Front. Agr. Sci. Eng.
https://doi.org/10.15302/J-FASE-2020374
Verso: Front. Agr. Sci. Eng.
Recto: Chunli ZHANG et al. high expression of *FNC* lead to fruit netted-cracking
Available online at http://journal.hep.com.cn/fase
RESEARCH ARTICLE

FUNCTIONAL GAIN OF FRUIT NETTED-CRACKING IN AN INTROGRESSION LINE OF TOMATO WITH HIGHER EXPRESSION OF THE *FNC* GENE

Chunli ZHANG*, Taotao WANG*, Jing LI, Danqiu ZHANG, Qingmin XIE, Shoaib MUNIR, Jie YE, Hanxia LI, Yongen LU, Changxian YANG, Bo OUYANG, Yuyang ZHANG, Junhong ZHANG, Zhibiao YE (✉)

Key Laboratory of Horticultural Plant Biology (Ministry of Education), Huazhong Agricultural University, Wuhan 430070, China

* These authors contribute equally to the work

Received September 16, 2020;
Accepted November 30, 2020.

Correspondence: zbye@mail.hzau.edu.cn

SUPPLEMENTARY MATERIALS

Table S1 Indel marker primers used for fine mapping of the *FNC* gene

Primer name	Primer sequence
M1	Fw： GGGGCAAGGCAATAATTTTACTAC
	Rv： AATGGTTGTCATCCAAACTCTGC
M2	Fw： TTGCAATTCGTTTTTCTCATGTC
	Rv： CAAGTTGCATCAAATAAATACGAAA
M3	Fw： TTGCAATTCGTTTTTCTCATGTC
	Rv： CATCAAGTTGCATCAAATAAATACG
M4	Fw： TCATGAACTTTCAAGCAAAAACAAT
	Rv： TGCTAATACTATTGCCCTATCCCA
M5	Fw： TGACCAAATTCAAACACTTAGTAGCA
	Rv： GTGAAGTTTGAGTCTTGGCCATT
M6	Fw： TATTGCCAGTCAGTTCGCTTTTAT
	Rv： GTAAGGGTGGAGTTCAATAGATGC
M7	Fw： GCATAGCAATAACGTCATGACTCA
	Rv： AAATTAAGTGTCGAAAAACATGTGG
M8	Fw： TAACAGACGTGTAAAACATCCTTGC
	Rv： ATTGGCCTTGCTTATGAATCAGA
M9	Fw： ATTCATTGTTTGAATATGAGCTTCG
	Rv： GATAAGCCTTTTAGCACCGTCAA
M10	Fw： GATCTTACTAGGTTCAATTTGTGGGA
	Rv： AAATTTTGGAGATTGCCTAGAGATG
M11	Fw： GTGCTCCAATGGTTCACTCTAAGA
	Rv： TTGGTGCTGATGAGAAAAGTAGGT
M12	Fw： TTCGAACATTGATAAGCTACGTAGTG
	Rv： TAGGCAATTTTTTATGAGTTAGGCA
M13	Fw： ACGGACTATCTTCTTCCACTTGGT
	Rv： GACATGTATTGGAATATTGTGGCAG
M14	Fw： ACTGGCGGCACTACTTTGAACTA
	Rv： ATGAGCATTTGGGCTTATGAACTT
M16	Fw： GTCTCTTTCTATTTGCCTCTTTTGG
	Rv： ATTTCTCGAAGATGAGTCAAACTGA
M17	Fw： CTGTATCTGTTAAATCACATTCGCTT
	Rv： CGTTCTGATGACTTTACTTCCAATAG
M19	Fw： AACCGTCCGTGTCTTTTCTTATT
	Rv： CTTTACTCATCTCTCCTGGAATCTTAC
M20	Fw： TTACCACAACGCTCAACAAGATTTA
	Rv： TTGCCTACTGGTCAAGGATAGATTT
M21	Fw： AGTCTCTTTGATGCTTTATGTCCAG
	Rv： TCTCTGTCTGTGCTTGTGTTGATAA
M22	Fw： TCCTGAAATATGACAGTAGAACCCA
	Rv： GGATCAGTGCTATTCCTTGTACATT

