
Thank You For
Shopping

researchers have been working with. One banana genotype was rather flavourless and starchy (Prata Ana), but two others emphasized what we in the temperate countries miss: Garantida II with citrus flavours overlaying a sweet smooth texture, while Caipira had a more savoury and vanilla custard taste. But the

Banana genotypes

Sbmenu: Blog.nwsource.com

ESPRESSO
TALL/GRANDE/VENTI

- Espresso
- Caffè Americano
- Caffè Latte
- Cappuccino
- Caramel Macchiato

Add Extra Shot/Syrup

- Vanilla Latte
- Skinny Vanilla Latte
- Caffè Mocha
- White Chocolate Mocha
- Espresso Truffle

- Pike
- Today
- Caffè

Add Espre

TEA - Brewed Hot or Shaken Ic
TALL/GRANDE/VENTI

Repetitive DNA and its evolution in the Musa genome

Polymorphisms
DNA
Evolution
Breeding
Conservation

Epigenomics

W067: Banana (Musa) Genomics
Plant and Animal Genome 2011

Pat Heslop-Harrison, Faisal Nouroz, Farah Badakshi, Asha Nair, Anath B Das, Gerhard Menzel, Thomas Schmidt, Trude Schwarzacher

Thanks:
IAEA
Joint FAO/IAEA Programme
Nuclear Techniques in Food and Agriculture
ANNALS OF BOTANY
AoBBlog.com
musa genomics

University of Leicester
phh4@le.ac.uk
www.molcyt.com

Red AAA

Palayam codan AAB (two bunch yellow, one green)

Peyan ABB (green cooking banana),

Njalipoovan AB (yellow)

Robusta AAA (green ripe)

Nendran AAB

Poovan AAB (one yellow bunch)

Red AAA

Peyan

Wild banana species:
Musa acuminata – A genome
Musa balbisiana – B genome

Varkala, Kerala, India

Wild banana species:

