

G8 Locus, 25 cM, Chromosome 6

Christopher Martin and Douglas Maxwell
University of Wisconsin Madison, August 25, 2006

Primers

CMG8F3, CATGGATAAAGGCCCAAACAATGAGG

CMG8R3, CCTCTCCGACATGTCATATTCTCG

PR_G8F3-R3: 656 bp;

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1      CATGGATAAA GGCCCAAACA ATGAGGTATT TGATCCTAAA GTAAAATTGC CAGTGAAGCA
61     AACTTTACAG GTAAGCAAAA TCTGTTTTCA TGTGGAGAGC TTACAAAATT TTAAGTCACT
121    AAATATGAAG GTATTGGTTA AGAAGTATAA TTCTTTTTAA AAAAAAAAAA ATAATTCTGC
181    AGGTTAGAGT ATATATGGGA GATGGGTGGC GCTTGGATTT CAGCCACACA CATTTTGATG
241    CCTATTCACC ACCAGACTTC TACACAAAGG TTAGTGACAG TGACTIONTCC CTCTCCACG
301    ACTCATTGTC TTACCTGAAT TAACACATTC GTAGCTTTGA CCCTGTCCTG AGCTCATAAT
361    TAAGGTGTTA TGTTTCTTGT TTGGTGTGTC CTTGCCTTTT TACTTTACAT ATTTGTATGG
421    TCATTGATGT TCTGCTTTAT ACTCCAAGAG GCTGCAGGAA CTTATTATAA CTCTATTGAT
481    CCTTATGTCG CAGCTATATT TAGTTGGAGT TCCTGCAGAT AGTCGTAAGA AAAAGACAAG
541    GATACTGGAG GATGACTGGT GTCCCGTATG GGATGAAGAG TTTAATTTTC CATTGACAGT
601    ACCAGAGCTG GCTTTGCTTC GAATTGAAGT ACGAGAATAT GACATGTCGG GAGAGG
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74_G8F3-R3: 655 bp;

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1      CATGGATAAA GGCCCAAACA ATGAGGTATT TGATCCTAAA GTAAAATTGC CAGTGAAGCA
61     AACTTTACAG GTAAGCAAAA TCTGTTTTCA TGTGGAGAGC TTACAAAATT TTAAGTTACT
121    AAATATGAAG GTATTGGTTA AGAAGTATAA TTCTTTTTAA AAAAAAATA AAATTCTGCA
181    GGTTAGAGTA TATATGGGAG ATGGGTGGCG CTTGGATTTT AGCCACACAC ATTTTGATGC
241    CTATTCACCA CCAGACTTCT ACACAAAGGT TAGTGACAGT GACTGTTCCC TCTTCCACGA
301    CTCATTTGCT TACCTGAATT AACACATTCG TAGCTTTGAC CCTGTCCTGA GCTCATAATT
361    AAGGTGTTAT GTTTCTTGTT TGGTGTGTCC TTGCCTTTT ACTTTACATA TTTGTATGGT
421    CATTGATGTT CTGCTTTATA CTCCAAGAGG CTGCAGGAAC TTATTATAAC TCTATTGATC
481    CTTATGTCGC AGCTATATTT AGTTGGAGTT COTGCAGATA GTCGTAAGAA AAAGACAAGG
541    ATACTGGAGG ATGACTGGTG TCCCGTATGG GATGAAGAGT TTAATTTTCC ATTGACAGTA
601    CCAGAGCTGG CTTTGCTTCG AATTGAAGTA CGAGAATATG ACATGTCGGG AGAGG
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88_CMG8F3-R3: 640 bp;

