

COS Marker T0774, 18.0 cM, Chr. 6

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Primer Name	Sequence (5' to 3')
T0774F2	CTGGAAGAAACTAGAAATAAAGG
T0774R2	CAGTACAAGGATATC CCA TTC CTCATG

100a_T0774F2-R2: 602 bp;

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1      CTGGAAGAAA CTAGAAATAA AGGGGTGGTG CTCGCCCTAT ATGAAGCTTT GAGCTCACGT
61     GACGTTGACA AGGTCCAGAA ACTTCTGGCC TCTGACCTTG AGTGGTGGTT CCATGGTCCA
121    CCTTCACATC AATTTTTGAT GCGCATACTA ACTGGTACTG CCAACTCCGA TCACTATTTT
181    TTCAAATTCA TTCCTCAAAG TATTGACGCC TTTGGATCTA CTGTCCTTGT CGAAGGTTGC
241    GATCCTGATC ACTCTATTAC TTGGGTTTAC GCTTGGACTG TTAATGATGG GATAAATTACT
301    CAGGTTAGGG AGTATTTCAA TACCTCTCTC ACTGTCACTC GACTTGACAA TAGCAATAAT
361    AATAATAATT GCCCTAAATC GGATTTGTCT TCCATTGCTG CTACACGGCA TTGCCCTTCT
421    CTTTGGGAGA GTAGTTTACC TAATCGGGTG GGTAAGTCGG TTCCGGGTCT TGTTCTTGCT
481    CTCTGAGTTC CGCGAGGATG TAAGTTTTTA ACGGTTGATT TGGGGGTTTT CGTCGCATTG
541    TTTTAATTTT ATTATCTGCA ATTTTAATTT GGGACCATGA GGAATGGGAT ATCCTTGTAC
601    TG
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Purple Russian T0774F2-R2: 602 bp;

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1      CTGGAAGAAA CTAGAAATAA AGGGGTGGTG CTCGCCCTAT ATGAAGCTTT GAGCTCACGT
61     GACGTTGACA AGGTCCAGAA ACTTCTGGCC TCTGACCTTG AGTGGTGGTT CCATGGTCCA
121    CCTTCACATC AATTTTTGAT GCGCATACTA ACTGGTACTG CCAACTCCGA TCACTATTTT
181    TTCAAATTCA TTCCTCAAAG TGTTGACGCC TTTGGATCTA CTGTCCTTGT CGAAGGTTGC
241    GATCCTGATC ACTCAATTAC TTGGGTTTAC GCTTGGACTG TTGATGATGG GATAAATTACT
301    CAGGTTAGGG AGTATTTCAA TACCTCTCTC ACAGTCACTC GACTTGACAA TAGTAATAAT
361    AATAATAATT GCCCTTCATC GGATTTGTCT TCCATTGCTG CTACACGGCA TTGCCCTTCT
421    CTTTGGGAGA GTAGTTTACC TAATCGGGTG GGTAAGTCGG TTCCGGGTCT TGTTCTCGCT
481    CTCTGAGTTC CGCCAGRATG TAAGTTTTTA ACGGTTGATT TGGGGGTTTT CGTCGCATTG
541    TTTTGATTTT ATTATCTGCA ATTTTAATTT GGGACCATGA GGAATGGGAT ATCCTTGTAC
601    TG
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Blast Search:

DEFINITION *Lycopersicon esculentum* cDNA, clone: FC09DF07, HTC in fruit.
ACCESSION AK224717
AUTHORS Tsugane,T., Watanabe,M., Yano,K., Sakurai,N., Suzuki,H. and Shibata,D.
TITLE Expressed sequence tags of full-length cDNA clones prepared from the laboratory-grown miniature tomato (*Lycopersicon esculentum*) cultivar Micro-Tom
JOURNAL Plant Biotechnol. 22, 161-165 (2005)

SGN BAC Clone Search

No Match

Comparison With Other Breeding Lines from Guatemala:

All tested resistant breeding lines matched identically (100a=19a=113a=68a). The susceptible breeding lines (PR=Mandarina) matched with each other identically but differed from the resistant by 10 SNP (PR≠100a, 10 SNP). Therefore, the resistant lines likely contain an introgression related to begomovirus resistance in this region.