

## Supplementary materials information

**Title: An alternative strategy for targeted gene replacement in plants using a dual-sgRNA/Cas9 design**

**Authors:** Yongping Zhao<sup>1,#</sup>, Congsheng Zhang<sup>1,2,#</sup>, Wenwen Liu<sup>1</sup>, Wei Gao<sup>1</sup>, Changlin Liu<sup>1</sup>, Gaoyuan Song<sup>1</sup>, Wen-Xue Li<sup>1</sup>, Long Mao<sup>1</sup>, Beijiu Chen<sup>2</sup>, Yunbi Xu<sup>1, 3</sup>, Xinhai Li<sup>1</sup>, Chuanxiao Xie<sup>1,\*</sup>

**Author affiliations:**

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<sup>3</sup> International Maize and Wheat Improvement Center, El Batán, 56130, Mexico

### I. The list of 5 supplementary figures.

**Supplementary Figure 1.** A scheme illustrating the designed targeted chromosome deletion region within the *AtTFL1* region within gene structure.

Empty rectangle, UTR region; black rectangle, exons; dash lines, introns; vertical arrows, the sgRNA CRISPR/Cas9 targeted sites.

**Supplementary Figure 2. The design and sequence detail of dual-sgRNA CRISPR/Cas9 for deleting target region of *AtMIR169a* locus.**

**A.** Expressed sgRNA1 targeting *AtMIR169a* at site 1. The PAM sequence AGG is underlined. PAM, protospacer-adjacent motif sequence (sequence NGG underlined in red).

**B.** Expressed sgRNA2 targeting *AtMIR169a* at site 2. The PAM sequence AGG is underlined. The sequences underlined in bold (A panel and B panel in this figure) are expected to be joined together after precision repair of both DSB lesions induced by the two sgRNAs.

**Supplementary Figure 3.** Screening of targeted deletion mutation lines of *mir169a* mutant in the T<sub>1</sub> generation.

M: DNA size marker (GeneRuler™ 100-bp DNA Ladder; Fermentas, Beijing); WT, Columbia

Col0 wild type; 8, 12, 31, 32, 33, 34, 35, 36, 39, 42: the 10 lines in which the heterozygous targeted mutation was identified.

**Supplementary Figure 4.** The observed left (sgRNA1) or right (sgRNA2) indel mutations induced by single or dual sgRNAs rather than deletion of the entire target region in effort of deleting *AtMIR827* target region.

PAM, proto-adjacent motif; LD6, 6-bp deletion at the left sgRNA1-mediated site; RD1, 1-bp deletion at the right sgRNA2-mediated site. The number plus multiplication symbol indicates the observed individuals. For instance, for “3×” in figure panel B, 3 individuals had a 6-bp deletion mutation at the left sgRNA1 site (LD6) with no change at the sgRNA2 site.

**Supplementary Figure 5.** The sequencing evidences of the full length of the amplicon of the targeted replacement events. The full sequence could be seen in Supplementary File 1. The combined 4 junctions in one amplicon could identify a replacement event. Only junction sites 1-4 were shown. B: The junction site 1 sequence was shown; C: The junction site 2 was shown; D: The reverse complementary sequence of the junction 3. E: The reverse complementary sequence of the junction 4.

Note: Four raw sequencing file harboring 4 Junction sites had been provided as Supplementary File 2, 3, 4, and 5.

## **II. The list of 12 supplementary files.**

**Supplementary File 1.** The desired sequence detail of partial *AtTFL1* was replaced with eGFP.

**Supplementary File 2.** The raw sequencing peaks surrounding the junction 1 of the replacement event.

**Supplementary File 3.** The raw sequencing peaks surrounding the junction 2 of the replacement event.

**Supplementary File 4.** The raw sequencing peaks of the reverse complementary sequence surrounding the junction 3 of the replacement event.

**Supplementary File 5.** The raw sequencing peaks of the reverse complementary sequence surrounding the junction 4 of the replacement event.

**Supplementary File 6.** The raw sequencing peak of the reverse complementary sequence harboring re-joining junction site after DNA donor had been target deleted in plant.

**Supplementary File 7, 8 and 9.** Three more biological replicates of the sequencing evidence for harboring re-joining junction site after DNA donor had been target deleted in plants.

**Supplementary File 10.** The sequence of the mentioned key elements of CRISPR/Cas9 expression cassette in this study.

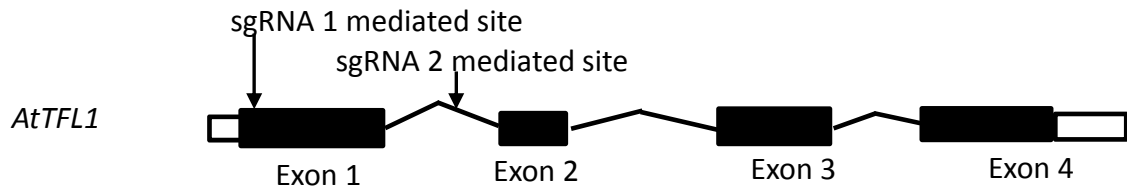
**Supplementary File 11.** The list of primers used in this study.

**Supplementary File 12.** The sequence detail of DNA donor template before and after deletion to supply for HDR repair.

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## Supplementary Figure 1

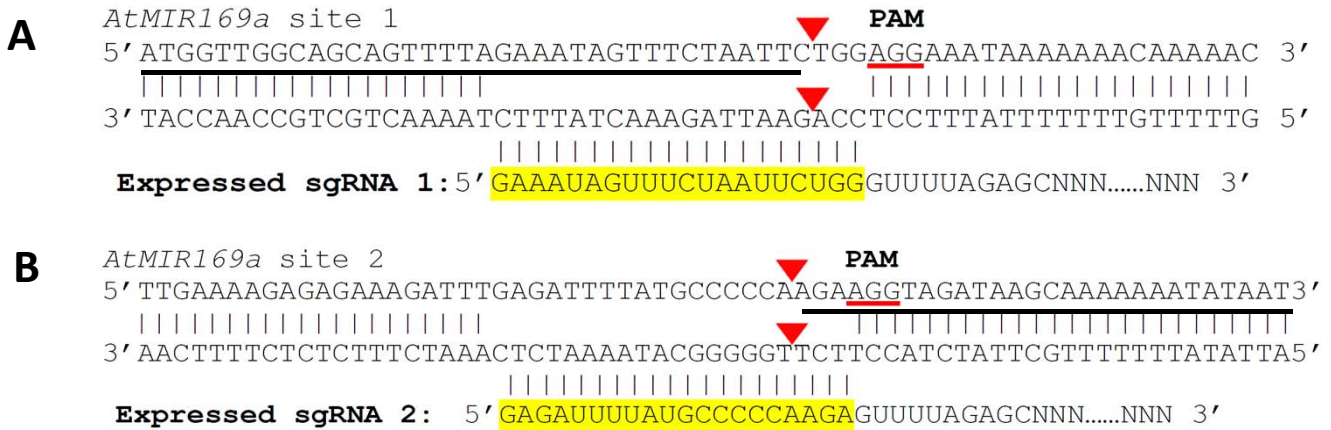


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## Supplementary Figure 2



### Supplementary Figure 2. The design and sequence detail of dual-sgRNA CRISPR/Cas9 for deleting target region of *AtMIR169a* locus.

