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Multiple evolutionary trajectories have led to the emergence of races in Fusarium oxysporum f. sp. lycopersici

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Supplemental material for "Multiple evolutionary trajectories have led to the emergence of races in *Fusarium oxysporum* f. sp. *lycopersici.*", Biju V.C. et al.

Supplemental material and methods Details of the assembly of clone 9G3

Sequencing of BAC clone 9G3 and *de novo* assembly resulted in three scaffolds, notably 47 (approximately 35 kb in length), 56 (31 kb) and 53 (22 kb), hence in a contiguous sequence with two gaps (Supplemental figure 2A). The three scaffolds could easily be ordered because of the presence of BAC vector sequences at one end of both scaffold 47 and 53. Using primer pairs 4241/4242 and 4239/4240 corresponding to sequences flanking the two gaps in the 9G3 sequence (Supplemental figure 2A and Supplemental table 1), fragments could be PCR-amplified (Supplemental figure 2B) and sequenced.

The gap between scaffolds 56 and 53 appeared to be a sequence of 6122 bp representing a *Helitron (HelB)*. The gap between scaffolds 56 and 47 was found not to be a real gap but rather the result of a mis-assembly, most likely due to the presence of another *Helitron* copy (*HelA*) at the end of scaffold 47. Comparing the 9G3 gap closed sequence with the genome sequence of the Fol reference strain (Fol4287) revealed that it fully aligns with a genomic region in the lineage specific (LS) chromosome 14, namely with supercontig (sc) 2.22: 651200 to 712754, except for a unique fragment containing *AVR1* (Supplemental figure 2A).

Sc2.22 is composed of a large number of contigs of which four (partly) align with 9G3, namely contigs 852, 853, 854 and 855 (Supplemental figure 2A). These contigs are separated by sequence gaps and the availability of 9G3 allowed closing of these gaps. Using primer pair 4618/4619 (Supplemental table 1) a 6.4 kb fragment could be amplified from both Fol4287 genomic DNA and 9G3 DNA (data not shown). Sequencing confirmed the identity of the amplified fragments and let us conclude that the gap between contigs 852 and 853 was the result of a mis-assembly due to the presence in this region of an *NHT2*-like retrotransposon. Similarly, PCR analysis using primer pair 4620/4621 (Supplemental table 1) and sequencing indicated that the gap between contigs 853 and 854 can be explained by a mis-assembly due to the presence of a *Fot5* DNA transposon (data not shown).

The third gap (between contigs 854 and 855) appeared to be located within a copy of transposable element *Yaret2* that precedes a second *Yaret2* copy on contig 855, suggesting the presence of two *Yaret2* copies in a row. However, in 9G3 only one copy was identified.

Using primer set 4625/4630 (Supplemental table 1) a 3.7 kb fragment could be amplified from genomic DNA of both Fol4287 and Fol004 as well as from and 9G3 DNA (data not shown). Sequence analysis confirmed the presence of two *Yaret2* copies in tandem sharing the LTR that separates the open reading frame of the two copies. This suggests that during assembly of the 9G3 insert sequence one copy was missed due to a high level of sequence similarity. The length of the full 9G3 insert was found to be 98694 nucleotides in total.



Figure S1. Analysis of BAC clones with an insert containing the AVR1 locus

(A) DNA of BAC clones 2G2, 9C1, 9G3 and 14I-2, selected from a Fol004-BAC library, was digested with either NotI or SwaI alone or with both enzymes. NotI was chosen to cut out the insert from the BAC vector (the vector pBleoBAC11 contains two NotI sites in the region flanking the insert). SwaI was chosen to estimate the approximate location of AVRI in the insert (The analysis of 2.8 kb AVRI genomic region revealed a SwaI site 294 bp downstream of AVRI stop codon; the vector pBleoBAC11 does not carry a SwaI site). DNA fragments were separated on a 1% agarose CHEF gel at 5- to 15-s linear ramp time, 6 V/cm, 14°C in 0.5× TBE buffer for 18 h, and stained with ethidium bromide. The 7.5 kb band present in the NotI digests (indicated by arrows) corresponds to the cloning vector. A: clone 2G2, B: clone 9C1, C: clone 9G3, D: clone 14I-2, E: Lamda ladder, F: 8-48 kb ladder, G: GeneRuler 1 kb DNA Ladder (0.25 – 10 kb). (B) Schematic representation of the relative positions of the BAC inserts containing AVRI. The insert sizes and the positions of NotI and SwaI sites are deduced from the restriction analysis. The position of AVRI was inferred from the position of the SwaI site.





Figure S2. Assembly of the 9G3 insert.

(A) Schematic representation of 9G3 insert mapped to a genomic region in supercontig (sc) 2.22 of chromosome 14 of Fol4287. The order of three scaffolds corresponding to the sequence of the 9G3 insert is shown above. Arrows indicate the location of the primers used to fill the gaps between the scaffolds. Red lines indicate the contigs of sc2.22 corresponding to this genomic region. Arrows indicate the location of the primers used to fill the gaps between the contigs. (B) Left: amplification of a PCR product of 6.2 kb using the primer pair 4240/4239. Right: amplification of a PCR product of 600 bp using the primer pair 4242/4241. W: water control, M1: GeneRuler 1 kb DNA Ladder (0.25 - 10 kb), M2: MassRuler DNA Ladder Mix (0.08 - 10 kb), W: Water control.



Figure S3. Confirmation of the absence of Helitron B (HelB) in some race 1 isolates.

PCR experiment showing the presence/absence of a 1.8 kb fragment in the genomic DNA of different race 1 isolates (lanes 1-8) using primer pair 4345/4340 (these primers correspond to the 5' and 3' flanking sequences of *HelB*, respectively). Lane 1: Fol001, lane 2: Fol003, lane 3: Fol004, lane 4: Fol006, lane 5: Fol009, lane 6: Fol010, lane 7: Fol011, lane 8: Fol016, lane 9: water control, M: MassRulerTM Low Range DNA Ladder (80-1031 bp).



Figure S4. Fol4287 and Fol033 contain a *Hop3* insertion at the 5' end of *HelAB*.

(A) Amplification of PCR fragments from the genomic DNA of Fol4287 with primer pairs A-J. The absence of a PCR product with primer pair B indicates a *Hop3* insertion at the 5' end of *HelAB*. (B) A product of 624 bp was amplified only from Fol4287 and Fol033 using primer pair 4304/4298. (C) A product of 723 bp was amplified only from Fol4287 and Fol033 using primer pair 4303/4297. M: Marker, 1: Fol004, 2: Fol002, 3: Fol4287, 4: Fol033, W: water control.



Figure S5: Six5 is absent in Fol097.

We used PCR to determine whether, in addition to AVR2, Six5 is absent from Fol097. The left three lanes show presence and absence of amplicons obtained using primer pair 962+963 (corresponding to a 273 bp fragment) in water (W, negative control), Fol007 and Fol097. We confirmed the absence of AVR2 (SIX3) in Fol097. The middle three lanes show presence and absence of amplicons obtained using primer pair 1993+1994 (corresponding to a 524 bp fragment) in water, Fol007 and Fol097. We show the absence of Six5 in Fol097. The right three lanes are our positive control: primer pairs 157+158 correspond to a 274 bp region in the Fem1 promoter. Primers are listed in Suplemental table 1 and we used MassRuler DNA Ladder Mix (ThermoFisher) as a marker for fragment sizes.