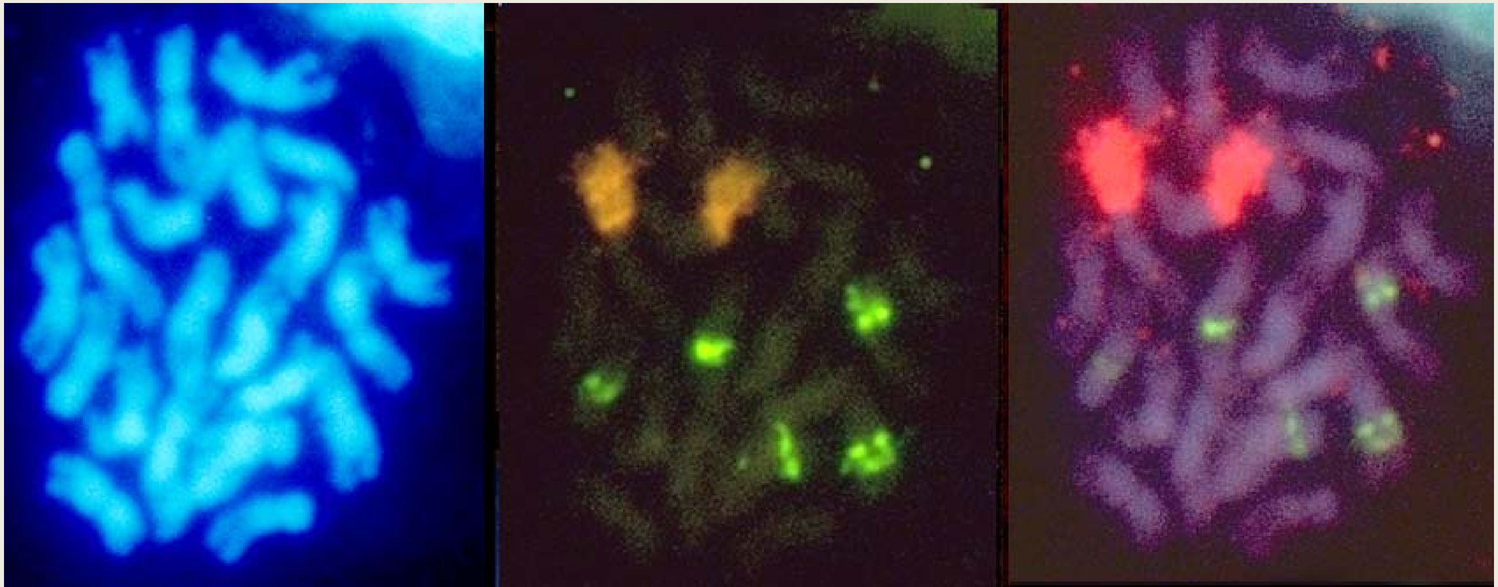
Musa acuminata – A genome

Basic chromosome number n=x=11

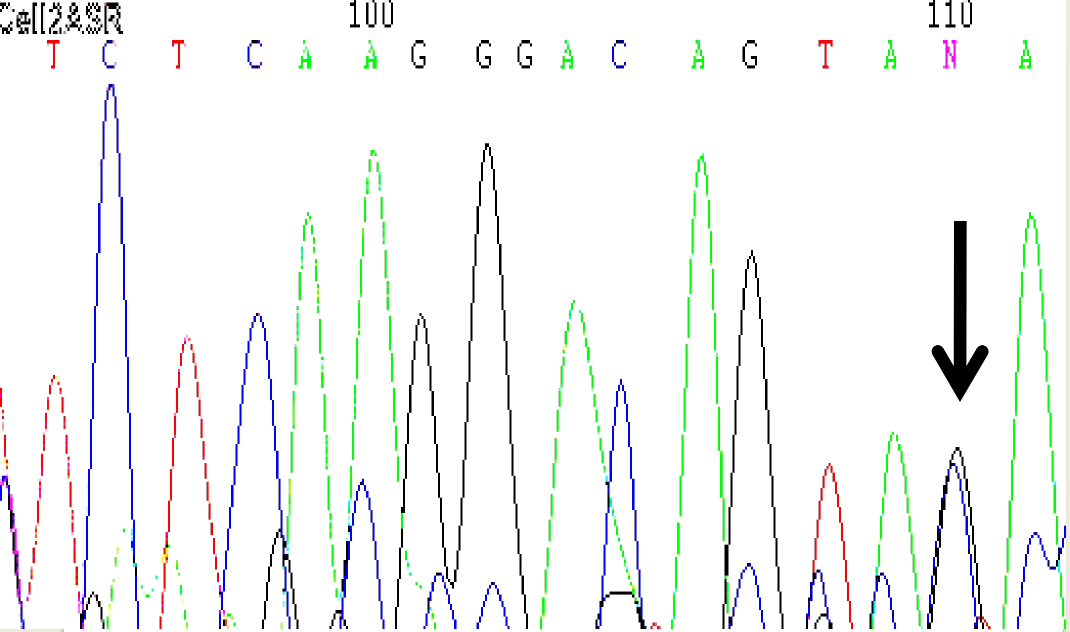
Most cultivated hybrids are 2n=3x=33

Musa balbisiana – B genome

Genome size c. 550 Mbp



Polymorphisms



SNP heterozygosity in cellulose synthase

Gene polymorphisms:
Heterozygosity
Intraspecific (population)
Interspecific

-Ploidy

-Transposable elements

-Microsatellites

- Satellite DNA sequences

-Gene sequences

5 ACE consensus sequence alignments with reference BAC sequence

```
                  0
BAC Ref MA4_64C22  CCATAGGGTTGAAGCTCCTGTTTCTAATATGAAAGTACCGATTATAATTT
Calcutta4          CCATAGGGTTGAAGCTCCTGTTTCTAATATGAAAGTACCGATTATAATTT
Mala Allele 1      CCATAGGGTTGAAGCTCCTGTTTCTAATATGAAAGTACCGATTATAATTT
Mala Allele 2      CCATAGGGTTGAAGCTCCTGTTTCTAATATGAAAGTACCGATTATAATTT
Pahang Allele 1    CCATAGGGTTGAAGCTCCTGTTTCTAATATGAAAGTACCAATTATAATTT
Pahang Allele 2    CCATAGGGTTGAAGCTCCTGTTTCTAATATGAAAGTACCGATTATAATTT
Pahang Doub Hap    CCATAGGGTTGAAGCTCCTGTTTCTAATATGAAAGTACCAATTATAATTT
                  51
MA4_64C22          CAGCTGTACAATAATTAAAGAAGAGCCTACCAATTCCTAGACCTTTGTGT
C410TF             CAGCTGTACAATAATTAAAGAAGAGCCTACCAATTCCTAGACCTTTGTGT
Mala05TF           CAGCTGTACAATAATTAAAGAAGAGCCTACCAATTCCTAGACCTTTGTGG
Mala allele2       CAGCTGTACAATAATTAAAGAAGAGCCTACCAATTCCTAGACCTTTGTGT
Pah06TR            CAGCTGTACAATAATTAAAGAAGAGCCAACCAATTCCTAGACCTTTGTGT
Pah19TR            CAGCTGTACAATAATTAAAGAAGAGCCTACCAATTCCTAGACCTTTGTGT
PDH07TF            CAGCTGTACAATAATTAAAGAAGAGCCAACCAATTCCTAGACCTTTGTGT
                 101
MA4_64C22          ACAGGCCCTTGTTCTCATGTCAATGCACAAAGGATGCACCTCAACACACA
C410TF             ACAGGCCCTTGTTCTCATGTCAATGCACAAAGGATGCACCTCAACACACA
Mala05TF           ACAGGCCCTTGTTCTCATGTCAATGCACAAAGGATGCACCTCAACACACA
Mala allele2       ACAGGCCCTTGTTCTCATGTCAATGCACAAAGGATGCACCTCAACACACA
Pah06TR            ACAGGCCCTTGTCCTCATGTCAATGCACAAAGGATGCACCTCAACACACA
Pah19TR            ACAGGCCCTTGTTCTCATGTCAATGCACAAAGGATGCACCTCAACACACA
PDH07TF            ACAGGCCCTTGTCCTCATGTCAATGCACAAAGGATGCACCTCAACACACA
                 151
MA4_64C22          CCAAACTCCAGTTGACTCATCTATACTTGGCCTAAATTGGACGGACTTGG
C410TF             CCAAACTCCAGTTGACTCATCTATACTTGGCCTAAATTGGACGGACTTGG
Mala05TF           CCAAACTCCAGTTGACTCATCTATACTTGGCCTAAATTGGACGGACTTGG
Mala allele2       CCAAACTCCAGTTGACTCATCTATACTTGGCCTAAATTGGACGGACTTGG
Pah06TR            CCAAACTCCAGTTGACTCAGCTATACTTGGCCTAAATTGGACAGACTTGG
Pah19TR            CCAAACTCCAGTTGACTCATCTATACTTGGCCTAAATTGGACGGACTTGG
PDH07TF            CCAAACTCCAGTTGACTCAGCTATACTTGGCCTAAATTGGACAGACTTGG
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MA4_64C22          TAGGACTTGACCTAATTTGGTCAAGCTGGGACAAATTGACCAATTCCAAC
C410TF             TAGGACTTGACCTAATTTGGTCAAGCTGGGACAAATTGACCAATTCCAAC
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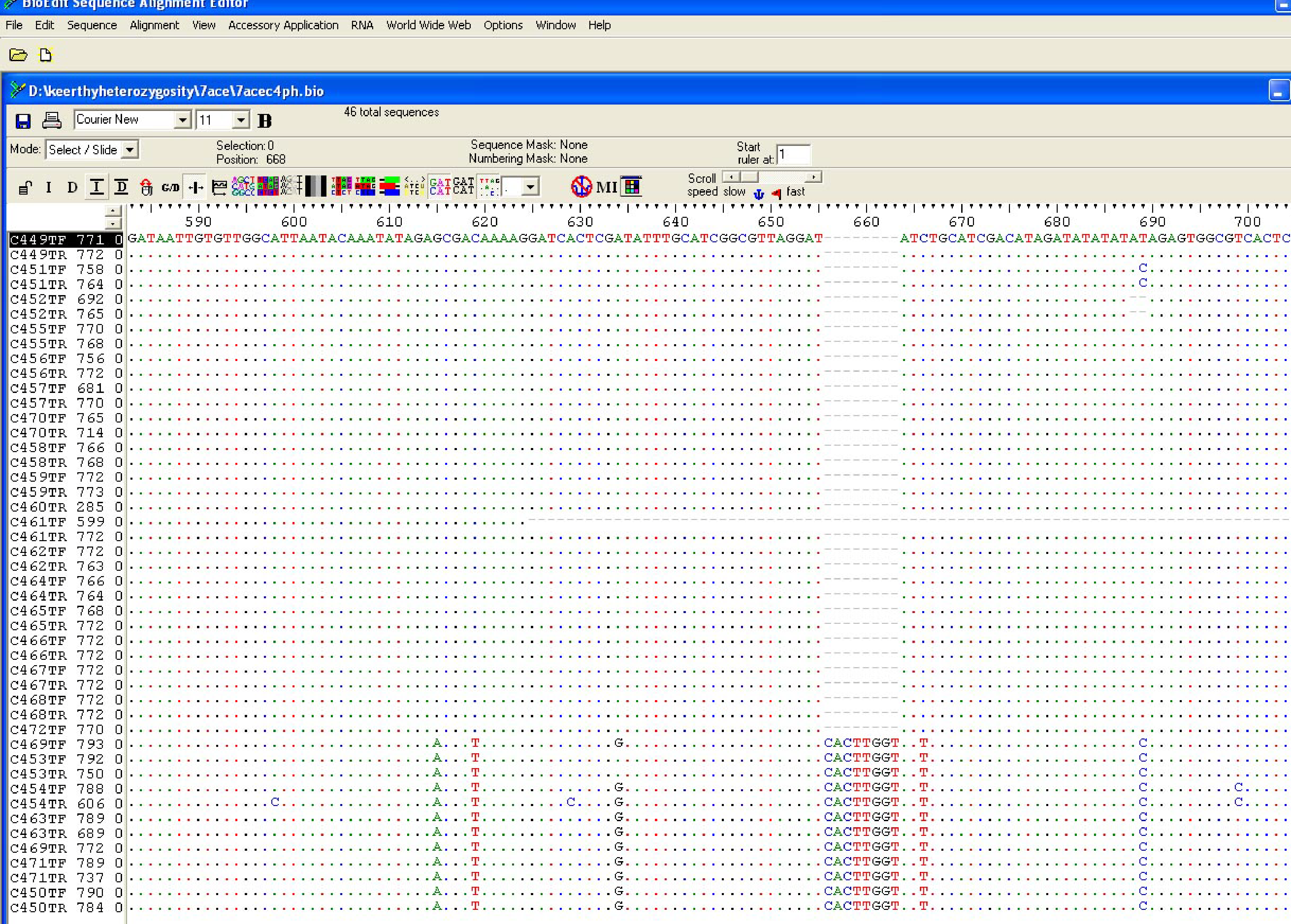

D:\keerthyheterozygosity\7ace\7acec4ph.bio

46 total sequences

Courier New 11

Mode: Select / Slide

Selection: 0
Position: 668

Sequence Mask: None
Numbering Mask: None

Start ruler at: 1

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                 590       600       610       620       630       640       650       660       670       680       690       700
C449TF 771 0 GATAATTGTGTTGGCATTAATACAAATATAGAGCGACAAAAGGATCACTCGATATTTGCATCGGCGTTAGGAT--------ATCTGCATCGACATAGATATATATATAGAGTGGCGTCACTC
C449TR 772 0 .........................................................................--------.........................................
C451TF 758 0 .........................................................................--------.........................C...............
C451TR 764 0 .........................................................................--------.........................C...............
C452TF 692 0 .........................................................................--------........................--...............
C452TR 765 0 .........................................................................--------........................--...............
C455TF 770 0 .........................................................................--------.........................................
C455TR 768 0 .........................................................................--------.........................................
C456TF 756 0 .........................................................................--------.........................................
