

Introgression at 81 cM on Chromosome 3 associated with Gc171

Douglas P. Maxwell, University of Wisconsin-Madison
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BACKGROUND: Dr. Y. Ji, University of Florida indicated that there was an introgression associated with Ty4 gene on chromosome 3 near 76-85 cM. Originally, Ty4 was thought to be on chromosome 6 between 40-80 cM. Our UW-team scanned this region at 5-cM intervals and did not find any evidence for an introgression in Gc171, which gives the SCAR marker for Ty4. With this new information, Maxwell designed primers for markers at 76 cM, 68 cM, 81 cM, and 84 cM.

Primers:

P3-81F1 5' ACTACATTGATTCCAAACTCCAATGAAGGTGG
P3-81-F5 5' GCGGACTTGGATGATGACATGGCCTGTGC
P3-81F6 5' ATTTAACCGTGTCTGGGCAACTCAATGG
P3-81R2 5' AAATCCATATCTTCTTTGCAATTCTC
P3-81R4 5' GCTCACTTTGCAAATCACATCCCCATTTCCACC

These primers were designed from a match of the unigene (U216063) of tomato for C2_At4g17300 with *Oryza sativa* (AP00384) and *Arabidopsis* (AJ222644 and Z97343). Eleven primers were designed and so far, 8 primer pairs have been evaluated. Single bands were obtained with P3-81F1/R2 (1.2 kb), P3-81F1/R4 (1.5 kb), P3-81F5/R4 (600 bp), P3-81F6/R4 (1,000 bp).

PCR program: TGEN53 (53 C annealing temperature)

Sequences:

HUJ-VF-F1-R4: 1441 bp; HUJ-VF has a DSI = 6 (scale 0-6) in Guatemala.

Composition 382 A; 264 C; 276 G; 519 T; 0 OTHER
Percentage: 26.5% A; 18.3% C; 19.2% G; 36.0% T; 0.0% OTHER
Molecular Weight (kDa): ssDNA: 444.44 dsDNA: 888.20
ORIGIN

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1     ACTACATTGA TTCCAAACTC CAATGAAGGT GGAGATTAC CAGTTAGTGC TATTCCTACT
61     ACTGAGTCTG GTTCTGTTGA CTGGTCACAA GTAAGTCAA TCATCAAACA GGGTGCTTTG
121    CCCATTTTAG AGTGAATCTA TTAGCTAGCA GTTTAAGAGC CTGCTTGAAT TGGGCAGCTT
181    ATTTACATAA TAATAGCTTT TAAGCAGTTT GTTAGTGTTT GGGTCAAATA AACAGTGCTT
241    TTGGACTCTT GTTTTTAAGC CAAAATAACA AAAATAATTT AAAAGTTATA AGCCCATCCA
301    AACAGGCTTG AAGTCTGTTT ATATCCTTAC AAGCAATGTG AACTTTTTAA TTTTCAGAAAG
361    TTAATAGGTA CATGCATTTG ATGTTGGATT TCTGCATTAA CTGTCTAATT ATCTTTTGTA
421    AATTGCATCC GTGTTGCAGG ACTTCTTTGG GAAACGAGCA TATTTAACCG TGTCTGGGCA
481    ACTCAATGGT GAAACATATG CTACTGCGCT CTCCGATGTA GAGTCTCCTT TCACTTTTTA
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541      GTTTCATATG CTACCTTCTC TGGCTTGTA  TCATTTTTCC CAACTTTATC TTTTGGTCAC
601      AGAATCCTTC ATGCTATTTT CTTCAATCTT TCATATTTCTG ACAATGTCAA CTTTTGGTTC
661      AGATCTACAC CTTTGGCCCT ACATTCAGAG CAGAAAAC TC AACACTTCC AGGCACTTGG
721      CTGAATCTG  GGTAAGCTTA TACTCTAAAA CTGATAAAAT ATAGTAGAAC TTCTTTGTAT
781      ATTTCTTTCC ATACTTGTGG GCAGAAACAA ATAAAATGTT GACACTAAGT TCTTTTGTGT
841      AAGATGATTG AACCAGAACT AGCTTTTGCG GACTTGGATG ATGACATGGC CTGTGCTACT
901      GCCATCTCC  AGTATGTAGT ATGTTACCTT TCACATCTCG CTGTTCCCTTA GTGAATATTT
961      ATTACTTTGT TCTCACAAC T AGACTTTTGC ATTGACGTAT CTGCTTGAAA GGTGCAACAT
1021     GTGTTGGAGA ATTGCAAAGA AGATATGGAT TTTTTTGACA CCTGGATTGA GAAAGGGATC
1081     ATCAATAGAC TTACCGTATG AATTTCTATG ATTTTGATGT GTTTACTTCT CAACGTATTC
1141     TCCACTCTGC TTGGGGTCTA TAGTGTGCTC CTAATAGTTG GTCTAATTTG TGATCATATG
1201     CTCCACAGGA TGTGTGTTGAG AAGAACTTTG TGCAGTTGAG TTACACTGAT GCTGTTGAGC
1261     TTCTATTGAA AGCAAAAAG AAGTTCGATT TCCCGGTAGG TGTGCTTTTA TTTGCATGCT
1321     TTCTCACATG CATTTTTTGG CCAGTCTCTC TCCATCCGTA CTTCTGTAC TTTTCCTTAA
1381     ATTGTAATGA GCTGCTTCTG CATATGGTAG GTGAAATGGG GATGTGATTT GCAAAGTGAG
1441     C