Table S1. Primers used in this study

NumberSequenceImpetting gene genome position in 4.87 4590AAGCUAGAGAAAACGGAAAC518 bp upstream HeIA4298TGAACCUAAGAAACGGAAAAC518 bp upstream HeIA4297TGCCUTTIGUTIGUTIGAAGG316 bp upstream HeIA4297TGCCUTTIGUTIGATAGSpecific to 3 end of Helitmons4212ACAAGTCACAAAGCATCAC201 bp downstream HeIA4214TTGACGACACGTTTAGATAG429 bp upstream HeIA4345TAGCTGGUCATTGATAG429 bp upstream HeIA4346ACACGGGGACATTGATGGC1382 bp downstream HeIB4347TGGGTACTGATGGTAATG3369 bp downstream HeIB4348TGGGTATGCATGGTAATG3369 bp downstream HeIB4349TTGCGAGCAGCACTGCG155 bp upstream HeIB4340TGCGAGCAGCACTGACATCG155 bp downstream HeIB4341TGGGTAGCACATGACC155 bp upstream HeIC4341TGGGTAGCACATCAACC154 bp downstream HeIC4342TGCGGTCGCAATCAAGCACC154 bp downstream HeIC4343ACGGGTCATGACGTCCTCGChrl 4 SC229705 -970964344TGGCTACAATGGTCCTTCGChrl 4 SC229705 -970964345TTGCCGACAGAGTTATCAGGChrl 4 SC229701 -990414346TAGGGTCATTGCAGACCChrl 4 SC229701 -92073 -92054380TGCAACACGTACTCCChrl 4 SC229701 -920734380TGCACATGACTGCACTCCChrl 4 SC229701 -920734380TGCACATAGCCGTCCTCGChrl 4 SC229701 -920734380TGCACATAGCCGTTACTGCGCATTCChrl 4 SC229701 -920734380TGCACATAGCACCACTCCChrl 4 SC229701 -92073 <td< th=""><th></th><th>0</th><th></th></td<>		0	
4390AAUCUAGUAAAACUAGUA996 be pisteam HeIA4391TGAAGCACAAGTAACGAGCA158 be pisteam HeIA4293TGACCACAAGTAACGAGGA316 be pisteam HeIA4294TGAAGCACAAGTAACGAICACSpecific to 5" and of Heitman4214TIAGCGACACGTICAACAC201 bp downsteam HeIB4314TIAGCGACACGTICAACAC201 bp downsteam HeIB4315ACAAGGGACAATGAICAGC236 bp downsteam HeIB4316TAGCGACACGTICGACATC236 bp downsteam HeIB4317TGCGGACTCGCAATGAICG236 bp downsteam HeIB4318ACACGGACACCGGATTGG3470 bp downsteam HeIB4319TGTGATAGCACGCGGATTGG348 bp downsteam HeIB4310TGTGATAGCACATCAAGGACCC155 bp downsteam HeIC4311TGTGCTAACGCACTCAGG156 bp downsteam HeIC4311AGGGTGCAATGAGTCTTGG156 bp downsteam HeIC4311AGGGTGCAATGAGTCTTGG156 bp downsteam HeIC4312TGGGTAGCCACATCAGGChrl * 8C22 9706 - 970254380TGCAAAGCCACTCAGGChrl * 8C22 9706 - 970254380TGCAAAGTCACATGGTCCTTGGChrl * 8C22 9490 - 990414381ACGGGTAATCAAAGCACCChrl * 8C22 9491 - 9198674380TGCCACATCAGGTCCTGGChrl * 8C22 9491 - 9198674380TGCCACTGGACAATGGCChrl * 8C22 9491 - 9198624380TGCCACTGGACACGGCChrl * 8C22 9491 - 9198624381ACTGGCTACTGCGAACCCChrl * 8C22 9491 - 9198674384ATGGCTTGCTGCAAGACCGCChrl * 8C22 9491 - 9198674385TCCCCTGTGACAGCGCGCCCChrl * 8C22 9491 - 919867<	Number	Sequence	Targeting gene/genomic position in 4287
2390 AARD TLAGGACCOCATACC 515 80 puptican Ite/A 2397 TGCCTCTTTGCTCGACGG Specific b 5 end of Helitoms 2421 ACAGCACACATTACTACG Specific b 3 end of Helitoms 2422 ACAGTCACACATTCATACC Specific b 3 end of Helitoms 2431 TIGACGACACCATTCATAGC 19 bu pustem Hela 2433 TAGCTGGCACATTCATAGC 138 bu downstream Hela 2434 TAGCTGGCACATTCATAGC 138 bu downstream Hela 2435 AAGAGGACATTGATGGC 138 bu downstream Hela 2436 TGGGTACGGGACATTGATGG 149 by downstream Hela 2437 TGGGGTACGGACATCGG 149 by downstream Hela 2438 TGGGTAGCGACATCGACCC 159 bu pustem Hela 2436 TGTCATACATTGAGGACTCG 159 bu pustem Hela 2436 TGTGCTAGCCACACCACC 159 bu pustem Hela 2436 TGTGCTAGCACCACATCAGC 159 bu pustem Hela 2437 TGGCTGGAATCGACACCACC 158 bu pustem Hela 2438 TGTGCTAGCACACACCACC 158 bu pustem Hela 2449 TGTGCTAGACACACACCC 154 bu puwnsteam Hela 2451 TGGTGTAGACAGGACTCG 154 bu puwnsteam Hela 2451 TGGTGCAGACTGGACATCG 154 bu puwnsteam Hela 2451 TGGTGCAGACTGGACATCG 154 bu puwnsteam Hela 2451 <td>4539</td> <td>AAGCGAGAGAAAACGGAAGC</td> <td>5956 bp upstream HeIA</td>	4539	AAGCGAGAGAAAACGGAAGC	5956 bp upstream HeIA
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1430 11GTOAGGAACCOTITGG 1472 by 0 downstream HelB 4395 TCCTCACAATGGTGACATCG 1550 bp upstream HelC 4391 AGCGTGGACTTGAGTTGCC 38 bp downstream HelC 4511 TGTCGTCACACTGACATCG 82 bp downstream HelC 4521 TGGGTCCAATGGTCCAAGCC 154 bp downstream HelC 4566 TAAGGTCTCAATGGTCCTTCG Chr14: SC229706-970625 4867 TTGCGACGAAGTTATCAG Chr14: SC229001-9041 4967 TCGCGACGAAGTATCAG Chr14: SC2291091-9041 4968 TTGCCGACGAAGTATCGC Chr14: SC2291091-9041 4967 TCAGAAACACGACATTC Chr14: SC2210941-219867 5023 AATCCATCTCCGAATCACC Chr14: SC2210914-129362 5024 TTATCAGACATACTCAGC Chr14: SC2221917-129362 5025 TCAGAAACAACGCACTTC Chr14: SC22234580-34389 5026 ATGGGCTGAAACG Chr14: SC2235590-353711 5026 TGGACACATAGTCGGCGAAACG Chr14: SC2235590-353711 5036 ATGGCCTGTAGTATGGC Chr14: SC2235590-355700 5047 TGCTACATATGCCTAGTACGG Chr14: SC2255590-355700 4759 <td< td=""><td>4354</td><td>TTOTOCACCOACCOACTTTOC</td><td>142(0) L L L L</td></td<>	4354	TTOTOCACCOACCOACTTTOC	142(0) L L L L
4306101CATACATIOAGOTGO14/12 ph downstream HelC4371AGCGTGGACTICAGTTCAGC1550 by petream HelC4371AGCGTGGACTACAATGGCCACATCAG82 by downstream HelC4541TGTGCTCACCACATGGTCCTTCG1435 bp downstream HelC4542TGGGTCGCAATGGTCCTTCGCht4: SC229705-970964867TTGGGACTGACGACGACGCCht4: SC229109-5970964870TGGATAATGTGTGTGCAAGCCht4: SC229109-5970964890TGATAATGTGTGTGCAAGCCht4: SC229109-5970964897TGCGATGGACGACGACGCCht4: SC229109-5970964898TGCCCATGGAAGACTGCCht4: SC229109-592134891ACTGGATTTCTGGTGAAGCGCCht4: SC221064295023AATCCATCTGCAAAGCACGTCCht4: SC221064295024TTATCAGACATACTCGATTCCht4: SC222300114874ATCTGGCGTGTGGCGAACGCht4: SC222300714875TTATTAGAGAGGGAGACGCht4: SC223300714874ATCTTGGCTGTGGCGGAACGCht4: SC2233104790TGTATTATAGGAGGAGAGCCht4: SC2235104790TGTATTCAAGGCCTAACTGGCht4: SC2235104790TGTATCATAGGCCTAAGTGCCht4: SC2253104781TGTGTGGTATAGAAGTCCCht4: SC2253194783AGCCGCTCGCTTAGGTAAGGCht4: SC2253194784TGTGTGGTAATAGAAGTCGCht4: SC2253194781TGGTATCGATAGCACGCCht4: SC2253194791TGTATCATAGGCTAACGGCht4: SC2253194792TGTATCATAGGACTTAGGCht4: SC2253194793TGTATCATAGCATAGGCCht4: SC2253394794TGTATCATAGGACTGAACG<	4309		14369 bp downstream HelB
13301CC LACAA IGC LOKATCO1500 bp dpstall nPCC1371AGGCTIGACTTCIAGCTTCIC18 bp downstream HeIC1452TGGCTCAATCGAACCACC1545 bp downstream HeIC1452TGCGACGCAATCAAACCACC1545 bp downstream HeIC1486TGCGACGAGATTATCAGChrl4: SC229705. 570961487TGCGACGAGATTATCAGChrl4: SC2299193. 982131489ACIGGATTICTCCGTGACACCChrl4: SC2291060. 776251489ACIGGATTICTCCGGAACACTGCChrl4: SC2291060. 1064391502TGCCACTGGAACACTGCChrl4: SC22201061. 2090111496TTGCCACACGGAACACTCCChrl4: SC222019. 1064391502TCAGAAAACAACAACACATTCChrl4: SC222019. 1290711502CAGACAACAGCACATTCChrl4: SC222019. 1290711503ATICCGCGTGGGGAAACGChrl4: SC22230051. 2300711514TTTATTAGCGAAGGCGAACTGGChrl4: SC22230051. 2300711515TTTATTAGCGAAGGCGAACGChrl4: SC2230051. 2300711517TGCTACATATGCCTTAGTATGGChrl4: SC2230051. 2300711518TGCTACATATGCCCTAGTACGChrl4: SC2230051. 2307111517TGCTACATATGCCTTAGGAACCGChrl4: SC2230051. 2307111518TGCTACATATGCCCTAGGTACGChrl4: SC2230051. 2307111519TGCTACATATGCCTTAGGAACCGChrl4: SC2230051. 2307111520TGCTACATATGCCTTAGGAACCGChrl4: SC2250150. 5507001531TGCTACATATGCCTTAGGAACCGChrl4: SC2250150. 5507001542TTATTAGCGAAGCGGAACCGChrl4: SC2250150. 5507001531TGCTACATATGCATACGGAACCGChrl4: SC22-207159. 5691131532 <td< td=""><td>4306</td><td></td><td>14//2 op downstream HelB</td></td<>	4306		14//2 op downstream HelB
4311ACCONTOCAL TOCAC55 0p downstream HelC4341CIGGETCAGCACATICAAGCAC1545 bp downstream HelC4352TCGGTCGCAATCAAAGCACC1545 bp downstream HelC4366TAAGGTCTCATGCATGCACTCGChrl4 SC229705 - 570964367TIGCGGACGAATGTATCAGChrl4 SC2299021 - 990414390TGGATATGTCGTGCAAGCChrl4 SC2299021 - 990414490ACTGGATTGTCATTGTCGTGCACGCChrl4 SC22106320 - 106439480TGCCCACTGGAAGAACAACChrl4 SC22106320 - 1064395023AATCCATCTTCCAGAATCAACChrl4 SC2221071 - 2193625024TTATCAGACATACTGCGAAGCACACChrl4 SC22221971 - 219365025TCGGACGACAGAGCACATTCChrl4 SC22221971 - 219365026ATGCCGTTACTGTCGGAGCChrl4 SC2223071 - 2297365026ATGGCCGTATACTGCCGAGACGChrl4 SC22231580 - 236014875TTATTAGCGACGGGAAGAGCChrl4 SC22231580 - 236014874ATCTTGGCTGGTGGCGAACGChrl4 SC2235050 - 535194880AGGGTGCTTAGGTATTGGChrl4 SC2255080 - 566104881TATCCTGCTAGTATAGGAChrl4 SC2255080 - 566104881TATCCTGCTAGTATAGGAChrl4 SC2255080 - 566104781TGGTATCATGCCTTAGGAACGGChrl4 SC2255080 - 562354752TTATTAAGACTTACGGChrl4 SC2256803 - 652334753TGCTCATTAGCATTACGGChrl4 SC2256803 - 652334754TGCTCCTTGTGAGAACGGChrl4 SC2268035 - 692364752TTGATAGCATTACGGATACGGChrl4 SC2270159 - 703594753TGCTCATTGATAGGATACGGChrl4 SC2270159 - 703594754TCCTCCTGTGAGATACGC <td>4393</td> <td></td> <td>28 km downstream HalC</td>	4393		28 km downstream HalC
1.1.11.0100 ECACCCATCAAAGCACC1624 by bownstream Helc4542TCGGTCGCAATCAAAGCACC1545 by downstream Helc4866TAGGGTCCAATGGTCCTTCGChr14: SC2239705-970964870TGCGACGAGAGTTATCAGChr14: SC2239193-982134891ACTGGATTCTCTCGCACGCChr14: SC2239193-982134967TCGGAAGACTTGTTCGCTGCChr14: SC22210643-1064395023AATCCATCTTCCAGAATCACChr14: SC22210847-2198675024TTATCAGACATACTCGCATTCChr14: SC22210847-2198675025TCAGCAAAGCACATTCChr14: SC222219847-2198675026ATCGCCGTTACTGTCGCGAACGChr14: SC222201981-2300014875TTTATTAGCGAAGGAGACCChr14: SC2222019847-2198675026ATCGCCGTGCGTGGCGAAACGChr14: SC22230051-2300714874ATCTTGCTGGTGGCGAAACGChr14: SC22230051-2300714875TTTATTAGCGAAGGGAGACCChr14: SC22230051-2300714876TGCTACATATGCCCTAGTACGChr14: SC22350500-536104877TGTATCATAGCCTAGTACGChr14: SC2256500-556104881TACCGCGTCATATGCCATACGGChr14: SC2256190-563134752TGTACAATAGCCGTATACGGChr14: SC2256190-561014751TGGTACATATGCCTATACGGChr14: SC2256190-562334752TTATAAGCAGCGTAAGCCChr14: SC2256190-562334752TTATAAGCAAGCGAGAGACGGChr14: SC22-697364753AACCACGCATTCCCTCTGTAGATAGCChr14: SC22-697364754TGCTACATTGCAGAGAGCGGChr14: SC22-697364752TGCTACATTGCCTGAAGCAGGChr14: SC22-697364753TACGCGCAATACCAGCGGCGTTGGC	45/1		38 Up downstream HelC
1.3.21.3.5 <th< td=""><td>4541</td><td>TEGETEGEAATEAAAGEACE</td><td>1545 hp downstream HelC</td></th<>	4541	TEGETEGEAATEAAAGEACE	1545 hp downstream HelC
100017ARODIC 1CANTGOClinit - SC22:9606 - 976254867TTGCGGACGAAGTTATCAGChil + SC22:99103 - 982134891ACTGGATTICTCGTGGACACCACCChil + SC22:9020 - 990414967TCCAGAAGACTTGTATTTGCChil + SC22:10608 - 1061034968TTGCCCACTGGAAGACTCCChil + SC22:10642 - 1064395023AATCCATCTTCCAGAATCACCChil + SC22:10642 - 1064395024TTATCAGACATACTGGATGCChil + SC22:2051 - 2300715025TCAGACAACAAGCACATTCChil + SC22:2051 - 2300715026ATGGCCGTTACTGTGGAGACCChil + SC22:235880 - 2450014874ATCTTGGCTGGGGGAGACCChil + SC22:235880 - 2450014875TTTATTAGGGAAGGGAGAGCChil + SC22:23710 - 5327314780TGCTACATAGCCTAGTACGChil + SC22:2510 - 5327314780TGCTACATAGCCTAGGAATTGGChil + SC22:56590 - 5566104811TATCGTGAAAGCTGACAACCGChil + SC22:56590 - 5566104752TTATTAGAGCTAAGAACCGChil + SC22:26082 - 5619134752TTATTAGAGCTATAGCCChil + SC22:26082 - 5619134752TTATTAGAGCAACCGChil + SC22:26083 - 562834618TGCCCAATTTCACTTACACAGChil + SC22:26935 - 69379464752TTGCGGCTCTGGTAGAACCGChil + SC22:20835 - 69379464753AACCACGCATCTCTTGGACACGChil + SC22:20835 - 69379464764TTCATCCTCTGTAAAACCGChil + SC22:20835 - 69379464773AACCACGCATCCTTTGGACCACGChil + SC22:20835 - 69379464784TTCGTCACATAGCGACCGCTTGGGChil + SC22:20835 - 69379464795TTCCGCCTAATGAACGGChil + SC22	4342	TAAGGTCTCAATGGTCCTTCG	Chr14: SC22:07075_07006