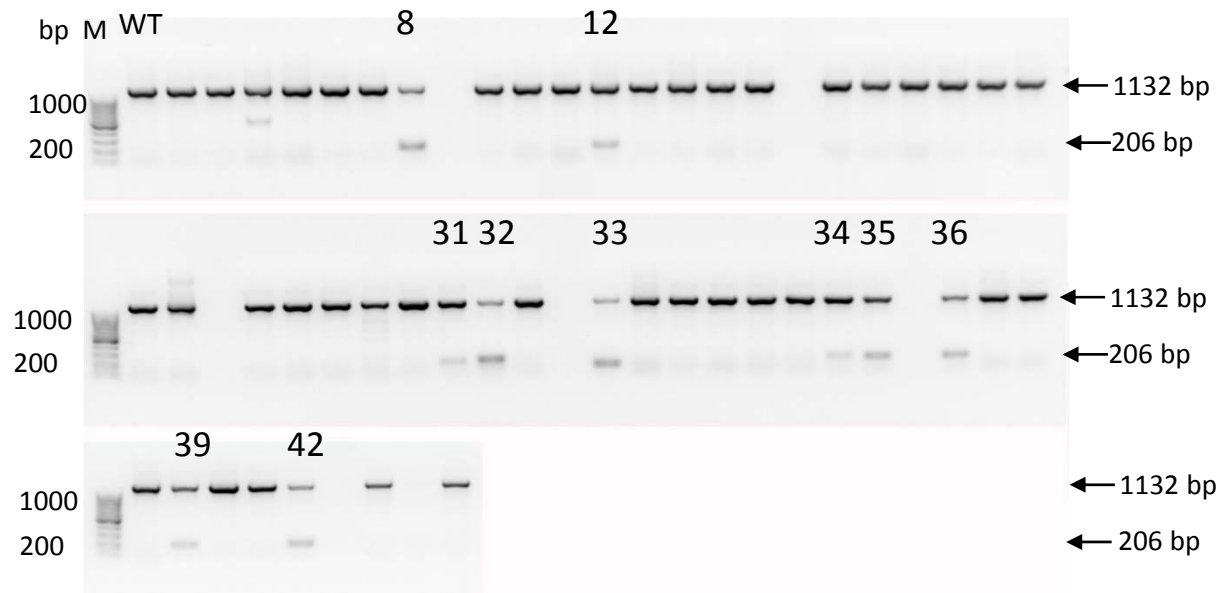
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### Supplementary Figure 3



**Supplementary Figure 3.** Screening of targeted deletion mutation lines of *mir169a* mutant in the  $T_1$  generation.

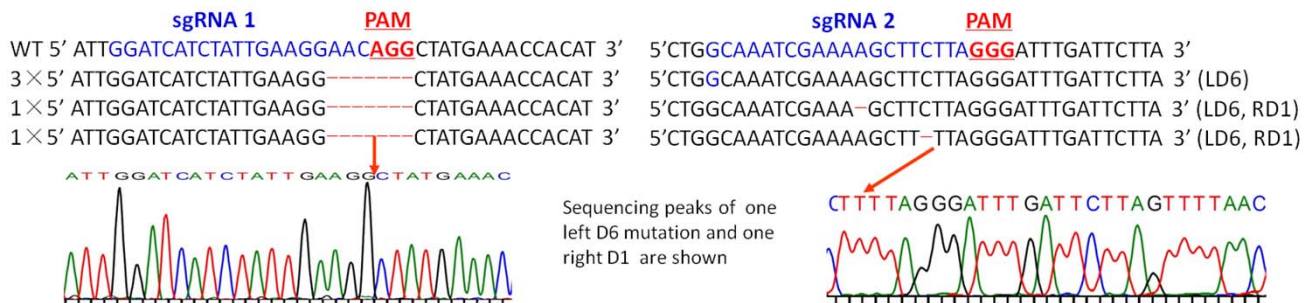
M: DNA size marker (GeneRuler™ 100-bp DNA Ladder; Fermentas, Beijing); WT, Columbia Col0 wild type; 8, 12, 31, 32, 33, 34, 35, 36, 39, 42: the 10 lines in which the heterozygous targeted mutation was identified.

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## Supplementary Figure 4

The observed mutations other than deletion induced by single and/or both sgRNAs



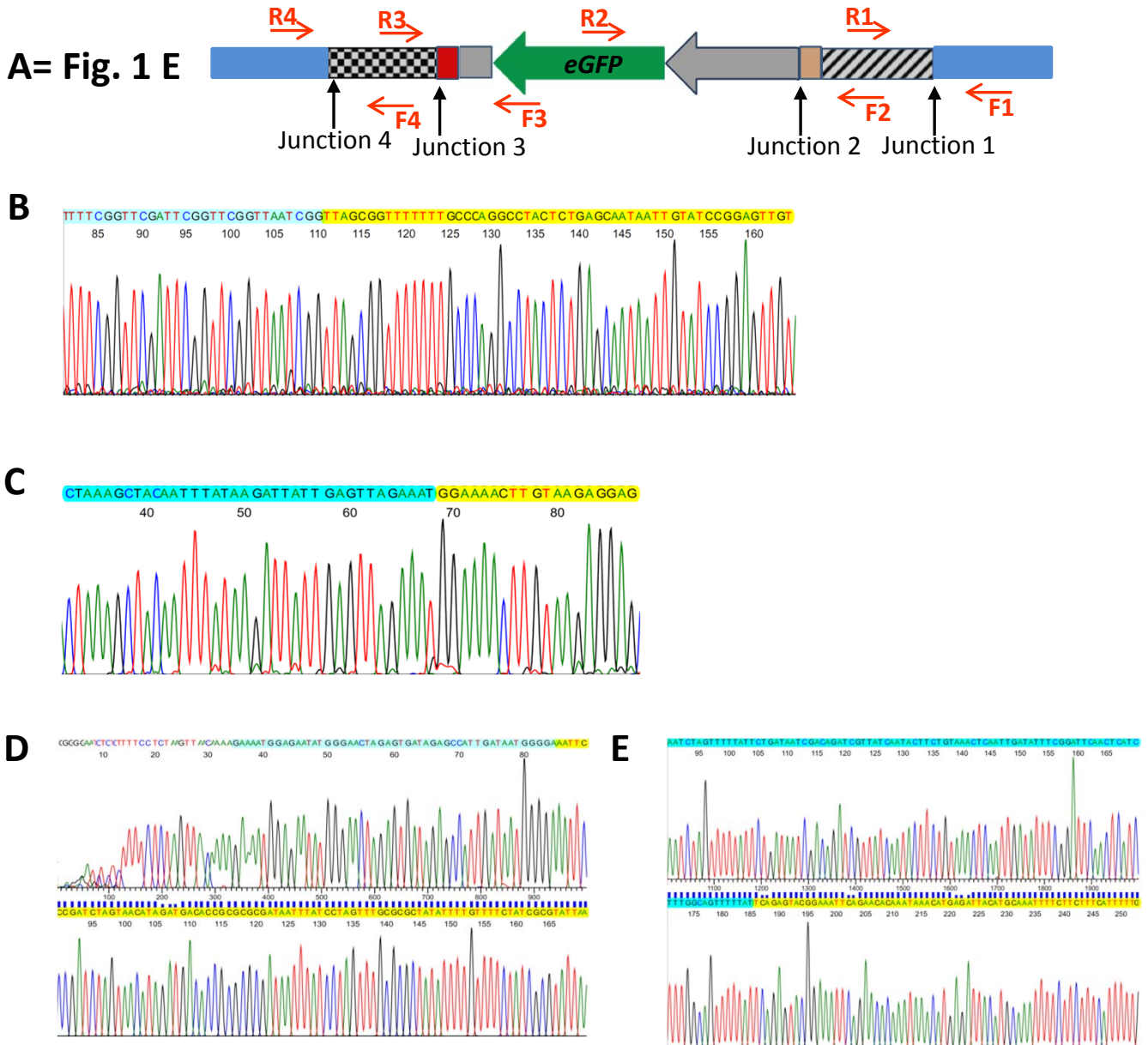
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PAM, proto-adjacent motif; LD6, 6-bp deletion at the left sgRNA1-mediated site; RD1, 1-bp deletion at the right sgRNA2-mediated site. The number plus multiplication symbol indicates the observed individuals. For instance, for “3 ×” in figure panel B, 3 individuals had a 6-bp deletion mutation at the left sgRNA1 site (LD6) with no change at the sgRNA2 site.

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## Supplementary Figure 5



**Supplementary Figure 5.** The sequencing evidences of the full length of the amplicon of the targeted replacement events. The full sequence could be seen in Supplementary File 1. The combined 4 junctions in one amplicon could identify a replacement event. Only junction sites 1-4 were shown. B: The junction site 1 sequence was shown; C: The junction site 2 was shown; D: The reverse complementary sequence of the junction 3. E: The reverse complementary sequence of the junction 4.

Note: Four raw sequencing file harboring 4 Junction sites had been provided as Supplementary File 2, 3, 4, and 5.