M23	Fw：	GCTCTGATACTCAACTTTTGGCATA
	Rv：	CTGGCTATTAAACGCTACAACAAGA
M24	Fw：	TGCGGCTTCATTTTCATCTGTAA
	Rv：	ATCCTCAAAATGTATGACGCCCT
M25	Fw：	AGCTTGAATGATTGCAACACTGAC
	Rv：	TTGTGGTGAGTTGCTAAAGCTGTAT
M26	Fw：	ACTTTGTGGTGTCTATTTGGATTGA
	Rv：	TGAATTGCATCCACCTGTAAAGTT
M27	Fw：	TGCATACTCCTCTTGTTATTTGACTT
	Rv：	TCTCAATCTTCACCTCAGAACAGTAC
M28	Fw：	TAACTCCTGCTCAGAGAGGCTAAC
	Rv：	TAGCTATATTGACTCATGGACAGGC
M29	Fw：	ATGGTTGGATTATGGTGAAGGAGT
	Rv：	GTCATGCTTCTCAGTTTGTCTACCA
M30	Fw：	GAACCAGACACCATTAACTTTAGGC
	Rv：	GAGAACTGTTTCGAGGATCTATCATG
M31	Fw：	CCTGTTGCCATTGAACTATCACTAA
	Rv：	GCACTTGATAGAGGTTCAGTCGATA
M32	Fw：	ACTTTGTGGTGCCAATGTTTTCT
	Rv：	TCTGCTTTTCTGCAACTTTGACTAC
M33	Fw：	CGTCCAAGTCTAAAAGAGTCTATGATG
	Rv：	CTTCTGATTTAGCCTTTTCATCTTCT
M34	Fw：	ATTCATTTGGTAGGTAGGTTTTAGCT
	Rv：	CCAAGCATCACCATCCATTATATTA
M35	Fw：	AAGTACCTGAAGTTCCAGATTTAGCT
	Rv：	TGGTGTCTGTTCTTCCACATCAT
M41	Fw：	TGCCAATATTGCATAATTTCTCACT
	Rv：	CTCTAATTCGTGTTTTATGTCCGTT
M42	Fw：	CCATATGTCACTTTGCATGTAATTG
	Rv：	TCAATCCCTAGCGTTTTCCTATC
M46	Fw：	ATCGTTTTGATTGTGGTATGTGAAG
	Rv：	AATTGTTGTTATACACAGGAGCACC
M47	Fw：	CATGATCACTAACAAGGGATGAAAA
	Rv：	GATGTTGTTCCTCCCACCTCTAATA
M48	Fw：	AAACGCATTATTTTGTATGTGGAG
	Rv：	TTCCCTCGTTTTAGCTAATGTGAT
M49	Fw：	GCACCTTTCAACTCAACTCATAACA
	Rv：	TAACAATTTTTCTCATTTCCAGGAC
M50	Fw：	CATCAGACCATACACTCCTCCAAAT
	Rv：	TTGTAAGGAGGATGAGTTAAAGGGA
M51	Fw：	TTGGACTCGTCAAAGGCTAATCA
	Rv：	CCATCTCTACCTTCAATTCAACTGTC
M52	Fw：	TGCGATACAACAAACATAACCCT
	Rv：	ATGACCACTAATAACACAGACAACTTC

Table S2 Primers used in this work

Primer name	Gene ID	Primer sequence
FNC-Q		Fw：TCCAACCAGGTATTCATGTGCTGTC RV：CGCAGATTTTCTCGTCATTCACTTC
FNC-101YFP		Fw：ATATGGGATCTACTAGTGAATTCATGTGTATAGTAGTGTTTATTTGG RV：TCGAGCCCGGGGGTACCGTCGACTTGCATTTGGAGTTTTTCAATCCG
FNC-OE-FW		Fw：CATTTGGAGAGGACACGCTCGAGATGTGTATAGTAGTGTTTATTTGGGAAGC RV：TCTCATTAAAGCAGGACTCTAGATTATTGCATTTGGAGTTTTTCAATC
4CL-Q	Solyc06g068650.2.1	Fw：TGTATTTGTACGTTAAACCACCTGC RV：ATACATACATTTTTCTCCTTTTGCC
PAL-Q	Solyc10g086180.1.1	Fw：CACCTGCCTCTATACGGTTAAAATT RV：ACACCAGCCATGTCCCTTACAGTCA
NLTP9-Q	Solyc09g082270.2.1	Fw：AACTCCACCTCTTAGCCAATGCAAT RV：GAACTCTGTTAGATCCACGTCCTGA
LTP-Q	Solyc09g065430.2.1	Fw：CAAACTCCTCCACTTAGTCGATGCA RV：AGATGAACCAGTTGGAGCAGGGGAA
Laccase13-Q	Solyc06g082240.2.1	Fw：CCTATGTGTGAGCCATCAGGGTTTA RV：TCTTTCTTGAGAGGTACTTGCACAT
PG-Q	Solyc08g060970.2.1	Fw：ATGGAGGGCCAAGCACTTATCTT RV：TACCAGCAACACTTCTTTCAATAAGAAA
Desaturase-Q	Solyc12g044950.1.1	Fw：ATGGGAGGTGGTGGTAATATGTCTG RV：ACTCTTTCGAGAGGATTTTTCTTCTG
EXPA11-Q	Solyc04g081870.2.1	Fw：TTCGGGATTTGAAGTTTATGAGTTT RV：AATAAAAGAAGACAGAGGAAGGGGG
SlGPAT5-Q	Solyc04g011600.2.1	Fw：GTTATTGTCAAGGGCAAACCACCAC RV：ATCGAGAGATTGAGTACGTCACGGC
SlASFT-Q	Solyc03g097500.2.1	Fw：TGGCTCAGGTGACAAAGTTCAAATG RV：AAACCTCTCGCAATTTCACCCCAAG
GDSL-Q	Solyc02g090210.2.1	Fw：ATTGAAGGAGAACGAGTGTGTGGAG RV：AAAAGTTGCTCCGTCGAGTTCTTTG
FAR-Q	Solyc06g074390.2.1	Fw：CTGCATATGTATCAGGGGAAAAAAG RV：CTCTCAGCTGTTTCAATGTTTCCTC
KCS-Q	Solyc03g005320.2.1	Fw：TCTTGCTAAACAACTATTGCAGGTG RV：TCCATACTCACCACAAGTGCATAAG