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Gc171-F1-R4: 1446 bp; Gc171 has a DSI = 0.5 (scale 0-6) in Guatemala and resistance is introgressed from *S. chilense* LA1932

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Composition  386 A; 266 C; 272 G; 522 T; 0 OTHER
Percentage:  26.7% A; 18.4% C; 18.8% G; 36.1% T; 0.0% OTHER
Molecular Weight (kDa): ssDNA: 445.87 dsDNA: 891.27
ORIGIN

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1      ACTACATTGA TTCCAAACTC CAATGAAGGT GGAGATTCAC CAGTTAGTGC TATTCCTACT
61     ACTGAGTCTG GTTCTGTTGA CTGGTCACAA GTAAGTCAAA TCATCAAACA GGGTGCTTAG
121    CCCATTTTAG ATGAATTCTA TTAGCTAGCA GTTTAAGAGC CTGCTTGAAT TGGGCAGCTT
181    ATTTACATAA TAATAGCTTT TAAGCAGTTT TTTAGTGTTT GGGTGAAATA AACAGTGGCT
241    TTAGACACTT GTTTTAAAGC CAAAATAACA AAAATACTTT AGAAGTTATA AGCCCATCCA
301    AACAGGCTTG AAGTCTGTTT ATATCCTTAC AAGCAACGTA AACTTTTTTA TTTCAGAAAG
361    TTAATAGGTG CATGCATTTG ATGTTGGATT TCTGCATTA CTGTCTAATT ATTTCTTGTA
421    AATTGCATCC ATGTTGCAGG ACTTCTTTGG GAAACGAGCA TATTTAACCG TGTCTGGGCA
481    ACTCAATGGT GAAACATATG CTACTGCGCT CTCCGATGTA GAGTCTCCTC TCACTTTTTTA
541    GTTTCATATG CTACTGTCTT CTCTGGCTTT TAACCATTAT TCCCAACTTT ATCTTTTGGT
601    CACAGAATCC TTCATTCAT TTTCTTCATT CTTTCATATT CTAACAATGT CAACTTTTGG
661    TTTTCAGATC TACACCTTTG GCCCTACATT CAGAGCAGAA AATTC TAACA CTTCCAGGCA
721    CTTGGCTGAA TTCTGGGTAA GCTTATACTC TAAAAC TGAT AAACATAGTA GAACTTCTTT
781    GTATATTTCT TTCCATATAT GTGGGCAGAA ACCAATAAAA TGTGACACT AAGTTCTATT
841    GTGTAAGATG ATTGAACCAG AACTAGCTTT TGCGGACTTG GATGATGACA TGGCCTGTGC
901    TACTGCCTAT CTCCAGTATG TAGTATGTTA CTTTTCACAT CTCGCTGTTC CTTAGTGAAT
961    ATTTATTACT TTGTTCTCAC AACTAGACTT TTGCATTGAC ATATCTGCTT GAAAGGTGCA
1021   ATATGTGTTG GAGAATTGCA AAGAAGATAT GGATTTTTTT GACACCTGGA TTGAGAAAGG
1081   GATCATCAAT AGACTTACCG TATGAATTTT TATGATTTTG ATGTGTTTTT TTCTCAACGT
1141   TTTCTCCACT ACGCTGGGGG TCTATTGTGT GCACCTAATA GTTGGTCTTA TTGTTGATCA
1201   TATGCTCCAC AGGATGTTGT TGAGAAGAAC TTTGTGCAGT TGAGTTACAC TGATGCTGTT
1261   GAGCTTCTAT TGAAAGCAAA AAAGAAGTTC GATTTCCCGG TAGGTGTGCT TTTATTTGCA
1321   TGCTTTTTCA CATGCATTTT TTGGCCAGTC TCTCTCCATC CGTACTTCTG TCACTTTTCC
1381   TTAAAATAGT AATGAGCTGC TTCTGCATAT GGTAGGTGAA ATGGGGATGT GATTTGCAA
1441   GTGAGC