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**Supplementary file 1. The desired sequence detail of partial AtTFL1 was replaced with eGFP.**

This sequence was confirmed with assembled sequencing from 1 amplicon using primer pair of F1 and R4.

```

                                F1 primer
1   ctttggtttt catttggta tcgGTTATTA ACCTAACCGA AACCGAAACC GAAATCTAAG
61  ACATATAATA TTCAACCGGT TATTTAAGC TATCCAAACC TGAACCGAAC CATGTTTTTC
                                Junction 1
121 GGTTCGATTC GGTTCGGTTA ATCGGTTAGC GGTTTTTTTG CCCAGGCCTA CTCTGAGCAA
181 TAATTGTATC CGGAGTTGTA ATAGAATCAA AGTACGATGA GAGTGTTTTT ATGACAAATA
241 TCTTAATCTT GGCCAATTAT ATGTTCTACT GAAATCTTTT TTGAATTCAT CGACCAGTGA
301 GACTTAAAAA TAGCTTTTTA TTCGCCGAGG TATATATAGC TAGGAATTTT GTCGAAATTT
361 AGACGTTAGT GGGTTTTGTT CTTCTGTGACA CAAAAGATAT TCTATATATT AACGAAATCT
421 AGCGATCGAT ATGGTATTTA TATAAAGTCT TGGTCATAGA TAGGGGTTGA AACTTGA AAC
481 CATGCATGAT ATGCCAATGT TGCTGAAGCA GTCAATGTTG CTGAAGAAGT CAAACGTAAT
541 TATATAGTGA ATACCAAAAA AGTGATATTT CTAATTCAA TTAATATAA TTATAGTTTT
601 AAATCACCTA AAATAAGTTA CTTATTA AAA CCCCCAAAT TACTTTAAT ATAGTTGGTG
661 TACATGTTTG AGAAAGCAA CAAAAGAAA AAGAAAAAGA AAAAAAAG AGAAAGAGGT
721 TAGTACACAT AATTGGAAT TAATGTCTAT TGATTCTTTT ATCTTTCTCT CTCTCTCTAA
                                F2 and R1 primer site
781 GACGAAAAC CCCTATAAAT AGatgtctcg gtegtctctt tctctCCAA ATCACTACAA
                                start codon of AtTFL1