Table S3 Genes ID of the candidate region

Gene ID	Annoted Function
Solyc04g082500.2.1	ATP binding / serine-threonine kinase
Solyc04g082510.2.1	Serine/threonine-protein kinase
Solyc04g082520.1.1	Ring zinc finger protein (Fragment)
Solyc04g082530.2.1	Bromodomain-containing protein
Solyc04g082540.1.1	Ser/Thr-rich protein T10 in DGCR region
Solyc04g082550.1.1	Trehalose-6-phosphate phosphatase
Solyc04g082560.2.1	Actin cytoskeleton-regulatory complex protein PAN1
Solyc04g082570.2.1	U-box domain-containing protein
Solyc04g082580.2.1	Kelch repeat-containing F-box family protein
Solyc04g082590.2.1	Canopy homolog 2
Solyc04g082600.2.1	Serine/threonine phosphatase family protein
Solyc04g082610.2.1	Glutamate-gated kainate-type ion channel receptor subunit GluR5
Solyc04g082620.2.1	Serine threonine-protein kinase
Solyc04g082630.2.1	Glyceraldehyde-3-phosphate dehydrogenase B
Solyc04g082640.2.1	Unknown Protein
Solyc04g082650.2.1	Palmitoyltransferase erf2
Solyc04g082660.2.1	Peptidyl-prolyl cis-trans isomerase
Solyc04g082670.2.1	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1
Solyc04g082680.2.1	Chloroplast channel forming outer membrane protein
Solyc04g082690.1.1	Ring finger protein
Solyc04g082700.2.1	Solute carrier family 2%2C facilitated glucose transporter member 12
Solyc04g082710.2.1	Cathepsin B-like cysteine proteinase 3
Solyc04g082720.2.1	Small heat shock protein
Solyc04g082730.1.1	Unknown Protein
Solyc04g082740.2.1	Heat shock protein-like protein
Solyc04g082750.2.1	3-beta hydroxysteroid dehydrogenase/isomerase family protein
Solyc04g082760.2.1	SWI/SNF complex subunit SMARCC1
Solyc04g082770.2.1	RNA-binding protein 68390-68829
Solyc04g082780.2.1	Cinnamoyl CoA reductase-like 1
Solyc04g082790.2.1	Atp-dependent RNA helicase
Solyc04g082800.2.1	Unknown Protein
Solyc04g082810.2.1	AT-hook DNA-binding protein (Fragment)
Solyc04g082820.2.1	ARID/BRIGHT DNA-binding domain-containing protein
Solyc04g082830.2.1	Auxin efflux carrier family protein
Solyc04g082840.2.1	Cell division protein kinase 2
Solyc04g082860.1.1	UDP-glucose glucosyltransferase
Solyc04g082870.1.1	Pentatricopeptide repeat-containing protein
Solyc04g082880.2.1	Diphosphate--fructose-6-phosphate 1-phosphotransferase