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Alignment:

HUJ-VF has DSI = 4; Gc171 has DSI = 0.5 (recent field test in Guatemala, Jan. 2008)

Top = HUJ-VF; bottom = Gc171

HUJ-F6-R4:171-F6-R4 identity= 97.55%

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1 ATTTAACCGTGTCTGGGCAACTCAATGGTGAAACATATGCTACTGCGCTCTCCGATGTAG
  |||
1 ATTTAACCGTGTCTGGGCAACTCAATGGTGAAACATATGCTACTGCGCTCTCCGATGTAG
61 AGTCTCCTTTTCACTTTTTAGTTTCATATGCTAC...CTTCTCTGGCTTGTAATCATTTTTT
  |||
61 AGTCTCCTCTCACTTTTTAGTTTCATATGCTACTGTCTTCTCTGGCTTTTAACCATTATT
118 CCCAACTTTTATCTTTTGGTCACAGAATCCTTCATGCTATTTTCTTCATTCTTTCATATTC
  |||
121 CCCAACTTTTATCTTTTGGTCACAGAATCCTTCATTCTATTTTCTTCATTCTTTCATATTC
178 TGACAATGTCAACTTTTGG...TTCAGATCTACACCTTTGGCCCTACATTTCAGAGCAGAAA
  |
181 TAACAATGTCAACTTTTGGTTTTCAGATCTACACCTTTGGCCCTACATTTCAGAGCAGAAA
236 ACTCTAACACTTCCAGGCACTTGGCTGAATTCTGGGTAAGCTTATACTCTAAAAC TGATA
  |
241 ATTCTAACACTTCCAGGCACTTGGCTGAATTCTGGGTAAGCTTATACTCTAAAAC TGAT.
296 AAATATAGTAGAACTTCTTTGTATATTTCTTTCCATACTTGTGGGCAGAAACAAATAAAA
  |||
300 AAACATAGTAGAACTTCTTTGTATATTTCTTTCCATATATGTGGGCAGAAACCAATAAAA
356 TGTTGACACTAAGTTCTTTTGTGTAAGATGATTGAACCAGAACTAGCTTTTGC GGACTTG
  |||
360 TGTTGACACTAAGTTCTATTTGTGTAAGATGATTGAACCAGAACTAGCTTTTGC GGACTTG
416 GATGATGACATGGCCTGTGCTACTGCCTATCTCCAGTATGTAGTATGTTACCTTTCACAT
  |||
420 GATGATGACATGGCCTGTGCTACTGCCTATCTCCAGTATGTAGTATGTTACCTTTCACAT
476 CTCGCTGTTCCTTAGTGAATATTTATTACTTTGTTCTCACAAC TAGACTTTTGCATTGAC
  |||
480 CTCGCTGTTCCTTAGTGAATATTTATTACTTTGTTCTCACAAC TAGACTTTTGCATTGAC
536 GTATCTGCTTGAAAGGTGCAACATGTGTTGGAGAATTGCAAAGAAGATATGGATTTTTTTT
  |||
540 ATATCTGCTTGAAAGGTGCAACATGTGTTGGAGAATTGCAAAGAAGATATGGATTTTTTTT
596 GACACCTGGATTGAGAAAGGGATCATCAATAGACTTACCGTATGAATTTCTATGATTTTGG
  |||