841 ATCTCTCTTT TCCTCTAAGT TAACAAAAGA AAATGGAGAA TATGGGAACT AGAGTGATAG
                                sgRNA1 targeted residue and Junction 2
901 AGCCATTGAT AATGGGAAA TTCCCGATCT AGTAACATAG ATGACACCGC GCGCGATAAT
961 TTATCCTAGT TTGCGCGCTA TATTTGTTT TCTATCGCGT ATTAATGTA TAATTGCGGG
1021 ACTCTAATCA TAAAAACCA TCTCATAAAT AACGTCATGC ATTACATGTT AATTATTACA
1081 TGCTTAACGT AATCAACAG AAATTATATG ATAATCATCG CAAGACCGGC AACAGGATTC
1141 AATCTTAAGA AACTTTATTG CCAAATGTTT GAACGATCGG GGAAATTCGA GCTCGGTACC
                                SV40 NLS
1201 CGGGCGATCA TACCTTCTC TTCTTCTGG GAGAACCCCC TTTGTACAGC TCGTCCATGC
1261 CGTGAGTGAT CCCGGCGGCG GTCACGA ACT CCAGCAGGAC CATGTGATCG CGCTTCTCGT
1321 TGGGTCTTT GCTCAGGGCG GACTGGGTGC TCAGGTAGTG GTTGTGGGC AGCAGCACGG
1381 GGCCGTCGCC GATGGGGTG TTCTGCTGGT AGTGGTCGGC GAGCTGCACG CTGCCGTCCT
1441 CGATGTTGTG GCGGATCTTG AAGTTCACCT TGATGCCGTT CTTCTGCTTG TCGGCCATGA
1501 TATAGACGTT GTGGCTGTTG TAGTTGTA CT CCAGCTTGTG CCCCAGGATG TTGCCGTCCT
1561 CCTTGAAGTC GATGCCCTC AGCTCGATGC GGTTCACCAG GGTGTCGCC TCGAACTTCA
1621 CCTCGGCGCG GGTCTGTAG TTGCCGTCGT CCTTGAAGAA GATGGTGC GC TCCTGGACGT
1681 AGCCTTCGGG CATGGCGGAC TTGAAGAAGT CGTGTCTGCTT CATGTGGTCG GGGTAGCGGC
1741 TGAAGCACTG CACGCCGTAG GTGAAGTGG TCACGAGGGT GGGCCAGGGC ACGGCAGCT
1801 TGCCGGTGGT gcagatgaacttcagggtca GCTTCCGTA GGTGGCATCG CCCTCGCCT
1861 CGCCGGACAC GCTGAACTTG TGGCCGTTA CGTCGCCGTC CAGCTCGACC AGGATGGGCA
                                R2 primer (in GFP)