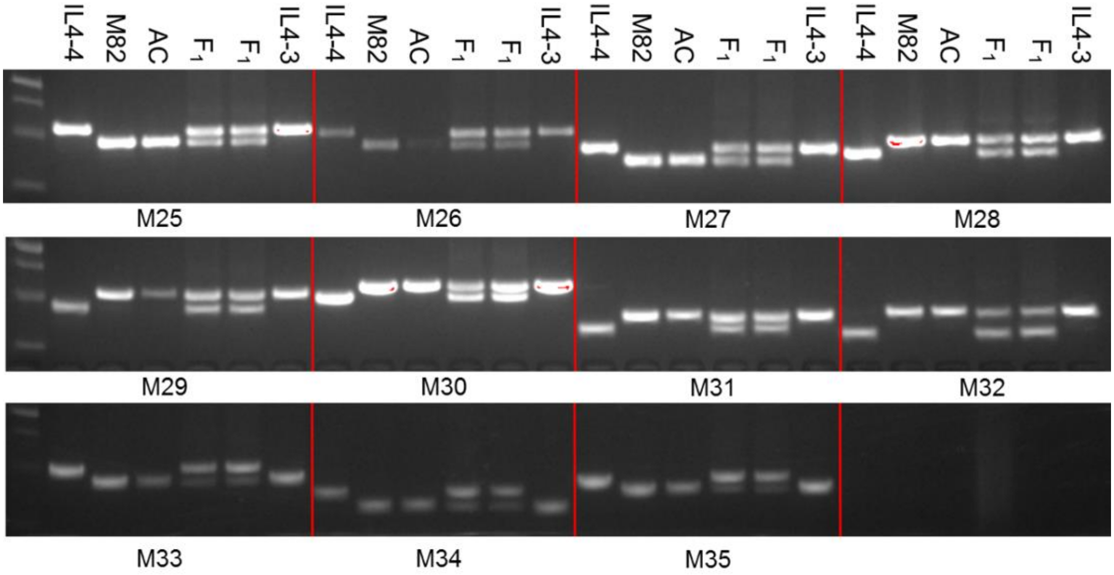
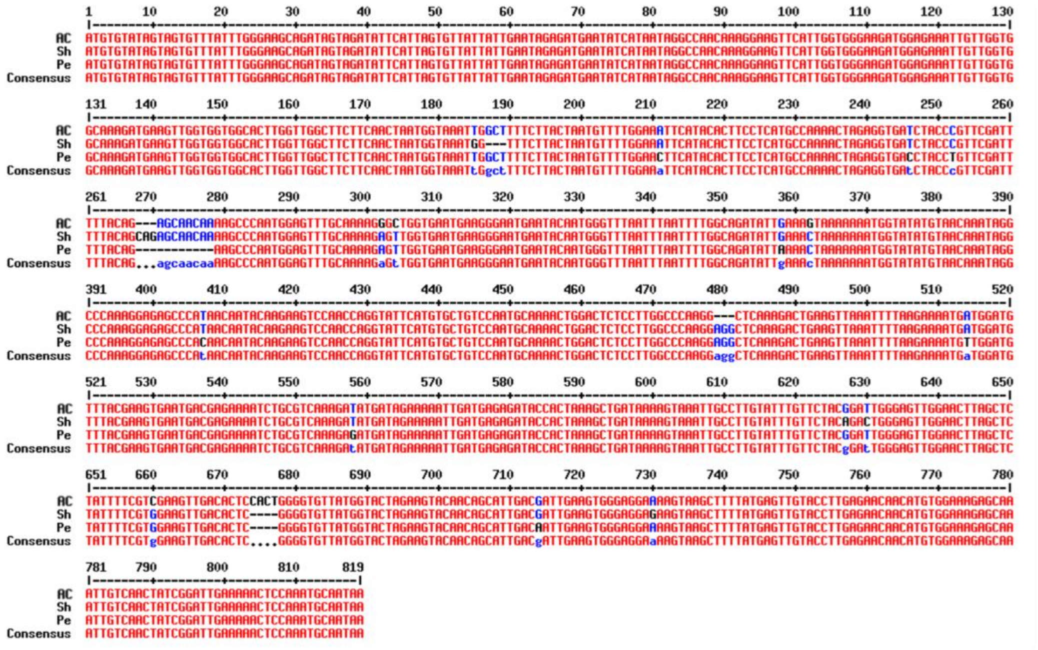
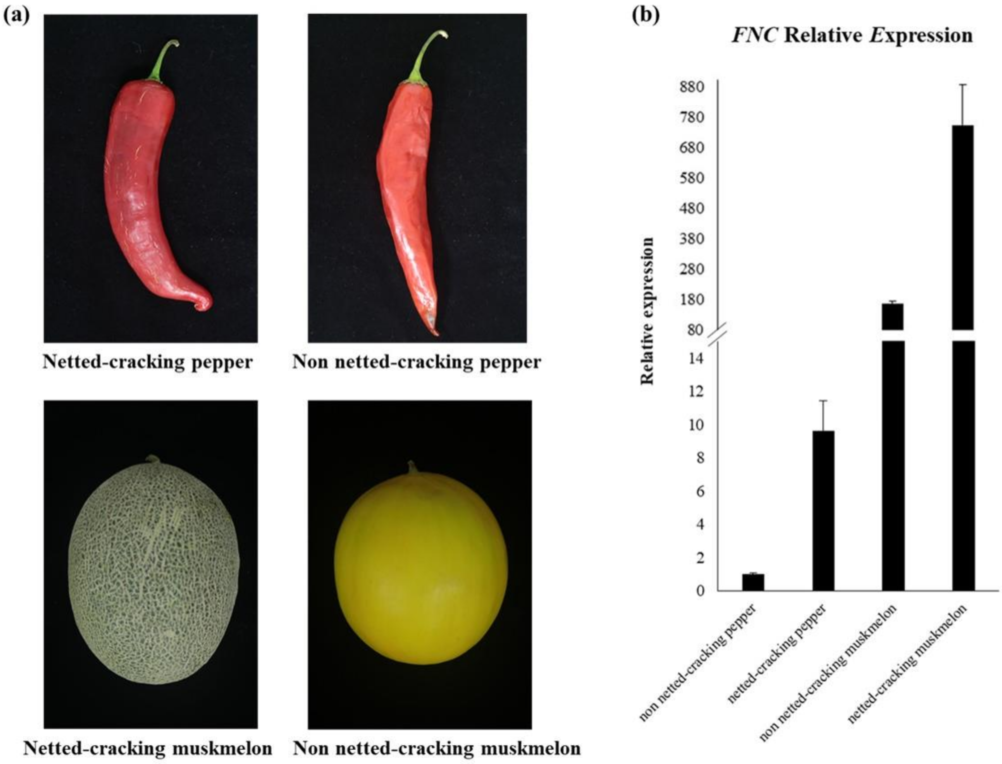