600 GACACCTGGATTGAGAAAGGGATCATCAATAGACTTACCGTATGAATTTCTATGATTTTGG
656 ATGTGTTTACTTCTCAACGTATTCTCCACTCTGCTTGGGGTCTATAGTGTGCTCCTAATA
  |||
660 ATGTGTTTTTCTTCTCAACGTTTTTCTCCACTACGCTGGGGGTCTATTGTGTGCACCTAATA
716 GTTGGTCTAATTGTTGATCATATGCTCCACAGGATGTTGTTGAGAAGA AACTTTGTGCAGT
  |||
720 GTTGGTCTTATTGTTGATCATATGCTCCACAGGATGTTGTTGAGAAGA AACTTTGTGCAGT
776 TGAGTTACACTGATGCTGTTGAGCTTCTATTGAAAGCAAAAAAGAAGTTTCGATTTCCCGG
  |||
780 TGAGTTACACTGATGCTGTTGAGCTTCTATTGAAAGCAAAAAAGAAGTTTCGATTTCCCGG
836 TAGGTGTGCTTTTATTTGCATGCTTTCTCACATGCATTTTTTTGGCCAGTCTCTCTCCATC
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840  |||
TAGGTGTGCTTTTATTTGCATGCTTTTTCACATGCATTTTGGCCAGTCTCTCTCCATC

896  CGTACTTCTGTCACTTTTCCCTT . AAATTGTAATGAGCTGCTTCTGCATATGGTAGGTGAA
|||
900  CGTACTTCTGTCACTTTTCCCTTAAAATAGTAATGAGCTGCTTCTGCATATGGTAGGTGAA

955  ATGGGGATGTGATTTGCAAAGTGAGC
|||
960  ATGGGGATGTGATTTGCAAAGTGAGC

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Assemble of PCR fragment sequences to get sequence from P3-81F1 to F3-81R4 (1140 bp):

Bold green areas are primers, green areas are the exons, which have 100% nt id with the SGN-U317629 from SGN site for the COS II marker. Some restriction sites are marked in orange. All the SNPs and indels are associated with introns except for one SNP in one exon.

Upper line: HUI-VF-F1-R4, from 1 to 1441
Lower line: Gc171-F1-R4, from 1 to 1446

HUI-VF-F1-R4:Gc171-F1-R4 identity= 97.01%(1397/1440) gap=0.48%(7/1447)

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P3-81F1
1  ACTACATTGATTCCAACTCCAATGAAGGTGGGAGATTCACCAGTTAGTGCTATTCCTACT
|||
1  ACTACATTGATTCCAACTCCAATGAAGGTGGGAGATTCACCAGTTAGTGCTATTCCTACT

61  ACTGAGTCTGGTTCTGTTGACTGGTCACAAGTAAGTCAAATCATCAAACAGGGTGCTTTG
|||
61  ACTGAGTCTGGTTCTGTTGACTGGTCACAAGTAAGTCAAATCATCAAACAGGGTGCTTAG