110COORCUMPTICAGChill + SC22:98103 -982134890TIGATAATGATGTTGTAGAAGACChill + SC22:9803 -982134891ACTGGATTTCTCGTGGACTGCChill + SC22:10688 - 1061034967TCAGAAGACTTGTAATTTTGCChill + SC22:10689 - 10683 - 1061034968TTGCCCACTGGAAGACTGCChill + SC22:10847 - 2198675023AATCCATCTTCCAGAATCAACChill + SC22:20812 - 390375024TTATCAGACATACTGGAGACChill + SC22:20812 - 329075025TCAGACAACAAGCACATTCChill + SC22:20815 - 320074874ATCTTGGCTGGTGGGGAAACGChill + SC22:23800 - 243894795TGTATTCAGGCACATCGGChill + SC22:23808 - 243894794TGTATTCAGGCTCAGATCGChill + SC22:253490 - 5335194880AGGGTGGCTAAGTATGGChill + SC22:55809 - 5536104881TATCGTGGTAATAGAAGTCCChill + SC22:56809 - 558194792TTATTAAGAGCTGAGAACCGChill + SC22:56809 - 5682334718TGGTATCATTACCCATTACCGChill + SC22:56809 - 5692364721TCTGGCTCTGTAGAAAGCCChill + SC22:69395 - 6934154732TCTATAAGAGCTGAGAACCGChill + SC22:69395 - 693314733AACCACGCATCCTCGTGACAChill + SC22:69394 - 6983334309TTGTGGGGGAGCCGCTTGGChill + SC22:69341 - 503594416TTCACGTCTGAATAGAGAGGChill + SC22:71136 - 7113564517TCATCACTGAATGGAACCGChill + SC22:71136 - 7113564618TCAGGATGCAATCCAGGCTGCJ274 bp downstream J/RJ stop codon4518TGCCAATTGACTGAATCGJ274 bp downstream J/RJ stop codon4524AATCAGGAAACTGAACAGC <t< td=""><td>4800</td><td>TTGCGGACGAAGTTATCAG</td><td>Chr 14: SC 22:97075 - 97090</td></t<>	4800	TTGCGGACGAAGTTATCAG	Chr 14: SC 22:97075 - 97090
100110011001100110014891ACTGGATTICTTCGTCGACTGCCh14:SC22:0021900414967TCAGAAGACTTGTTATTTGCCh14:SC22:106021064395023AATCCATCTTCCAGAATCAACCh14:SC22:106421064395024TTATCAGACATACTCGATTCCh14:SC22:2021298675025TCAGACAACAAGCACATTCCh14:SC22:2058123007114874ATCTTGGCTGGTGGGAACCGCh14:SC22:2308712397364875TTTATTAGGCAAGGCACACTGGCh14:SC22:23701-5327314780TGCTACATATGCCTAGTACGCh14:SC22:23701-5327314780TGCTACATATGCCTAGTACGCh14:SC22:35710-5327314881TATCGTCGTTAAGGTAATGGCh14:SC22:5509556104752TTATTAGACATATGCCATTACGGCh14:SC22:50509556104752TGTATCATATGCCATTACGGCh14:SC22:6025156925364752TCTCGCCTCTGTAGATAGCCCh14:SC22:60395693334752TCTCGCCTCTGTAGATAGCCCh14:SC22:7035956934154752TCTCGCACATTCACCTTACCAGCh14:SC22:7035956934154752TCTCGCACATTCACGTACGGCh14:SC22:7035956934154752TCTCGCACATTCACGTACGGCh14:SC22:7035956934154753TACCCCCTGTAAGACACGCh14:SC22:7035956934154754TGCTCACATGCGACATCGCh14:SC22:7035956934154752TCTCCGCAGATCACGTGAGCGCh14:SC22:703	4807		Chr14: SC22.97000 - 97023
1011ACTOGRAT ICCURCTORClinit 4: S222:06083 - 1061034967TCAGAAGACTTGTTATTTGCClinit 4: SC22:106483 - 1061034968TTGCCCACTGGAAGACTGCClinit 4: SC22:1941 - 2198675023AATCCATCTTCCAGAATCACClinit 4: SC22:2197 - 2297365024TTATCAGACATACTGGATTCClinit 4: SC22:2197 - 2297365025TCAGACAACAAGCACATTCClinit 4: SC22:21980 - 2480114875TTTATTAGGCGAAGGAGAGCClinit 4: SC22:2380 - 2480114874ATCTTGGCTGGTGGCGAAACGClinit 4: SC22:3580 - 248094790TGTATTCAAGGCTCACATCGGClinit 4: SC22:35290 - 5353194880AGGCGTGCTTAGGTATGGClinit 4: SC22:55809 - 556104881TATCGTCGTAATAGAAGTCCClinit 4: SC22:55809 - 556104881TGCCAATTACGCCAATACGGClinit 4: SC22:5515 - 625334752TTATTAAGACTGAGAACCGClinit 4: SC22:6930 - 568234618TGCCCACTTCCTGTAGAAGCCClinit 4: SC22:6935 - 6933144753TGCCGCTCTGTAGAAGCCClinit 4: SC22:69395 - 6931454753TCCGCTCTGTAGAAGCCClinit 4: SC22:69395 - 693344618TGCCCACTTGACTAGGCClinit 4: SC22:69395 - 693344752TCTCGCTCTGTAGAAGCCClinit 4: SC22:69341 - 6398534753TGCCGCATCGGTGGGClinit 4: SC22:70355 - 7035794754TGCCTCTGTATAAGACAGGClinit 4: SC22:70359 - 7035794755TGCGCTGTGGAGTGGGGGGClinit 4: SC22:70359 - 7035794756TGCCTCTGGTAGATCGClinit 4: SC22:711639-71169947577TGCCTCCTGGTAGAGCGClinit 4: SC22:711639-7116994758TGCCCAATTGAG	4890	ACTGGATTTCTCGTCGACTGC	Chr 14: SC 22:98193 - 98213
770Tecton No. CriterianClinity Science790Tracca Carta Cric Gaa Garta CaacClinity Science5023AATCCATCTTCC AGAATCAACClinity Science5024TTATCA GACAATACTCGATTCClinity Science5025TCA GACAACAAGCACATTCClinity Science5026ATGECCGTTACTGTCGA GACClinity Science4874ATCTTGGCTGGTGGCGAAACGClinity Science4875TTTATTAGCGAAGGCACACTCGGClinity Science4749TGCTTACAATATGCCCTAGTACGClinity Science4750TGCTAACATATGCCCTAGTACGClinity Science4880AGGCGTCGCTTAGGATTGGClinity Science4881TACCTCGTAATAGAAGTCCClinity Science4752TTATTAAGCTGAGAACGClinity Science4752TTATTAAGCTGAGAACGGClinity Science4752TCTCGCTCTGTATAGAACCGClinity Science4752TCTCGCTCTGTAAAGACCGClinity Science4752TCTCGCTCTGTAAGACCGClinity Science4753AACCACGCATCCTCTGTGACClinity Science4754TGCGCCTTTAGGATAGCCClinity Science4755TTGCGAGCGCTTGGGCClinity Science4752TCTCGCTGTAAAGACAGGClinity Science4752TCTCGCTGTAAAGACAGGClinity Science4753TACCACGCATCACTGGACCGClinity Science4754TGCTGCTTGGACACCGClinity Science4755TTGCTCTGTAAAGACAGCGClinity Science4756TGCCCTTTGGACACCGClinity Science4757TTATCAGCACACGTTGGACCClinity Science4758	4891	TCAGAAGACTTGTTATTTGC	Chr14: SC22:99021 -99041 Chr14: SC22:106083 -106103
7730FIGUE ALTOCINETICChr 14SC22:2193412193625024TTATICAGACATACTCGATTCChr 14: SC22:2193412198675025TCAGACAACAGCACATCChr 14: SC22:2193412198675026ATGGCGTTACTGTGAGACChr 14: SC22:2300512290715027TTATTAGCGAAGGCAAACGChr 14: SC22:2308012436014874ATCTTGGCTGGTGGCGAAACGChr 14: SC22:2308012438094749TGTATTCAAGCTCACATCGGChr 14: SC22:332105335194880AGGCGTCGCTTAGGTATGGChr 14: SC22:3534995335194880AGGCGTCGCTTAGGTATAGCGChr 14: SC22:5505905566104881TATCCGTCGTAATAGCATTACGGChr 14: SC22:56189561014881TATCCGTCGTAATAGCATTACGGChr 14: SC22:692355692334618TGCCCAATTTCACTTACACAGChr 14: SC22:69355634154732TTATTAAGAGTGAGACACGChr 14: SC22:69356334154733AACCACGCATCTCTGTAAAGACCGChr 14: SC22:69356334154734AACCACGCACCCTTCTGTGACAChr 14: SC22:7035477035794306TGTCATACATTGAGACAGGChr 14: SC22:7035477035794309TTGTGGAAGGAGCGCGTTTGGChr 14: SC22:71135661714616TCCATCACTTGGTCACATCG1505 bp upstream HelC4297TGCCTCTTGCTAGCAAGG1274 bp downstream APR 1 stop codon4219TGTGCATACAGGTAACG29718 bg downstream APR 1 stop codon4229ATCATCACAGTACAGCTACC28915 bp downstream APR 1 stop codon4230TGTCCATACAGAGACACG29815 bp downstream APR 1 st	4968	TTGCCCACTGGAAGACTGC	Chr14: SC22:106039 -106109
3024THATCAGACHACHCORATTCChrl 4: S022:2198472198675025TCAGACAACAGCACATTCChrl 4: S022:2219172297165026ATGGCCGTTAGTACTGCGAGCChrl 4: S022:2300512300714874ATCTTGGCGGGGGGAAACGChrl 4: S022:2415802436014875TTTATTAGCGAAGGGAGAGCChrl 4: S022:2318492438894780TGTATTCAAGGCTCACATCGGChrl 4: S022:3310-5327314750TGCTACATATGCCCTAGTACGChrl 4: S022:3510-5335194880AGGCGTCGCTAGTATGGATTGGChrl 4: S022:55690-566104881TATCGTCGTAATAGCACATTACGGChrl 4: S022:55690-5619134752TTATTAAGAGTGAGAACCGChrl 4: S022:561892-5619134752TTATTAAGAGTGAGAACCGChrl 4: S022:6613-628234618TGCCCCATTTCGATATAGCCChrl 4: S022:69395-6934154732TCTCGCTCGTAATAGCCChrl 4: S022:69395-6934154733AACCACGCATCCTCTGTGACChrl 4: S022:69395-6934154734AACCACGGATCCTCTGTGGACChrl 4: S022:07359-7035794306TGTCATACATTGAGATCAGChrl 4: S022:07359-7035794306TGTCGACACGTTGG1550 bp upstream HelC4297TGCTCTTGGTAACAAGG1560 chrl 4: S022:07364-7113564617TCATCACATGACACACGC1570 bp upstream A/RI stop codon4628TCCACATGCATCACATGG19278 bp downstream A/RI stop codon4799TGCTCTTAGCTAAGCACACCG28915 bp downstream A/RI stop codon4710TCATCACATGACATACCACGCACG28915 bp downstream A/RI	5023		Chr14: SC22:100420 -100439
023ITACAGRAACAAGCACATTCChr14: SC22:29717-229736026ATGGCGTTACTGTCGAGACChr14: SC22:20311-3200714874ATCTTGGCTGGTGGCGCAAACGChr14: SC22:243580-2436014875TTTATTAGCGAAGGACAGCChr14: SC22:23380-2436014876TGTATTCAAGGCTCACATCGGChr14: SC22:233210-5327314790TGTATTCAAGGCTCACATGGGChr14: SC22:532710-5327314881TATCGTCGTAATGAGAACGGChr14: SC22:557050-5570704881TATCGTCGTAATGAGAACCGChr14: SC22:557050-5570704751TGGTATCATATGCCATTACGGChr14: SC22:602515-6025364752TTATTAAGAGCTGAGAACCGChr14: SC22:602515-6025364732TCTCGCTCTCGTAGATAGCCChr14: SC22:602515-6025364732TCTCGCTCTCGTAGATAGCCChr14: SC22:60215-6092364733AACCACGCACTCTCTGTGACChr14: SC22:703941-7039614734ACCCACGCATCCTCTGTGACAChr14: SC22:703941-7039614735TCTCACACATGGAGACGGChr14: SC22:70136-7113664736TGCTATACATTGAGGATGGChr14: SC22:70136-7113664737TCCCCACATGCTGACCAGGChr14: SC22:711336-7113664747TCATCACTCTCCTCGTGTCCChr14: SC22:711376-7113664717TCATCACTCACTGCATAGCAPR/4797TGCCTCTTGCTGCAATGCAPR/4797TGCCTCAATGCGACACGCTAAGP278 bp downstream APR/ stop codon4297TGCCTCACTGCCATACCAPR/4297TGCCCCGTAATGCACACGCTGAG19278 bp downstream APR/ stop codon4219ACTCAGGAACCACGCTGAATC28921 bp downstream APR/ stop codon4229ACTCAGCAATGACACGCT	5024	TTATCAGACATACTCGATTC	Chr14: SC22:219341 -219302
3020ATGGCGGTTACIGTCGAGACChrl+1: SC22:230051-2300714874ATCCTTGGCIGGTGGCGAAACGChrl+1: SC22:230051-2300714875TTTATTAGGAAGGGAGAGCChrl+1: SC22:233869-2438894749TGTATTCAAGGCTCACATCGGChrl+1: SC22:333194750TGCACATATGCCCTAGTACGChrl+1: SC22:556590-5566104880AGGGTGGCTAAGATAGGAGCCChrl+1: SC22:556189-5507074751TGGTATATAGAAGCCGAGAACCGChrl+1: SC22:561890-5506104881TATCGTCGTAATAGCAGTACGGChrl+1: SC22:561890-5506104752TTATTAAGACTGAGAACCGChrl+1: SC22:69230-5628234618TGCCCAATTTCACTTACACAGChrl+1: SC22:69315-692364732TCTCGCTCTGTAGATAGCCChrl+1: SC22:69395-6934154733AACCACGCATCCTCTGTGACChrl+1: SC22:69395-6934154734TGTCGAGGCAGCCGTTTGGChrl+1: SC22:70359-7035794626TTCATCCTCTGTGAACAGGChrl+1: SC22:70359-7035794739TGTCGAACATGATCGATCCAGChrl+1: SC22:703941-7039614616TTCGGTGGAATCGATCCAGChrl+1: SC22:703941-7039614617TCATCACTCTCTCGTGTCCChrl+1: SC22:711367-7116994395TCCTCACAATGCTGACACGSpecific to 5' end of Helinons1091TCAGCATACAGCTACGCATCC12747 bp downstream <i>JRI</i> stop codon4219ATTGGAACTACAGCTACGSpecific to 5' end of Hej34239TGTTGCATACAGCTACGCATCC31210 bp downstream <i>JRI</i> stop codon4211TACACGAACCAGCTAACGSpecific to 5' end of Hoj34304TACTGGAACGGAAACCTAACGSpecific to 5' end of Hoj34304TACTGGAACGGAAAACCTAA<	5024	TCAGACAACAAGCACATTC	Chr14: SC22:219647 -219667