Fig. S1 Screening indel markers for the *FNC* gene fine mapping.



```
           1        10        20        30        40        50        60        70        80        90        100       110       120       130
           |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
       AC  ATGTGTATAGTAGTGTTTATTTGGGAAGCAGATAGTAGATATTCATTAGTGTTATTATTGAATAGAGATGAATATCATAATAGGCCAACAAAGGAAGTTCATTGGTGGGAAGATGGAGAAATTGTTGGTG
       Sh  ATGTGTATAGTAGTGTTTATTTGGGAAGCAGATAGTAGATATTCATTAGTGTTATTATTGAATAGAGATGAATATCATAATAGGCCAACAAAGGAAGTTCATTGGTGGGAAGATGGAGAAATTGTTGGTG
       Pe  ATGTGTATAGTAGTGTTTATTTGGGAAGCAGATAGTAGATATTCATTAGTGTTATTATTGAATAGAGATGAATATCATAATAGGCCAACAAAGGAAGTTCATTGGTGGGAAGATGGAGAAATTGTTGGTG
Consensus  ATGTGTATAGTAGTGTTTATTTGGGAAGCAGATAGTAGATATTCATTAGTGTTATTATTGAATAGAGATGAATATCATAATAGGCCAACAAAGGAAGTTCATTGGTGGGAAGATGGAGAAATTGTTGGTG

           131      140       150       160       170       180       190       200       210       220       230       240       250       260
           |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
       AC  GCAAAGATGAAGTTGGTGGTGGCACTTGGTTGGCTTCTTCAACTAATGGTAAATTGGCTTTTCTTACTAATGTTTTGGAAATTCATACACTTCCTCATGCCAAAACTAGAGGTGATCTACCCGTTCGATT
       Sh  GCAAAGATGAAGTTGGTGGTGGCACTTGGTTGGCTTCTTCAACTAATGGTAAATGG---TTTCTTACTAATGTTTTGGAAATTCATACACTTCCTCATGCCAAAACTAGAGGTGATCTACCCGTTCGATT
       Pe  GCAAAGATGAAGTTGGTGGTGGCACTTGGTTGGCTTCTTCAACTAATGGTAAATTGGCTTTTCTTACTAATGTTTTGGAACTTCATACACTTCCTCATGCCAAAACTAGAGGTGACCTACCTGTTCGATT
Consensus  GCAAAGATGAAGTTGGTGGTGGCACTTGGTTGGCTTCTTCAACTAATGGTAAATtGgctTTTCTTACTAATGTTTTGGAAaTTCATACACTTCCTCATGCCAAAACTAGAGGTGAtCTACCcGTTCGATT

           261      270       280       290       300       310       320       330       340       350       360       370       380       390
           |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
       AC  TTTACAG---AGCAACAAAAGCCCAATGGAGTTTGCAAAAGGGCTGGTGAATGAAGGGAATGAATACAATGGGTTTAATTTAATTTTGGCAGATATTGAAAGTAAAAAAATGGTATATGTAACAAATAGG
       Sh  TTTACAGCAGAGCAACAAAAGCCCAATGGAGTTTGCAAAAGAGTTGGTGAATGAAGGGAATGAATACAATGGGTTTAATTTAATTTTGGCAGATATTGAAACTAAAAAAATGGTATATGTAACAAATAGG
       Pe  TTTACAG-----------AAGCCCAATGGAGTTTGCAAAAGAGTTGGTGAATGAAGGGAATGAATACAATGGGTTTAATTTAATTTTGGCAGATATTAAAACTAAAAAAATGGTATATGTAACAAATAGG
Consensus  TTTACAG...agcaacaaAAGCCCAATGGAGTTTGCAAAAGaGtTGGTGAATGAAGGGAATGAATACAATGGGTTTAATTTAATTTTGGCAGATATTgAAAcTAAAAAAATGGTATATGTAACAAATAGG

           391      400       410       420       430       440       450       460       470       480       490       500       510       520
