATATCC	817
GH13_TG590F2-R2	TCATTAAcAATACTTTGtCTGTAGCCTAcgGATATATCC	813
LA1777_TG590F2-R	TCATTAAcAATACTTTGtCTGTAGCCTATCGATATATCC	800
LA2779_TG590F2-R	TCATTAAcAATACTTTGtCTGTAGCCTATCGATATATCC	815
Consensus	tcattaa aatactttg ctgtagccta gatatatcc	