C456TR 772 0 .........................................................................--------.........................................
C457TF 681 0 .........................................................................--------.........................................
C457TR 770 0 .........................................................................--------.........................................
C470TF 765 0 .........................................................................--------.........................................
C470TR 714 0 .........................................................................--------.........................................
C458TF 766 0 .........................................................................--------.........................................
C458TR 768 0 .........................................................................--------.........................................
C459TF 772 0 .........................................................................--------.........................................
C459TR 773 0 .........................................................................--------.........................................
C460TR 285 0 .........................................................................--------.........................................
C461TF 599 0 .........................................---------------------------------------------------------------------------------
C461TR 772 0 .........................................................................--------.........................................
C462TF 772 0 .........................................................................--------.........................................
C462TR 763 0 .........................................................................--------.........................................
C464TF 766 0 .........................................................................--------.........................................
C464TR 764 0 .........................................................................--------.........................................
C465TF 768 0 .........................................................................--------.........................................
C465TR 772 0 .........................................................................--------.........................................
C466TF 772 0 .........................................................................--------.........................................
C466TR 772 0 .........................................................................--------.........................................
C467TF 772 0 .........................................................................--------.........................................
C467TR 772 0 .........................................................................--------.........................................
C468TF 772 0 .........................................................................--------.........................................
C468TR 772 0 .........................................................................--------.........................................
C472TF 770 0 .........................................................................--------.........................................
C469TF 793 0 ................................A...T..............G.....................CACTTGGT..T......................C...............
C453TF 792 0 ................................A...T....................................CACTTGGT..T......................C...............
C453TR 750 0 ................................A...T....................................CACTTGGT..T......................C...............
C454TF 788 0 ................................A...T..............G.....................CACTTGGT..T......................C.........C.....
C454TR 606 0 ...............C................A...T.........C....G.....................CACTTGGT..T......................C.........C.....
C463TF 789 0 ................................A...T..............G.....................CACTTGGT..T......................C...............
C463TR 689 0 ................................A...T..............G.....................CACTTGGT..T......................C...............
C469TR 772 0 ................................A...T..............G.....................CACTTGGT..T......................C...............