           |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
       AC  CCCAAAGGAGAGCCCATAACAATACAAGAAGTCCAACCAGGTATTCATGTGCTGTCCAATGCAAAACTGGACTCTCCTTGGCCCAAGG---CTCAAAGACTGAAGTTAAATTTTAAGAAAATGATGGATG
       Sh  CCCAAAGGAGAGCCCATAACAATACAAGAAGTCCAACCAGGTATTCATGTGCTGTCCAATGCAAAACTGGACTCTCCTTGGCCCAAGGAGGCTCAAAGACTGAAGTTAAATTTTAAGAAAATGATGGATG
       Pe  CCCAAAGGAGAGCCCACAACAATACAAGAAGTCCAACCAGGTATTCATGTGCTGTCCAATGCAAAACTGGACTCTCCTTGGCCCAAGGAGGCTCAAAGACTGAAGTTAAATTTTAAGAAAATGTTGGATG
Consensus  CCCAAAGGAGAGCCCAtAACAATACAAGAAGTCCAACCAGGTATTCATGTGCTGTCCAATGCAAAACTGGACTCTCCTTGGCCCAAGGaggCTCAAAGACTGAAGTTAAATTTTAAGAAAATGaTGGATG

           521      530       540       550       560       570       580       590       600       610       620       630       640       650
           |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
       AC  TTTACGAAGTGAATGACGAGAAAATCTGCGTCAAAGATATGATAGAAAAATTGATGAGAGATACCACTAAAGCTGATAAAAGTAAATTGCCTTGTATTTGTTCTACGGATTGGGAGTTGGAACTTAGCTC
       Sh  TTTACGAAGTGAATGACGAGAAAATCTGCGTCAAAGATATGATAGAAAAATTGATGAGAGATACCACTAAAGCTGATAAAAGTAAATTGCCTTGTATTTGTTCTACAGACTGGGAGTTGGAACTTAGCTC
       Pe  TTTACGAAGTGAATGACGAGAAAATCTGCGTCAAAGAGATGATAGAAAAATTGATGAGAGATACCACTAAAGCTGATAAAAGTAAATTGCCTTGTATTTGTTCTACGGATTGGGAGTTGGAACTTAGCTC
Consensus  TTTACGAAGTGAATGACGAGAAAATCTGCGTCAAAGAtATGATAGAAAAATTGATGAGAGATACCACTAAAGCTGATAAAAGTAAATTGCCTTGTATTTGTTCTACgGAtTGGGAGTTGGAACTTAGCTC

           651      660       670       680       690       700       710       720       730       740       750       760       770       780
           |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
       AC  TATTTTCGTCGAAGTTGACACTCCACTGGGGTGTTATGGTACTAGAAGTACAACAGCATTGACGATTGAAGTGGGAGGAAAAGTAAGCTTTTATGAGTTGTACCTTGAGAACAACATGTGGAAAGAGCAA
       Sh  TATTTTCGTGGAAGTTGACACTC----GGGGTGTTATGGTACTAGAAGTACAACAGCATTGACGATTGAAGTGGGAGGAGAAGTAAGCTTTTATGAGTTGTACCTTGAGAACAACATGTGGAAAGAGCAA
       Pe  TATTTTCGTGGAAGTTGACACTC----GGGGTGTTATGGTACTAGAAGTACAACAGCATTGACAATTGAAGTGGGAGGAAAAGTAAGCTTTTATGAGTTGTACCTTGAGAACAACATGTGGAAAGAGCAA
Consensus  TATTTTCGTgGAAGTTGACACTC....GGGGTGTTATGGTACTAGAAGTACAACAGCATTGACgATTGAAGTGGGAGGAaAAGTAAGCTTTTATGAGTTGTACCTTGAGAACAACATGTGGAAAGAGCAA

           781      790       800       810      819
           |--------+---------+---------+--------|
       AC  ATTGTCAACTATCGGATTGAAAAACTCCAAATGCAATAA
       Sh  ATTGTCAACTATCGGATTGAAAAACTCCAAATGCAATAA
       Pe  ATTGTCAACTATCGGATTGAAAAACTCCAAATGCAATAA
Consensus  ATTGTCAACTATCGGATTGAAAAACTCCAAATGCAATAA
```