36.50ATGOCCOTTOCOTONICOChile SC22243580 -2436014874ATCTTGGCTGGTGGCGCGAAACGChile SC22243580 -2436014755TTTATTACCGAAGGCACATCGGChile SC22233210 -5327314750TGCTACATATGCCCTAGTACGChile SC22:53210 -5327314751TGCTGCTGTAATGAGATTTGGChile SC22:53700 -5566104881ATCGTCGTGTAATGAGAACCGChile SC22:55050 -5570704751TGGTATCATATGCCATTACGGGChile SC22:56280 -568134752TTATTAAGACTGAGAACCGChile SC22:66280 -5628234753TCCCCAATTTCACTTACACAGChile SC22:692515 -692564752TTCATCAGCTCGTGAGAACCGChile SC22:69393 - 6034154753ACCACCGCATCCTCTGTGACAChile SC22:69393 - 6034154753ACCACCGCATCCTCTGTGACChile SC22:703941 -7039614754TTCATCCTCTGTAATAGACACGChile SC22:7039704755TTCATCACTCACTGAGATGGAChile SC22:703941 -7039614766TTCATCCTCTGTAATAGACACGChile SC22:703941 -7039614761TCCACAATGCTGACATCCAGChile SC22:711336 -7113564771TCATCACTCACTTAGCATCCAGChile SC22:710397116994795TCCTCACAAGCACACTGG1520 bp upstream HelC4296TGTGCATACAGACACCTGAG19278 bp downstream A/RJ stop codon4210ATCATCACGACACCTACACTACC12747 bp downstream A/RJ stop codon4220ACATAGCCATACACGCTACC28915 bp downstream A/RJ stop codon4221TGACATAGCATACACGCATACACGSpecific to 5' end of Hej34304TACTGGACATCACGTTACCTG289215 bp downstream A/RJ stop codon4220ACATAGCCATCACCTCACCC	5025	ATGGCCGTTACTGTCGAGAC	Chr14: SC22:229717 -229750
arriteTHATTAGCOAGGGAGAGCChrl4: SC22:24389 2438894749TGTATTCAAGGCTCACATCGGChrl4: SC22:537114750TGCTACATATGCCCTAGTACGChrl4: SC22:53710 -5327314880AGGCGTCGCTTAGGTATTGGChrl4: SC22:5500 -5566104881TATCGTCGTAATAGAAGTCCChrl4: SC22:5500 -5570704751TGGTATCATATGCCATTACGGChrl4: SC22:50150 -5570704752TTATTAAGAGCTGAGAACCGChrl4: SC22:69203 -5628234618TGCCCAATTTCACTTACACAGChrl4: SC22:69203 -5628234732TCTCGCTCTGTGTAAACACGCChrl4: SC22:69395 -6934154733AACCACGCATCCTCTGTGACChrl4: SC22:69319 -6953464744TCTCGCTCTGTATAAGACACGChrl4: SC22:69319 -695334755TCCTCCTCTGTATAAGACACGChrl4: SC22:70359 -7035794766TGCCAACATGATCCAGGChrl4: SC22:70359 -7035794766TTCATCCTCTCGTGTCCChrl4: SC22:70136 -7113564777TGCGCTCTACACATGAGGCAGGGChrl4: SC22:711639 -7115694789TGTGCAACATGATCCAGG1550 bp upstream <i>HVR1</i> stop codon4790TCAGGCTTCACTTAGCATAC <i>HVR1</i> oor codon4791TGCCCATACACGCTCGG12747 bp downstream <i>AVR1</i> stop codon4792TGCCCATACACGCTACGC28915 bp downstream <i>AVR1</i> stop codon4793TATGACAGTACACCGCTCG12747 bp downstream <i>AVR1</i> stop codon4794ATCATACACGTACACATGG28915 bp downstream <i>AVR1</i> stop codon4794ATCATACACGTACACATGG28915 bp downstream <i>AVR1</i> stop codon4794ATCATACACGTACACATGG33849 bp downstream <i>AVR1</i> stop codon4795ACATACA	4874	ATCTTGGCTGGTGGCGAAACG	Chr14: SC22:230031 -233601
1749TGTATTCAAGCTCACATCGGChrl4: SC22:532710.:5327314750TGCTACATATGCCACATCGGChrl4: SC22:55490.:556104880AGCGTCGCTTAGGTATTGGChrl4: SC22:555050.:5570704751TGGTATCATATGCCATTACGGChrl4: SC22:551282.:5619134752TTATTAAGAGCTGAGACCGChrl4: SC22:652803.:5628234753TGCCCAATTTCACTTACACAGChrl4: SC22:692515.:6925364732TCTCGCTCTGTAGATAGCCChrl4: SC22:69395.:6934154733AACCACGCATCCTCGTGACChrl4: SC22:69395.:6934154734AACCACGCATCCTCTGTGACChrl4: SC22:69335.:9035794306TGTCATCCTCTGTAAAGACACGChrl4: SC22:09395.:9035794306TGTCATACATTGAGGATGGChrl4: SC22:09359.:7035794306TGTCATACATGAGGATGGChrl4: SC22:71136.:7113564617TCATTCACTCTCTGTGTCCChrl4: SC22:71136.:7113564618TCCCCAATGCTGACATCG1550 bp upstream HelC4297TGCCTCACTACACATCG1550 bp upstream HelC4293TGTGTCAACAACAGCGTAGG19278 bp downstream <i>AVRI</i> stop codon4219TGATCATACAGCACACGCTCG12147 bp downstream <i>AVRI</i> stop codon4220AATCAGGAACTCACGCTCAGC3120 bp downstream <i>AVRI</i> stop codon4621TGACTATGAATTGAGCTAACG28915 bp downstream <i>AVRI</i> stop codon4622ACTAGGAATACAGACAGCC33849 bp downstream <i>AVRI</i> stop codon4623ACCGGTGAAAACCGCSpecific to 5' end of Hop34630TATCGACGTAAACGCACACGCSpecific to 5' end of Hop34641TGCACTCACTGTCATACATTC28915 bp downstream <i>AVRI</i> stop codon4622AC	4875	TTTATTAGCGAAGGGAGAGC	Chr14: SC22:243869 -243889
1750TGCTACATATGCCCTAGTACGChrl4: SC22:533499 -5335194880AGGCGTCGCTTAGGTATTGGChrl4: SC22:5509 -5566104881TATCGTGTAATAGAAGTCCChrl4: SC22:5509 -55670704751TGGTACATATGCCATTACGGChrl4: SC22:561892 -5619134752TTATTAAGAGCTGAGAACCGChrl4: SC22:6930 -5628234618TGCCCAATTCACTTACACAGChrl4: SC22:693095 -6934154732TCTCGCTCTCGTAGATAGCCChrl4: SC22:693295 -6979464264TCATCCTCTGTTAAGACACGChrl4: SC22:693295 -6979464265TTCATCCTCTGTTAAGACACGChrl4: SC22:703559 -7035794306TGTCATCACATTGAGATGGChrl4: SC22:70359 -7035794306TGTCATCACTTGGAATCGAGChrl4: SC22:71136 -7113564617TCATTCACCTCTCGTGTCCChrl4: SC22:71136 -7113564617TCATTCACTCTCTGGTGTCCChrl4: SC22:71136 -7113564617TCATTCACTTCTCGTGTGCChrl4: SC22:71136 -7113564617TCATTCACTTCTCGTGGACGI550 bp upstream <i>HVR</i> 4299TGTTGCATACAGCATCAG <i>JVRI</i> ORF4299TGTTGCATACAGCATCAC <i>JVRI</i> ORF4240AATCAGGAACTCACGCTTCG12477 bp downstream <i>JVRI</i> stop codon4621TGACTATCACATGACATCC3849 bp downstream <i>JVRI</i> stop codon4625ACCGTGGTACTGCATACACTG3849 bp downstream <i>JVRI</i> stop codon4626ACATAGCATCACACTACCAC3853 bp downstream <i>JVRI</i> stop codon4621TGACTATGAATAGAGCAGAGG38453 bp downstream <i>JVRI</i> stop codon4622ACATAGCATCACACTGTCATACC3849 bp downstream <i>JVRI</i> stop codon4623ACCTGGTAAATACCAGGTGACA </td <td>4749</td> <td>TGTATTCAAGGCTCACATCGG</td> <td>Chr14: SC22:532710 -: 532731</td>	4749	TGTATTCAAGGCTCACATCGG	Chr14: SC22:532710 -: 532731
4880AGGCGTCGCTTAGGTATTGGChrl4: SC22:556590 -5566104881TATCGTCGTAATAGAAGTCCChrl4: SC22:56590 -5570704751TGGTATCATATGCCATTACGGChrl4: SC22:562803 -5628234618TGCCCAATTTCACTTACACAGChrl4: SC22:692515 -6925364732TCTCGCTCTGTAGATAGCCChrl4: SC22:69395 -6934154733AACCACGCATCCTCTGTGACChrl4: SC22:69395 -6979464626TTCATCCTCTGTAAAGACACGChrl4: SC22:69395 -6979464626TGCATACATTGAGGATGGChrl4: SC22:703597 -0035794306TGTCATACATTGAGGATGGChrl4: SC22:703591 -7035794616TCCGGTTGGAAATGGATCCAGChrl4: SC22:711336 -7113564617TCATTCACTCTCGTGTCCChrl4: SC22:711336 -7113564617TCATCACTCTCGTGTCCChrl4: SC22:711336 -7116994995TCCTCACAATGCTGACACGJP27 NB4997TGCTCTCACTTACGAACGSpecific to 5' end of Helitrons1091TCAGGCTTACCAGACGCTGAG19278 bp downstream <i>AVRI</i> stop codon4239TGTTGCATACAGCACAGCTCAATTC28921 bp downstream <i>AVRI</i> stop codon4620ACCATACAGCATCACGCTAACC28915 bp downstream <i>AVRI</i> stop codon4621TGACTATGAATTGAGCTAACG28915 bp downstream <i>AVRI</i> stop codon4622ACCGTGGTACTGTCATACATTG3849 bp downstream <i>AVRI</i> stop codon4630TATCGCAATACAGACGCSpecific to 5' end of Hop34303ACTTCCCAGTGACAAACGCSpecific to 5' end of Hop34304TATCGGACATTACACTGGSpecific to 5' end of Hop34303ACTCCCAGTGACAAACGCSpecific to 5' end of Hop34304TATCGGA	4750	TGCTACATATGCCCTAGTACG	Chr14: SC22:533499 -533519
4881TATCGTCGTAATAGAAGTCCChrl4: SC22:557050 -5570704751TGGTATCATATGCCATTACGGChrl4: SC22:561892 -5619134752TTATTAAGAGCTGAGAACCGChrl4: SC22:562803 -5628234618TGCCCAATTTCACTTACACAGChrl4: SC22:692315 -692364732TCTCGCTCTGTAGATAGCCChrl4: SC22:693395 -6934154733AACCACGCATCCTCTGTGACChrl4: SC22:69813 -6985334309TTGTGGAGGCAGCCGTTTGGChrl4: SC22:703559 -7035794306TGCTCATACATTGAGATGGGChrl4: SC22:703941 -7039614616TTCGGTGGAATGCAGChrl4: SC22:711336 -7113564617TCATTGATGGAATCCAGChrl4: SC22:71136 -7113564618TCCGCTCTTGGACATCGChrl4: SC22:71136 -7113564793TGCTCTTGGCATCCAGGChrl4: SC22:71136 -7113564617TCATCACTCTCTCGTGTCCChrl4: SC22:71136 -7113564794AATCAGCATCCAGCTCAGG1550 bp upstream HelC4297TGCCTCTTGCTCGAAGGSpecific to 5' end of Heiltrons1091TCAGGCTTACTTAGCTAACAA//R / ORF4239TGTTGCATACAGGACGCTGAG19278 bp downstream A//R / stop codon4240AATCAGGAATCCACGCTTCG212147 bp downstream A//R / stop codon4621TGACTATGACTTAACATTC28921 bp downstream A//R / stop codon4622ACCATGGAATCCACCATCACC31210 bp downstream A//R / stop codon4623ACTTGCAATGAGAACGCSpecific to 5' end of Hop34630TATGGAACAGTGAACGCSpecific to 5' end of Hop34733GCCGAATACAGAAAACCCTAAA//R / ORF4744GGAAGTAACCAGTGACAAGCGSpecific to 5' end of H	4880	AGGCGTCGCTTAGGTATTGG	Chr14: SC22:556590 -556610
4751TGGTATCATATGCCATTACGGChrl4: SC22:561892-5619134752TTATTAAGAGCTGAGAACCGChrl4: SC22:562803-5628234618TGCCCAATTTCACTTACACAGChrl4: SC22:692515-6925364732TCTCGCTCTGTAGATAGCCChrl4: SC22:697926-6979464626TTCATCCTCTGTATAAGACACGChrl4: SC22:69813-6985334309TGTGGAGGCAGCCGCTTGGChrl4: SC22:703559-7035794306TGTCATACATTGAGATCGAChrl4: SC22:703591-7035794306TGTCATACATTGAGATCGAChrl4: SC22:711366-7113564617TCATTCACTCTCTGTGTGCChrl4: SC22:711367-7113564618TCCATCAATGCTGACAATCG1550 bp upstream HelC4395TCCTCACAATGCTGACAGCG59eeiffe to 5' end of Helitrons1091TCAGGCTTCACTTAGCATACA/// I ORF4239TGTTGCATACAGACAGCTGAG19278 bp downstream $AVRI$ stop codon4240AATCAGGAATCACGCTCG12747 bp downstream $AVRI$ stop codon4620ACATAGCATCACACTACC28915 bp downstream $AVRI$ stop codon4621TGACTATCAACGTAACG28915 bp downstream $AVRI$ stop codon4622ACTGGAACTCACCCATCC31210 bp downstream $AVRI$ stop codon4630TATGGACAATACAGAGAGCG34839 bp downstream $AVRI$ stop codon4630TATGGACAATACAGAGACGSpecific to 5' end of Hop3333ACTCCCAGTGAACCCTAAC $A'RI$ ORF4240ACTCCCAGTGAACACGCSpecific to 5' end of Hop34304TACCCGAACAACCCCACGC28915 bp downstream $AVRI$ stop codon4620ACATAGCAATACAGAGAGAG38849 bp downstream $A'RI$ stop codon4621TGACTATG	4881	TATCGTCGTAATAGAAGTCC	Chr14: SC22:557050 -557070
4752TTATTAAGAGCTGAGAACCGChrl4: SC22:562803 -5628234618TGCCCAATTTCACTTACACAGChrl4: SC22:692515 -6923664732TCTCGCTCTGTAGATAGCCChrl4: SC22:693395 -6934154733AACCACGCACTCTGTGACChrl4: SC22:693395 -6939464626TTCATCCTCTGTATAAGACACGChrl4: SC22:703599 -7035794809TTGTGGAGGCAGCCGTTTGGChrl4: SC22:703599 -7035794816TTCGGTTGGAATCGATCCAGChrl4: SC22:703599 -7035794816TTCGGTTGGAATCGATCCAGChrl4: SC22:711336 -7113564617TCATCACTTCTCTCGTGTCCChrl4: SC22:711679-7116994395TCCTCACAATGCTGACATCG1550 bp upstream HelC4297TGCCTCTTTGCTCTGAAGGSpecific to 5' end of Helitrons1091TCAGGCTTCACGAGCTGAG19278 bp downstream AVRI stop codon4240AATCAAGCATCCACGCTCG1210 bp downstream AVRI stop codon4621TGCATACACGTAGCTCAATCC28915 bp downstream AVRI stop codon4622ACCGTGGTACTGCATACACG28915 bp downstream AVRI stop codon4630TATGGACAATACAGAGAGC3483 bp downstream AVRI stop codon4630TATGGACAATACAGAGACGSpecific to 5' end of Hop34304TACTCCAGGGACAAACGCSpecific to 5' end of Hop34305TACTCCAGGAGAGCAGTTTAIR2 ORF4304TACTCCAGGACAAACGCSpecific to 5' end of Hop34304TACTCCAGGAGAGCAGTTTAIR3 ORF4304TACTCCAGGCACAGTTAIR3 ORF4304TACTCCAGGAAAGCCAGATTAIR3 ORF4304TACTCCAGCGACAGAGCAAIR3 ORF4305ATGCGCGACGACAGCAG	4751	TGGTATCATATGCCATTACGG	Chr14: SC22:561892 -561913
4618TGCCCAATTTCACTTACACAGChrl4: SC22:692515 - 6925364732TCTCGCTCCGTAGATAGCCChrl4: SC22:693395 - 6934154733AACCACGCATCCTCTGTAGCChrl4: SC22:69726 - 6979464266TTCATCCTCTGTATAGACACGChrl4: SC22:69726 - 6979464309TTGTGGAGGCAGCCGTTTGGChrl4: SC22:703559 - 7035794306TGTCATACATTGAGGATGGChrl4: SC22:703941 - 7039614616TTCGGTTGGAATCGATCCAGChrl4: SC22:71136 - 7113564617TCATTCACTCTCTGTGTCCChrl4: SC22:71136 - 7113564797TGCCTCTTTGGCTGACATCG1550 bp upstream HelC4299TGCTGCATACAGCTGAGAGGSpecific to 5' end of Helitrons1091TCAGGCTTCACTACGCTGAG12747 bp downstream AVRI stop codon4240AATCAAGGAACTCACGCTGAG12747 bp downstream AVRI stop codon4251TGATGCATACAGTTAGCTCAATTC28921 bp downstream AVRI stop codon4620ACATAGCCATCCACTCATTCC31210 bp downstream AVRI stop codon4621TGACTATGAATTGAGCTAACG28915 bp downstream AVRI stop codon4630TATGGACAATACAGGCAGCG38453 bp downstream AVRI stop codon4630TATGGACAATACAGAGACGSpecific to 5' end of Hop31033GCCGACCGAAAACCCTAAAVRI ORF2934CCAGCCAGAAAACCCTAAAVRI ORF2934CCAGCCGCAAAAACCCTAAAVRI ORF2934CCAGCCGCAAAAACCTAGCSpecific to 5' end of Hop31033GCCGCCCGAGAAAACCCTAAAVRI ORF2934CCAGCCGCAAAAACCCTAAAVRI ORF2934CCAGCCGCAAAAACCCTAAAVR2 ORF303AATTGCA	4752	TTATTAAGAGCTGAGAACCG	Chr14: SC22:562803 -562823