1921 CCACCCCGGT GAACAGctcc tcgccttgc tcaccatCCC GGGGATCCTC TAGAGTCCC
1981 CGTGTCTCT CCAATGAAA TGAACCTCCT TATATAGAGG AAGGTCTTG CGAAGGATAG
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2041 TGGGATTGTG CGTCATCCCT TACGTCAGTG GAGATATCAC ATCAATCCAC TTGCTTTGAA  
 2101 GACGTGGTTG GAACGTCTTC TTTTCCACG ATGCTCCTCG TGGGTGGGGG TCCATCTTTG  
 2161 GGACCACTGT CGgagagge atcttcaacg atGGCCTTTC CTTTATCGCA ATGATGGCAT

F3 primer region

2221 TTGTAGGAGC CACCTTCCTT TTCCACTATC TTCACAATAA AGTGACAGAT AGCTGGGCAA  
 2281 TGGAAATCCGA GGAGGTTTCC GGATATTACC CTTTGTGAA AAGTCTCAAT TGCCCTTTGG  
 2341 TCTTCTGAGA CTGTATCTTT GATATTTTG GAGTAGACAA GTGTGTCGTG CTCCACCATG  
 2401 TTGACGAAGA TTTTCTTCTT GTCATTGAGT CGTAAGAGAC TCTGTATGAA CTGTTCGCCA  
 2461 GTCTTTACGG CGAGTTCTGT TAGGTCCTCT ATTTGAATCT TTGACTCCAT GGCCTTTGAT  
 2521 TCAGTGGGAA CTACCTTTTT AGAGACTCCA ATCTCTATTA CTTGCCTTGG TTTGTGAAGC  
 2581 AAGCCTTGAA TCGTCCATAC TGGAAATGTA CTTCTGATCT TGAGAAATAT ATCTTTCTCT  
 2641 GTGTTCTTGA TGCAGTTAGT CCTGAATCTT TTGACTGCAT CTTTAACTT CTTGGGAAAG  
 2701 TATTTGATTT CCTGGAGATT ATTGCTCGGG TAGATCGTCT TGATGAGACC TGCTGCGTAA  
 2761 GCCTCTCTAA CCATCTGTGG GTTAGCATT TTTCTGAAAT TGAAGGCT AATCTGGGGA

Junction 3 and the sgRNA2 targeted residue were bold letters

2821 **CCTGCAGGCA TGCAAGCTCC TCTTACAAGT TTCCATTTC** TAACTCAATA ATCTTATAAA  
 2881 TTGTAGCTTT AGTTTTATC ATTCTTTTT CCAGTCTTT TTTTAAATG GTAAAACCA

R3 and F4 primers region

2941 ACcgaaatgc aaacaggtc atgATAGACC CAGATGTTCC AGGTCCTAGT GACCCCTTTC  