121  CCCATTTTAGAGTGAATCTATTAGCTAGCAGTTTAAGAGCCTGCTTGAATTGGGCAGCTT
|||
121  CCCATTTTAGATGAATTCTATTAGCTAGCAGTTTAAGAGCCTGCTTGAATTGGGCAGCTT
EcoRI

181  ATTTACATAATAATAGCTTTTAAGCAGTTTGTAGTGTGGGTGAAATAAACAGTGCTT
|||
181  ATTTACATAATAATAGCTTTTAAGCAGTTTTTAGTGTGGGTGAAATAAACAGTGGCT
DraI

241  TTGGACTCTTGTTTTTAAGCCAAAATAACAAAATAATTTAAAAGTTATAAGCCCATCCA
|||
241  TTAGACACTTGTTTTTAAGCCAAAATAACAAAATACTTTAGAAAGTTATAAGCCCATCCA
DraI

301  AACAGGCTTGAAGTCTGTTTATATCCTTACAAGCAATGTGAAGTTTTAAATTTCAGAAAG
|||
301  AACAGGCTTGAAGTCTGTTTATATCCTTACAAGCAACGTAAACTTTTAAATTCAGAAAG

361  TTAATAGGTACATGCATTTGATGTTGGATTTCTGCATTAAGTGTCTAATTATCTTTTGTA
|||
361  TTAATAGGTGCATGCATTTGATGTTGGATTTCTGCATTAAGTGTCTAATTATTTCTTGTA
P3-81F6

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421 AATTGCATCCGTGTTGCAGGACTTCTTTGGGAAACGAGCATATTTAACCGTGTCTGGGCA
|||||
421 AATTGCATC**CATG**TTCAGGACTTCTTTGGGAAACGAGCATATTTAACCGTGTCTGGGCA
|||||
481 **ACTCAATGGT**GAAACATATGCTACTGCGCTCTCCGATGTAGAGTCTCCTTTCACTTTTTA
|||||
481 ACTCAATGGT**GAAACATATGCTACTGCGCTCTCCGATGTAGAGTCTCCTTTCACTTTTTA**
|||||
541 GTTTCATATGCTAC...CTTCTCTGGCTTGTAATCATTTTTCCCAACTTTATCTTTTGGT
|||||
541 GTTTCATATGCTACTGTCTTCTCTGGCTTTTAACCATTTATCCCAACTTTATCTTTTGGT
|||||
598 CACAGAATCCTTCATGCTATTTTCTTCATTCTTTTCATATTCGACAATGTCAACTTTTGG
|||||
601 CACAGAATCCTTCATTCTATTTTCTTCATTCTTTTCATATTC**TAACAATGTCAACTTTTGG**
|||||
658 ..TTCAGATCTACACCTTTGGCCCTACATTCAGAGCAGAAAAC**TCTAACACTTCCAGGCA**
|||||
661 TTTTCAGATCTACACCTTTGGCCCTACATTCAGAGCAGAAAATTC**TAACACTTCCAGGCA**