4732TCTCGCTCTCGTAGATAGCCChr14: SC22:693395 -6934154733AACCACGCATCCTCTGTGACChr14: SC22:69726 -6979464626TTCATCCTCTGTATAAGACACGChr14: SC22:69813 -6985334309TTGTGGAGGCAGCCGTTTGGChr14: SC22:703941 -7039614316TTCGGTTGGAATCGATCCAGChr14: SC22:711336 -7113564617TCATCACTCTCGTGTCCChr14: SC22:711376 -7116994395TCCTCACAATGCTGACATCGI550 bp upstream HelC4397TGCCTCTTGGTGCACATCGSpecific to 5' end of Helitrons1091TCAGGCTTCACTTAGCATACAVRI ORF4240AATCAGGAACTCACGCTTCG12747 bp downstream AVRI stop codon4240AATCAGGAACTCACGCTTCG32819 bp downstream AVRI stop codon4619ATCATACACGTTAGCTCAACTC32811 bp downstream AVRI stop codon4620ACATAGCAATCAACACC32815 bp downstream AVRI stop codon4625ACCGTGGTACTGTCATACATG33849 bp downstream AVRI stop codon4626TATGACATCAAGACAGCSpecific to 5' end of Hop34303TATGGACAATACAGAGACG34833 bp downstream AVRI stop codon4625ACCGTGGTACTGTCATACATTG33849 bp downstream AVRI stop codon4626ACCATCAACAGAGACGSpecific to 5' end of Hop34304TACTCGAACGATAAACGCSpecific to 5' end of Hop34304TACTCGAACGATAAACGCSpecific to 5' end of Hop34304TACTCGAACGATAAACTGGSpecific to 5' end of Hop34304TACTCGAACGATAAACTGGSpecific to 5' end of Hop34304TACTCGCAGAAGCCTAAACTGGSpecific to 5' end of Hop34333GCCGCCCG	4618	TGCCCAATTTCACTTACACAG	Chr14: SC22:692515 -692536
1732AACCACGCATCGTCTGTGACChr14: SC22:697926 -6979464733AACCACGCATCCTCTGTGACChr14: SC22:69813 -6985334309TTGTGGAGGCAGCCGTTTGGChr14: SC22:703559 -7035794306TGTCATACATTGAGATGGChr14: SC22:703941 -7039614616TTCGGTTGGAATCGATCCAGChr14: SC22:711336 -7113564617TCCTACATGCTGACATCG1550 bp upstream HelC4297TGCCTCTTGCTTGACATACAVRI ORF4293TGTGCATACATGAGACAGCTGAG19278 bp downstream AVR1 stop codon4210AATCAGGAACTCACGCTTCG12747 bp downstream AVR1 stop codon4220AATCAGGAACTCACGCTTCG12747 bp downstream AVR1 stop codon4239TGTGCATACAGACAGCTGAG28921 bp downstream AVR1 stop codon4240AATCAGGAACTCACGCTTCG21210 bp downstream AVR1 stop codon4251TGACTATGAATTGAGCTAACG28915 bp downstream AVR1 stop codon4620ACATAGCCATCACATCACC31210 bp downstream AVR1 stop codon4621TGGACATAGAGAGAGGG38453 bp downstream AVR1 stop codon4630ACTTCCCAGTGACAAACGCSpecific to 5' end of Hop34303ACTTCCCAGTGACAAACGCSpecific to 5' end of Hop34304TACTCGAACGATAAACTGGSpecific to 5' end of Hop34303ACTTCCCCGGAATAACTGGCAVR1 ORF2934CCAGCCGAAAAACCCTAAAVR1 ORF2934CCAGCCGAAAAACCCTAAAVR2 ORF1002TATCCCTCCGGAATTTGACCAVR3 ORF116GGAATAACCAGGTGCTAVR3 ORF127CGATGGCAAGGCAAGGTAVR2-upstream1238GGTGTGTGAAAGGTCCCTT	4732	TCTCGCTCTCGTAGATAGCC	Chr14: SC22:693395 -693415
HighInterfectionChrl H Sch2ory Strange4626TTCATCCTCTGTATAAGACACGChrl H SC22:69813 - 6985334309TTGTGGAGGCAGCCGTTTGGChrl H SC22:703541 - 7039614616TTCGGTTGGAATCGATCCAGChrl H SC22:711336 - 7113564617TCATTCACTCTCTCGTGTCCChrl H SC22:711679 - 7116994395TCCTCACAATGCTGACATCG1550 bp upstream HelC4297TGCTCACTTAGCATACAVR I ORF4239TGTTGCATACAGACAGCGCAGAG19278 bp downstream AVR I stop codon4240AATCAGGAACTCACGCTTCG12747 bp downstream AVR I stop codon4240AATCAGGAACTCACGCTCAGTC28921 bp downstream AVR I stop codon4252ACCATAGCATCACACTCAATTC28921 bp downstream AVR I stop codon4620ACATAGCATCACGCTAACG28915 bp downstream AVR I stop codon4621TGACATGACATCACACTCACTG31849 bp downstream AVR I stop codon4622ACCGTGGTACTGTCATACG28915 bp downstream AVR I stop codon4630TATGGACAATACAGAGACG38453 bp downstream AVR I stop codon4303ACTTCCCAGTGACAACGCSpecific to 5' end of Hop34304TACTCGAACGATAAACTGGSpecific to 5' end of Hop34303GCCGCCGAAAAACCCTAAAVR I ORF2934CCAGCCAGAAGGCCAGTTTAVR 2 ORF964GGCAATTAACACATGGCAVR 3 ORF363AATAGACCAGTGAAAGCTAVR 3 ORF364GGAAGTACCAGTGATCATGTTEF-1a ORF889TCGTCGTCAACGGTACATGTTAVR2-upstream1236GATGGTGTAAACGTTAGCCTTAVR2-downstream1238GGTGTGTTGAACAGGTGCT<	4733	AACCACGCATCCTCTGTGAC	Chr14: SC22:697926 -697946
4309TIGTGGAGCCAGCCGTTTGGCh14: SC22:703559 -7035794306TGTCATACATTGAGGATGGChr14: SC22:70359 -7035794306TGTCATACATTGAGGATGGChr14: SC22:71136 -7113564617TCATTCACTCTCGTGTCCChr14: SC22:711679-7116994395TCCTCACAATGCTGACATCG1550 bp upstream HelC4297TGCCTCTTTGCTCGAAGGSpecific to 5' end of Helitrons1091TCAGGCTTCACTTAGCATAC $AVRI$ ORF4239TGTTGCATACAGACAGCTGAGG19278 bp downstream $AVRI$ stop codon4240AATCAGGAACTCACGCTCAGC28921 bp downstream $AVRI$ stop codon4250ACATACCAGTAGCTCAATTC28915 bp downstream $AVRI$ stop codon4620ACATAGCCATCCACTCATCC31210 bp downstream $AVRI$ stop codon4621TGACTATGAATTGAGCTAACG28915 bp downstream $AVRI$ stop codon4630TATGGACAATACAGAGACG3849 bp downstream $AVRI$ stop codon4303ACTTCCCAATGCAAACGCSpecific to 5' end of Hop34304TACTCGAACGATAAACGGSpecific to 5' end of Hop34303GCCGACCAAAAACCCTAA $AVRI$ ORF2934CCAGCCAGAAGGCCAGTTT $AVR2$ ORF964GGCAATTAACCACTGTGCC $AVR3$ ORF1416GAAGTACCAGTGATCATGTT $EF-Ia$ ORF889TCGTCGTCACAGGAAAGCTAGG $AVR2$ -upstream1237TTCGTGGCAAGTCACGTT $AVR2$ -downstream1238GGTGTTGACTGACAGGTGCT $AVR2$ -downstream1238GGTGTTGACAGGGGCCT $AVR2$ -downstream	4626	TTCATCCTCTGTATAAGACACG	Chr14: SC22:69813 -698533
4306TGTCATACATTGAGGATGGCh14: SC22:703941 -7039614616TTCGGTTGGAATCGATCCAGCh14: SC22:711336 -7113564617TCATTCACTCTCTCGTGTCCCh14: SC22:711679-7116994395TCCTCACAATGCTGACATCG1550 bp upstream HelC4297TGCCTCTTTGCTCTGAAGGSpecific to 5' end of Helitrons1091TCAGGCTTCACTAGCATAC $AVRI$ ORF4239TGTTGCATACAGACAGCTGAG19278 bp downstream $AVRI$ stop codon4240AATCAGGAACTCACGCTTCG12747 bp downstream $AVRI$ stop codon4619ATCATACAGCATCCACTCATC28921 bp downstream $AVRI$ stop codon4620ACATAGCATCCACTCATCC31210 bp downstream $AVRI$ stop codon4621TGACTATGAATTGAGCTAACG28915 bp downstream $AVRI$ stop codon4625ACCGTGGTACTGTCATACATTG33849 bp downstream $AVRI$ stop codon4630TATGGACAATACAGAGACGSpecific to 5' end of Hop34304TACTCCAATGGAAACGCSpecific to 5' end of Hop34303GCCGACCGAAAAACCCTAA $AVRI$ ORF2934CCAGCCAGAAGGCCAGTTT $AVR2$ ORF1033GCCGACCGAAAAACCCTAA $AVR3$ ORF363AATAGAGCCTGCAAAGCATG $AVR3$ ORF363AATAGAGCCTGCAAAGCATG $AVR3$ ORF116GGAACTACCAGTGATCATGTT $EF-Ia$ ORF889TCGTCGTCATCGCCAAGTC $EF-Ia$ ORF1236GGTGTTGAACAGGTGCT $AVR2$ -upstream1238GGTGTTGAACAGGTGCT $AVR2$ -downstream1238GGTGTTTGAACAGGTGCT $AVR2$ -downstream	4309	TTGTGGAGGCAGCCGTTTGG	Chr14: SC22:703559 -703579
4616TTCGGTTGGAATCGATCCAGChrl4: SC22:711336 -7113564617TCATTCACTCTCTCGGGTCCChrl4: SC22:711679-7116994395TCCTCACAATGCTGACATCG1550 bp upstream HelC4297TGCCTCTTGGTCTGAAGGSpecific to 5' end of Helitrons1091TCAGGCTTCACTTAGCAATCCAVRI ORF4239TGTTGCATCACGACAGCTGAG19278 bp downstream AVRI stop codon4240AATCAGGAACTCACGCTTCG12747 bp downstream AVRI stop codon4619ATCATACACGTTAGCTCAATTC28911 bp downstream AVRI stop codon4620ACATAGCCATCCCATCC31210 bp downstream AVRI stop codon4621TGACTATGAATTGAGCTAACG28915 bp downstream AVRI stop codon4625ACCGTGGTACTGTCATACATTG33849 bp downstream AVRI stop codon4630TATGGACAATACAGAGACGSpecific to 5' end of Hop34303ACTTCCCAGTGACAAACGCSpecific to 5' end of Hop34304TACTCGAACGATAAACTGGSpecific to 5' end of Hop34303GCCGACCGAAAAACCCTAAAVRI ORF2934CCAGCCAGAAGGCCAGTTTAVR2 ORF964GGCAATTAACCACTCTGCCAVR3 ORF1002TATCCCTCCGGATTTGAGCAVR3 ORF1416GGAAGTACCAGTGATCATGTTEF-1a ORF889TCGTCGTCATCAGCAAAGGCAGGAVR2-upstream1236GGTGTTGAACAGGTGCTAVR2-downstream1238GGTGTTGAACAGGTGCTAVR2-downstream	4306	TGTCATACATTGAGGATGG	Chr14: SC22:703941 -703961
4617TCATTCACTCTCTCGTGTCCChrl4: SC22:711679-7116994395TCCTCACAATGCTGACATCG1550 bp upstream HelC4297TGCCTCTTTGCTCTGAAGGSpecific to 5' end of Helitrons1091TCAGGCTTCACTTAGCATACA/RI ORF4239TGTTGCATACAGACAGCTGAG19278 bp downstream A/RI stop codon4240AATCAGGAACTCACGCTTCG12747 bp downstream A/RI stop codon4240AATCAGGAACTCACGCTAGC38921 bp downstream A/RI stop codon4240AATCAGGAACTCACGCTAATTC28921 bp downstream A/RI stop codon4619ATCATACACGTTAGCTAATCC31210 bp downstream A/RI stop codon4620ACATAGCCATCACTCATCC31210 bp downstream A/RI stop codon4621TGACTATGAATTGAGCTAACG28915 bp downstream A/RI stop codon4625ACCGTGGTACTGTCATACATTG33849 bp downstream A/RI stop codon4303ACTTCCCAGTGACAAACGCSpecific to 5' end of Hop34304TACTCGAACGATAAACTGGSpecific to 5' end of Hop34303GCCGACCGAAAAACCCTAAA/RI ORF2934CCAGCCAGAAGGCCAGTTTA/R2 ORF1002TATCCTCCGGGATTTGAGCA/R3 ORF116GGAAGTACACATGATCATGTTE/F-Ia ORF889TCGTCGTCATCGGCCACGTCE/F-Ia ORF1236GGTGTTGAACAGGTGCTA/R2-upstream1238GGTGTGTTGAACAGGTGCTA/R2-downstream	4616	TTCGGTTGGAATCGATCCAG	Chr14: SC22:711336 -711356
4395TCCTCACAATGCTGACATCG1550 bp upstream HelC4297TGCCTCTTTGCTCTGAAGGSpecific to 5' end of Helitrons1091TCAGGCTTCACTTAGCATACA/RI ORF4239TGTTGCATACAGACAGCTGAG19278 bp downstream A/RI stop codon4240AATCAGGAACTCACGCTTCG12747 bp downstream A/RI stop codon4619ATCATACACGTTAGCTCAATTC28921 bp downstream A/RI stop codon4620ACATAGCCATCCACTCC31210 bp downstream A/RI stop codon4621TGACTATGAATTGAGCTAACG28915 bp downstream A/RI stop codon4625ACCGTGGTACTGTCATACATTG33849 bp downstream A/RI stop codon4630TATGGACAATACAGAGACGSpecific to 5' end of Hop34303ACTTCCCAGTGACAAACGCSpecific to 5' end of Hop34304TACTCGAACGATAAACTGGSpecific to 5' end of Hop34303GCCGACCGAAAACCCTAAA/RI ORF2934CCAGCCAGAAGGCCAGTTTA/R2 ORF1002TATCCCTCCGGATTTGAGCA/R3 ORF116GGAAGTACCAGTGACAAGGTA/R3 ORF1416GGAAGTACCAGTGACAAGGTA/R3 ORF1236AGTGGTAACGGCAGGTTA/R2-upstream1237TTCGTGGCAGTTCCCCTTA/R2-upstream1238GGTGTGTTGAACAGGTGCTA/R2-downstream	4617	TCATTCACTCTCTCGTGTCC	Chr14: SC22:711679-711699
4297TGCCTCTTTGCTCTGAAGGSpecific to 5' end of Helitrons1091TCAGGCTTCACTTAGCATAC $AVRI$ ORF4239TGTTGCATACAGACAGCTGAG19278 bp downstream $AVRI$ stop codon4240AATCAGGAACTCACGCTTCG12747 bp downstream $AVRI$ stop codon4619ATCATACACGTTAGCTCAATTC28921 bp downstream $AVRI$ stop codon4620ACATAGCCATCCACTCATCC31210 bp downstream $AVRI$ stop codon4621TGACTATGAATTGAGCTAACG28915 bp downstream $AVRI$ stop codon4625ACCGTGGTACTGTCATACATTG33849 bp downstream $AVRI$ stop codon4630TATGGACAATACAGAGACGSpecific to 5' end of Hop34303ACTTCCCAGTGACAAACGCSpecific to 5' end of Hop34304TACTCGAACGATAAACTGGSpecific to 5' end of Hop31033GCCGACCGAAAACCCTAA $AVRI$ ORF964GGCAATTAACACTCTGCC $AVR2$ ORF1002TATCCCTCCGGATTTTGAGC $AVR3$ ORF116GGAAGTACCAGTGATCATGTT $EF-Ia$ ORF889TCGTCGTCACGCCAGTT $AVR2$ -upstream1236AGTGGTAAATGTTAGGCAAG $AVR2$ -upstream1238GGTGTGTTGAACAGGTGCT $AVR2$ -downstream1238GGTGTGTTGAACAGGTGCT $AVR2$ -downstream	4395	TCCTCACAATGCTGACATCG	1550 bp upstream HelC