 3001 TAAAAGAACA CCTGCACTGG TACGTTTAAAT TTATTTATTC TTTCTTTTCA TTTTGGCCCC  
 3061 ATATTCCATA TACATTGCAT TAAATCATT TCGTTATAAC CCTAATAAAG TTTTTTTTGG  
 3121 GTGTAAGTTA TATACATTTG AGTTGGTCAA AGATCTCCAT CGCCATGAGT TCTCAGAACT  
 3181 TTTTCTGTAA AGTAATAATA TTAGTATTGT TGAATGTTT AATAGGATCG TTACAAACAT  
 3241 TCCCGGCACA ACAGATGCTA CGTTTGGTAA GGCCTCTTCA TGAATCTTGT AATTTAAATA  
 3301 CTTATACATA TATCATGTTA TATAGAAATA AAAATATTG CATTGTAATA TAGGCAAAGA  
 3361 GGTGGTGAGC TATGAATTGC CAAGGCCAAG CATAGGGATA CATAGGTTT TGTGTTCTCT  
 3421 GTTCAGGCAG AAGCAAAGAC GTGTTATCTT TCCTAATATC CCTTCGAGAG ATCACTTCAA  
 3481 CACTCGTAAA TTTGCGGTCG AGTATGATCT TGGTCTCCCT GTCGCGGCCG TCTTCTTTAA  
 3541 CGCACAAAGA GAAACCGCTG CACGCAAACG CTAGTTTCAT GATTGTCATA AACTGCAAAA  
 3601 ATGAAAGAAG AAAATTTGCA TGAATCTCA TGTTTATTG TGTCTGAAT TTCCGTAICT  
 3661 TGAATAAAAA CTGCCAAAGA TGAGTTGAAT CCGAAATATC AATTGAGTTT ACAGAAGTAT

Junction4

3721 TGATAACGAT CTGTCGATTA TCAGAATAAA AACTAGATTA ATTGCATATC ATGTTTAGCA  
 3781 TTGTAATACT AAAAAATAG TAAACTCTTG ATTAATTAAT AAAATCTAAG TTGCTGTAGT  
 3841 ATATAATCA TAAATCctc atacatgget tgataggtea c

R4 primer region

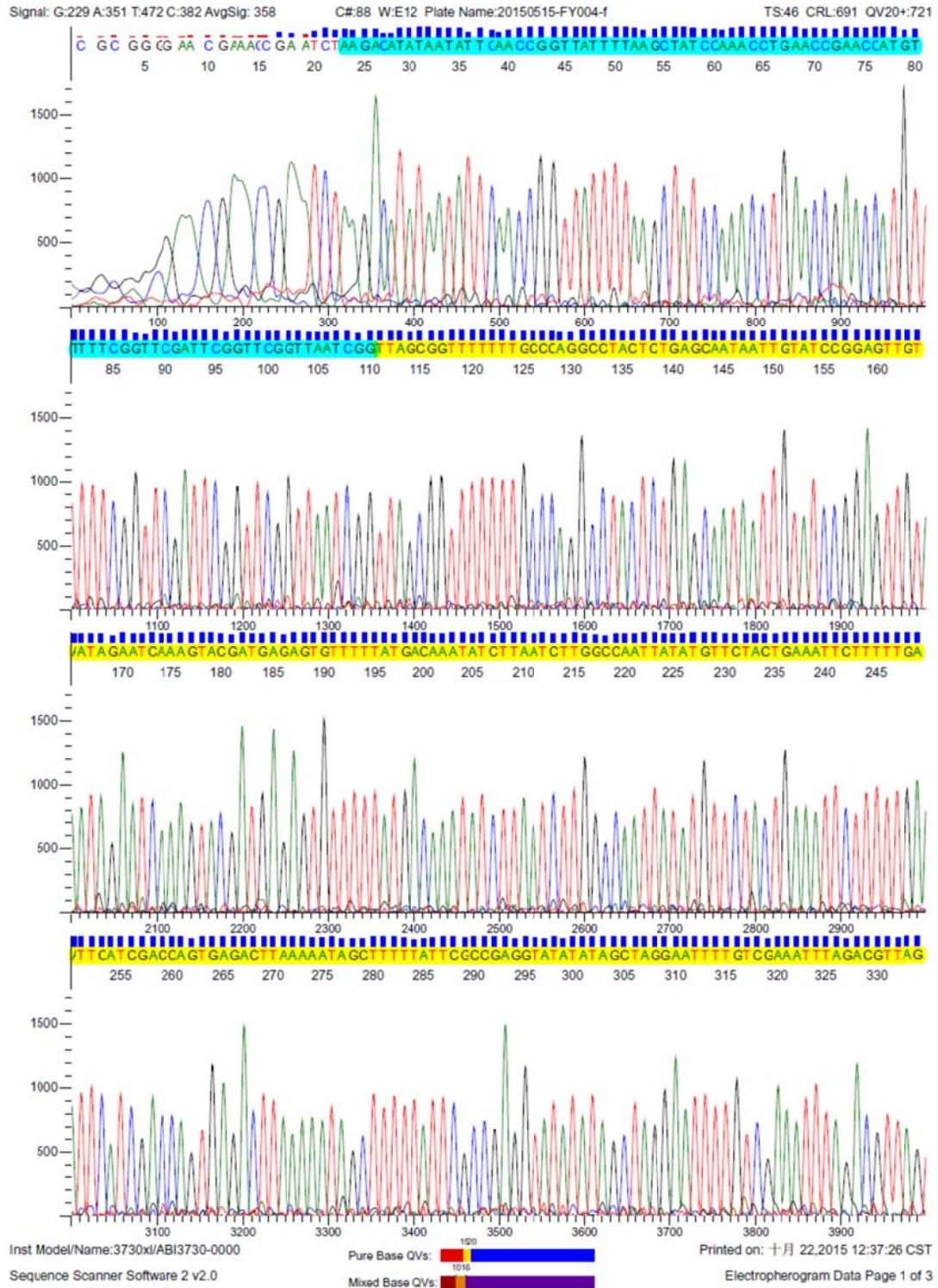
### Captions:

- Sequence in red letters is the replaced sequence harboring the expression cassette of eGFP.
- Sequence with light blue shadowed is the sequence of the homologs arms.
- All primer regions were underlined in lowercase letters.
- At the middle junction sites.