C471TF 789 0 ................................A...T..............G.....................CACTTGGT..T......................C...............
C471TR 737 0 ................................A...T..............G.....................CACTTGGT..T......................C...............
C450TF 790 0 ................................A...T..............G.....................CACTTGGT..T......................C...............
C450TR 784 0 ................................A...T..............G.....................CACTTGGT..T......................C...............
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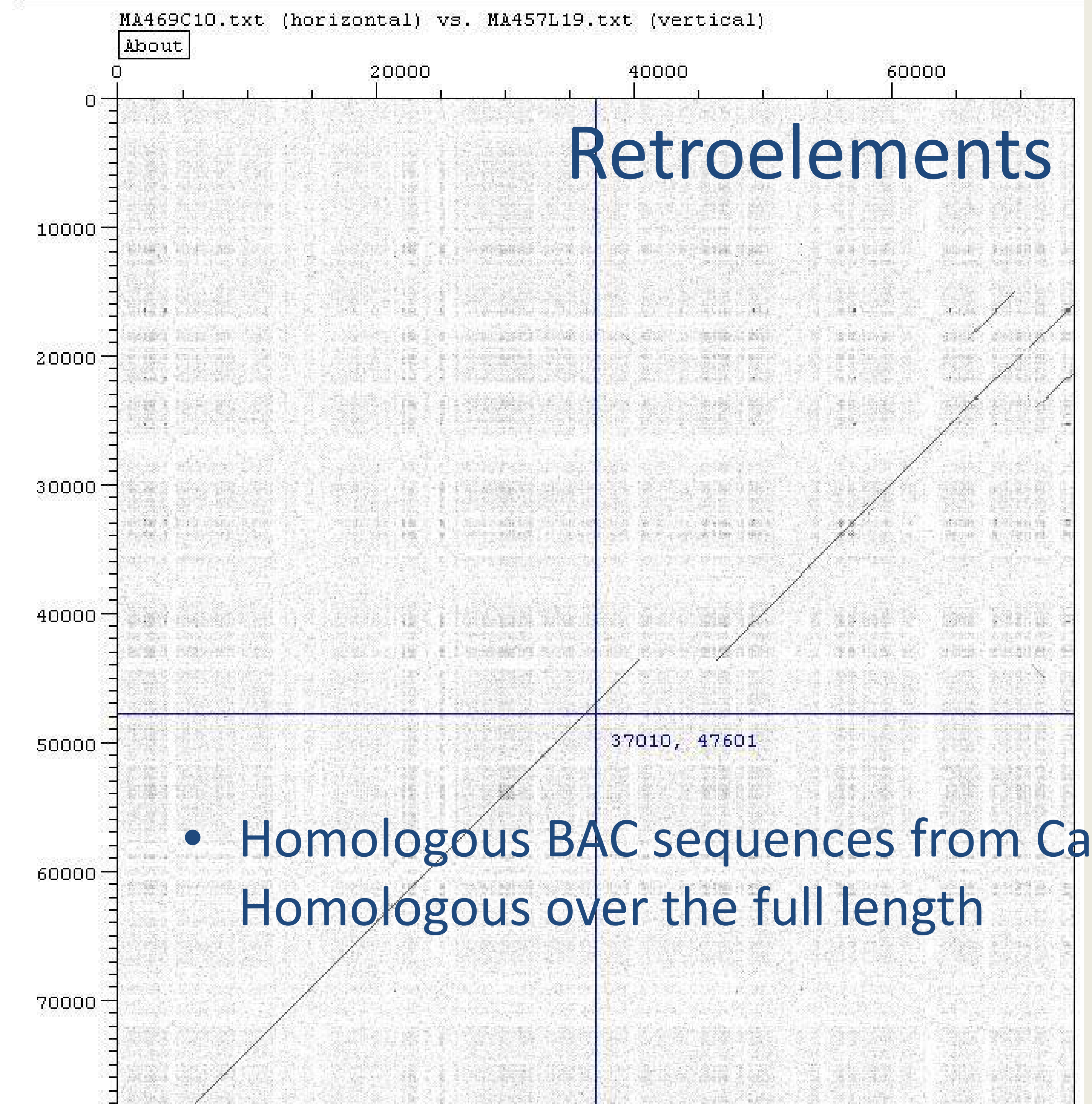
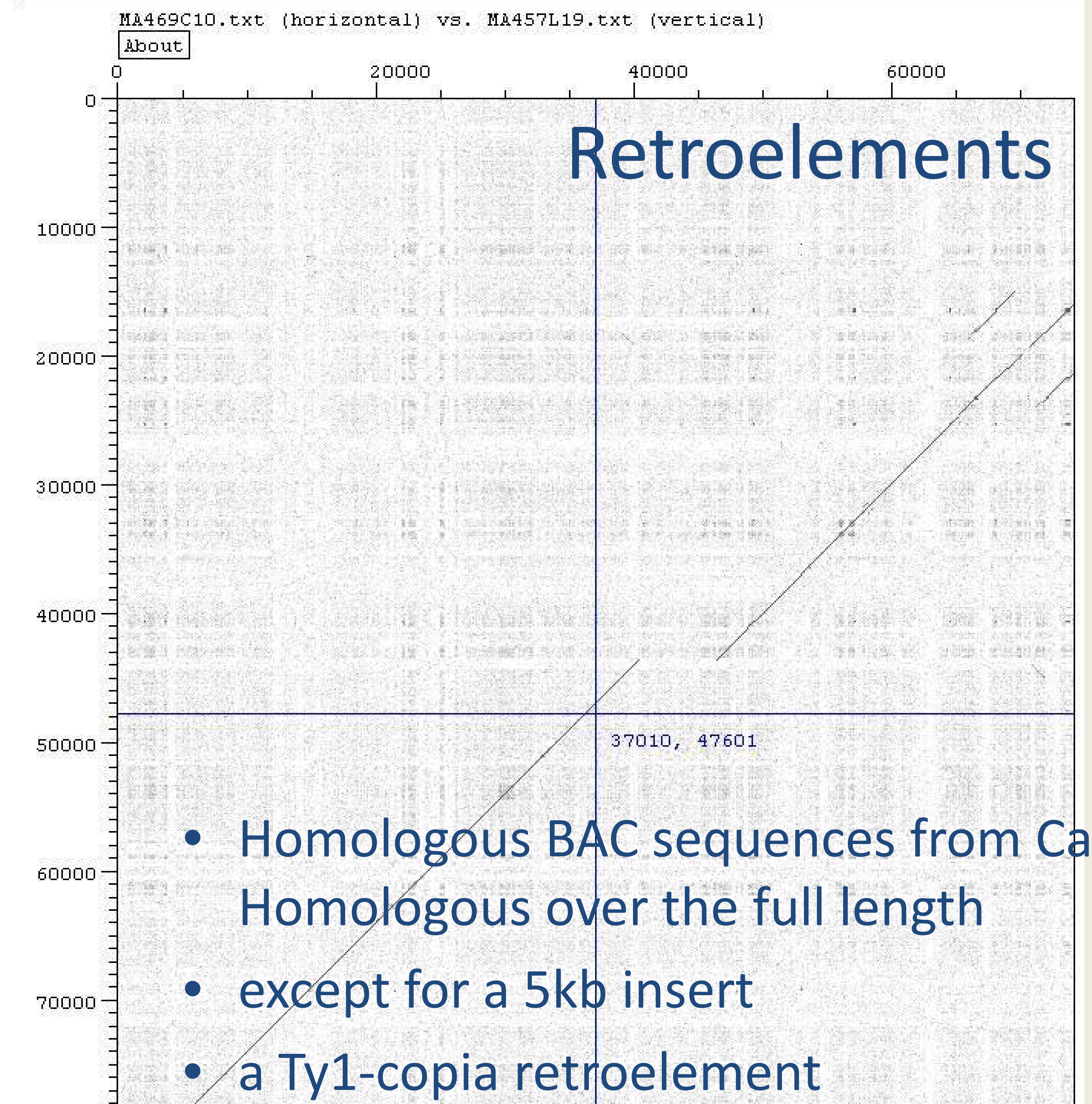
Collaborations: Chris Town, Foo Cheung JVCI; Angelique d'Hont, Isabel Hippolyte CIRAD; Nicolas Roux Bioversity

Retroelements



- Homologous BAC sequences from Calcutta 4
Homologous over the full length

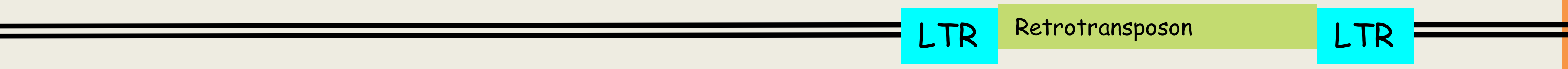
Retroelements



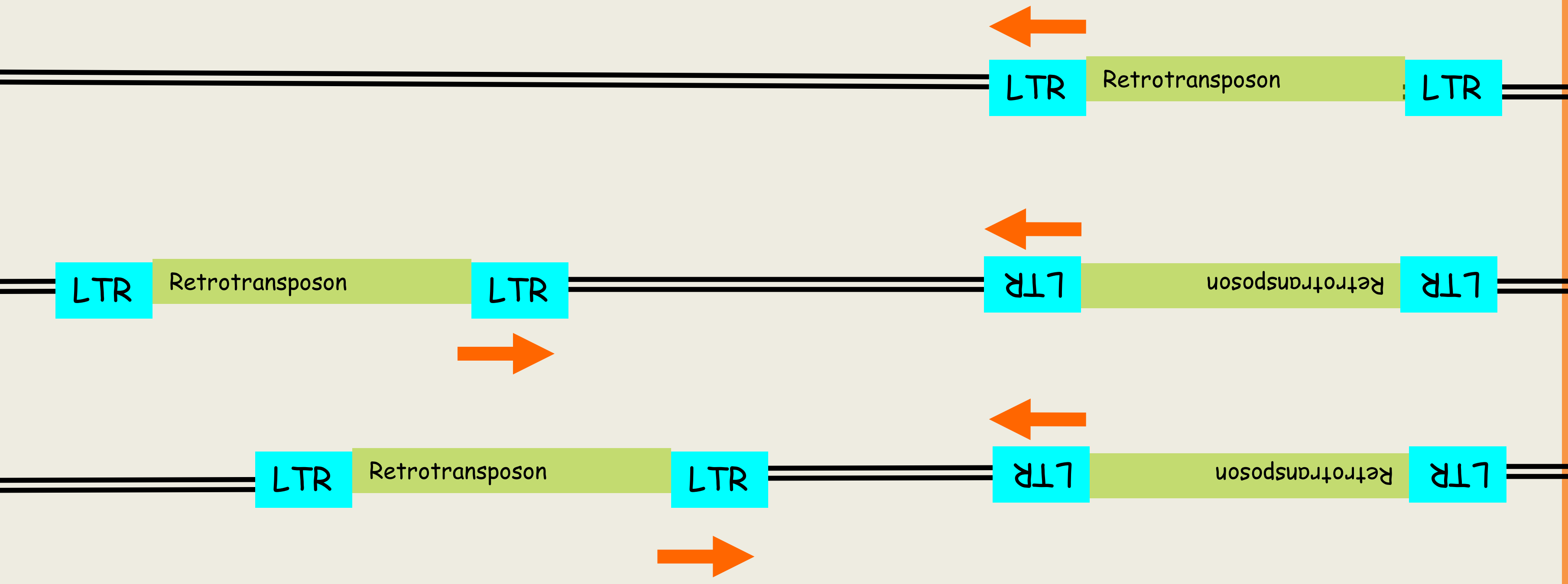
- Homologous BAC sequences from Calcutta 4
  Homologous over the full length
- except for a 5kb insert
- a Ty1-copia retroelement

Retroelement Markers

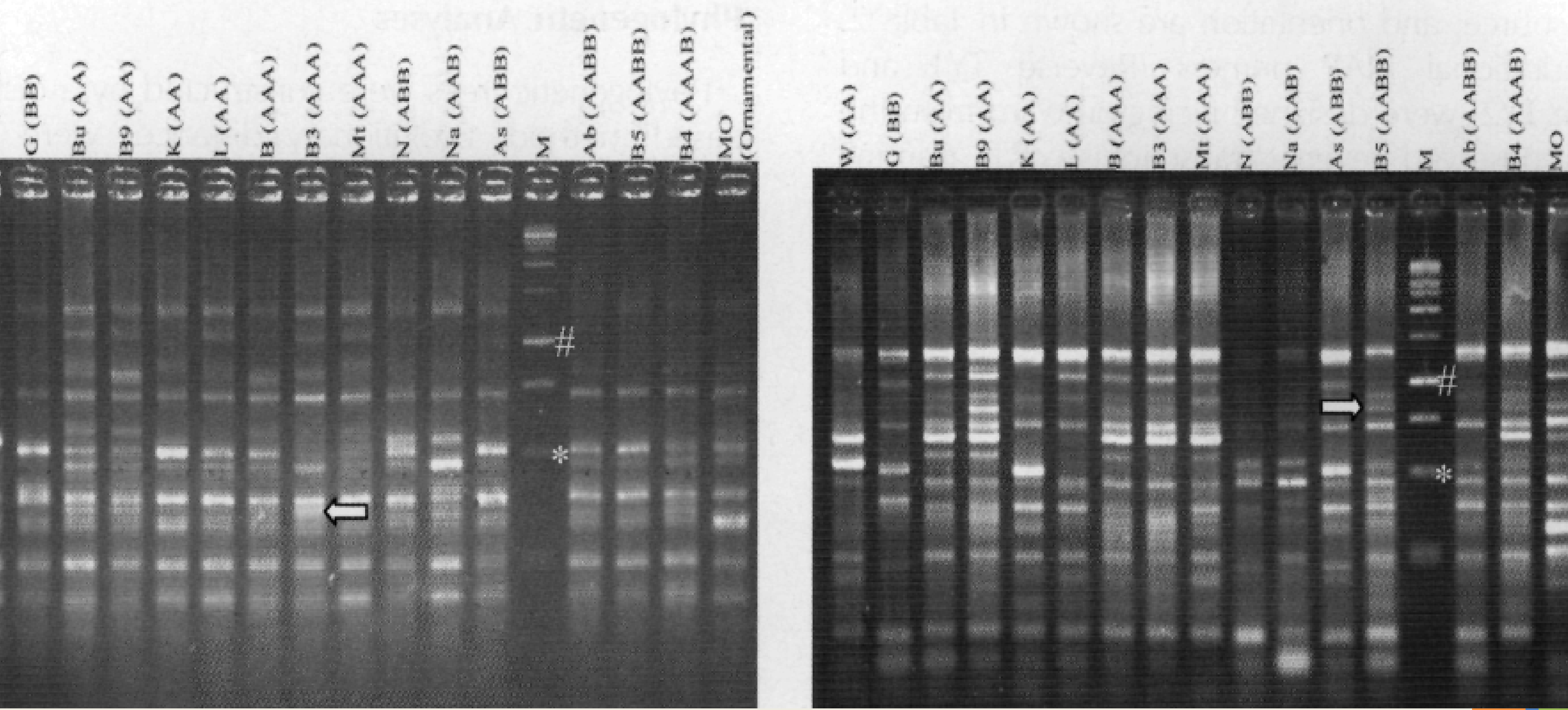
Insertion



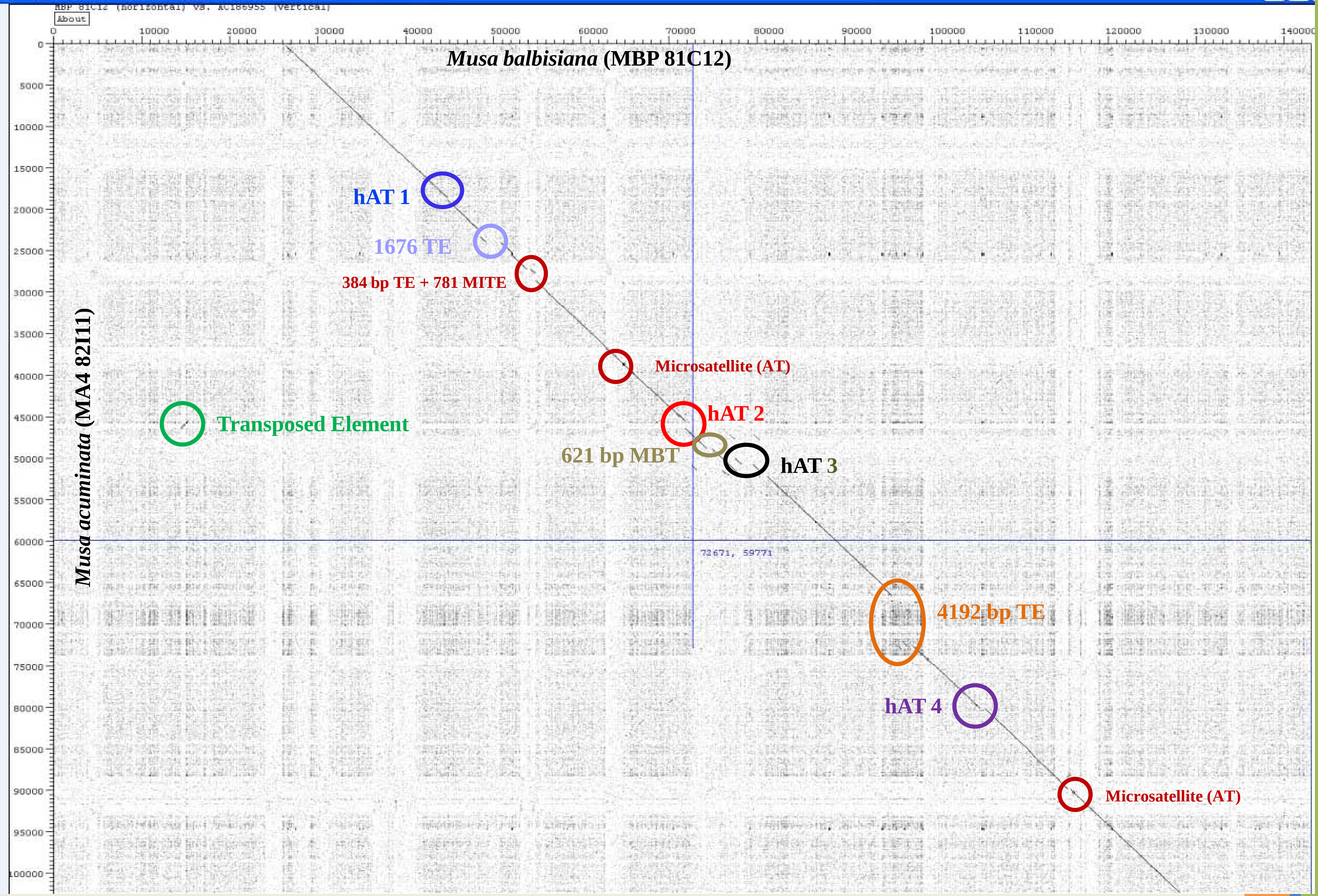
IRAP - InterRetroelement PCR



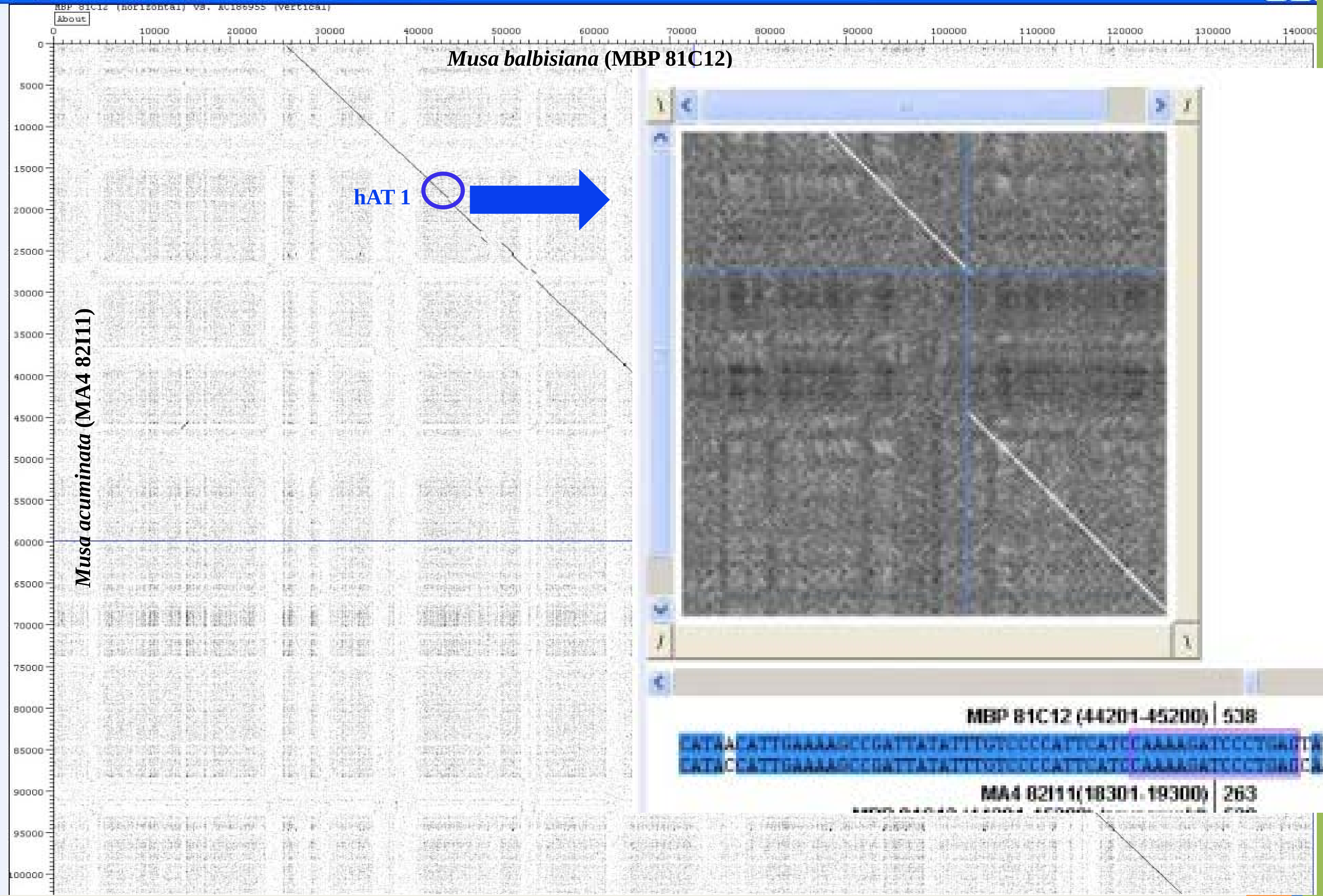
IRAP diversity in Musa



Teo, Tan, Ho, Faridah, Othman, HH, Kalendar, Schulman 2005 *J Plant Biol*
Nair, Teo, Schwarzacher, HH 2006 Euphytica
Desai, Maha..., HH et al. in prep.



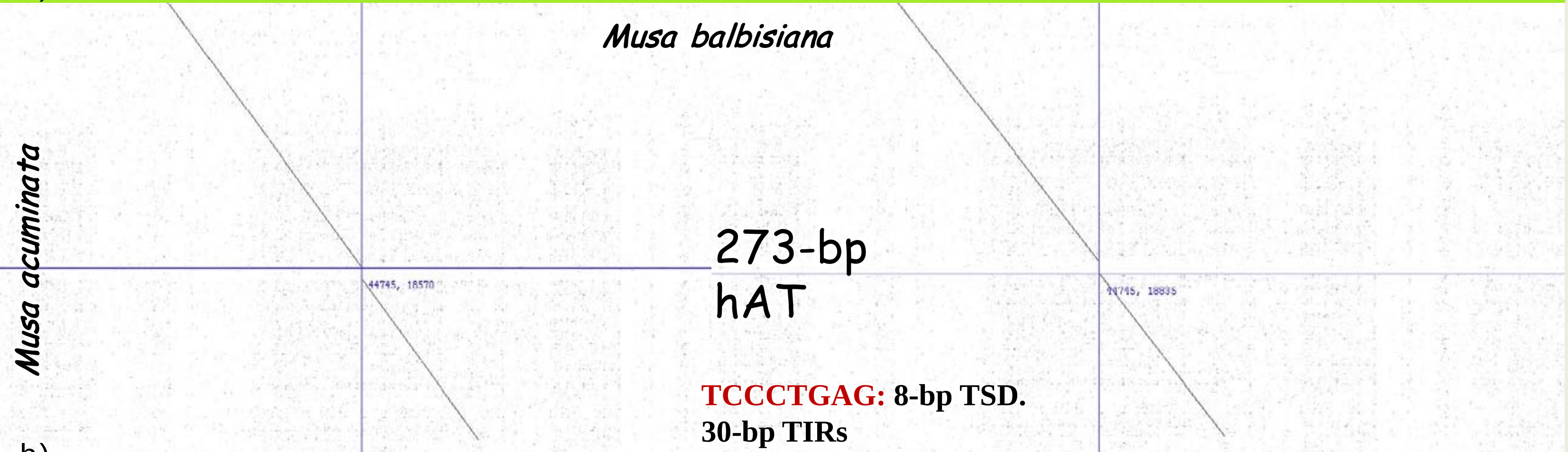
MBP 81C12 (*M. balbisiana*) x MA4 82I11 (*M. acuminata*) BACs.



MBP 81C12 (*M. balbisiana*) x MA4 82I11 (*M. acuminata*) BACs.

ACCCACCTGGCTCTTGTGTCATACCATTGAAAAGCCGATTATATTTGTCCCCATTCATCCAAAAG
A**TCCCTGAG**CAAGGTCTGCCATACCGTACCGTACCGGCGTTTCGACCCGGGCTCGGTACGGT
ACCGGTGTACCGGGCAGTACATCAGGGTGTACCGAATGGTACACCCTGATGTACCGAACAATTT
TATACTTTTTCATACTGTAGCAGTGCTACAGTATAATACTGTAGCACTGTAGCGGTATCGGGCGGT
CCGCGTACCGGTAACCTGTCGGACCGGTACATACCGCCCGGTATCGGCGGTACGCTTCGGTAT
GACAGACCTTG**TCCCTGAG**TATATATCTCTTTTCTAAATTTATGACCACTCCAAGGCAACTTGCC
AAAGAAAATGAAAAGAAGAAAAAAATTAGGGGAATGAAGATTCTCCACAATTCCTTATTCTTT
GATTTGAGATAAATAATGTCCATAGTAAAACATATCTTATGATCATCATTGCTGATTAATCAAAAT
ACCTGATTCTATAGTCTCAAGCTTTAGTGGTCAAAACACATTCGC

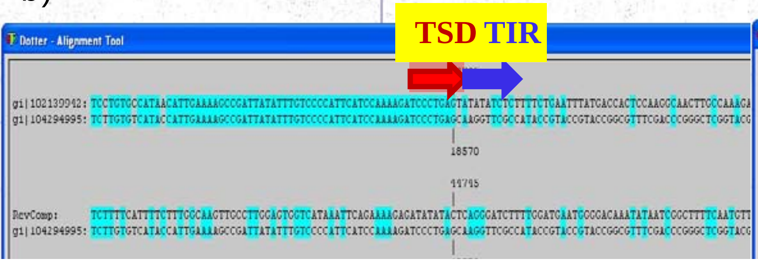
a)

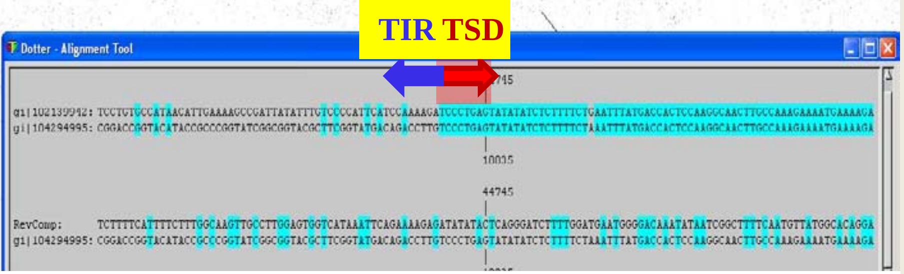


273-bp
hAT

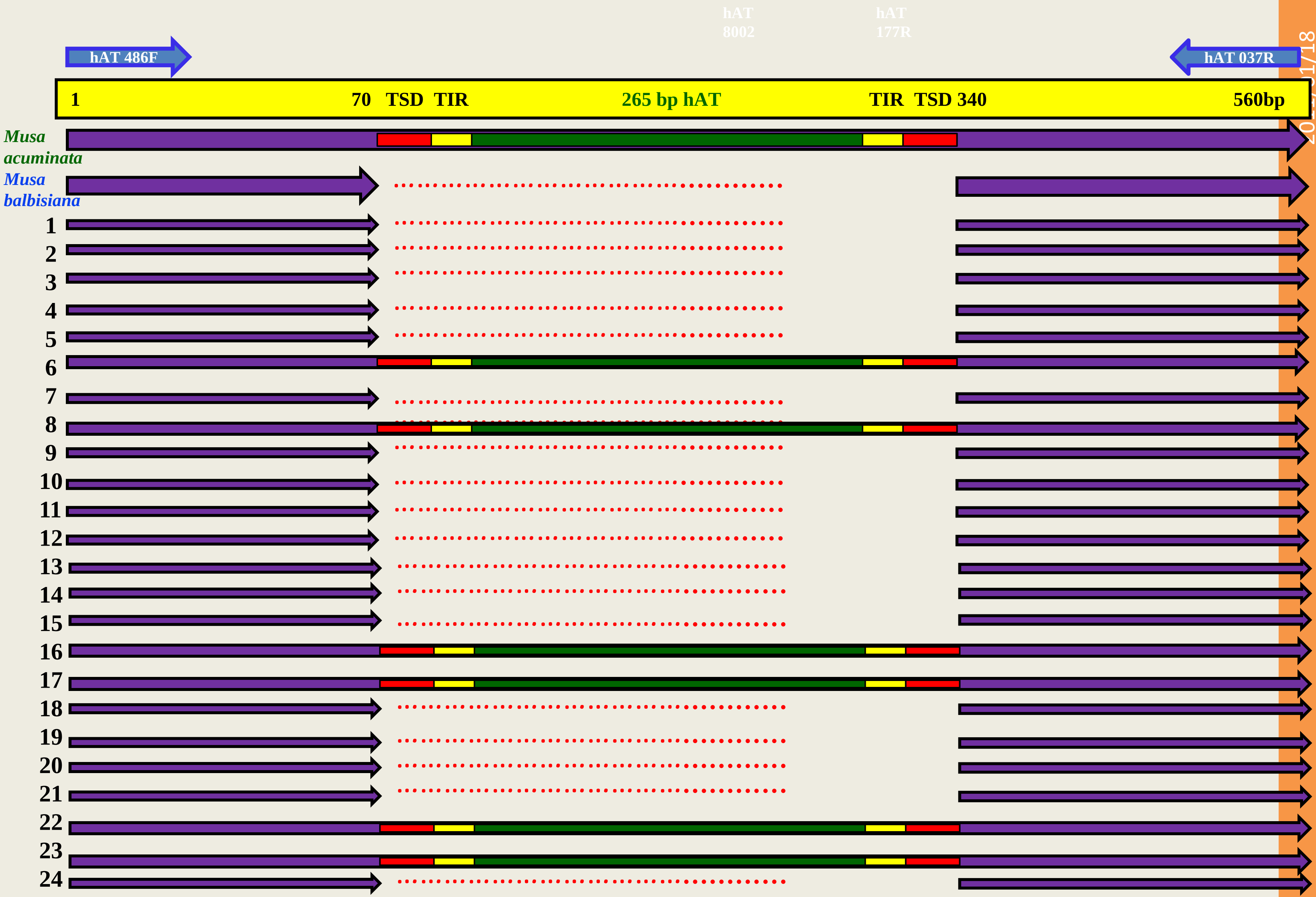
TCCCTGAG: 8-bp TSD.
30-bp TIRs

b)

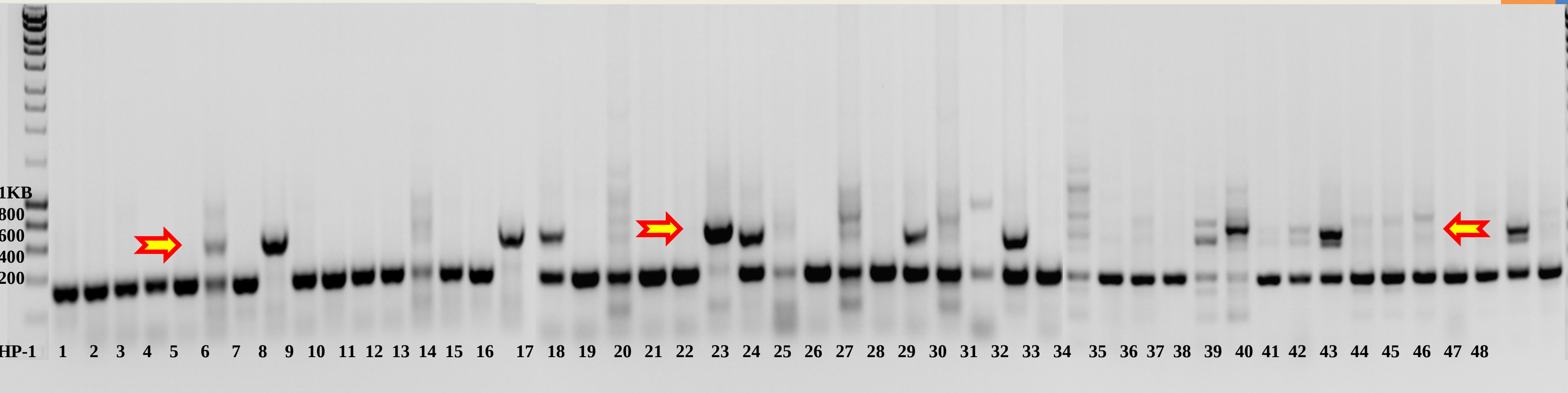


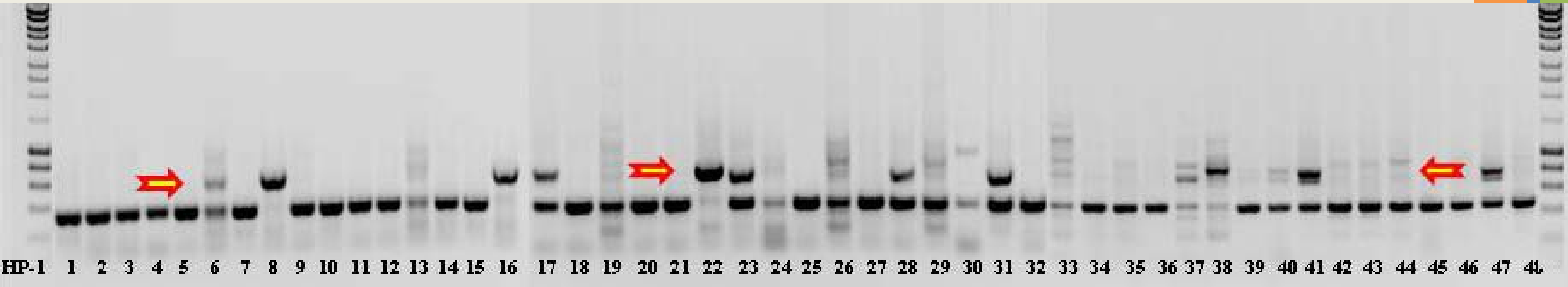


hAT1 in *Musa acuminata*
F and R primers indicated by blue arrows in sequence



The hAT1 **insertion sites in *Musa with* hAT486F and hAT037R in: 6) *acuminata,* 8) *acuminata,* 16) *acuminata,* 17) AAB, 22) *acuminata,* 23) AB cv.**

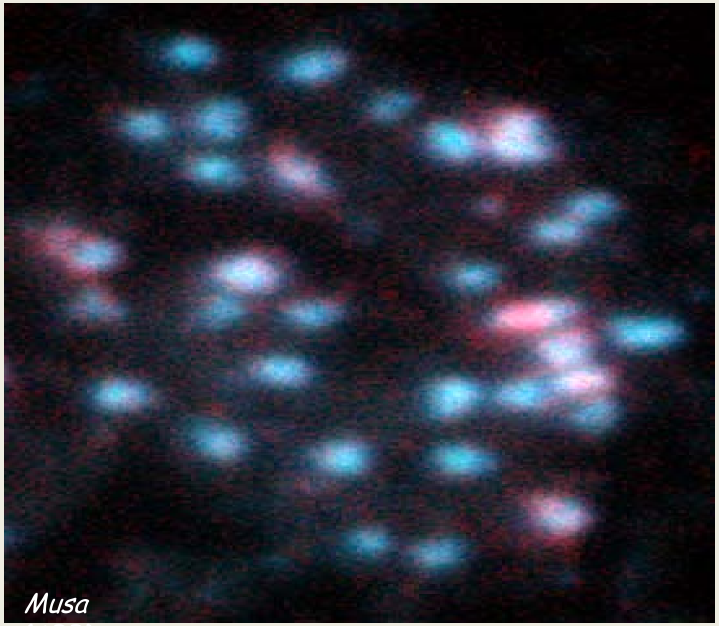


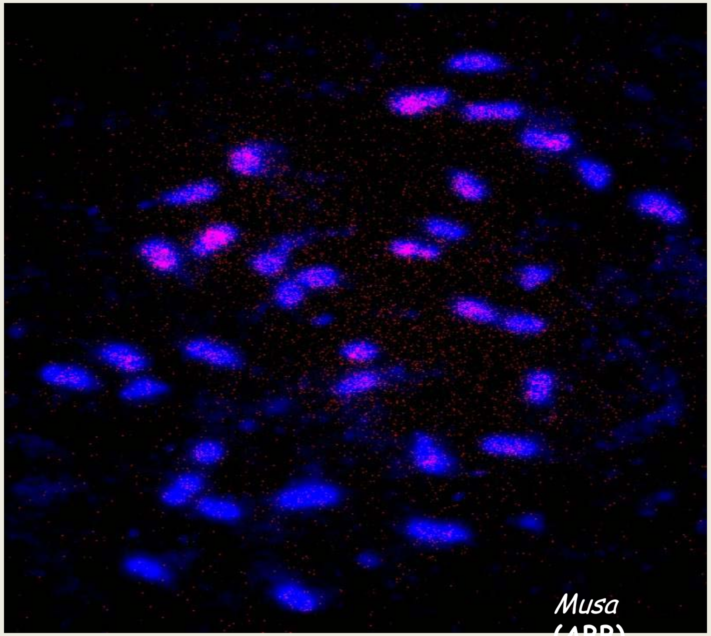


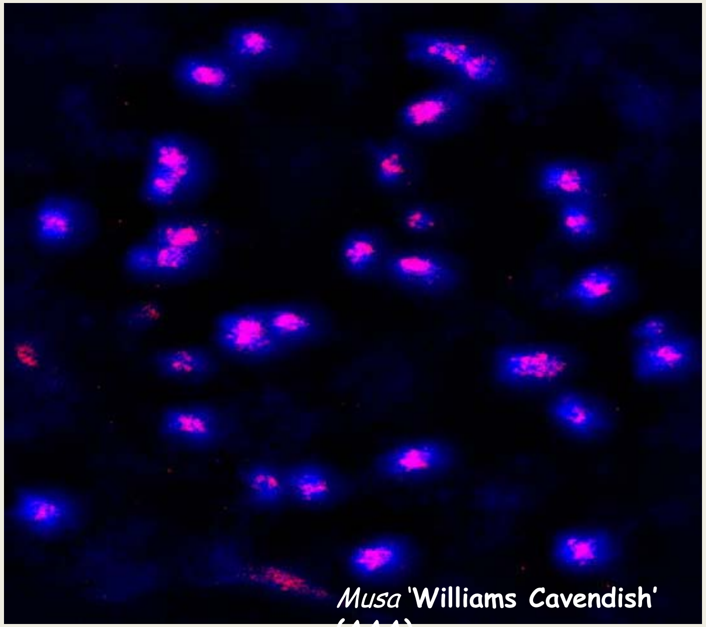
***hAT1* insertion sites in *Musa* diversity collection**

hAT486F and hAT037R

Top bands (560-bp) amplified hAT element and lower bands amplifying the flanking sequences only


Musa (ABB)

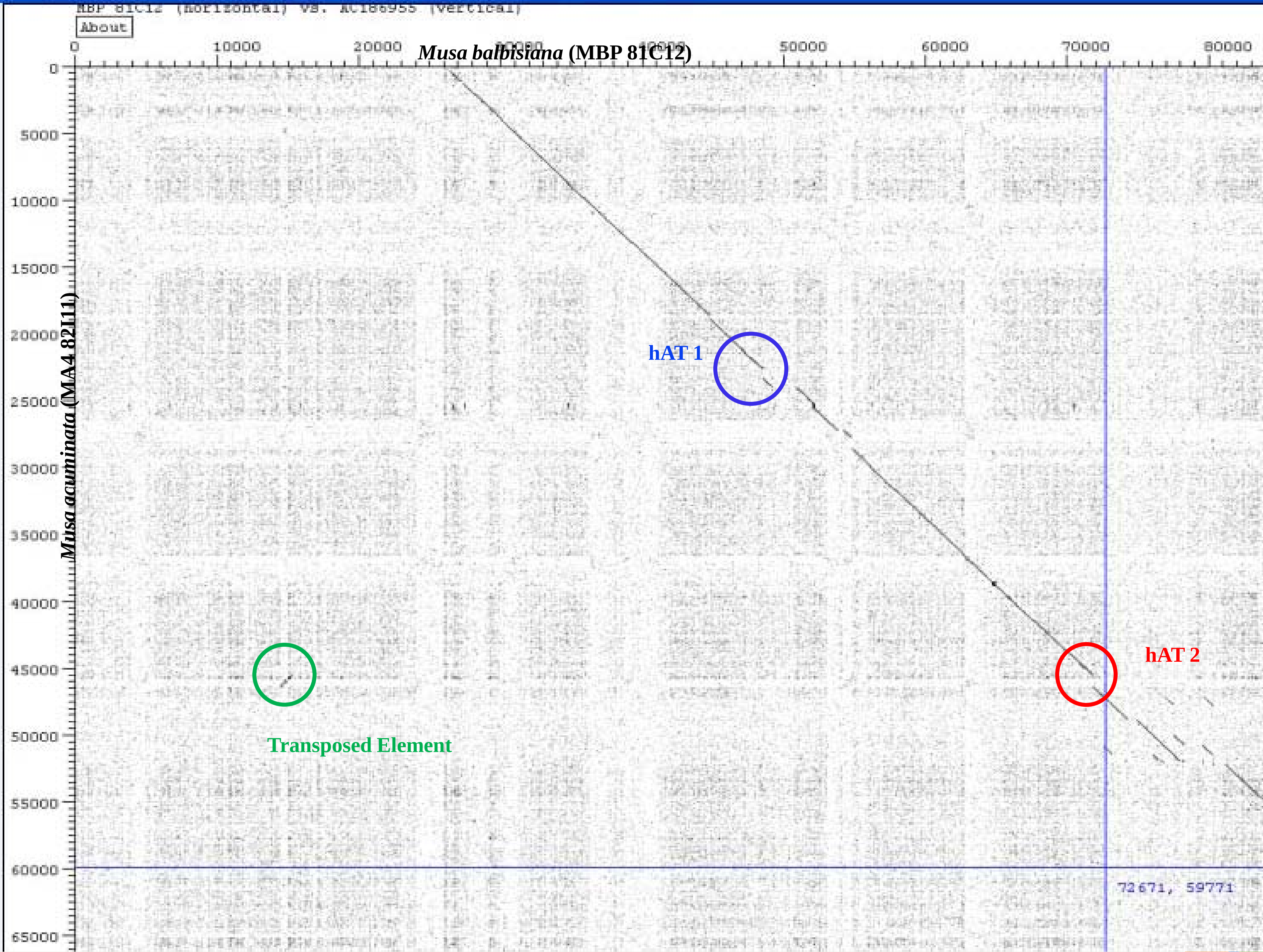

Musa (ABB)

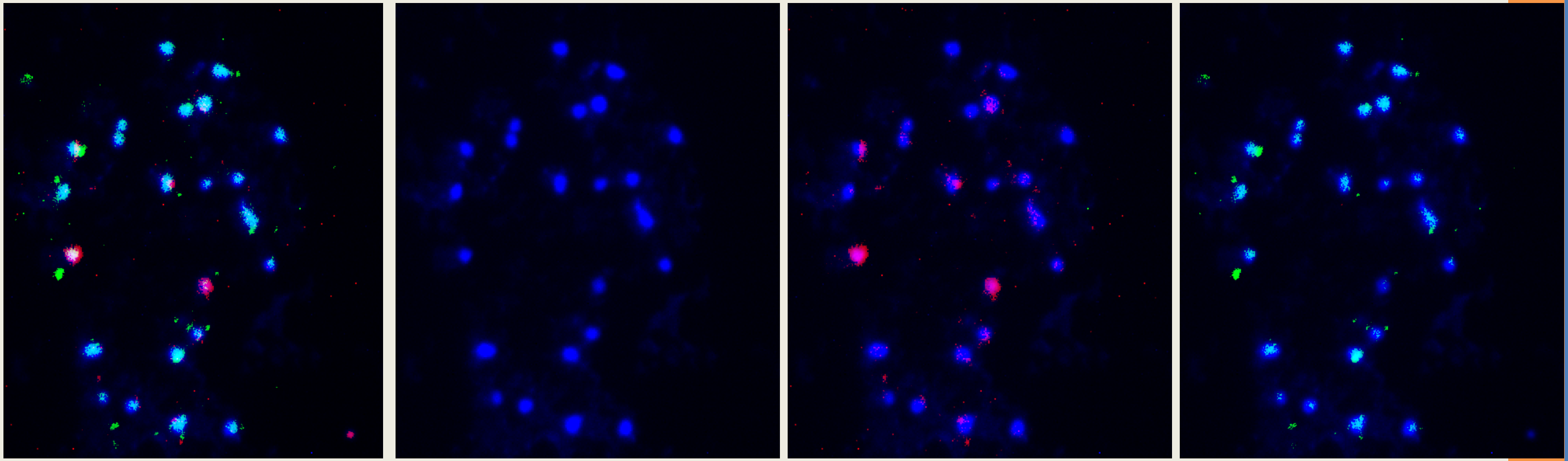

Musa 'Williams Cavendish' (AAA)

A-genome specific hAT in three *Musa* hybrids (2n=3x=33)

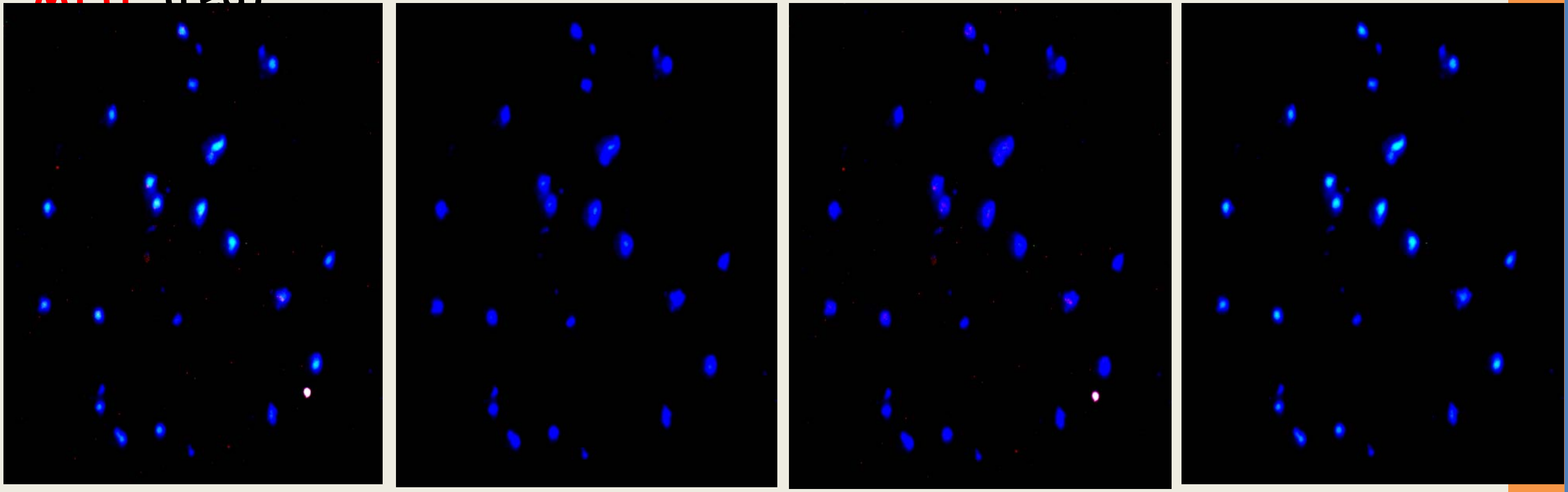
ACTCCTTGTGTTTATAGGTTAATATTTTGATCATACCTAGGTGGATGGTGCACAATAATAGGGTTTGTTTATGACTTGATTTGTTG
AGTGATGTTGCACATACTTTATATAAGCTAACTCAT**GGTAGTCATTATTCATGCCATC**ATTGCTTAATATTTATTCATGTTATATG
ACAATTCCATCTAGTTATATCATGTCATTGACTTGTTTTGG**T**A**GTG**C**TA***ACC**AGTGATTTaAAaAG***CGCTAAGCGCCAAGCGGCA
AAATGCGTCAAGGTCAAAAAACGCCCGAGGCGCTAGGCGCTCGCCCAAGCGAAGCGAGACGCTAAAATATAAAAATATATAAT
ATAATTAATAAATATAATTATTTAAATAAAAAATATGCTATTAAATAAATAAAATTTAATGGTATTAAAATCAAAATAATATATTATT
AATCTAATAAATAAAAATATTATTATTAGTATATAGTTAGAAGTATACTGTTAACAGTATAATGAGAAGAGTGTGAGAAGACCGA
GGCTGCTGTGGCAACGACAGCGGTAGCAGGTGGCAGTCATAGCTGGAGCGAGAGCAGCGAGCGACGGCAATAACGAGAGCA
ACGACGACAGCGGGAGCGGGAGCTGCGAGTGGTAGCGGGAGCGGCGATAACAGCGACGAGTGACGACAACAACGACGAGC
GACGATTATGGCAGCGGCGAGCAGCGATTGTGGCAGTGGCGAGCAGCGACAATAGTGGCGAGCAGCGACAGTGGCAACGAC
AACGGAGAAGAAATCTCGGCGGCAAAATCGTGAGTGTTAGGGTTGGGGAAGTCGGGGAAATCGCGAGAGAGAGCCTGATAT
CGGTGATTTAGATGGTTCGATTGAACCAACTAAAGCATTGGAGACCAACCAGACCTAAAAATCTGGTTCGGTCGCCTGGTTTA
ACCCGGGCGCTCGCCCGAAGCGCCCGACGCCTGGGCTCGGGCGAGCGCCTAGGCGGTGCCCTCTTTGAAGCGAGGCGCCTG
GACATGAAGCGAGGCGCTCGGGCCTCGTCTCGCCTCGCCCGAGCGCCTAGGCGGGCACCCGAGTGC***CTaTTgAAATCACTGGT***
