

## COSII Marker C2\_At5g37260, 2.5 cM, Chr. 2

Luis Montes, Brenda Garcia, and Douglas Maxwell  
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Primer Name	Primer Sequence (5' to 3')
BG2-F1	AGAGCACAAAAAGTTCCTTGAAGC
BG2-R1	ACCGTACCAAATGCATCTGAACC

902BG2F1-R1: 529 bp:

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1      AGAGCACAAA AAGTTCCTTG AAGCATTAAA GCTTCATGGT AGGGCATGGC GACGAATAGA
61     AGGTAAACAA CTAATACAAT CAATGGATAT GGATTGTTTG AGTTGTCACT CCATACTAAA
121    GAGACCTTGT TTAATTCTCA GAGCATGTGG GAACTAAAAC TGCAGTTCAG ATTAGAAGCC
181    ATGCTCAGAA GTTCTTTTCA AAGGTTTTCG CCTCGCTCTT ATCCCATTTT ATTGTTTGTG
241    CTTGCATCTG TTTTGTATTG GCTGTTGACA TAAAAGTGTT TTCAGGTTGT TCGTGAATCG
301    AGTAATGGTG ATGCAAGCTC TGTGAAATCC ATTGAGATCC CTCCTCCTCG GCCTAAAAGA
361    AAGCCGATGC ACCCTTATCC AAGAAAAATG GCAACTCCAC TTAAAAGTGG AACCCCTGGCT
421    TCAGAGAAAT TGAACAGATC TGGTTCACCT GATCTCTGTC TCTCTGAGCC AGAGAATCAG
481    TCTCCTACCT CTGTGTTGTC TACCCTTGGT TCAGATGCAT TTGGTACGG
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### Blast Search

The sequence matches with 100% identity to:

DEFINITION *Lycopersicon chmielewskii* putative At5g37260 (CT251) gene,  
CT251-7206b allele, partial cds.  
AUTHORS Baudry,E., Kerdelhue,C., Innan,H. and Stephan,W.  
TITLE Species and recombination effects on DNA variability in the  
tomato genus  
JOURNAL *Genetics* 158 (4), 1725-1735 (2001)  
PUBMED [11514458](https://pubmed.ncbi.nlm.nih.gov/11514458/)

### SGN BAC Clone Search

No Match

### Comparison With Other Genotypes

All tested lines matched identically at this locus (902h=Cerasiforme). Therefore, there are no SNP or INDEL that distinguish the begomovirus resistant genotypes from the susceptible at this location on chromosome 2.