- The captions were inserted between the lines of the sequence.
- The junction sites 1-4 were indicated. The different color letters in word “junction” indicate the real junction site located in the sequence. For example, “Junction 1” indicates that the junction sites were located within “ATCGG**TTAGC**” showing different shadow colors. “**GT**” was the very junction site.

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**Supplementary File 2.** The raw sequencing peaks surrounding the junction 1 of the replacement event.

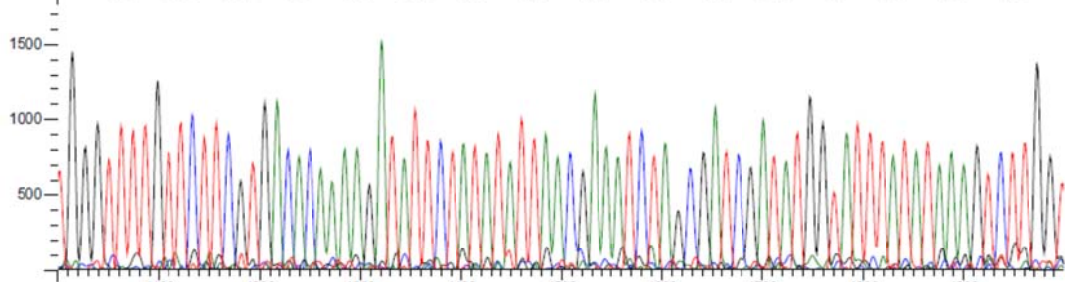


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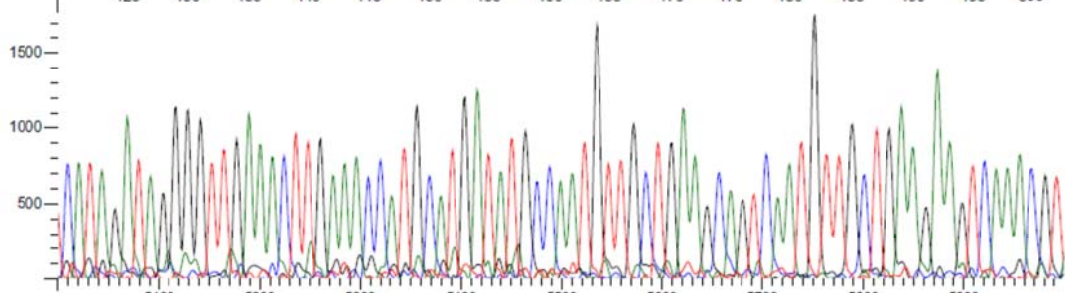
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TS:46 CRL:691 QV20+:721

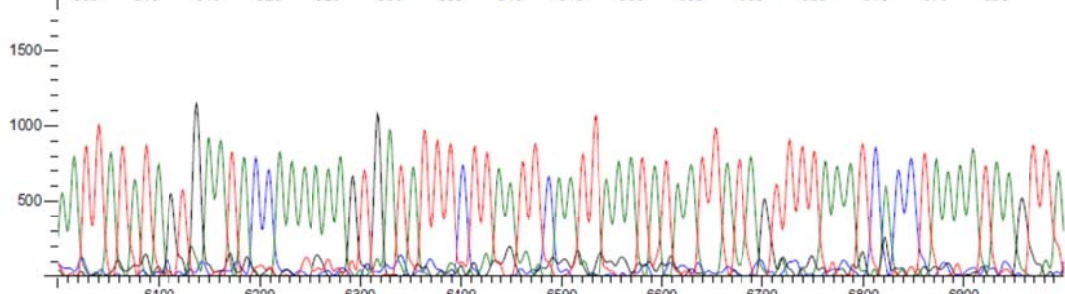
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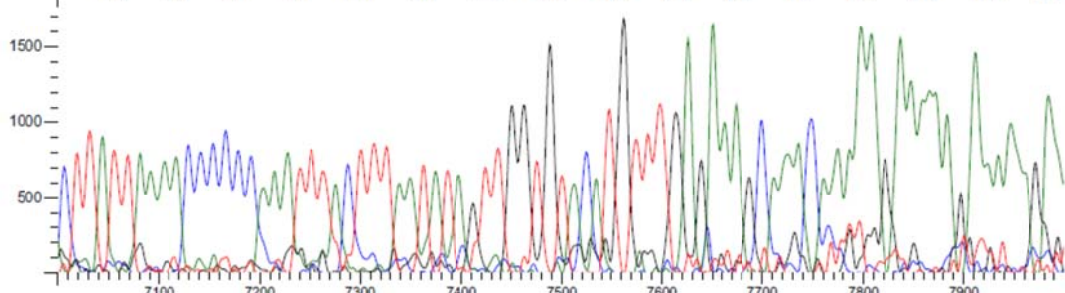
CAT AGAT AGGGGT T GAAACT T GAAACCA T GCA T GAT AT GCCAAT GT T GCT GAAGCAGT CAAT GT T GCT GAAAGAAGT CAAAC GT



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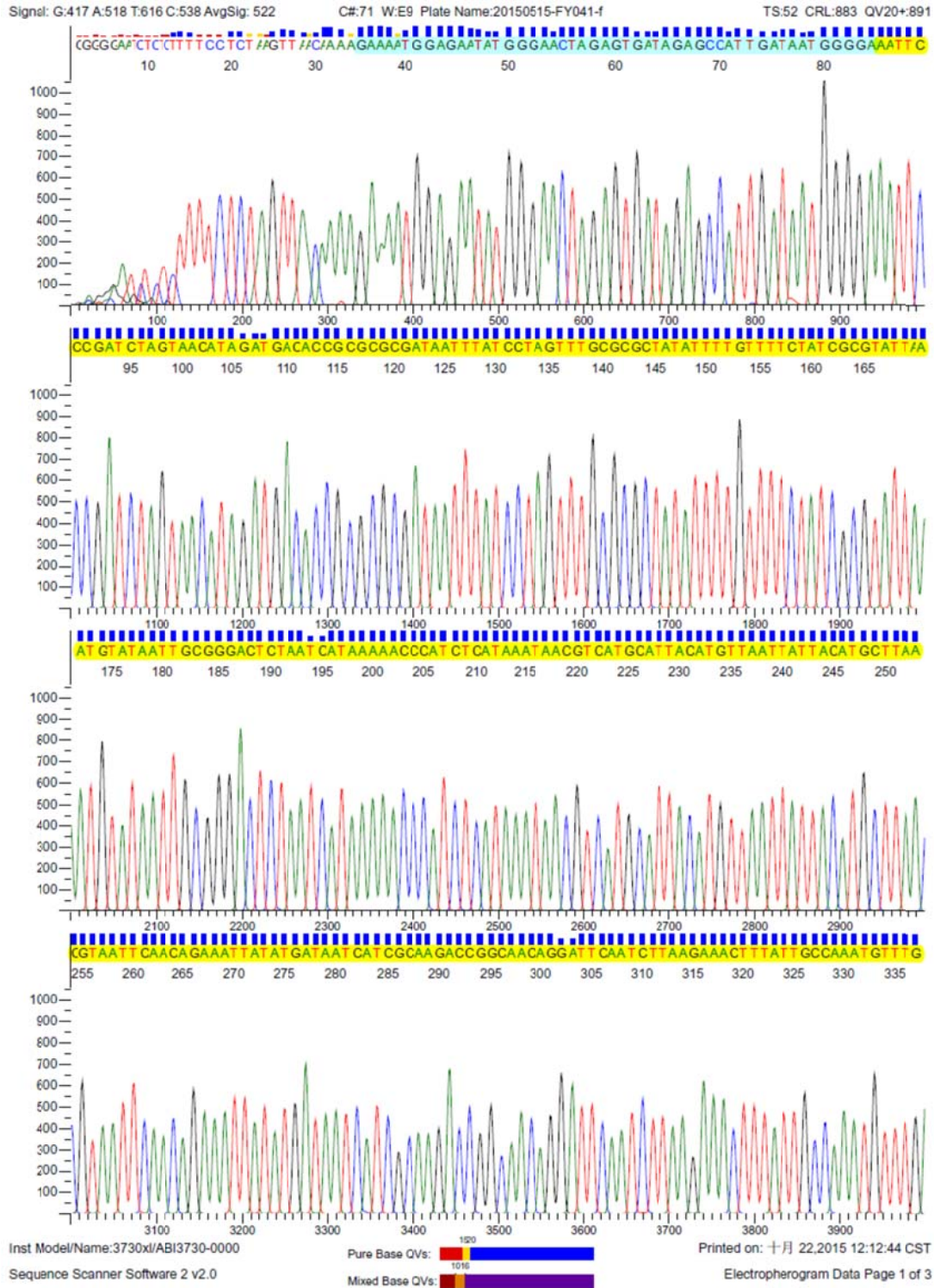
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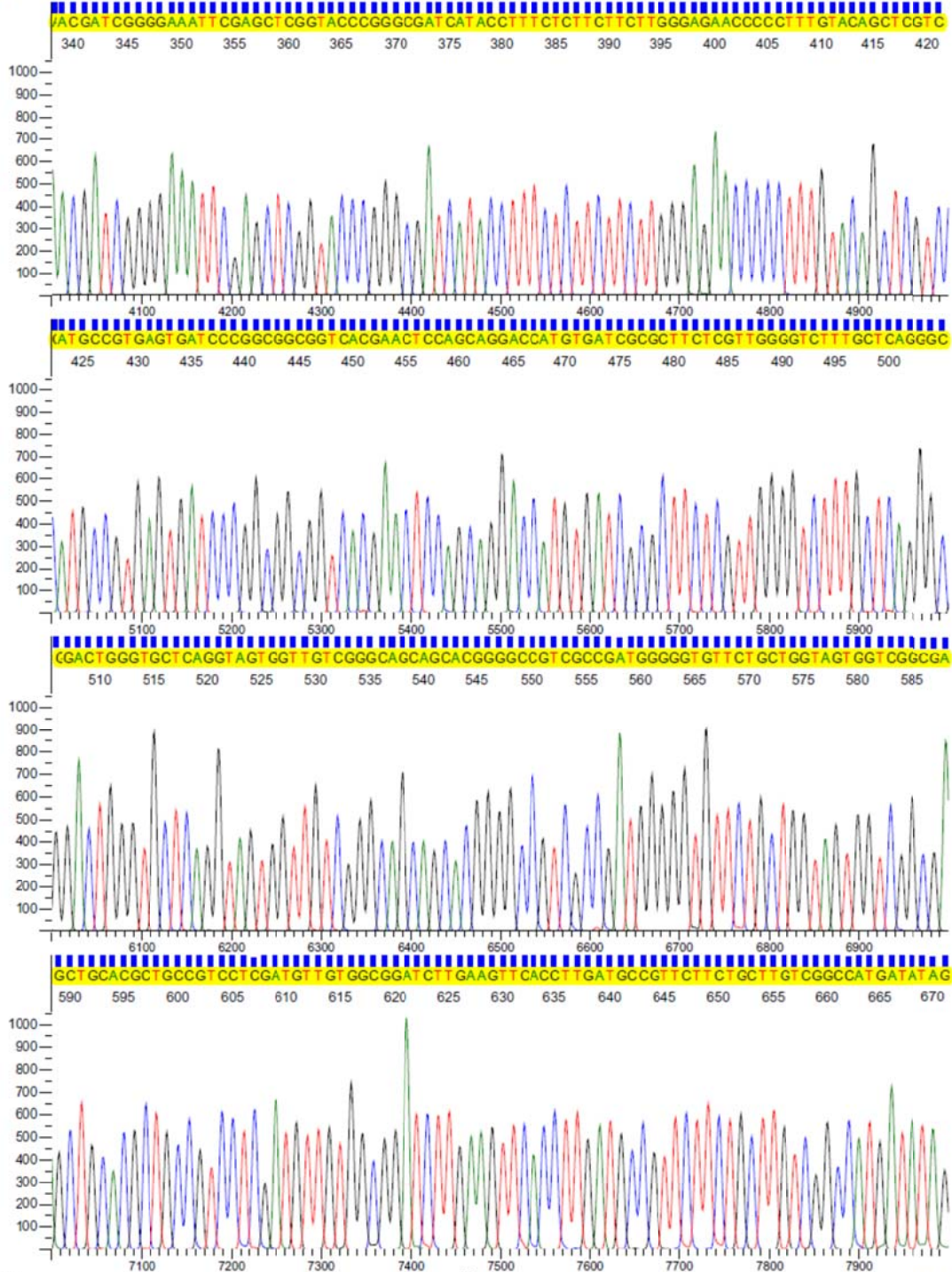


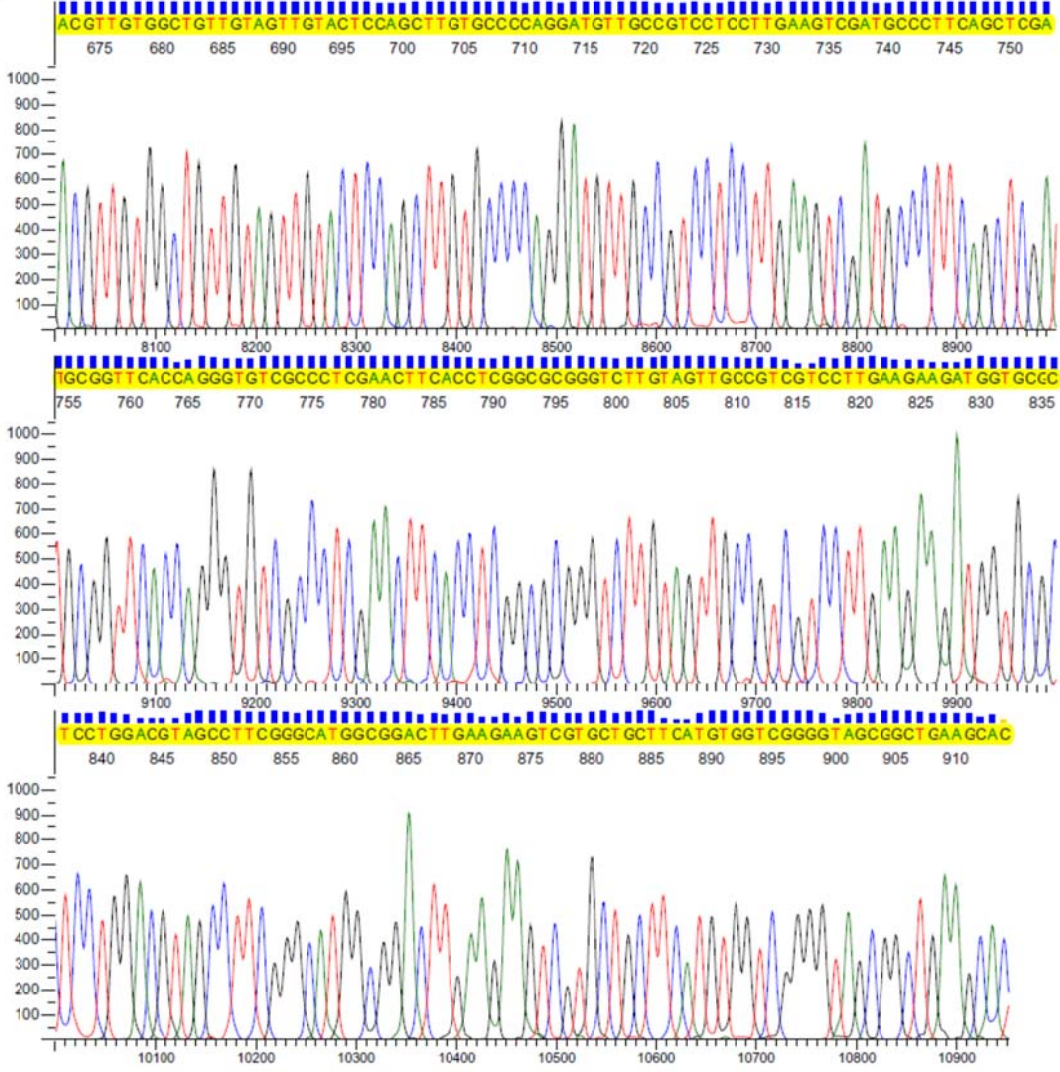
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**Supplementary File 3.** The raw sequencing peaks surrounding the junction 2 of the replacement event.



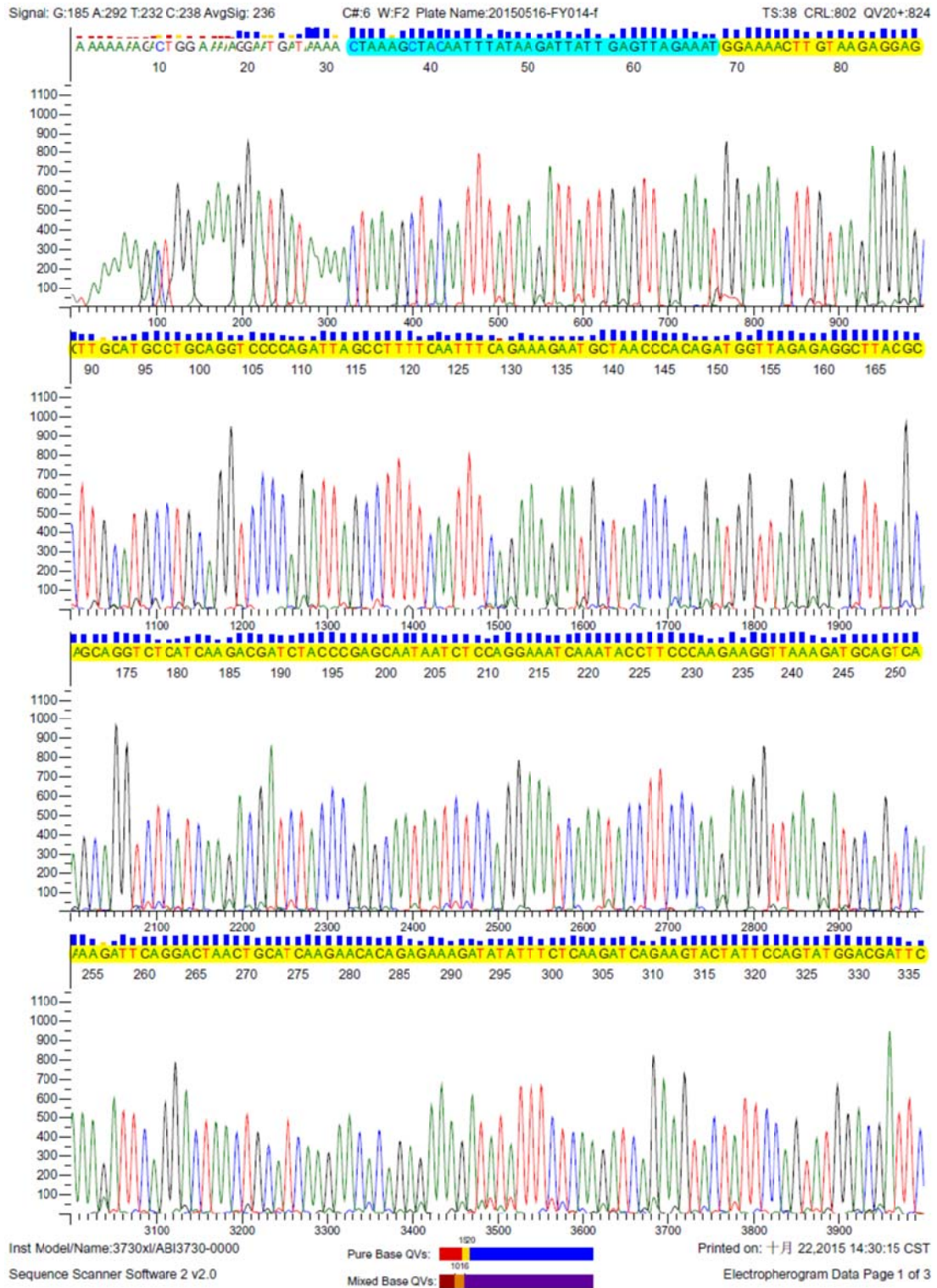