GTTAGCCCCCTAAAAGGCATATGATAACCATCTAGAAGTTCATATGCATGA***CACTCCTTACTGGACGGTAACC***AAGTGGCAATT
ATTAACCACAACCATTCTTTATTTCTTAAAGATTTAGATAAATTGTTTGAAAAATAAGATAGGTATTTTATTTCGATATAATTCATG
GTCCTAAATAGAGCTCAATAGCATGAAAAGAATAACTGATACCATGGCATGTTGTTTTTGTACGATTTGTATTTGC

hAT2 in *Musa acuminata* with TSD, TIRs and forward and reverse primers. Primers indicated by blue arrows, 6-bp TSD with red bold and TIR with blue *italic.* Subterminal inverted repeats and direct repeats highlighted by colours.


MBP 81C12 (horizontal) vs. AC186955 (vertical)
About
Musa balbisiana (MBP 81C12)
Musa acuminata (MA4 82I11)
0
10000
20000
30000
40000
50000
60000
70000
80000
0
5000
10000
15000
20000
25000
30000
35000
40000
45000
50000
55000
60000
65000
hAT 1
hAT 2
Transposed Element
72671, 59771



Musa acuminata “malaccensis” (AA: 2n=22) with hAT2 (green) and 781bp MITE (red)



Musa textilis with hAT1 (green) and hAT3 (red) showing the of A genome specific Tes signals (green), but no B genome signals.

CTCAACAACAACGGCAGAGAGTAGCTGGGAGCCAAAAGATGT***GTTGCAAC***CAAGGTCTGCATACCGAATCATACCGCTTGGTATGGGCGGTACGTA
CCGGTCCAACAGGCTCCCGGGCGGTACGTCCAAAAACCCCCCGTATCAGACAATACGGGGTAATATCGGGCGGTAACGGTCGAAATTTCGATCGTTA
CCACCCGGCACCACTCGATAACGGTTGAAATCGACCATTATCGCACTGTAGCAGTGCTACAGTGCTCCAACGGTCAATTTAATCGTTGGAGCCCTTT
CTCCTCCTATTTAAACCATTCTTCTCTCCCCTATTTCATTATACTCTCTTAAACTCTCTCTCAAACTTTTTTTTTCTCTCCTAAACTCTATAAAACA
ACGATTTGTAAATTCAATCGAGGCTAATTTGGGAAGATTAAGAGGAAGAACTTTCTAATCAAGAGGTATGTATTCGTTTTCTTTAATTAGAGAGTAA
TTAAGATTTTACACATGTCACTCAAGATTCAGATCATGGAACTCGACAAAGTACTAGTCAAGTTTATGCGTGGAAGGGGAAGGCAGTGGATGAATAT
GAACAAATGCGACAGAGCATACATGATATAGACACAGAAAGAGGCTCATCGTATTCACAACCATCGTATTATGGAGAATTATACGAGCAACAACAAT
ATGGTGATAGATGGTCATCCTTCTCTGAGCAACAACATGATACAGAATAGCACCAATATATGCCTCAAGAGCTGCCTCGGATAAATATGATTCATGA
CGATCAATCTACGATCAGCACCACATTGATGTATCAATGGCATACGGTGTATCAATACACTATGTCATGTGATCAATTTCATGATTGAGTCTAACAA
ACGTATCATATTGATATGTATCGAATCGAGGACCCAGATCCACCACCCGTGGAGGCTCGTCGTTCGTTTTGGTGGTAGAATCAACAATCAGGTATAT
CTAGATATGTGATTATTTAATTCATTTGAATTTTAGAGTTTATATTGTAACAAAATAGTCTAACAATTCAACTGATTTTTCTGTAGATATTTCAATA
TATAACGGGCTGAAATACGAACCTCGAACAAGACTACCTCAAAGCCCGAAAAAGATATATGATACTATTCTTACCTAATTTACATTGATTTTGCTAA
ACTTATACTATTACTATATTTATTTGTAACTTGAAAATCCTATCCTAACTTTTTTTTTATTTTCAGGTTCGGAGGGTTAAATCGATGAAATCAGGTG
TACCGCTCGGTACACCGTAACGAGCCCGGGTCGAAACGCCGATACGGTATGGTACGGCGAACCTTG***GTTGCAAC***TAAAGCAGAAGATTAAAGATTC
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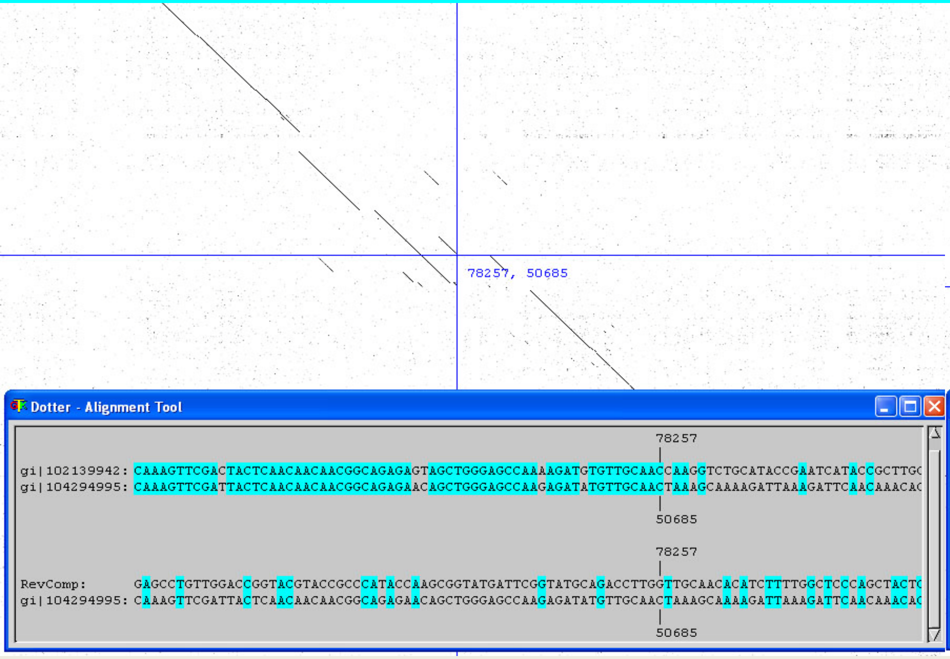

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                                                                            78257
                                                                              |
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gi|104294995: CAAAGTTCGATTACTCAACAACAACGGCAGAGAACAGCTGGGAGCCAAGAGATATGTTGCAACTAAAGCAAAAGATTAAAGATTCAACAAACAC
                                                                              |
                                                                            50685

                                                                            78257
                                                                              |
RevComp:      GAGCCTGTTGGACCGGTACGTACCGCCCATACCAAGCGGTATGATTCGGTATGCAGACCTTGGTTGCAACACATCTTTTGGCTCCCAGCTACTC
gi|104294995: CAAAGTTCGATTACTCAACAACAACGGCAGAGAACAGCTGGGAGCCAAGAGATATGTTGCAACTAAAGCAAAAGATTAAAGATTCAACAAACAC
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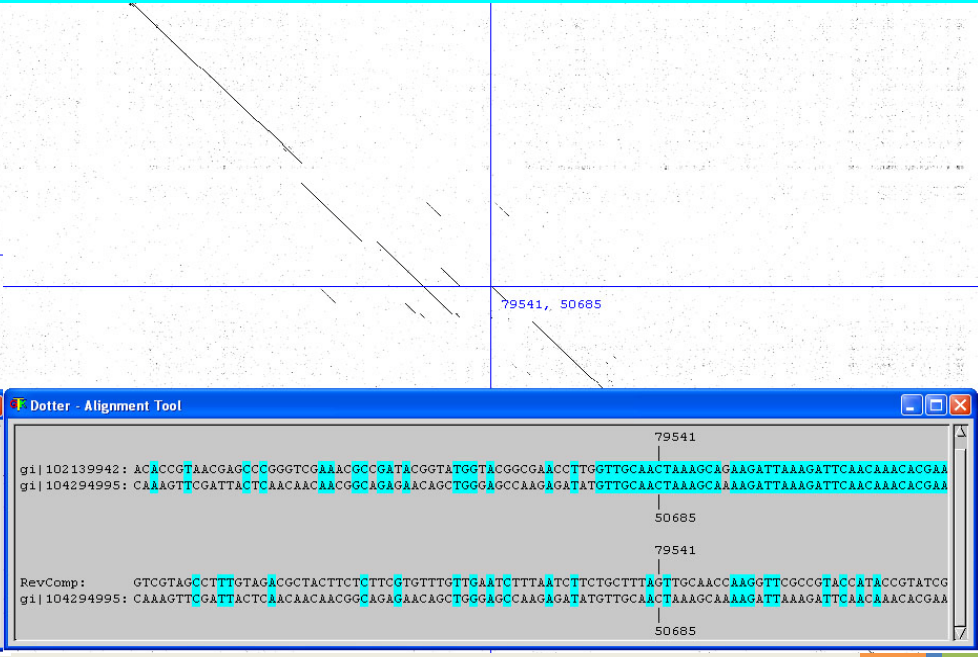

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                                                                            79541
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                                                                              |
                                                                            50685

                                                                            79541
                                                                              |
RevComp:      GTCGTAGCCTTTGTAGACGCTACTTCTCTTCGTGTTTGTTGAATCTTTAATCTTCTGCTTTAGTTGCAACCAAGGTTCGCCGTACCATACCGTATCG
gi|104294995: CAAAGTTCGATTACTCAACAACAACGGCAGAGAACAGCTGGGAGCCAAGAGATATGTTGCAACTAAAGCAAAAGATTAAAGATTCAACAAACACGAA
                                                                              |
                                                                            50685
```
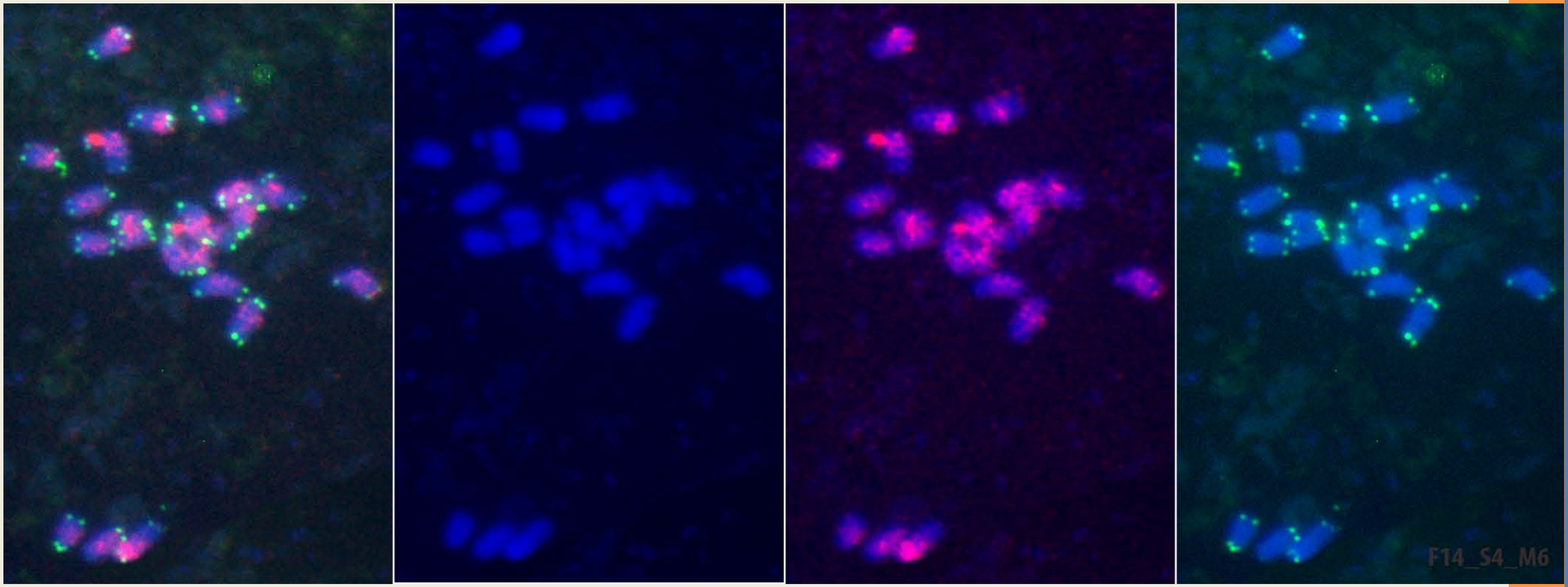
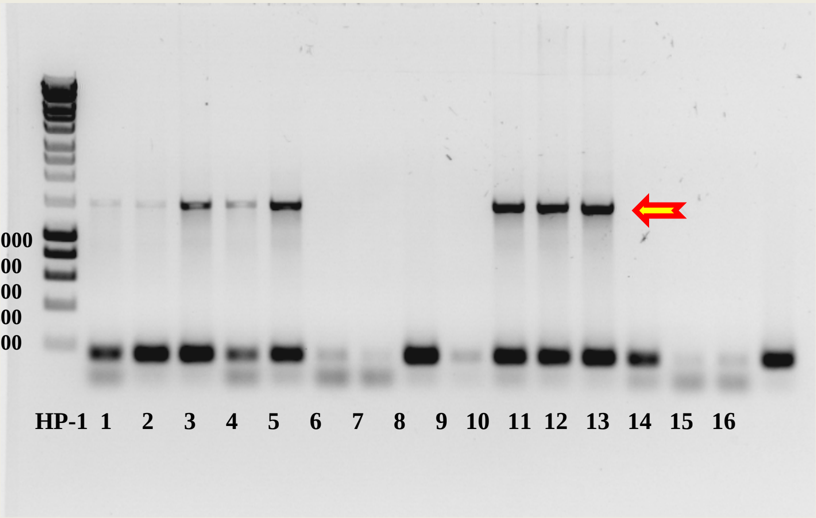
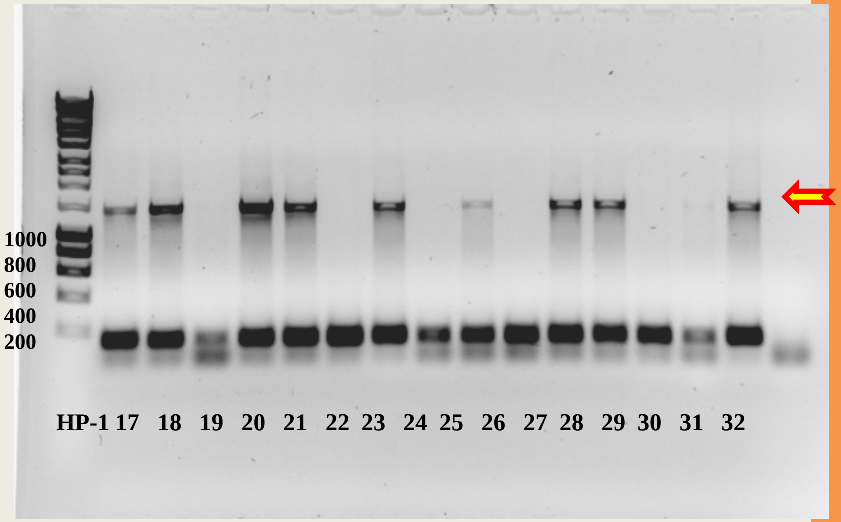

