

C2_At5g42740, Chromosome XII, 54.5 cM

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October 6, 2006

Primers: (See SGN web site)

Forward: AGCACCATTTGAGAAAATATACCTG

Reverse: ATCCAAGGAATGAAACATTCCACAC

PCR at 53 C gave a single 1,000-bp fragment. (Excellent fragment for direct sequencing of the PCR product.)

Breeding line, Gh902-b, 959 bp;

ORIGIN

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1      AATATACCTG TATGTCCCTG CTCATAGAAA CTTATGTTTA TGTTCTCTCT TATACTTAAT
61     TGTTCTGTTC TCTTATGCGT AGTGCTGTGA TATTTCTGTA ATGTTTCAGT GGTACCCTG
121    TGATGTAATT AGATCGGTGA GCGGCGCGTT CTGCCTTAGA GAGTTCAGAA GTCCAAACTG
181    AGGGGCTAAG TGA AACACA CACTTCACAA ACAATAAATA TTTTGTGAGA TTGTTTGATG
241    CAAATGTACG TGTGTGCTTA TATTGATGTA TAGCCTGTCT ACTTGTGTTT TCTCCATATC
301    TTAAGACTGG TAGCTTCATT CTACTCTTAG CCAATGAGGT GCTTTGTTGA TTAAGTTTGC
361    ATCTGTACCC AGATATTGAG CCAAGCCTGT ACCCTTGATT CGTTGTCGGA TTTAATTTTC
421    CCAGAGCAAT CAAACGGTTT GTAGTTTTAA TTGCATGATC AGCTGTTATA ACGATTGGGA
481    CAGTTCAGAC TTCAGTGA CTAGCCTGG TCCCGTCTGG CATGTTTGCA TTCTGATTGT
541    TCTTACCAAG CTAGTGAATC TGAAGTTTTT CCTTCTGTGG TTAAGCCTCT TTCTCTGTTA
601    CATTTTTGTT TCATAAGGAT CAAAGGTTTC CTAACTGCAG GCTCTGTTAC ACATTTTATA
661    CATACTTTT GTTGCTCTT TATTTCTCTG CAATGAATCC TCTTTGCTT TATTTTCTA
721    TATTTCCCTC ATTCTCTCCA TACTTCGAAC TCTTGAAGAT TCTTTTGCAA TACTTGCAC
781    CTTTGGTTAT TGGATTATTA CACCTCAATC CCAAGCATT TCTGCTAAGA ACAACTTTAT
841    ATTCTGCTTT TCTAGTCAGA TGTTTGATTT GCTTATATCA CATCACTAAA CTCTATTGCT
901    TGATTCTTAA TATCACATTC TTGTTTCAGG TGCTTTTAGG CTTGCTGAGT GTGTGGAAT
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The sequence for Heinz 1706, Gh902-a, Gh902-b, and Gh25 were identical.

BLAST searches:

No match with BAC full-length clones at SGN (Oct. 6, 2006).

GenBank: High identity with glucose-6-phosphate isomerase (DQ423167), *L. cheesmaniae*, *L. pimpinellifolium*, and *S. lycopersicum* (DQ423164) (100% id for 876 nt) and 97% id with *S. habrochaites* LA1777 for nt 42-926 (DQ423163) and *S. chilense* LA2930 nt 42-856.