

COS Marker T0507: SGN, Chr. 6, 25.00 cM

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July 5, 2005

Primer Name	Sequence (5' to 3')
T0507F2	GAGTCGAGTTATCCCGGTTTCG
T0507R1	GATGGTGGAGGTAGTTTCATAGCC

Note: This primer pair produced a PCR fragment of roughly 1000bp. Because of this size, the sequence at the ends was not good. As a result, the sequence reported here is smaller than the PCR band. In addition, not all tested lines gave good sequence of the same size. Thus, our comparison is limited to the areas where the sequences overlap

SEQ Gh13_T0507F2-R1: 857 bp;

ORIGIN

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1      TTTGGGTCCN GGTTTTCCCG GTTCGATACA GAATTTACCT GGGAGATACT CTCTGTTGCT
61     TATGAGAGGA AGTCTACACA AAAGAATGCN TTCNTTAACT ATGAGTTTCG CTAATTCTTC
121    CNTTCTTAAA GATCATCTGT TGGGCGATAT AGATCGATTG GTTAGGCTTA ATTTGGATTC
181    GTGGACCGGC AGGGTTTTCC TCATGGACGA GGCTAAGAAG GTAATCATT TATTTAATTA
241    TTTTTCAATT CGGATTGTTG AGTTTTGATG GATTAGAGAA TAACAACCTT AGTGTAGTTG
301    TGGTGGGGGT ATGATTACTT TTCCAAATTA ATTAATTAAT GGAGACATAG TATTATTATT
361    ATGTACAAGT AATTATTATG ATGATAACAC ATGTGAATGT GGTGTTATCA TGACTTTTTT
421    TTTTCTTTTT TTTGGGTTGT GGAAAATGTA ATTCAGTTTA TGGATGTATG GATGTGCAGA
481    TAACGTTTTAA TCTAACAGTG AAGCAGCTGA TGAGTTTTGA TCCATGTGAG TGGACAGAGA
541    ATCTGATGAA AGAGTATATG CTTGTTATTG AAGGTTTCTT CTGCATTCCT TTGCCTATTT
601    TCTCATCCAC CTATCGCAAG GCCATTCAAG TATGTATTAT AAATCCAATT CAATCAATTA
661    GCTTTACTTT TGTTGTATAT ATGTGATGAA TAATCATTTG CATATGTATT TTCAGGCGAG
721    AACGAAAGTA GCGGAGGCGT TGGGATTGGT AGTGAGAGAT CGGAGAAAAG AAAGAGAGAT
781    CGGAGAAAAA AGAAAGAATG ATATGTTGGA GGCATTGTTT GAAGGAGATG GAGTTGAAAG
841    GAGTAGGATT TTCCGAT
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SEQ Heinz_T0507F2-R1: 883 bp;

ORIGIN

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1      GAGTCGAGTT TTCCCGGTTT GATACAGAAT TTACTTGGGA GATACTCTCT GTTGCTTATG
61     AGAGGAAGTC TACACAAACG AATGCATTCA TTAACATATGA GTTTTGCTAA TTCTTCCATT
121    CTAAAGATC ATCTGTTGGG CGATATAGAT CGATTGGTTA GGCTTAATTT GGATTCATGG
181    ACCGGCAGGG TTTTCCTCAT GGACGAGGCT AAGAAGGTAA TCATTTTATT TAATTATTTT
241    TCAATTCGGA TTGTTGAGTT TTGATGGATT AGAGAATAAC AACTTTAGTG TAGTTGTGGT
301    GGGGTATGAT TACTTTTCCA AAATTAATTA ATTAATGGAG ACATAGTAGT ATTATTATGT
361    ACGAGTAATT ATTATGATGA TAACACATGT GAATGTGGTG TTATCATGAC TTTTTTTTTA
421    TTTTTAAATT TTTGGTTGTG ATGTATGTGC AGATAACGTT TAATCTAACA GTGAAGCAGT
481    TGATGAGTTT TGATCCATGT GAGTGGACAG AGAATCTGAT GAAAGAGTAT ATGCTTGTTA
541    TTGAAGGTTT CTTCTGCATT CCTTGCCTA TTTTCTCATC CACCTATCGC AAGGCCATTC
601    AAGTATGTAT TATAAATCTA ATTCAATTAA TTAGCTTTTA CTTGTTGGTG GTGAATAATC
661    ATTTTGTATG TATTTTTTCTG CCGGAGACGA AAGTAGCGGA GCGGTTGGGA TTGGTAGTGA
721    GAGATCGGAG AAAAGAACGA GACGGAGGAG AACGAAAGAA TGATATGTTG GAGGCATTGT
781    TCGAAGGAGA CGGAGTTGAA GGAGTAGGAT TTTCCGATGA GGAAAATTGT TGATTTTATA
841    CTGGCGTTGC TTGTTGCTGG CTATGAAACT ACCTCCCACC ATC
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SEQ LA1777 T0507F2-R1: 769 bp;