1091TCAGGCTTCACTTAGCATAC $A'RI$ ORF4239TGTTGCATACAGACAGCTGAG19278 bp downstream $AVRI$ stop codon4240AATCAGGAACTCACGCTTCG12747 bp downstream $AVRI$ stop codon4619ATCATACACGTTAGCTCAATTC28921 bp downstream $AVRI$ stop codon4620ACATAGCATCCACTCATCC31210 bp downstream $AVRI$ stop codon4621TGACTATGAATTGAGCTAACTG28915 bp downstream $AVRI$ stop codon4630TATGGACATTACAGGAACG34849 bp downstream $AVRI$ stop codon4630TATGGACAATACAGAGAACG34853 bp downstream $AVRI$ stop codon4630TATGGACAATACAGAGAACGSpecific to 5' end of Hop34303ACTTCCCAGTGACAAACGCSpecific to 5' end of Hop34304TACTCGAACGATAAACTGGSpecific to 5' end of Hop31033GCCGACCGAAAAACCCTAA $AVRI$ ORF2934CCAGCCAGAAGGCCAGTTT $AVR2$ ORF1002TATCCCTCCGGATTTGAGC $AVR3$ ORF1416GGAAGTACCAGTGATCATGTT $EF-Ia$ ORF1416GGAAGTACCAGTGATCATGTT $AVR2$ -upstream1236AGTGGTAAATGTTTAGGCAAG $AVR2$ -upstream1238GGTGTGTTGAACAGGTGCT $AVR2$ -downstream1238GGTGTGTTGAACAGGTGCT $AVR2$ -downstream	4297	TGCCTCTTTGCTCTGAAGG	Specific to 5' end of Helitrons
4239TGTTGCATACAGACAGCTGAG19278 bp downstream AVR1 stop codon4240AATCAGGAACTCACGCTTCG12747 bp downstream AVR1 stop codon4619ATCATACACGTTAGCTCAATTC28921 bp downstream AVR1 stop codon4620ACATAGCCATCCACTCATCC31210 bp downstream AVR1 stop codon4621TGACTATGAATTGAGCTAACG28915 bp downstream AVR1 stop codon4625ACCGTGGTACTGTCATACATGG33849 bp downstream AVR1 stop codon4630TATGGACAATACAGAGACG34853 bp downstream AVR1 stop codon4630ACTTCCCAGTGACAAACGCSpecific to 5' end of Hop34303ACTTCCCAGTGACAAACGCSpecific to 5' end of Hop34304TACTCGAACGATAAACTGGSpecific to 5' end of Hop31033GCCGACCGAAAAACCCTAAAVR1 ORF2934CCAGCCAGAAGGCCAGTTTAVR2 ORF964GGCAATTAACCACTCTGCCAVR3 ORF1002TATCCCTCCGGATTTGAGCAVR3 ORF1416GGAAGTACCAGTGATCATGTTEF-1a ORF1236AGTGGTAAATGTTAGGCAAGAVR2-upstream1238GGTGTTGAACAGGTGCTAVR2-downstream1238GGTGTTGAACAGGTGCTAVR2-downstream	1091	TCAGGCTTCACTTAGCATAC	AVR1 ORF
4240AATCAGGAACTCACGCTTCG12747 bp downstream $AVRI$ stop codon4619ATCATACACGTTAGCTCAATTC28921 bp downstream $AVRI$ stop codon4620ACATAGCCATCCACTCATCC31210 bp downstream $AVRI$ stop codon4621TGACTATGAATTGAGCTAACG28915 bp downstream $AVRI$ stop codon4625ACCGTGGTACTGTCATACATTG33849 bp downstream $AVRI$ stop codon4630TATGGACAATACAGAGACG34853 bp downstream $AVRI$ stop codon4303ACTTCCCAGTGACAAACGCSpecific to 5' end of Hop34304TACTCGAACGATAAACTGGSpecific to 5' end of Hop31033GCCGACCGAAAAACCCTAA $AVRI$ ORF2934CCAGCCAGAAGGCCAGTTT $AVR2$ ORF964GGCAATTAACCACTCTGCC $AVR3$ ORF363AATAGAGCCTGCAAAGCATG $AVR3$ ORF1416GGAAGTACCAGTGATCATGTT $EF-1a$ ORF1723CGATGCCTTGACCGAAAGCT $AVR2$ -upstream1236AGTGGTAAATGTTTAGGCAAG $AVR2$ -upstream1238GGTGTGTTGAACAGGTGCT $AVR2$ -downstream	4239	TGTTGCATACAGACAGCTGAG	19278 bp downstream AVR1 stop codon
4619ATCATACACGTTAGCTCAATTC28921 bp downstream $AVRI$ stop codon4620ACATAGCCATCCACTCATCC31210 bp downstream $AVRI$ stop codon4621TGACTATGAATTGAGCTAACG28915 bp downstream $AVRI$ stop codon4625ACCGTGGTACTGTCATACATTG33849 bp downstream $AVRI$ stop codon4630TATGGACAATACAGAGACG34853 bp downstream $AVRI$ stop codon4303ACTTCCCAGTGACAAACGCSpecific to 5' end of Hop34304TACTCGAACGATAAACTGGSpecific to 5' end of Hop31033GCCGACCGAAAAACCCTAA $AVRI$ ORF2934CCAGCCAGAAGGCCAGTTT $AVR2$ ORF964GGCAATTAACCACTCTGCC $AVR2$ ORF1002TATCCCTCCGGATTTTGAGC $AVR3$ ORF1416GGAAGTACCAGTGATCATGTT $EF-1a$ ORF889TCGTCGTCATCGGCCACGTC $EF-1a$ ORF1723CGATGCTTGACCGAAAGTT $AVR2$ -upstream1236AGTGGTAAAATGTTTAGGCAAG $AVR2$ -upstream1238GGTGTGTTGAACAGGTGCT $AVR2$ -downstream	4240	AATCAGGAACTCACGCTTCG	12747 bp downstream AVR1 stop codon
4620ACATAGCCATCCACTCATCC 31210 bp downstream $AVRI$ stop codon4621TGACTATGAATTGAGCTAACG 28915 bp downstream $AVRI$ stop codon4625ACCGTGGTACTGTCATACATTG 33849 bp downstream $AVRI$ stop codon4630TATGGACAATACAGAGACG 34853 bp downstream $AVRI$ stop codon4303ACTTCCCAGTGACAAACGCSpecific to 5' end of Hop34304TACTCGAACGATAAACTGGSpecific to 5' end of Hop31033GCCGACCGAAAAACCCTAA $AVRI$ ORF2934CCAGCCAGAAGGCCAGTTT $AVR2$ ORF964GGCAATTAACCACTCTGCC $AVR3$ ORF1002TATCCCTCCGGATTTTGAGC $AVR3$ ORF1416GGAAGTACCAGTGATCATGTT $EF-Ia$ ORF1416GGAAGTACCAGTGATCATGTT $EF-Ia$ ORF1723CGATGCCTTGACCGAAAGTT $AVR2$ -upstream1236AGTGGTAAATGTTTAGGCAAG $AVR2$ -upstream1238GGTGTGTTGAACAGGTGCT $AVR2$ -downstream	4619	ATCATACACGTTAGCTCAATTC	28921 bp downstream AVR1 stop codon
4621TGACTATGAATTGAGCTAACG28915 bp downstream $AVR1$ stop codon4625ACCGTGGTACTGTCATACATTG33849 bp downstream $AVR1$ stop codon4630TATGGACAATACAGAGACG34853 bp downstream $AVR1$ stop codon4303ACTTCCCAGTGACAAACGCSpecific to 5' end of Hop34304TACTCGAACGATAAACTGGSpecific to 5' end of Hop31033GCCGACCGAAAAACCCTAA $AVR1$ ORF2934CCAGCCAGAAGGCCAGTTT $AVR2$ ORF964GGCAATTAACCACTCTGCC $AVR3$ ORF1002TATCCCTCCGGATTTTGAGC $AVR3$ ORF1416GGAAGTACCAGTGATCATGTT $EF-Ia$ ORF1723CGATGCCTTGACCGAAAGTT $AVR2$ -upstream1236AGTGGTAAATGTTAGGCAAG $AVR2$ -upstream1238GGTGTGTTGAACAGGTGCT $AVR2$ -downstream1238GGTGTGTTGAACAGGTGCT $AVR2$ -downstream	4620	ACATAGCCATCCACTCATCC	31210 bp downstream AVR1 stop codon
4625ACCGTGGTACTGTCATACATTG 33849 bp downstream $AVR1$ stop codon4630TATGGACAATACAGAGACG 34853 bp downstream $AVR1$ stop codon4303ACTTCCCAGTGACAAACGCSpecific to 5' end of Hop34304TACTCGAACGATAAACTGGSpecific to 5' end of Hop31033GCCGACCGAAAAACCCTAA $AVR1$ ORF2934CCAGCCAGAAGGCCAGTTT $AVR2$ ORF964GGCAATTAACCACTCTGCC $AVR3$ ORF1002TATCCCTCCGGATTTTGAGC $AVR3$ ORF166GGAAGTACCAGTGATCATGTT $EF-Ia$ ORF1723CGATGCCTTGACCGAAAGTT $AVR2$ -upstream1236AGTGGTAAATGTTTAGGCAAG $AVR2$ -upstream1238GGTGTGTTGAACAGGTGCT $AVR2$ -downstream	4621	TGACTATGAATTGAGCTAACG	28915 bp downstream AVR1 stop codon
4630TATGGACAATACAGAGACG34853 bp downstream $AVRI$ stop codon4303ACTTCCCAGTGACAAACGCSpecific to 5' end of Hop34304TACTCGAACGATAAACTGGSpecific to 5' end of Hop31033GCCGACCGAAAAACCCTAA $AVRI$ ORF2934CCAGCCAGAAGGCCAGTTT $AVR2$ ORF964GGCAATTAACCACTCTGCC $AVR3$ ORF1002TATCCCTCCGGATTTTGAGC $AVR3$ ORF363AATAGAGCCTGCAAAGCATG $AVR3$ ORF1416GGAAGTACCAGTGATCATGTT $EF-Ia$ ORF1723CGATGCCTTGACCGAAAGTT $AVR2$ -upstream1236AGTGGTAAATGTTTAGGCAAG $AVR2$ -upstream1237TTCTGTGGCAGTTCCCCTT $AVR2$ -downstream1238GGTGTGTTGAACAGGTGCT $AVR2$ -downstream	4625	ACCGTGGTACTGTCATACATTG	33849 bp downstream AVR1 stop codon
4303ACTTCCCAGTGACAAACGCSpecific to 5' end of Hop34304TACTCGAACGATAAACTGGSpecific to 5' end of Hop31033GCCGACCGAAAAACCCTAA $AVR1$ ORF2934CCAGCCAGAAGGCCAGTTT $AVR2$ ORF964GGCAATTAACCACTCTGCC $AVR3$ ORF1002TATCCCTCCGGATTTTGAGC $AVR3$ ORF363AATAGAGCCTGCAAAGCATG $AVR3$ ORF1416GGAAGTACCAGTGATCATGTT $EF-1a$ ORF1723CGATGCCTTGACCGAAAGTT $AVR2$ -upstream1236AGTGGTAAATGTTTAGGCAAG $AVR2$ -upstream1237TTCTGTGGCAGTTCCCCTT $AVR2$ -downstream1238GGTGTGTTGAACAGGTGCT $AVR2$ -downstream	4630	TATGGACAATACAGAGACG	34853 bp downstream AVR1 stop codon
4304TACTCGAACGATAAACTGGSpecific to 5' end of Hop31033GCCGACCGAAAAACCCTAA $AVR1$ ORF2934CCAGCCAGAAGGCCAGTTT $AVR2$ ORF964GGCAATTAACCACTCTGCC $AVR3$ ORF1002TATCCCTCCGGATTTTGAGC $AVR3$ ORF363AATAGAGCCTGCAAAGCATG $AVR3$ ORF1416GGAAGTACCAGTGATCATGTT $EF-1a$ ORF889TCGTCGTCATCGGCCACGTC $EF-1a$ ORF1723CGATGCCTTGACCGAAAGTT $AVR2$ -upstream1236AGTGGTAAATGTTTAGGCAAG $AVR2$ -upstream1237TTCTGTGGCAGTTCCCCTT $AVR2$ -downstream1238GGTGTGTTGAACAGGTGCT $AVR2$ -downstream	4303	ACTTCCCAGTGACAAACGC	Specific to 5' end of Hop3
1033GCCGACCGAAAAACCCTAA $AVR1$ ORF2934CCAGCCAGAAGGCCAGTTT $AVR2$ ORF964GGCAATTAACCACTCTGCC $AVR2$ ORF1002TATCCCTCCGGATTTTGAGC $AVR3$ ORF363AATAGAGCCTGCAAAGCATG $AVR3$ ORF1416GGAAGTACCAGTGATCATGTT $EF-1a$ ORF889TCGTCGTCATCGGCCACGTC $EF-1a$ ORF1723CGATGCCTTGACCGAAAGTT $AVR2$ -upstream1236AGTGGTAAATGTTTAGGCAAG $AVR2$ -upstream1237TTCTGTGGCAGTTCCCCTT $AVR2$ -downstream1238GGTGTGTTGAACAGGTGCT $AVR2$ -downstream	4304	TACTCGAACGATAAACTGG	Specific to 5' end of Hop3
2934CCAGCCAGAAGGCCAGTTT $AVR2$ ORF964GGCAATTAACCACTCTGCC $AVR2$ ORF1002TATCCCTCCGGATTTTGAGC $AVR3$ ORF363AATAGAGCCTGCAAAGCATG $AVR3$ ORF1416GGAAGTACCAGTGATCATGTT $EF-1a$ ORF889TCGTCGTCATCGGCCACGTC $EF-1a$ ORF1723CGATGCCTTGACCGAAAGTT $AVR2$ -upstream1236AGTGGTAAATGTTTAGGCAAG $AVR2$ -upstream1237TTCTGTGGCAGTTCCCCTT $AVR2$ -downstream1238GGTGTGTTGAACAGGTGCT $AVR2$ -downstream	1033	GCCGACCGAAAAACCCTAA	AVR1 ORF
964GGCAATTAACCACTCTGCC $AVR2$ ORF1002TATCCCTCCGGATTTTGAGC $AVR3$ ORF363AATAGAGCCTGCAAAGCATG $AVR3$ ORF1416GGAAGTACCAGTGATCATGTT $EF-1a$ ORF889TCGTCGTCATCGGCCACGTC $EF-1a$ ORF1723CGATGCCTTGACCGAAAGTT $AVR2$ -upstream1236AGTGGTAAATGTTTAGGCAAG $AVR2$ -upstream1237TTCTGTGGCAGTTCCCCTT $AVR2$ -downstream1238GGTGTGTTGAACAGGTGCT $AVR2$ -downstream	2934	CCAGCCAGAAGGCCAGTTT	AVR2 ORF
1002TATCCCTCCGGATTTTGAGCAVR3 ORF363AATAGAGCCTGCAAAGCATGAVR3 ORF1416GGAAGTACCAGTGATCATGTTEF-1α ORF889TCGTCGTCATCGGCCACGTCEF-1a ORF1723CGATGCCTTGACCGAAAGTTAVR2-upstream1236AGTGGTAAATGTTTAGGCAAGAVR2-upstream1237TTCTGTGGCAGTTCCCCTTAVR2-downstream1238GGTGTGTTGAACAGGTGCTAVR2-downstream	964	GGCAATTAACCACTCTGCC	AVR2 ORF
363AATAGAGCCTGCAAAGCATGAVR3 ORF1416GGAAGTACCAGTGATCATGTTEF-1α ORF889TCGTCGTCATCGGCCACGTCEF-1a ORF1723CGATGCCTTGACCGAAAGTTAVR2-upstream1236AGTGGTAAATGTTTAGGCAAGAVR2-upstream1237TTCTGTGGCAGTTCCCCTTAVR2-downstream1238GGTGTGTTGAACAGGTGCTAVR2-downstream	1002	TATCCCTCCGGATTTTGAGC	AVR3 ORF
1416GGAAGTACCAGTGATCATGTTEF-1α ORF889TCGTCGTCATCGGCCACGTCEF-1a ORF1723CGATGCCTTGACCGAAAGTTAVR2-upstream1236AGTGGTAAATGTTTAGGCAAGAVR2-upstream1237TTCTGTGGGCAGTTCCCCTTAVR2-downstream1238GGTGTGTTGAACAGGTGCTAVR2-downstream	363	AATAGAGCCTGCAAAGCATG	AVR3 ORF
889TCGTCGTCATCGGCCACGTCEF-1a ORF1723CGATGCCTTGACCGAAAGTTAVR2-upstream1236AGTGGTAAATGTTTAGGCAAGAVR2-upstream1237TTCTGTGGCAGTTCCCCTTAVR2-downstream1238GGTGTGTTGAACAGGTGCTAVR2-downstream	1416	GGAAGTACCAGTGATCATGTT	<i>EF-1α</i> ORF
1723CGATGCCTTGACCGAAAGTTAVR2-upstream1236AGTGGTAAATGTTTAGGCAAGAVR2-upstream1237TTCTGTGGCAGTTCCCCTTAVR2-downstream1238GGTGTGTTGAACAGGTGCTAVR2-downstream	889	TCGTCGTCATCGGCCACGTC	<i>EF-1a</i> ORF
1236AGTGGTAAATGTTTAGGCAAGAVR2-upstream1237TTCTGTGGCAGTTCCCCTTAVR2-downstream1238GGTGTGTTGAACAGGTGCTAVR2-downstream	1723	CGATGCCTTGACCGAAAGTT	AVR2-upstream
1237TTCTGTGGCAGTTCCCCTTAVR2-downstream1238GGTGTGTTGAACAGGTGCTAVR2-downstream	1236	AGTGGTAAATGTTTAGGCAAG	AVR2-upstream
1238 GGTGTGTTGAACAGGTGCT <i>AVR2</i> -downstream	1237	TTCTGTGGCAGTTCCCCTT	AVR2-downstream
	1238	GG1GTGTTGAACAGGTGCT	AVR2-downstream