1292 bp : 8 bp TSD. Present in *Musa balbisiana* and absent in *Musa acuminata*.

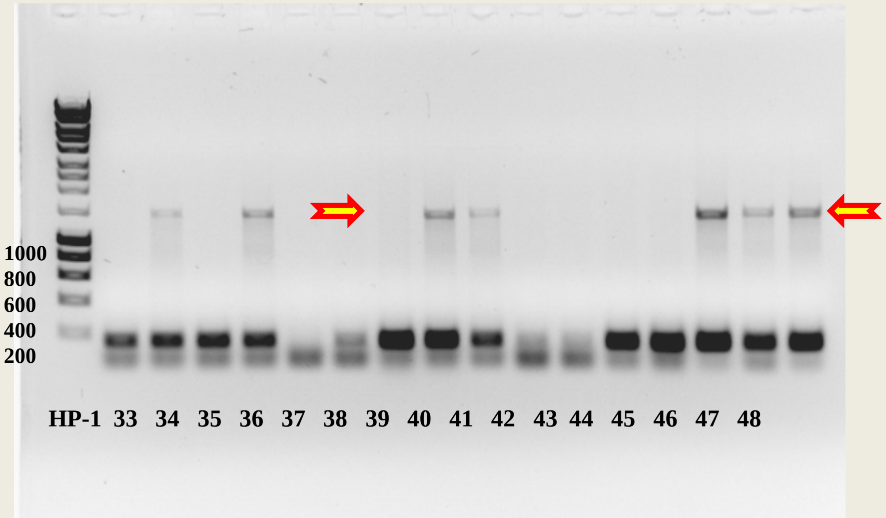


Musa balbisiana
(BB, ITC0545, 2n=2x=22)

Dispersed but not entirely uniform location of a B-genome specific hAT4 transposable element (red) and telomeres (green)







Agarose gel chromatograph illustrating hAT3 insertion sites in *Musa:* Amplification with degenerative primer pair hAT78,208F and hAT79,629R. Top bands (1441bp) showed the amplified element and lower bands amplifying the flanking sequences only. 1) AAB, 2) AAB, 3) AAB, *4) balbisiana, 5) balbisiana,* 6) *acuminata, 7) acuminata, 8) acuminata,* 9) ABB, 10) AAB, 11) ABB, 12) ABB, 13) AAA, 14) AAA, *15) acuminata, 16) acuminata,* 17) AAB, 18) ABB, 19) AAA, 20) ABB, 21) balbisiana, *22) acuminata,* 23) AB cv, 24) AAA, *25) acuminata,* 26) AAA, 27) AAB, 28) ABB, 29) AAA, 30) AS, 31) AB cv, 32) AAcv (18), 33) AAcv (2), 34) AAB, 35) AAA, 36) ABB, *37) acuminata,* 38) AAcv, *39) balbisiana, 40) balbisiana,* 41) ABB, 42) AAA, 43) AAA, 44) AAA, 45) AAB, 46) AAB, 47) ABBB, 48) AAB.

CAAGGATGAACCAAGCTTACATTGAGAGTGAAAGAGACACAATGCTAGATGTTAATTGAGGAAGCACAAGAACATACCTTATTTCATGTATC
GTAATACCAACAATGTCTTTACATTATCCTAACAATAGAACATGTAATGAATTTTTTGCTGATGAAAAATGAACATATTGAACAACATGATGA
GATAATTATGGCGGATTGCTCTTGAAATGAG**TTCAAATG*****CAAGGT***T***TG***CTGTACCGAATGATACCGCC**CGGTACGG**GTGGTACGTACCGGTC
CGACGGCATACCGGTACTCGGACCGCCCGCTACCGGGCGAAACAAAAAATAATAATAATATTATATATATATATATATATATATATATATATATA
TATATATATATATATATATATATATATATATATATTAATTAAAAAAAAAGCAATGTTCGGTGACGTTGCCAAGGCGACGTGACGTCGATATATAT
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GAGCGGTATACCATTCGGTATACCGTT**CCGTACCG***T*ACCGAGCGATCGTCGAAACTCTGGTACGGTACGAAATTT***CA***G***ACCTTG*****TTCAAATG**T
ACATAATTAACCATTATACTGGTGATGTGTCATTAAAGTATTAAACTATGTCTCAAGTATAAGAAAGAGTTTGGCTTCATTTTAGGTGTGATTT
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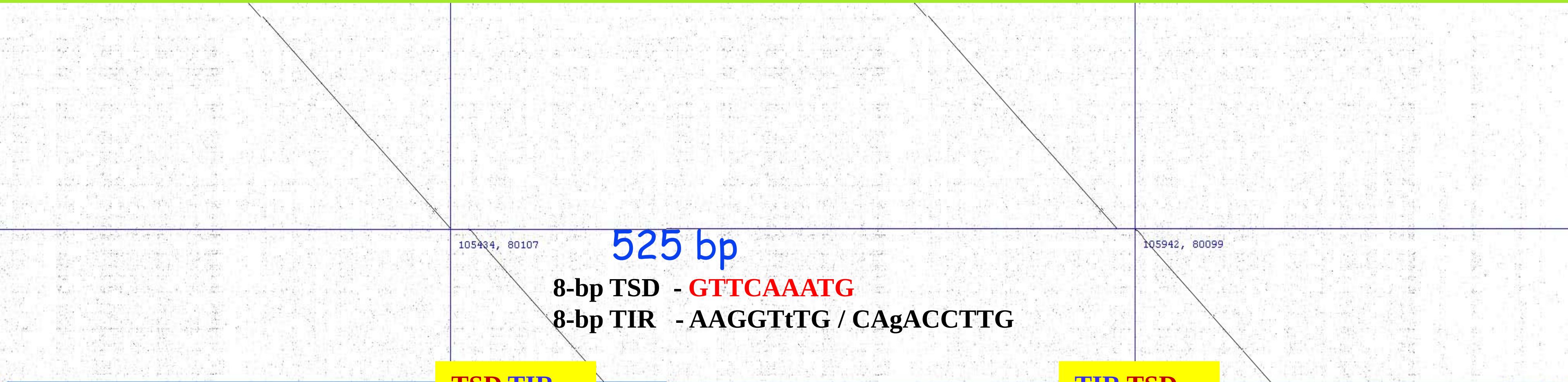
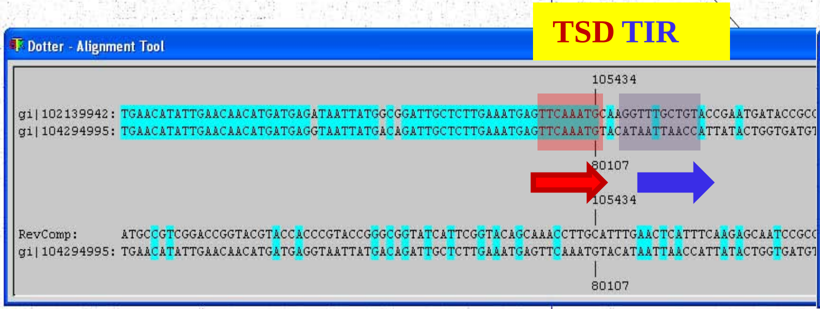


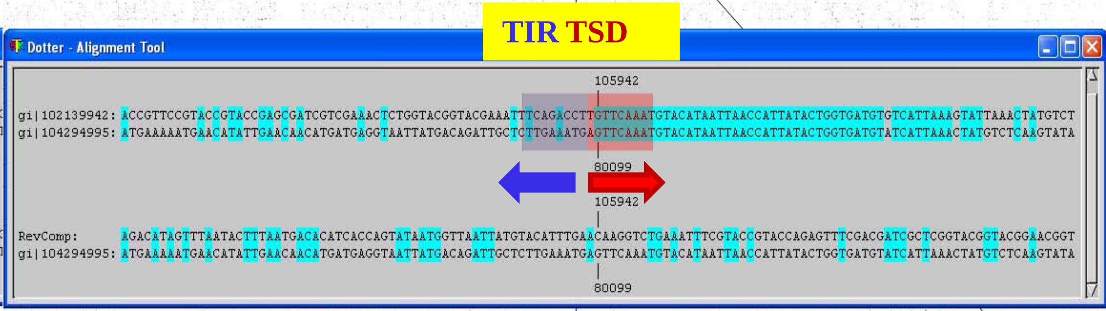
525 bp

8-bp TSD - GTTCAAATG

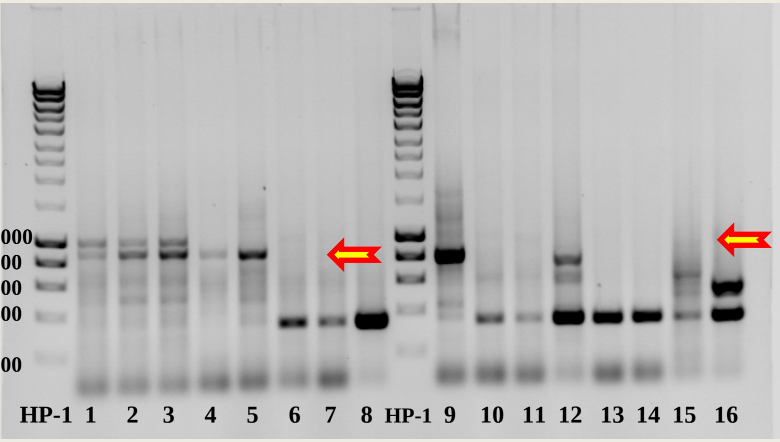
8-bp TIR - AAGGTtTG / CAgACCTTG

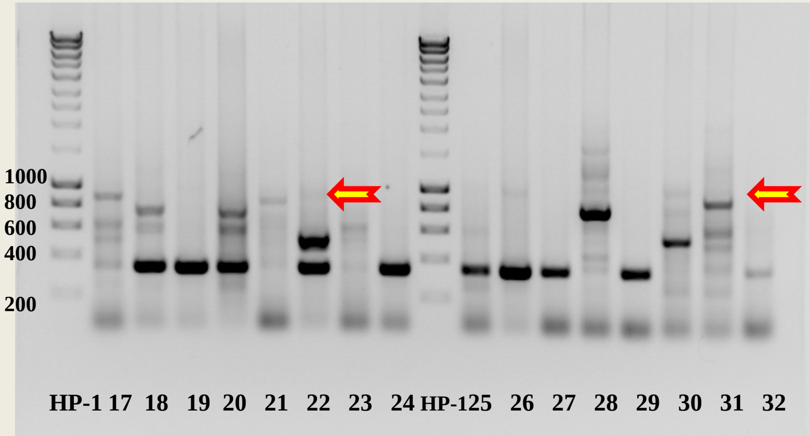


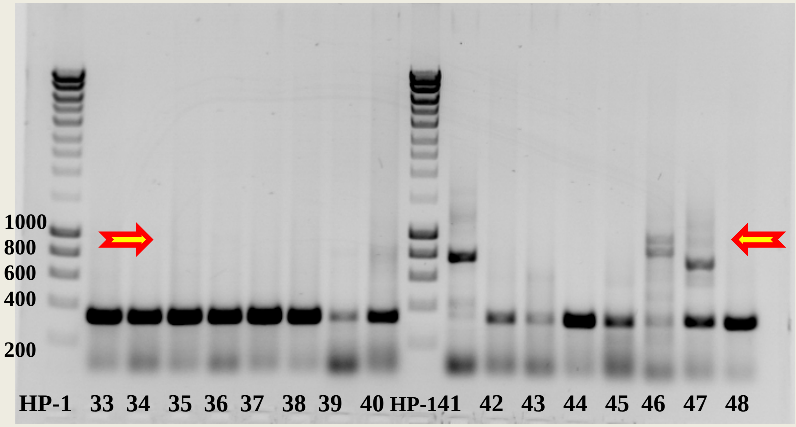
```
                                                              105434
                                                                |
gi|102139942: TGAACATATTGAACAACATGATGAGATAATTATGGCGGATTGCTCTTGAAATGAGTTCAAATGCAAGGTTTGCTGTACCGAATGATACCGCC
gi|104294995: TGAACATATTGAACAACATGATGAGGTAATTATGACAGATTGCTCTTGAAATGAGTTCAAATGTACATAATTAACCATTATACTGGTGATGT
                                                                |
                                                              80107

                                                              105434
                                                                |
RevComp:      ATGCCGTCGGACCGGTACGTACCACCCGTACCGGGCGGTATCATTCGGTACAGCAAACCTTGCATTTGAACTCATTTCAAGAGCAATCCGCC
gi|104294995: TGAACATATTGAACAACATGATGAGGTAATTATGACAGATTGCTCTTGAAATGAGTTCAAATGTACATAATTAACCATTATACTGGTGATGT
                                                                |
                                                              80107
```