Fig. S2 Alignment of *FNC* gene sequences from the tomato cultivar Ailsa Craig (AC), wild species *Solanum habrochaites* (Sh) LA1777 and S. pennellii (Pe) LA0716, showing the differences in *FNC* alleles.



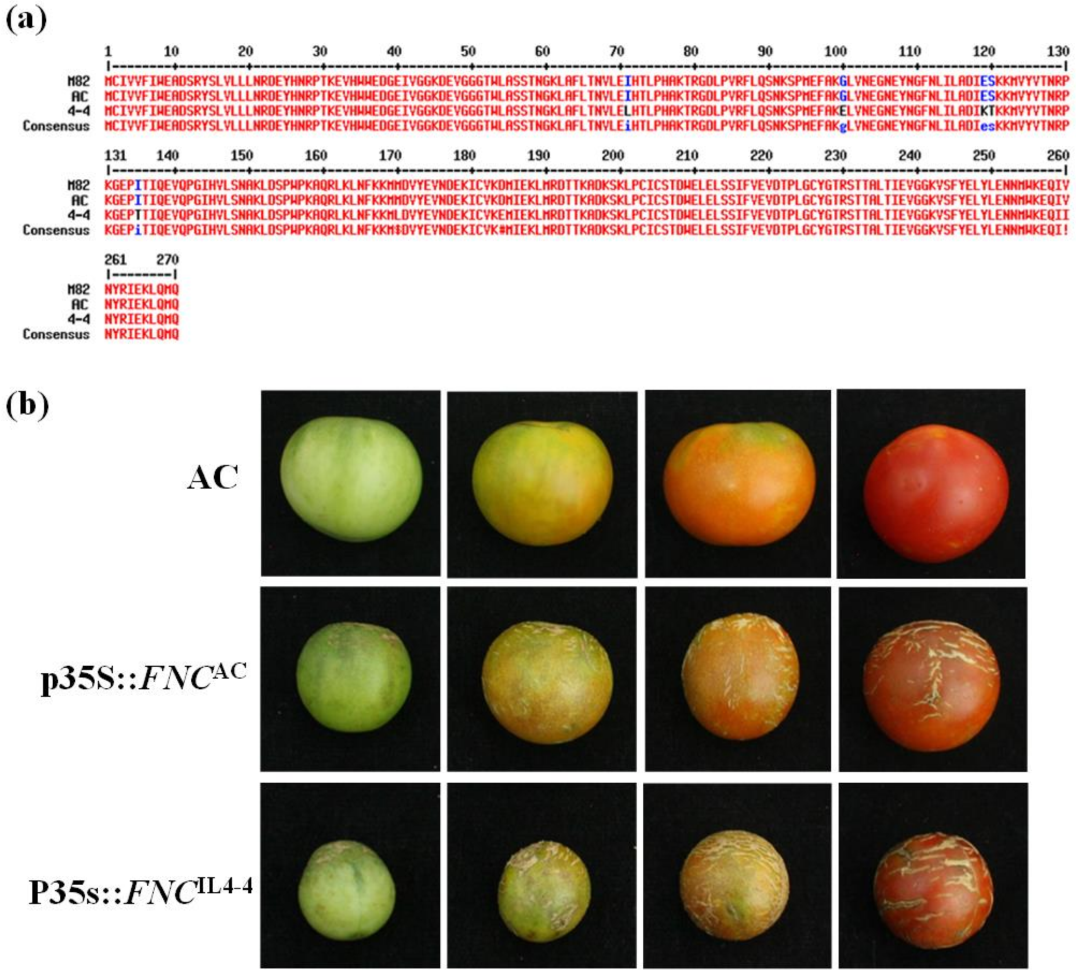
Netted-cracking pepper

Non netted-cracking pepper

Netted-cracking muskmelon

Non netted-cracking muskmelon

Fig. S3 Expressions of homologous *FNC* in netted-cracking/non-netted-cracking pepper and muskmelon. (a) Mature fruit of peppers and muskmelons with netted-cracking and non-netted-cracking phenotypes. (b) Expression of *FNC* in netted-cracking phenotypes was higher than that in non-netted-cracking ones.



```
          1        10        20        30        40        50        60        70        80        90        100       110       120       130
          |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
      M82 MCIVVFIWEADSRYSLVLLLNRDEYHNRPTKEVHWWEDGEIVGGKDEVGGGTWLASSTNGKLAFLTNVLEIHTLPHAKTRGDLPVRFLQSNKSPMEFAKGLVNEGNEYNGFNLILADIESKKMVYVTNRP
       AC MCIVVFIWEADSRYSLVLLLNRDEYHNRPTKEVHWWEDGEIVGGKDEVGGGTWLASSTNGKLAFLTNVLEIHTLPHAKTRGDLPVRFLQSNKSPMEFAKGLVNEGNEYNGFNLILADIESKKMVYVTNRP
      4-4 MCIVVFIWEADSRYSLVLLLNRDEYHNRPTKEVHWWEDGEIVGGKDEVGGGTWLASSTNGKLAFLTNVLELHTLPHAKTRGDLPVRFLQSNKSPMEFAKELVNEGNEYNGFNLILADIKTKKMVYVTNRP
Consensus MCIVVFIWEADSRYSLVLLLNRDEYHNRPTKEVHWWEDGEIVGGKDEVGGGTWLASSTNGKLAFLTNVLEiHTLPHAKTRGDLPVRFLQSNKSPMEFAKgLVNEGNEYNGFNLILADIesKKMVYVTNRP

          131      140       150       160       170       180       190       200       210       220       230       240       250       260
          |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
      M82 KGEPITIQEVQPGIHVLSNAKLDSPWPKAQRLKLNFKKMMDVYEVNDEKICVKDMIEKLMRDTTKADKSKLPCICSTDWELELSSIFVEVDTPLGCYGTRSTTALTIEVGGKVSFYELYLENNMWKEQIV
       AC KGEPITIQEVQPGIHVLSNAKLDSPWPKAQRLKLNFKKMMDVYEVNDEKICVKDMIEKLMRDTTKADKSKLPCICSTDWELELSSIFVEVDTPLGCYGTRSTTALTIEVGGKVSFYELYLENNMWKEQIV
      4-4 KGEPTTIQEVQPGIHVLSNAKLDSPWPKAQRLKLNFKKMLDVYEVNDEKICVKEMIEKLMRDTTKADKSKLPCICSTDWELELSSIFVEVDTPLGCYGTRSTTALTIEVGGKVSFYELYLENNMWKEQII
Consensus KGEPiTIQEVQPGIHVLSNAKLDSPWPKAQRLKLNFKKM$DVYEVNDEKICVK#MIEKLMRDTTKADKSKLPCICSTDWELELSSIFVEVDTPLGCYGTRSTTALTIEVGGKVSFYELYLENNMWKEQI!

          261      270
          |--------|
      M82 NYRIEKLQMQ
       AC NYRIEKLQMQ
      4-4 NYRIEKLQMQ
Consensus NYRIEKLQMQ
```

Fig. S4 The amino acid sequence alignment and overexpressing phenotype of FNC in different development stages of fruit. (a) Amino acid sequence alignment of FNC protein from AC, M82 and IL4-4. (b) Overexpression of *FNC*^IL4-4 and *FNC*^AC lead to the appearance of the netted-cracking in tomato during different stages of fruit.