|||||
716 **CTTGGCTGAAT**CTGGGTAAGCTTATACTCTAAAAC**TGATAAAATATAGTAGAACTTCTT**
|||||
721 CTTGGCTGAATCTGGGTAAGCTTATACTCTAAAAC**TGAT.AAACATAGTAGAACTTCTT**
|||||
776 TGTATATTTCTTTCCATACCTTGTGGGCAGAAACAAATAAAATGTTGACACTAAGTTCTTT
|||||
780 TGTATATTTCTTTCCATATATGTGGGCAGAAACCAATAAAATGTTGACACTAAGTTCTAT
P3-81F5
836 TGTGTAAGATGAT**TGAACCAGA**ACTAGCTTTT**GCGGACTTGGATGATGACATGGCCTGTG**
|||||
840 TGTGTAAGATGAT**TGAACCAGA**ACTAGCTTTT**GCGGACTTGGATGATGACATGGCCTGTG**
|||||
896 **CTACTGCCTATCTCCAGTATGTAGTATGTTACCTTTCACATCTCGCTGTTCCCTAGTGAA**
|||||
900 **CTACTGCCTATCTCCAGTATGTAGTATGTTACCTTTCACATCTCGCTGTTCCCTAGTGAA**
|||||
956 TATTTATTACTTTGTTCTCACAAC**TAGACTTTTGCATTGACGT**ATCTGCTT**GAAAGGTGC**
|||||
960 TATTTATTACTTTGTTCTCACAAC**TAGACTTTTGCATTGACATATCTGCTT**GAAAGGTGC
P3-81R2
1016 **AACATGTTGTTGGAGAATTGCAAAGAAGATATGGATTTTTTTTGACACCTGGATTGAGAAAAG**
|| |
1020 AATATGTGTTGGAGAATTGCAAAGAAGATATGGATTTTTTTTGACACCTGGATTGAGAAAAG
|| |
1076 **GGATCATCAATAGACTTACCGT**TATGAATTTCTATGATTTTGATGTGTTACTTCTCAACG
|||||
1080 **GGATCATCAATAGACTTACCGT**TATGAATTTCTATGATTTTGATGTGTTTCTTCTCAACG
|||||
1136 TATTTCTCCACTCTGCTTGGGGTCTATAGTGTGCTCCTAATAGTTGGTCTAATTGTTGATC
| |
1140 TTTTCTCCACTACGCTGGGGTCTATTTGT**GTGCAC**CTAATAGTTGGTCTTATTGTTGATC
| |
1196 ATATGCTCCACAG**GATGTTGTTGAGAAGA**ACTTTGTGCAGTTGAGTTACACTGATGCTGT
|||||
1200 ATATGCTCCACAG**GATGTTGTTGAGAAGA**ACTTTGTGCAGTTGAGTTACACTGATGCTGT
|||||
1256 **TGAGCTTCTATTGAAAGCAAAAAAGAAGTTCGATTTCCCGG**TAGGTGTGCTTTTATTTCG
|||||