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1      CATGGATAAA GGCCCAAACA ATGAGGTATT TGATCCTAAA GTAAAATTGC CAGTGAAGAA
61     AACTTTACAG GTAAGCAAAA TCTGTTTTCA TGTGGAGAGC TTACAAAATT TTAAGTTACT
121    AAATTTGAAG GTATTGGTTA AGAAGTATAA TTATTTTTTT CAAAAAAAT AATTCTGCAG
181    GTTAGAGTAT ATATGGGAGA TGGGTGGCGC TTGGATTTCA GCCATACACA TTTTGATGCC
241    TATTCACCAC CAGACTTCTA CACAAAGGTT AGTGACAGTG ACTGTTCCCT CTTCCACGAC
301    TCATTTGCTT ACCTGAACTA ACACATTCCT AGCTTTGACC CTGTCCTGAG CTCATAAGGT
361    GTTATGTTTT TTGTTTGGTG TGTCCTCGCC TTTTTACTTT ACATATTTGT ATGGTCATTG
421    ATGTACTGCA AGAGGCTGCA GGAACTTATT ATAACTCTAT TGATCCTTAT GTCGCAGCTA
481    TATTTAGTTG GAGTTCCTGC AGATAGTCGT AAGAAAAAGA CAAGGATACT GGAGGATGAC
541    TGGTGTCCCG TGTGGGATGA AGAGTTTAA TTTCCATTGA CAGTACCAGA GCTGGCTTTG
601    CTTCGAATTG AAGTACGAGA ATATGACATG TCGGGAGAGG
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100a_G8F3-R3: 645 bp;

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1      CATGGATAAA GGCCCAAACA ATGAGGTATT TGATCCTAAA GTAAAATTAC CAGTGAAGAA
61     AACTTTACAG GTAAGCAAAA TCTGTTTTCA TGTGGAGAGC TTACAAAATT TTAAGTTACT
121    AAATATGAAG GTATTGGTTA AGAAAAGTATA ATTCTTTTTT TTTAAAAAAT AAATAAATTC
181    TGCAGGTTAG AGTATATATG GGAGATGGGT GCGCCTTGGA TTTCAGCCAT ACACATTTTG
241    ATGCCTATTC ACCACCAGAC TTCTACACAA AGGTTAGTGA CAGTGACTGT TCCCTCTTCC
301    ACGACTCATT TGCTTACCTG AACTAACACA TTCGTAGCTT TGACTGTGC CTGAGCTCAT
361    AAGGTGTTAT GTTTCTTGTT TGGTGTGTCC TCGCCTTTTT ACTTTACATA TTTGTATGGT
421    CATTGATGTA CTGCAAGAGG CTGCAGGAAC TTATTATCAC TCTATTGATC CTTATGTTCG
481    AGCTATATTT AGTTGGAGTT CCTGCAGATA GTCGTAAGAA AAAGACAAGG ATACTGGAGG
541    ATGACTGGTG TCCCCTATGG GATGAAGAGT TTAATTTTCC ATTGACAGTA CCAGAGCTTG
601    CTTTGCTTCG AATTGAAGTA CGAGAATATG ACATGTCGGG AGAGG
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Blast Search

The Purple Russian sequence matched with 100% identity to the following:

DEFINITION *Lycopersicon esculentum* clone 56B23 chromosome 6, genomic
sequence.
ACCESSION AY678298
AUTHORS Guyot,R., Cheng,X., Su,Y., Cheng,Z., Schlagenhauf,E., Keller,B.
and Ling,H.Q.
TITLE Complex Organization and Evolution of the Tomato Pericentromeric
Region at the FER Gene Locus
JOURNAL *Plant Physiol.* 138 (3), 1205-1215 (2005)
PUBMED [16009996](https://pubmed.ncbi.nlm.nih.gov/16009996/)

SGN BAC Clone Search

No Match

Comparison With Other Breeding Lines

Upon Alignment 88 and 30a matched exactly, and PR matched with the BAC Clone exactly.
100a and 74 each had unique sequences, although 74 matched closely with PR. 88=30a ≠ 100a
(13SNP and 3 INDEL), PR = BAC Clone ≠ 74 (2 SNP and 1 INDEL).