157	ATGAAGTACACTCTCGCTACC	FEM1 ORF	
158	GGTGAAAGTGAAAGAGTCACC	FEM1 ORF	
962	TGAGCGGGCTGGCAATTC	AVR2 ORF	
963	CAATCCTCTGAGATAGTAAG	AVR2 ORF	
1993	GCGCTTCGAGTACATCTCTG	SIX5 ORF	
1994	CTAGGCCGCATCACAATAGA	SIX5 ORF	

Classification								
Order	Superfamily	Family	Designation	Size	LTR	TIR	TSD	Coordinates
ClassI								
LTR	Gypsy\Ty3		MAGGY-like	5717	152			44144 - 49860
	Copia\Ty1		NHT2-like	5610	176		8	75725 - 81334
			NHT2-like fragment	211				14114 - 4324
	Unclassified		Yaret2	4840	195			86539 - 91378
			Yaret2	4840	195			91184 - 96083
	Solo-LTR		MAGGY-like solo-LTR	152				74512 - 74663
			Skippy-solo-LTR	431				59963 - 60393
LINE			MGR583 like LiNE element	5353				8403 - 13755
			MGR583-like LINE element	665				17893 - 18557
			MGR583-like LINE element	86				6588 - 6673
			MGR505 like LINE element fragment	59				6944 7002
			MOR585-like LINE element hagment	39				0944 - 7002
SINE			Foxy fragment	156				7778 - 7933
Unrelated			Marsu	2328				20822 - 23149
Class II								
Subclass 1								
TIR	TC1\mariner	Pogo	Fot5	1869		42	2	53449 - 55317
		C	Fot5	1860		44	2	81947 - 83806
			Fot3-partial	247				75478 - 75724
			Fot3-nartial	603				81337 - 81939
		hAT	hAT-1	3093		11	8	55469 - 58559
			Tfol_partial	1644			0	49861 - 51504
			Hormin	750		15	0	26660 27427
			Voh AT7 frogmant	739		15	0	20009 - 2/42/
			Yah A T7 frogment	/1 529				20/44 - 20014
		Mastatan	f anA 1 / fragment	328				34923 - 33430
		Mutator	Hopo Iragment	2038				24031 - 20008
			Hop6 fragment	1308				2/436 - 28/43
		MITE	mimp3	215		27	2	24102 - 24316
			mimp1	222		27	2	4879 - 5101
			mimp1	223		27	2	5546 - 5767
			mimp4-partial	86				51652 - 51737
Class II								
Sudclass 2			Halitzan	6109				20015 24022
				6108				26815 - 54922
CI H			Helitron	6123				65981 - 72103
Class II Unclassified								
			Unclassified	233		26	2	3885 - 4120
			Unclassified	859		20	-	19969 - 20827
			Onenassinea	057		<u>~ 1</u>		17707 - 20027