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1260  |||||
      TGAGCTTCTATTGAAAGCAAAAAAGAAGTTCGATTTCCCGGTAGGTGTGCTTTTATTTGC
1316  ATGCTTTCTCACATGCATTTTTTTGGCCAGTCTCTCTCCATCCGTACTTCTGTCACTTTTC
      |||||
1320  ATGCTTTTTTCACATGCATTTTTTTGGCCAGTCTCTCTCCATCCGTACTTCTGTCACTTTTC
      |||||
      P3-81R4
1376  CTT.AAATTGTAATGAGCTGCTTCTGCATATGGTAGGTGAAATGGGGATGTGATTTGCAA
      ||| |||
1380  CTTAAAATAGTAATGAGCTGCTTCTGCATATGGTAGGTGAAATGGGGATGTGATTTGCAA
1435  AGTGAGC
      |||||
1440  AGTGAGC

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100% nt id for the seven exons in color below for this unigene and the sequence from HUU-VF, susceptible OP

SGN-U317629, associated with C2_At4g17300 (SGN site)

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AATGGCTGGTGTCTGTCTCCGGCCACCCTCTCCGCCTTAAGCCCTTCTACGCCGTCCGGTCTTTCAGTCAATACCGAAGACCTATCAA
AGTCTTAAACCCCAATTTCTACTCATCGTACCCTCCACAGCTGCCTCCAGCACCCCTACTTGAGCCGTCGACGGAGCTTTTGCTCTGTGGT
TTCCGCGCTATTTTCATCCGGAGAAGCAGTTGAAAGACCCAAATTTGAAAATATTGAGGCAAAGAGGGGGTAAAACTGAAAAGTTGG
GGAATTTCCGAAAAGGTTGAGGGTTGCGGACATAAAGGGAGGACCTGAAGAAGGTTTGGACCGTCTTGGTGAACTTTGGTGGTTAGAGG
ATGGGTTGCGACGGTTAGGGCTCAGAGCAGTGTGACGTTTATGATATTAATGATGGTCTTGTCTTCAAATATGCAATGTGTTATGGG
TCTGATGCTGAGGGTTATGATCAGGTGGAGAATGGCTTAATTTCAACTGGTGCATCAGTATGGATTGAAGGTACTGTCGTGAGCAGCCA
AGGGTCAAAGCAGAAAATTGAGTTGAAGGTTGAGAACTTGTAGTGGTTGGTAAAAGTGATCCTTCTTCCCATCCAGAAGAAAAGAGT
CAGCAGAGAATTTTGAAGAACAAAGGCTCACCTTCGCCCTCGAACAAACACTTTTGGTGGGTTTCCGAGGGTGAGGAAATGCTTTGTCTTA
TGCCACACACAAGTTTTTCAAAGAAAATGGCTTTGTTGGGCTCTAGTCCAATAATCACTGCTTCTGATTGTGAAGGAGCTGGCAGCA
ATTTCTGTGTTACTACATTGATTTCCAAACTCCAATGAAGGTTGGAGATTCAACCAGTTAGTGCTATTCCTACTACTGAGTCTGGTTCTGTGTA
CTGGTCAAA

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GACTTCTTTGGGAAACGAGCATATTTAACCGTGTCTGGGCAACTCAATGGTGAACATATGCTACTGCGCTCTCCGAT

AT

CTACACCTTTGGCCCTACATTGAGAGCAGAAACTCTAACACTTCCAGGCCTTGGCTGAATTCTG

GATGATTGAACCAGAAGTAGCTTT

TGCGGACTTGGATGATGACATGGCCTGTGCTACTGCCTATCTCCAGTATGTA

GTGCAACATGTGTTGGAGAATTGCAAAGAAGATATGGA

TTTTTTTGACACCTGGATTGAGAAAGGGATCATCAATAGACTTACC

GATGTTGTTGAGAAGAACTTTGTGCAGTTGAGTTACACTGATGC

TGTTGAGCTTCTATTGAAAGCAAAAAAGAAGTTCGATTTCCC

GGTGAATGGGGATGTGATTTGCAAAGTGAAGCATGAAAGATATATCAC

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CGAGGAGGCTTTTGGTGGTTGCCTGTGATTATTAGAGACTATCCGAAAGGACATCAAGGCATTTTACATGCGGCAGAACGATGATGGGAA
GACTGTTGCAGCCATGGATATGTTGGTACCTCGGGTTGGAGAACTTATGGTGGAAAGTCAAAGAGAGGAACGCCTTGAATACCTAGAGGA
ACGTTTGGATCACATGAACCTCAACAAAGAAAGCTTTTGGTGGTATCTTGATCTGCGACGTTATGGTTCAGTTCCTCATGCTGGATTGG
ACTAGGCTTTGAAAGGCTCGTTCAATTTGCGACTGGAATAGACAATATCAGAGATGCAATACCTTTCCCTCGAACACCTGGCTCTGCAGA
GTTTGGAGTTTGGACCTTAAAGGGTACTACTACTTTATAAAAAATGAATCGGTCCAAAAGGTGCAGTGTACCAATACTACCTTCTGT
AATCCTTTTTTGTCTTTTCACTATTCAATCATTATATAGATTTTGTAGAGCGTGTAAAATGGTGGAAAGTTATAGTCATTTCTCCGAAA
TAATTAGATATATGGAACACACCAAAAAACTGTGTTTTTCATAAAAACTTATAAGTTGTAGGGTTCCCAATGTAATGGTGCATTTATAA
TGGCTTTTTCCCCTCTATAAAGCACTGCACGGAAAAA

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