ORIGIN

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1 ATATAGATCG ATTGGTTAGG CTTAATTTGG ATTCGTGGAC CGGCAGGGTT TTCCTCATGG
61 ACGAGGCTAA GAAGGTAATC ATTTATTTAA TAATTTTTCA ATTCGGATTG TTGAGTTTTG
121 ATGGATTAGA GAATAACAAC TTTAGTGTAG TTGTGGTGGG GGTATGATTG CTTTTCCAAA
181 TTAATTAATT AATGGAGACA TAGTATTATT ATTATGTACA AGTAATTATT ATGATGATAA
241 CACATGTGAA TGTGGTGTTA TCATGACTCT TTTTTTTTTA TTTTTTTTTT GGTTGTGGAA
301 AATGTAATTC AGTTGATGTA TGGATGTGCA GATAACGTTT AATCTAACAG TGAAGCAGCT
361 GATGAGTTTT GATCCATGTG AGTGGACAGA GAATCTGATG AAAGAGTATA TGCTTGTTAT
421 TGAAGGTTTC TTCTGCATTC CTTTGCCTAT TTTCTCATCC ACCTATCGCA AGGCCATTCA
481 AGTATGTATT ATAAATCCAA TTCAATTAAT TAGCTTTACT TATTGGTATG TGATGATGAA
541 TAATCATTTN TATGTATTTT TCAGGCGAGA AGGAAAGTAG CGGAGGCTTT GGGATTGGTA
601 GTGAGAGATC GGAGAAAAGA AAGAGAAGGA GGAGAAAAAA GAAAGAATGA TATGTTGGAG
661 GCATTGTTTT AAGGANATGG ANTTGAAGGA NTAGGATTTT CCNATGAGGA AATTGTTGAT
721 TTTANACNGG CGTTGCTTGT TGCTGGCTAN GAAACTCCCN CCCCCATC
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SEQ LA2779 T0507F2-R1: 754 bp;

ORIGIN

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1 GAGTTTTTCC CCGTTNCNAN ACNGGAATTT AGMKTTRSAS ATNMYCYMWG TWGCTTWTGA
61 GRGGAAGTCT WCYCCAAAAG AATGCMTTTCM TTAAMTWYSM STTWCGCKAG GGATTCTTCC
121 ATTCTTAAAG ATCATCTGTT GGGCCATATA GATCGATTGG TTAGGCTTAA TTTGGATTCCG
181 TGGACCGGCA GGGTTTTCCCT CATGGACGAG GCTAAGAAGG TAATCMTTTT ATTTAATTAT
241 TTTTCAATTC GGATTGTTGA GTTTTGATGG ATTAGAGAAT AACAACTTTA GTGTATTTGT
301 GGNGGGGGTA TGATTACTTT TCCMAAATTA ATTAATTAAT GGAGACMTAG TATTATTATT
361 ATGTACAAGT AATTATTATG ATGATAACMC MTGTGAATGT GGTGTTATCM NGACNTTTTT
421 TTTTCNTTTT TTTTTTTGGT TGTGGAAAAT GTGATTCAGT TGATGTATGG ATGTATGTGC
481 AGATAACGTT TAATCTAACA GTGAAGCAGC TGATGAGTTT TGATCCATGT GAGTGGACAG
541 AGAATCTGAT GAAAGAGTAT ATGCTTGTTA TTGAAGGTTT CTTCTGCATT CCTTTGCCTA
601 TTTTCTCATC CACCTATCGC AAGGCCATTC AAGTATGTAT TATAAATCCA ATTCAATCAA
661 TTAGCTTTAC TTATTGGTGG TGTATAATCA TTTGTATGTA TTTTTCAGGC GAGAACGAAA
721 GTAGCGGAGG CGTTGGGATT GGTAGTGAGA GATC
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SEQ Gc9 T0507F2: 250 bp; Gc9 produced readable sequence with only the forward primer, and even then only over 250-bp. However, over that 250-bp the sequence was excellent. As such, comparisons in this area are valid. Upon alignment, Gc9 matched exactly with Gh13.

Blast Search

Lycopersicon esculentum clone 133672F, mRNA sequence, accession number BT014380.

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TITLE Direct Submission
JOURNAL Submitted (11-MAY-2004) The Institute for Genomic Research, 9712 Medical Center Drive, Rockville, MD 20850, USA

SGN BAC Clone Search: No Matches

Comparison With Germplasm From Guatemala:

Heinz ≠ Gh13 (25 SNP and 12 INDEL in 700-bp of overlap)

Heinz ≠ LA1777 (28 SNP and 5 INDEL in 700-bp of overlap)

Heinz ≠ LA2779 (18 SNP and 5 INDEL in 620-bp of overlap)

Gc9 = Gh13

Gh13 did not match either species, but was closer to the species than Heinz.