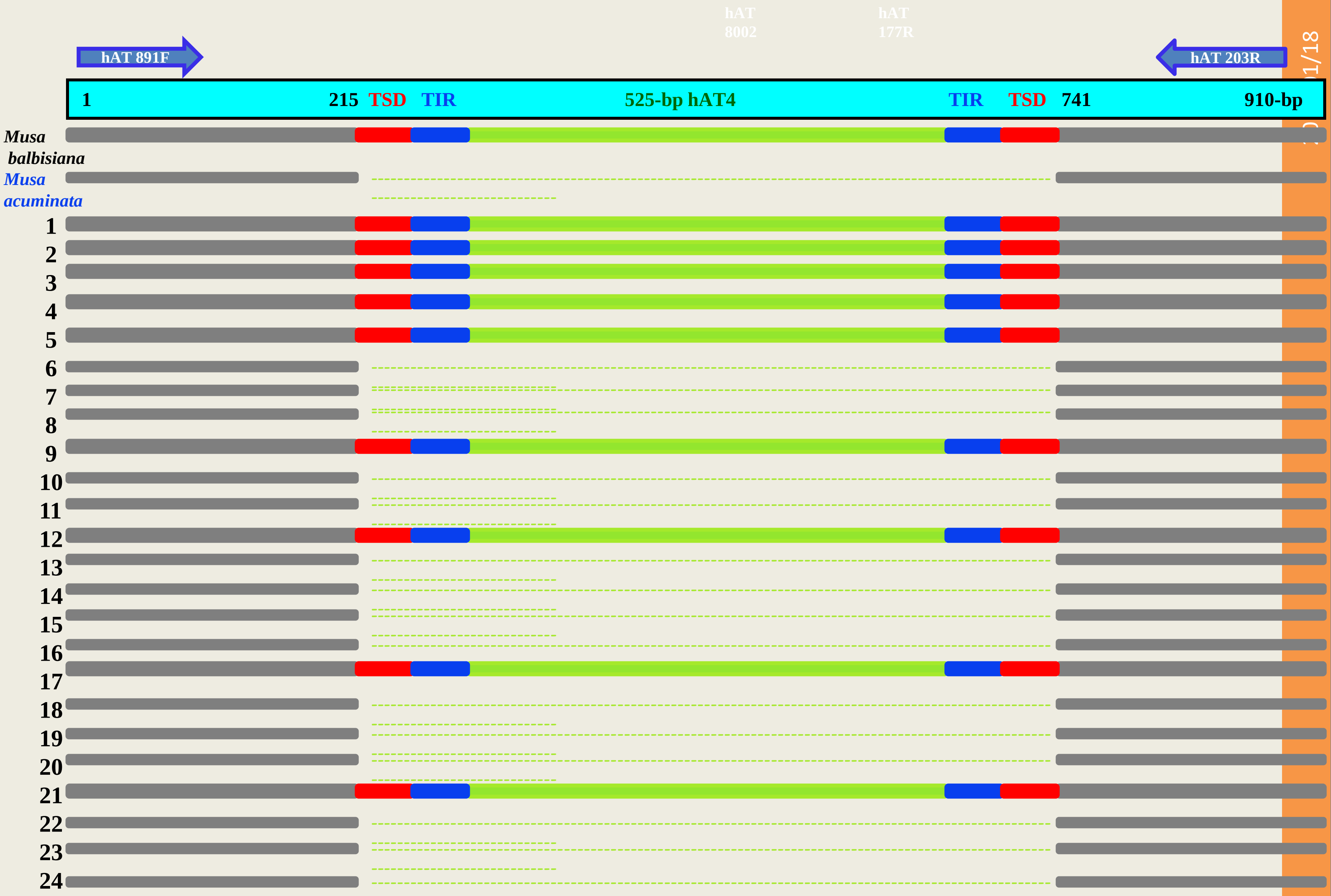
```
                                                                              105942
                                                                                |
gi|102139942: ACCGTTCCGTACCGTACCGAGCGATCGTCGAAACTCTGGTACGGTACGAAATTTCAGACCTTGTTCAAATGTACATAATTAACCATTATACTGGTGATGTGTCATTAAAGTATTAAACTATGTCT
gi|104294995: ATGAAAAATGAACATATTGAACAACATGATGAGGTAATTATGACAGATTGCTCTTGAAATGAGTTCAAATGTACATAATTAACCATTATACTGGTGATGTATCATTAAACTATGTCTCAAGTATA
                                                                                |
                                                                              80099

                                                                              105942
                                                                                |
RevComp:      AGACATAGTTTAATACTTTAATGACACATCACCAGTATAATGGTTAATTATGTACATTTGAACAAGGTCTGAAATTTCGTACCGTACCAGAGTTTCGACGATCGCTCGGTACGGTACGGAACGGT
gi|104294995: ATGAAAAATGAACATATTGAACAACATGATGAGGTAATTATGACAGATTGCTCTTGAAATGAGTTCAAATGTACATAATTAACCATTATACTGGTGATGTATCATTAAACTATGTCTCAAGTATA
                                                                                |
                                                                              80099
```







Agarose gel chromatograph illustrating insertion sites in *Musa:* **hAT4 amplification with degenerative primer pair hAT891F and hAT203R. Top bands (860-bp) showed the amplified hAT3 element and lower bands amplifying the flanking sequences only.** **1) AAB, 2) AAB, 3) AAB, *4) balbisiana, 5) balbisiana,* 6) *acuminata, 7) acuminata, 8) acuminata,* 9) ABB, 10) AAB, 11) ABB, 12) ABB, 13) AAA, 14) AAA, *15) acuminata, 16) acuminata,* 17) AAB, 18) ABB, 19) AAA, 20) ABB, 21) balbisiana, *22) acuminata,* 23) AB cv, 24) AAA, *25) acuminata,* 26) AAA, 27) AAB, 28) ABB, 29) AAA, 30) AS, 31) AB cv, 32) AAcv (18), 33) AAcv (2), 34) AAB, 35) AAA, 36) ABB, *37) acuminata,* 38) AAcv, *39) balbisiana, 40) balbisiana,* 41) ABB, 42) AAA, 43) AAA, 44) AAA, 45) AAB, 46) AAB, 47) ABBB, 48) AAB.**

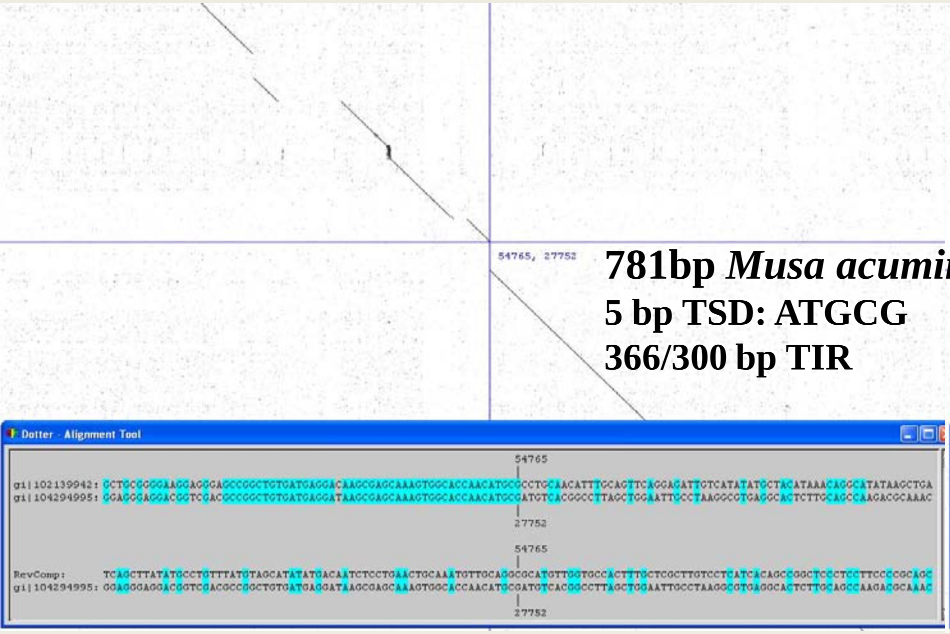


The insertion sites in *Musa with* hAT891F and hAT203R in: 1) AAB, 2) AAB, 3) AAB, 4) *balbisiana*, 5) *balbisiana*, 9) ABB, 17) AAB, 21) *balbisiana.*

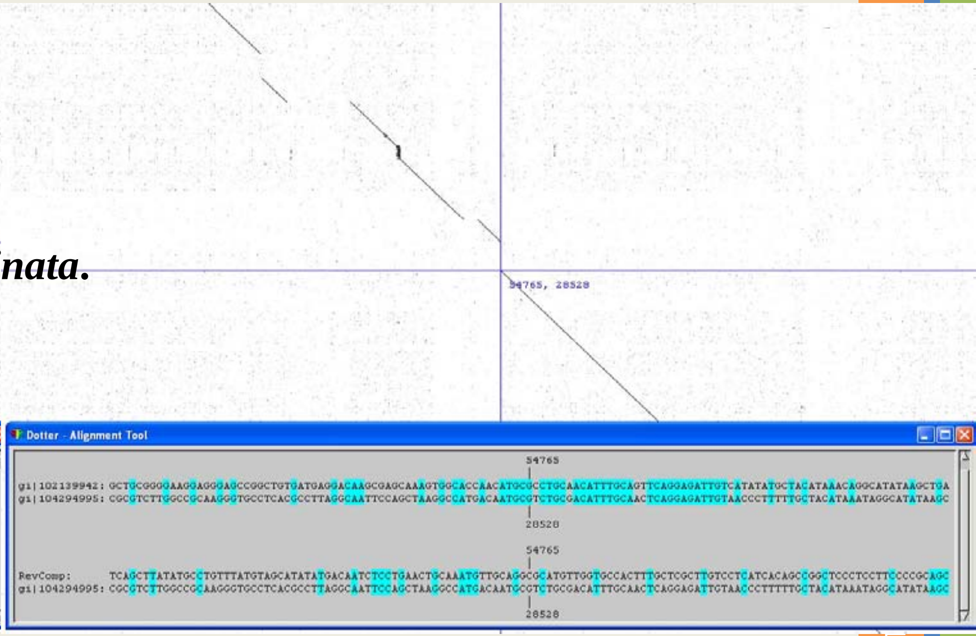
TSD AND TIRs OF TRANSPOSABLE ELEMENTS STUDIED IN MUSA

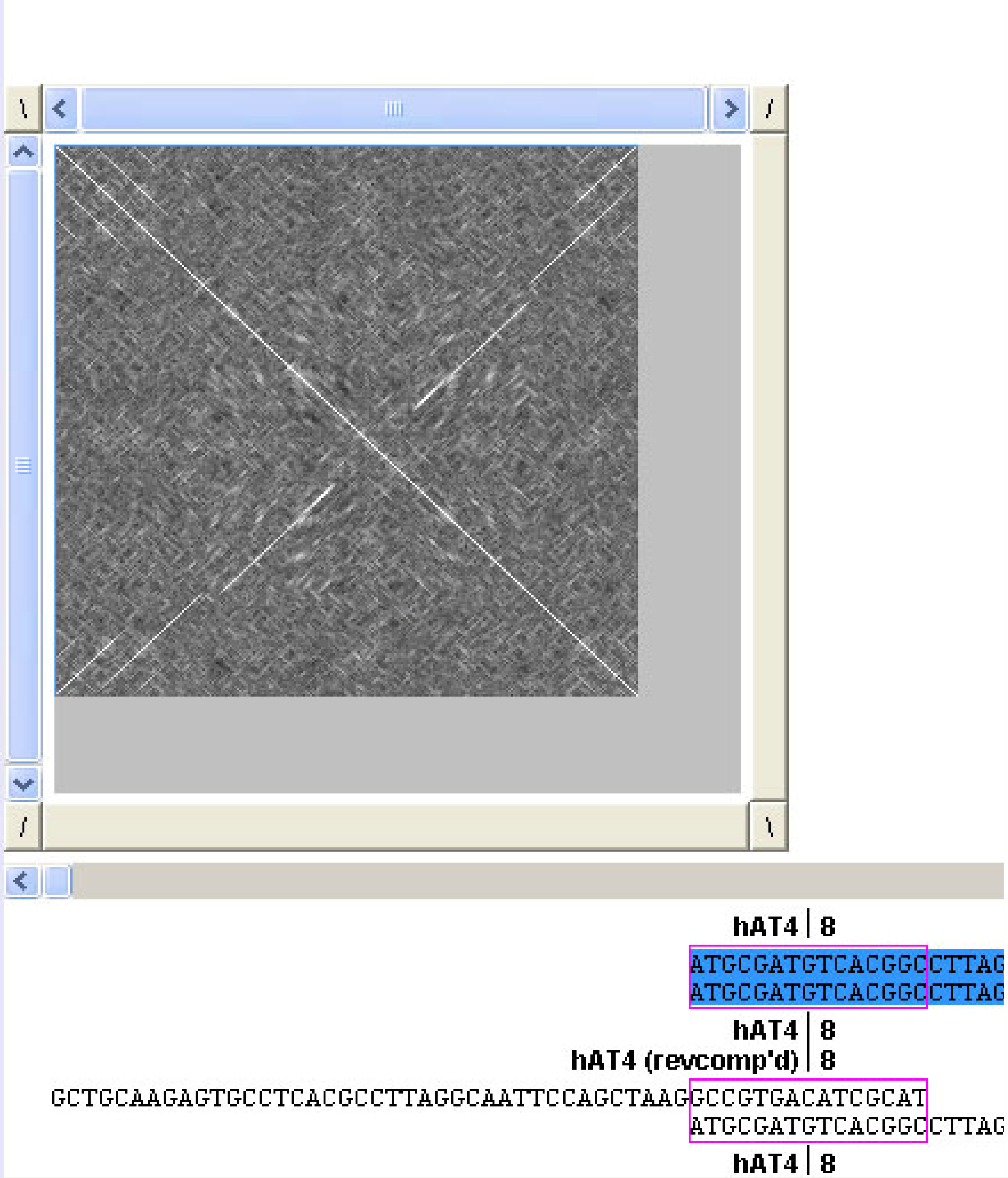
Superfamily	Species	Size	TSD bp	TSD seq.	TIRs bp	TIR sequence (5′-3′)
hAT1	*Musa acuminata*	273	8	TCCCTGAG	*30*	CAAGGTTCGCCATACCGTACCGTACCGGCG
hAT2	*Musa acuminata*	872	6	GTGcTA	*17*	ACCAGTGATTTaAAaAG
hAT3	*Musa balbisiana*	1292	8	GTTGCAAC	*24*	CAAGGTCTGCATACCGAATCATACCG
hAT4	*Musa balbisiana*	525	8	TTCAAATG	*8*	CAAGGTTTG
MITE	*Musa acuminata*	781	5	ATGCG	366	-----------------------
MBT	*Musa balbisiana*	621	3	ATG	Nil	-----------------------
MART	*Musa acuminata*	4192	5	CATAA	11	TGTAACACCCT
MBT384	*Musa balbisiana*	384	5	CGAGC	NIL	------------------------
MBT1676	*Musa balbisiana*	1676	5	CAAAG	NIL	-----------------------

