

## LE\_HBa0250I21, 5.5cM, Chromosome 6

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Primer Name	Primer Sequence (5'-3')
CM4-F1	CTTTAGAGTAGTGGCTTCCGTTC
CM4-R1	GCAGTACAACAAAATTGGTAGGCTC

### Gc143-2\_CM4-F1: 648 bp; *S. chilense* LA2779 introgression

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1      ATTTGGAAGA TGCACTATTG AAACGTGTAA TGGTCACACC TGAAGAAGTA ATAAAGAGAA
61     GTCTTGATCC TGATGCTGCA ACAGTTAGTA GAGATGGGCT TGCTAAAACA TTATATTCTC
121    GCTTGTTTGA CTGGTATGAT TCTATTGTCT CAACCAGATC GTGTGATGTG GTTTGTTACT
181    GATTATTTGA CACTAAGATG CACAGTTTTT AACTGCTTAC AGGTTGGTGG ACAAATAAAA
241    TAACTCAATT GGTCAAGATC CGAATTCAA ATCTCTTATT GGTGTTCTTG ACATTTATGG
301    TTTTGAAAGT TTTAAAATA ATAGGTAGGA GTCAAATCAT TGGAGTACAC AGGTTATTGT
361    TGAATGTGGT GTTTCGACAT TTGACTCTTT TGACTTTTGT GTACCAGTTT TGAACAATTC
421    TGCATTAATT TCACAAATGA GAAGCTGCAG CAACACTTTA ACCAGGTATT TGTAGTTGAA
481    ATTTTAGAGA ATTTCTGTCC ATATCTTCTA AGCCAAAAC TGAAGTGGG TATATTTGTT
541    TTCCAGCACG TGTTCAAGAT GGAGCAGGAG GAATACACTA GAGAAGAGAT CGATTGGAGC
601    CTACATAGAA ATTTGTGGGA TAATAAGGGA TGTTCTGGGA TCTTATGG
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### Gc43\_CM4-F1: 524 bp; *S. chilense* LA2779 introgression

```
1      AAGTCTTGAT CCTGATGCTG CAACAGTTAG TAGAGATGGG CTTGCTAAAA CATTATATTC
61     TCGCTTGTTT GACTGGTATG ATTCTATTGT CTCAACCAGA TCGTGTGATG TGGTTTGTTA
121    CTGATTATTT GACACTAAGA TGCACAGTTT TCAACTGCTT ACAGGTTGGT GGACAAAATA
181    AATAACTCAA TTGGTCAAGA TCCGAATTCA AAATCTCTTA TTGGTGTCTT TGACATTTAT
241    GGTTTTGAAA GTTTTAAAAC TAATAGGTAG GAGTCAAATC ATTGAGTAC ACAGGTTATT
301    GTTGAATGTG GTGTTTCGAC ATTTGACTCT TTTGACTTTT GTGTACCAGT TTTGAACAAT
361    TCTGCATTA TTTCAAAAT GAGAAGCTGC AGCAACACTT TAACCAGGTA TTTGTAGTTG
421    AAATTTTAGA GAATTTCTGT CCATATCTTC TAAGCCAAA AACTGAAACT AGGGTATATT
481    TGTTTTCCAG CACGTGGTTC AAGATGGGAG CAGGGAGGGA ATAC
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### Gc9\_CM4-R1: 575 bp; *S. chilense* LA2779 introgression

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1      GAAAGNNTTC CTCTTTTAGT TTAGCAGAGA AGTGCTCCNC CATATGTACA CCCATTTCTG
61     GTTCTCTGCA TTCTACTNGT CATGTGTCTA CTACANAAGT NANCCAGACA NGGAGAATNG
121    TTTAGTGAGT GTTGATCAGA ATTNCTTTGG ATTCTGACTT TCTAATACTN ATTTGCANGC
181    ATGTGTCGTG CACATAACTG ACAATGATCA AAATTGATCT ATCTAAAACC CAAATAAGTT
241    GCTTTAACTG GAAAGAGTTC TGTTGAAGAC ANTGATATAG ATTTTTCTTC TTCAAATCAA
301    GTCTTNTTTT CTNNGACTTN TTGTGCCTTT TTTTAAAATG TATGATGCCA ANATATATTC
361    TTGTCAAATT GTAGAAAGAT CAAATTGGTC TTAGTTTGAC AGTGATAGAC ACAGGTAGCT
421    TCCAAATAAA TNTGTTCGNN TGATATAAAA NCACNAGAAA NTATTCAATT GATGTAATTC
481    GAAGTTTTGA AAGAGAAATT CATCTCATT CATTTTATTT TAATNTTACT GATNGATTTT
541    GTTAGATCNT TTTAGTCTCN NTATCATGGT GTTCT
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### HUJ-VF\_CM4-F1: 528 bp; susceptible to begomoviruses, *S. lycopersicum*

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1      CTTGATCCTG ATGCTGCAAC AGTTAGTAGA GATGGGCTTG CTA AACATT ATATTCTCGC
61     TTGTTTGACT GGTATGATTC TATTGTCTCA ACCAGATCGT TTGATGTGGT TTGTTACTGA
121    TTATTTGACA CTAAGATGCA CAATTTTCAA CTGCTTACAG GTTGGTGGAC AAAATAAATA
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181   ACTCAATTGG TCAAGATCCA AACTCAAAAT CTCTTATTGG TGTTCTTGAC ATTTATGGTT
241   TTGAAAGTTT TAAAAC TAAT AGGTAGGAGT CAAATCATTG GAGTACACAG GATATTGTTG
301   AATGTGGTGT TTCGACATTT GACTCTTTTG ACTTTTGTGT ACCAGTTTTG AACAATTCTG
361   CATTAAATTC ACAAATGAGA AGCTGCAGCA ACACTTTAAC CAGGTATTTG TAGTTGAGAT
421   TTTAGAGAAT TTCTGTCAAT ATCTTCTAAG CCAAAAAC TG AACTAGGGTA TATTTGTTTT
481   CCAGCACGTG TTCAAGATGG AACAGGAGGA ATACACTAGA GAAGAGAT
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### **Summary**

Partial sequence was obtained for all four tested lines with the forward primer. Upon alignment, Gc143-2, Gc9, and Gc43 all matched identically (these all have a *S. chilense* introgression from LA2779 in this region). These differ from HUI-VF by 7 SNPs. This area is not suitable for the development of a SCAR marker linked to Ty1.