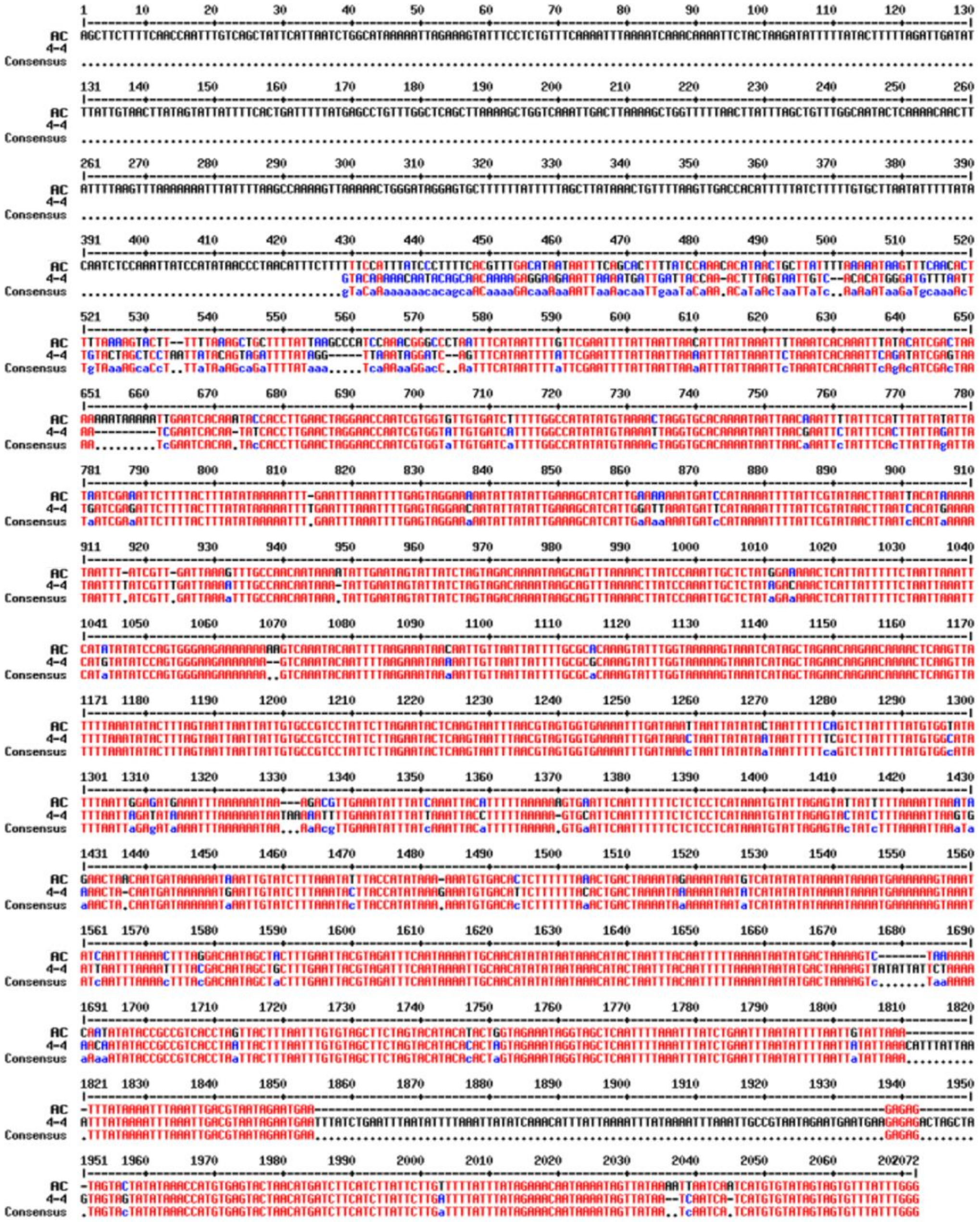


Fig. S5 Sequence alignment of *FNC* promoter regions from the netted-cracking IL4-4 and the non-cracking AC.

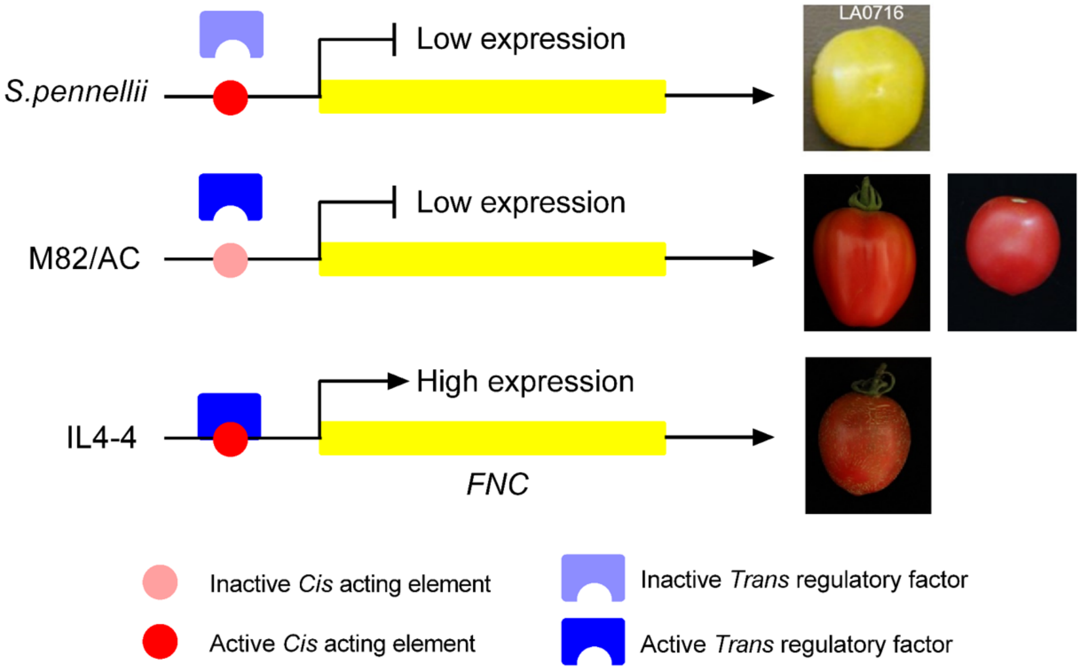


Fig. S6 The proposed mechanism of netted-cracking. The netted-cracks on tomato fruit are postulated to be a result of the synergism (in *cis*-*trans* acting) of two loci (*FNC* and another *trans*-regulatory factor) at different locations in the genomes. In *S. pennellii*, the inactive *trans*-regulatory was unable to bind to active *cis*-acting elements on *FNC* promoters, and the active *trans*-regulatory was also unable to bind to inactive *cis*-acting elements on *FNC* promoters in M82 and AC. However, in IL4-4, an active *trans*-regulatory was able to bind to active *cis*-acting elements on *FNC* promoters to increase its expression and cause the formation of netted-cracking.