Table S2. Transposable elements on the insert of 9G3

ORF	Size	Position in 9G3	Homologous gene	Position in strain 4287	Remarks
ORF1	2727	1140 - 3866	FOXG_14233	Chr14: Supercontig 22: 652339-655065 -	
ORF2	2600	15079 - 17678	FOXG_14234	Chr14: Supercontig 22: 666276-668875 +	Bifunctional catalase-
ORF3	6114	36089 - 42202	FOXG_06805 FOXG_07365 FOXG_16388	Chr03: Supercontig 7: 1924520-1931400 Chr06: Supercontig 9: 2323584-2330452 - Unpositioned: Supercontig 34: 451087-457955 -	Encode protein with Helicase domain and Rep domain
AVRI	793	52222 - 53014	No homologue		Avirulence gene corresponding to R gene <i>I</i> or <i>I</i> -1
ORF4	828	62898 - 63725	FOXG_22916 FOXG_14128 FOXG_12409	Unpositioned: Supercontig 68: 1286-2722 - Chr14: Supercont2.51:71494-72306 – Chr03: Supercontig 18: 68914-70292 -	Unknown
ORF5	2189	72260 - 74448	FOXG_14236	Chr14: Supercontig 22:689228-691416 +	Highly similar to secreted oxidoreductase ORX1
ORF6	942	74643 - 75584	FOXG_14237	Chr14: Supercontig 22: 691611-692552 +	recQ family helicase
ORF7	1136	85183 - 86318	FOXG_14238	Chr14: Supercontig 22: 702268-703400 +	recQ family helicase
ORF8	477	97014 - 97490	FOXG_14240	Chr14: Supercontig 22: 711073-711549 -	Unknown

 Table S3. Non-transposable ORFs on the insert of 9G3