AACGGGACGAGTCTTGAGAAGGTGCGATGGGCGTGGCGGAAGCCGCTGCGGGGAAGGAGGGAGGACGGTCGACGCCGGCTGTGATGAGGATAAGCGA{GCAAAGTGGCACCAAC**ATGCG**A***TGTCACGGCCTTAGCTGGAATTGCCTAAGGCGTGAGGCACTCTTGCAGCCAAGACGCAAACTTAGCTTGCGTTACCTAAGTCGCGAGGCACCCTTGCGACAAAGACGCGAACTTAGCTTGCGTTGCCTAAGTCGCGCTTCGCCCTTGAGATATTGCTCCGCAAAGATCAGCCCACTTGCAACCTCTCGCAGGTC***CCGAAGGACCTGTAAAAGAGAAAG***TTGATTAGTTCGAAAGAACGAGCGACGGACAAGTCCTAACATCTCGCGAAAAGAGGGGAAGCTTTACAAGCAATTCAGCGAGCATCTTGTGTGCACAAGAGAAAAGAAGAGAGGGAAAAAACAAAGACTTTAGAGGGTTGAACGAACAGCTGCAA***CGGGTGCCGGGCGCGACAACAAGTTCCCGTCAAGGTAACGTGCGAACTTGCGAAAGGTTGTTCAACACCCGACACCCGGTGAGCAGTTGTCTGCGGAC***TTACAGTTGTTCGTTCAACCCTCTAAAGTCCTTGTTTTCCCCCTCTCCCTCTTTTCTCTTATGCACGCAAGGTGCTCGCTAAATTGCTTGTAAAGCTTCTCCTCTTTTCGCGAGACGTTGGGACTTATCCGTCGCTTGTTCTTTCAAACTAATCAAGACCTGCGAGAGATTCCAAGTGGGCTGATCTTTGTGGAGCAATATCTCAAGGACGAAGCGCGACTTAGGTAACGCAAGCTAAGTTCGCGTCTTGGCCGCAAGGGTGCCTCACGCCTTAGGCAATTCCAGCTAAGGCCATGACA*****ATGCG**TCTGCGACATTTGCAACTCAGGAGATTGTAACCCTTTTTGCTACATAAATAGGCATATAAGCCGAGATATAAAAGAATGAATACCGAGCTGTTTGCATGAAAGACAAATAATTATGTCAAATAAAGGAGTAGCTTTT**GGCCTAAGCGGAGACATTTA**

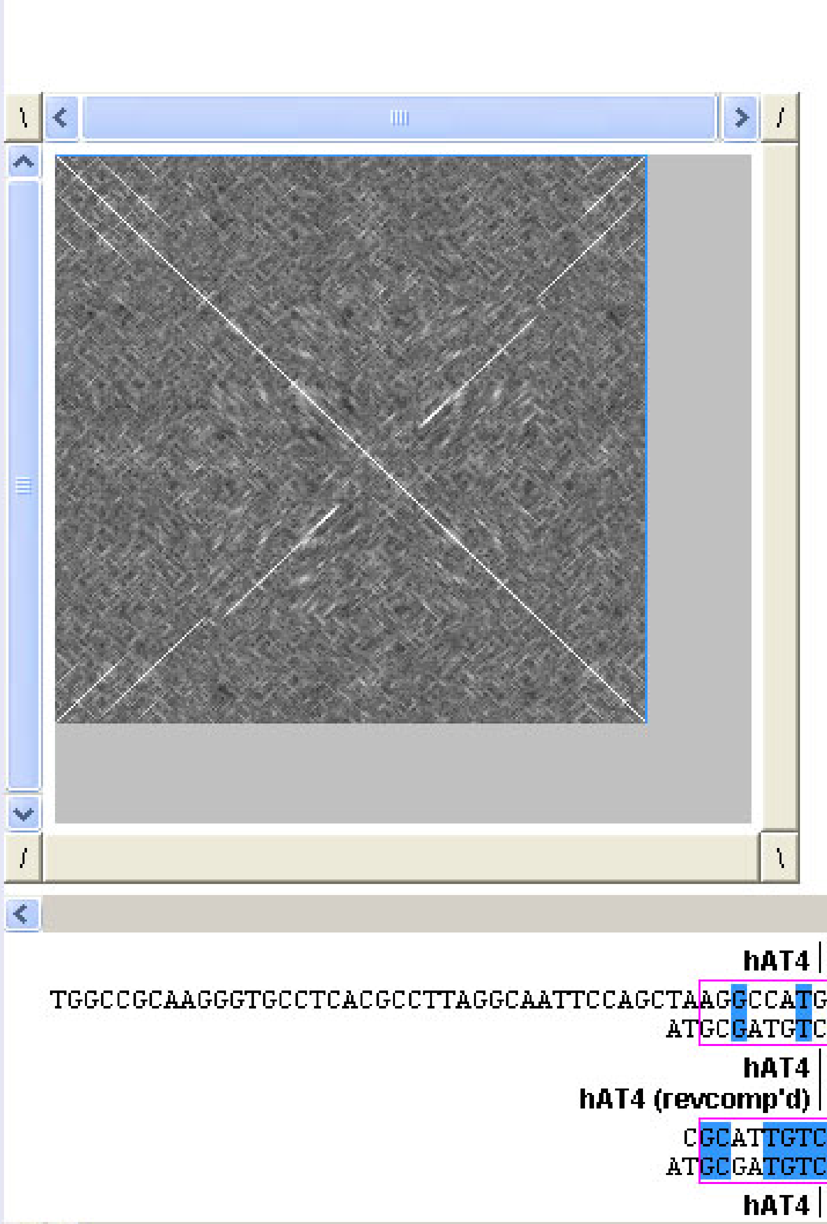


781bp *Musa acuminata*.
5 bp TSD: ATGCG
366/300 bp TIR



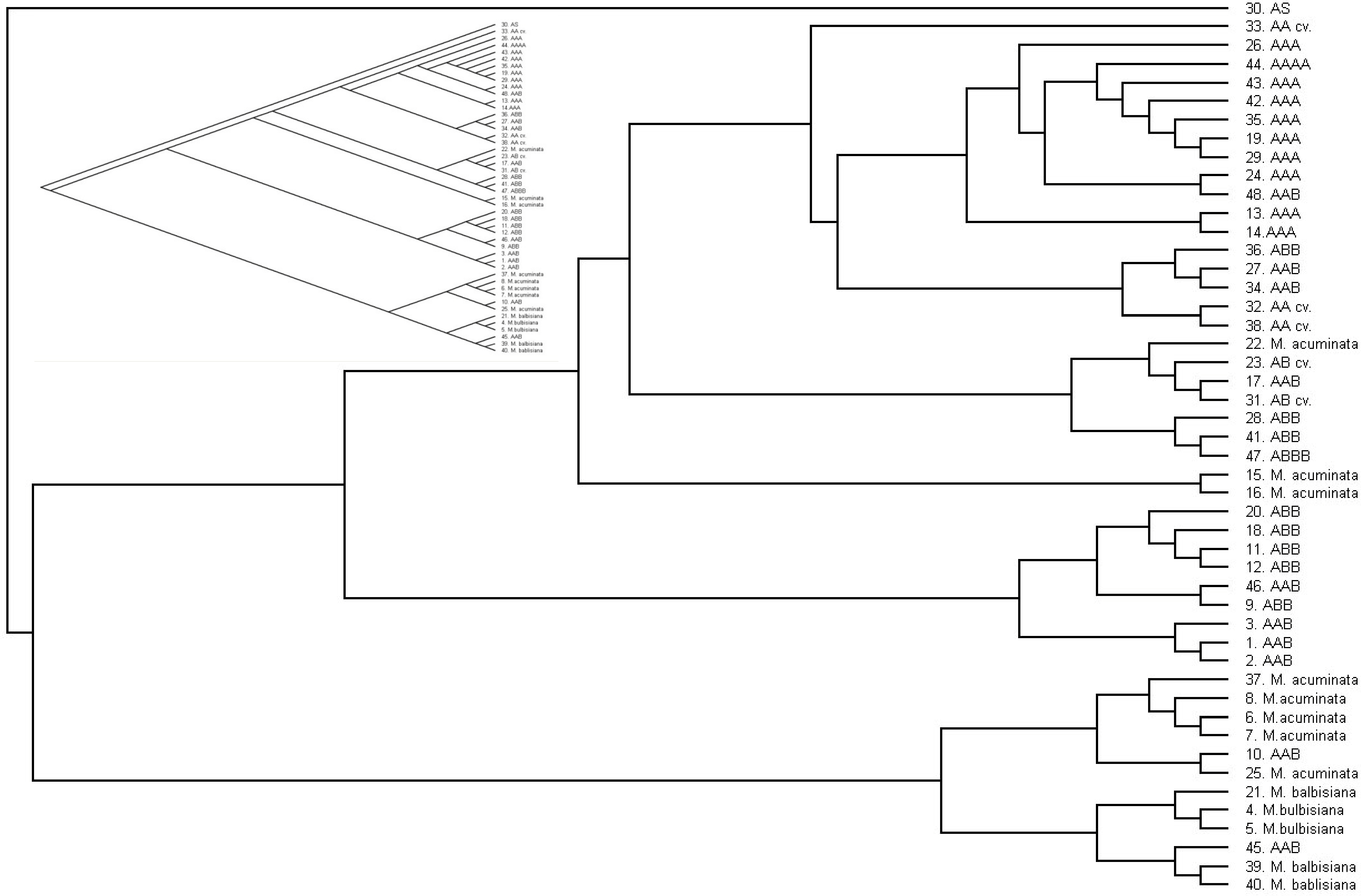


```
                                               hAT4 | 8
                                              ATGCGATGTCACGGCCTTAG
                                              ATGCGATGTCACGGCCTTAG
                                               hAT4 | 8
                                    hAT4 (revcomp'd) | 8
GCTGCAAGAGTGCCTCACGCCTTAGGCAATTCCAGCTAAGGCCGTGACATCGCAT
                                              ATGCGATGTCACGGCCTTAG
                                               hAT4 | 8
```

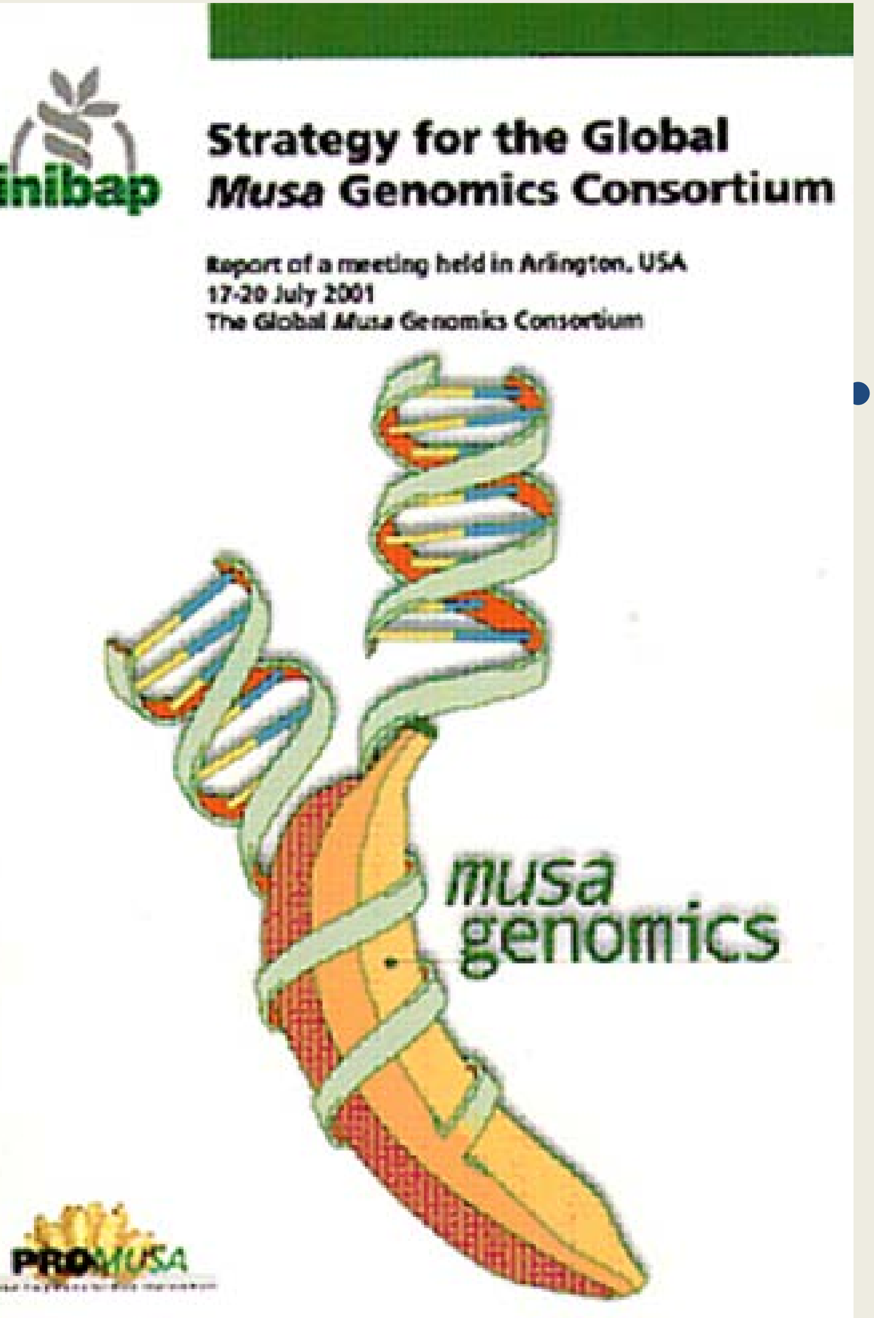


```
                                                     hAT4 |
TGGCCGCAAGGGTGCCTCACGCCTTAGGCAATTCCAGCTAAGGCCATG
                                          ATGCGATGTC
                                                     hAT4 |
                                         hAT4 (revcomp'd) |
                                            CGCATTGTC
                                          ATGCGATGTC
                                                     hAT4 |
```

Dot plot showing the complete Inverted repeat.



Phylogenetic analysis of *Musa* genomes by TRBIP



Strategy for the Global *Musa* Genomics Consortium

Report of a meeting held in Arlington, USA
17-20 July 2001
The Global *Musa* Genomics Consortium

The Global Musa Genomics Consortium

- To assure the sustainability of banana as a staple food crop by developing an integrated genetic and genomic understanding, allowing targeted breeding, transformation and more efficient use of Musa biodiversity

Repetitive DNA and its evolution in the Musa genome

Nature of polymorphisms
Sources of polymorphisms

Understanding evolution
Breeding

W067: Banana (Musa) Genomics
Plant and Animal Genome 2011

Pat Heslop-Harrison, Faisal Nouroz, Farah Badakshi, Asha Nair, Anath B Das, Gerhard Menzel, Thomas Schmidt, Trude Schwarzacher

Thanks:

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