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**Supplementary File 4.** The raw sequencing peaks of the reverse complementary sequence surrounding the junction 3 of the replacement event.

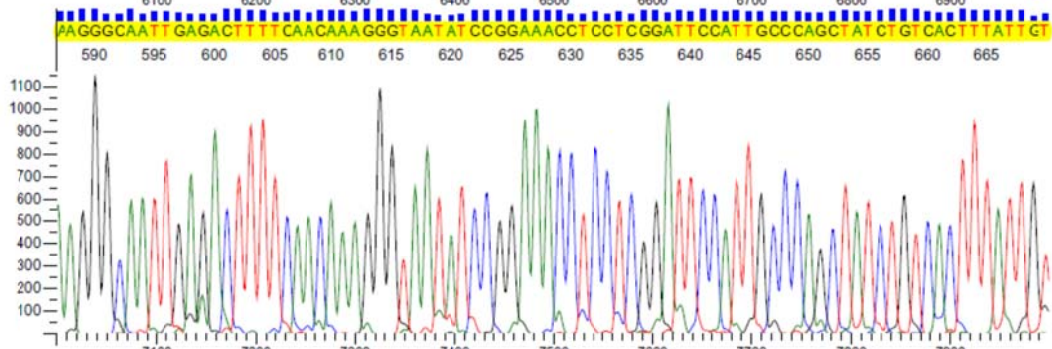
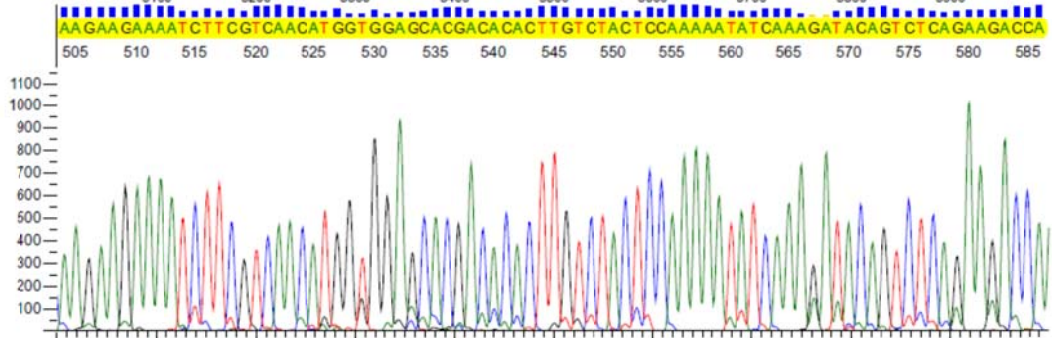
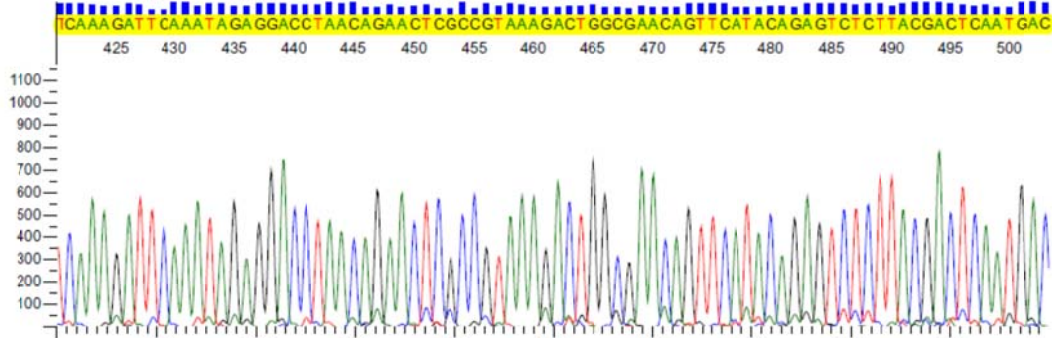
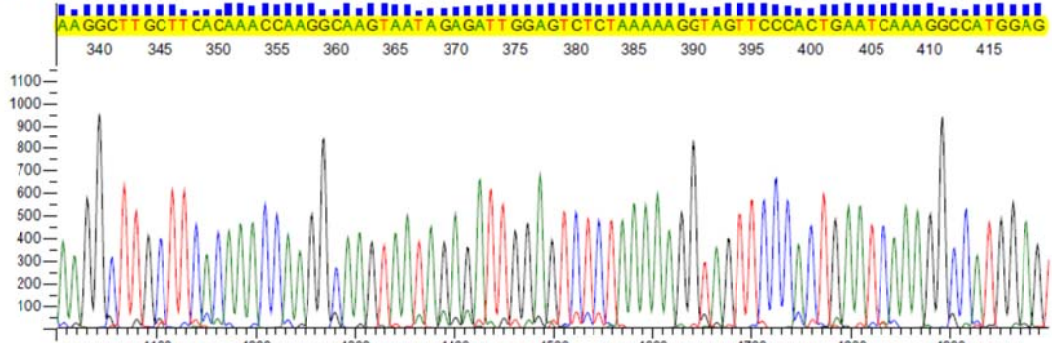




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C#:6 W:F2 Plate Name:20150516-FY014-f

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Sequence Scanner Software 2 v2.0



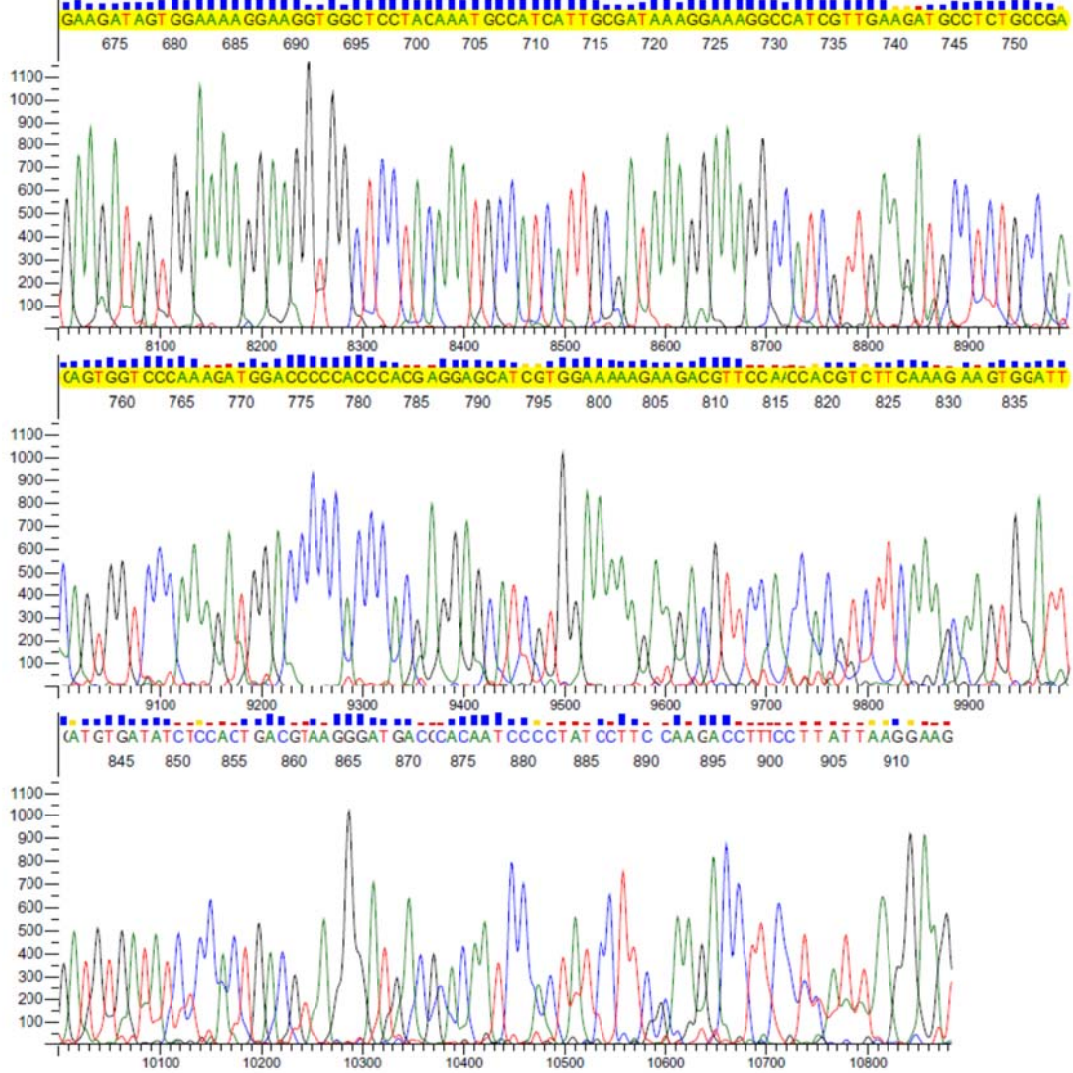
Printed on: 十月 22, 2015 14:30:15 CST

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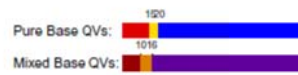
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C#:6 W:F2 Plate Name:20150516-FY014-f

TS:38 CRL:802 QV20+824



Inst Model/Name:3730xl/ABI3730-0000  
Sequence Scanner Software 2 v2.0



Printed on: 十月 22, 2015 14:30:15 CST  
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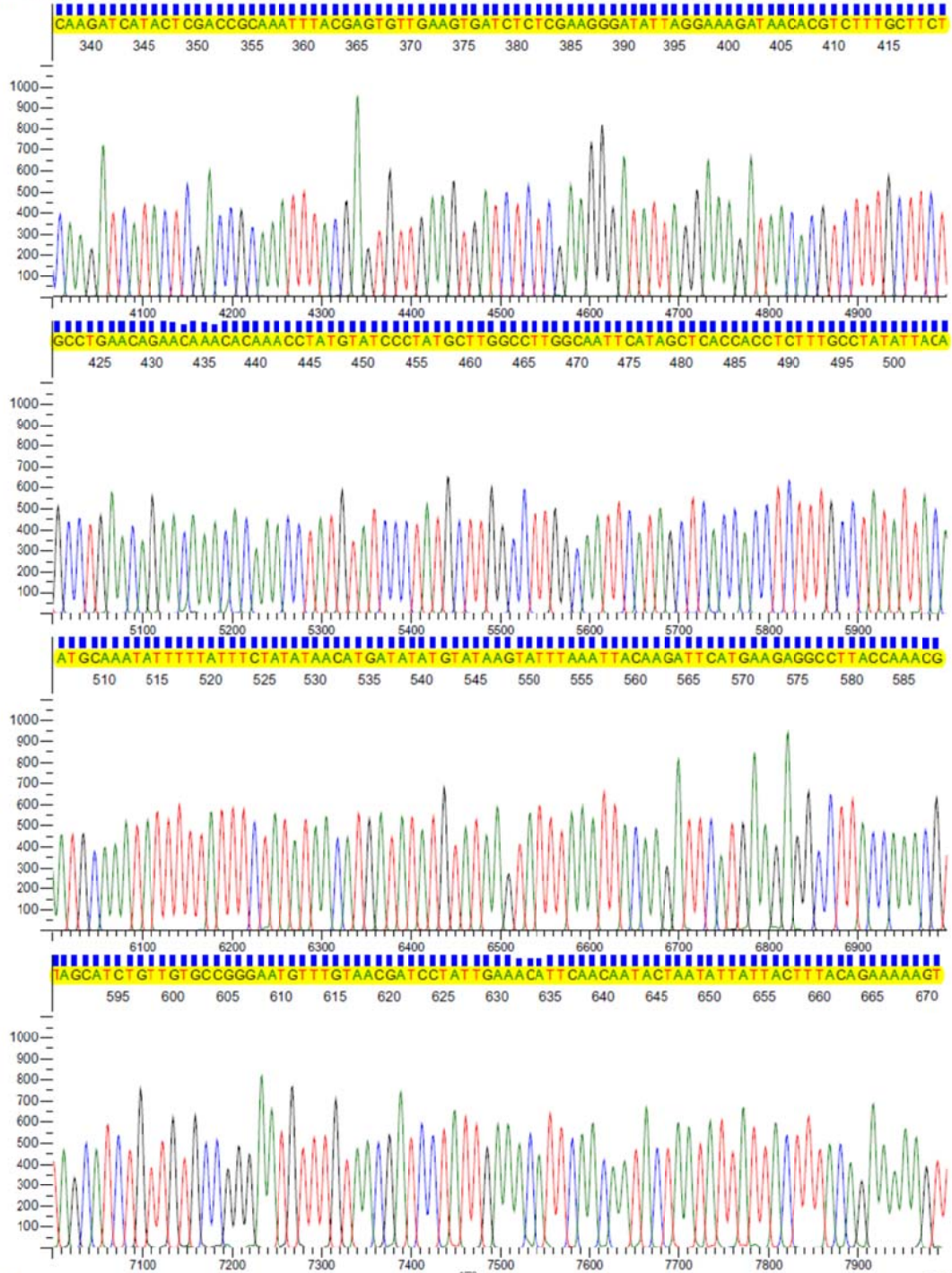
**Supplementary File 5.** The raw sequencing peaks of the reverse complementary sequence surrounding the junction 4 of the replacement event.



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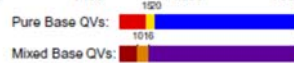
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Sequence Scanner Software 2 v2.0



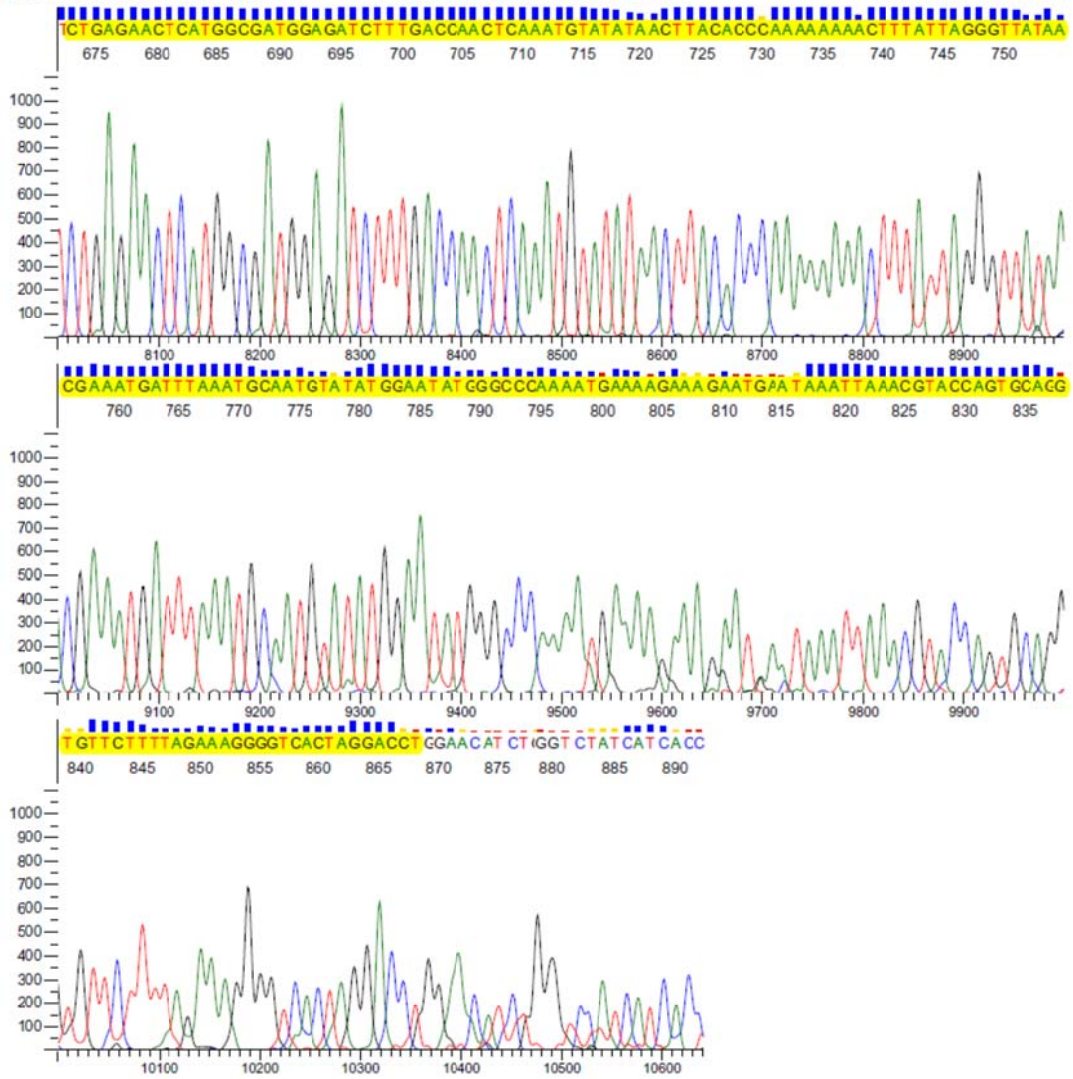
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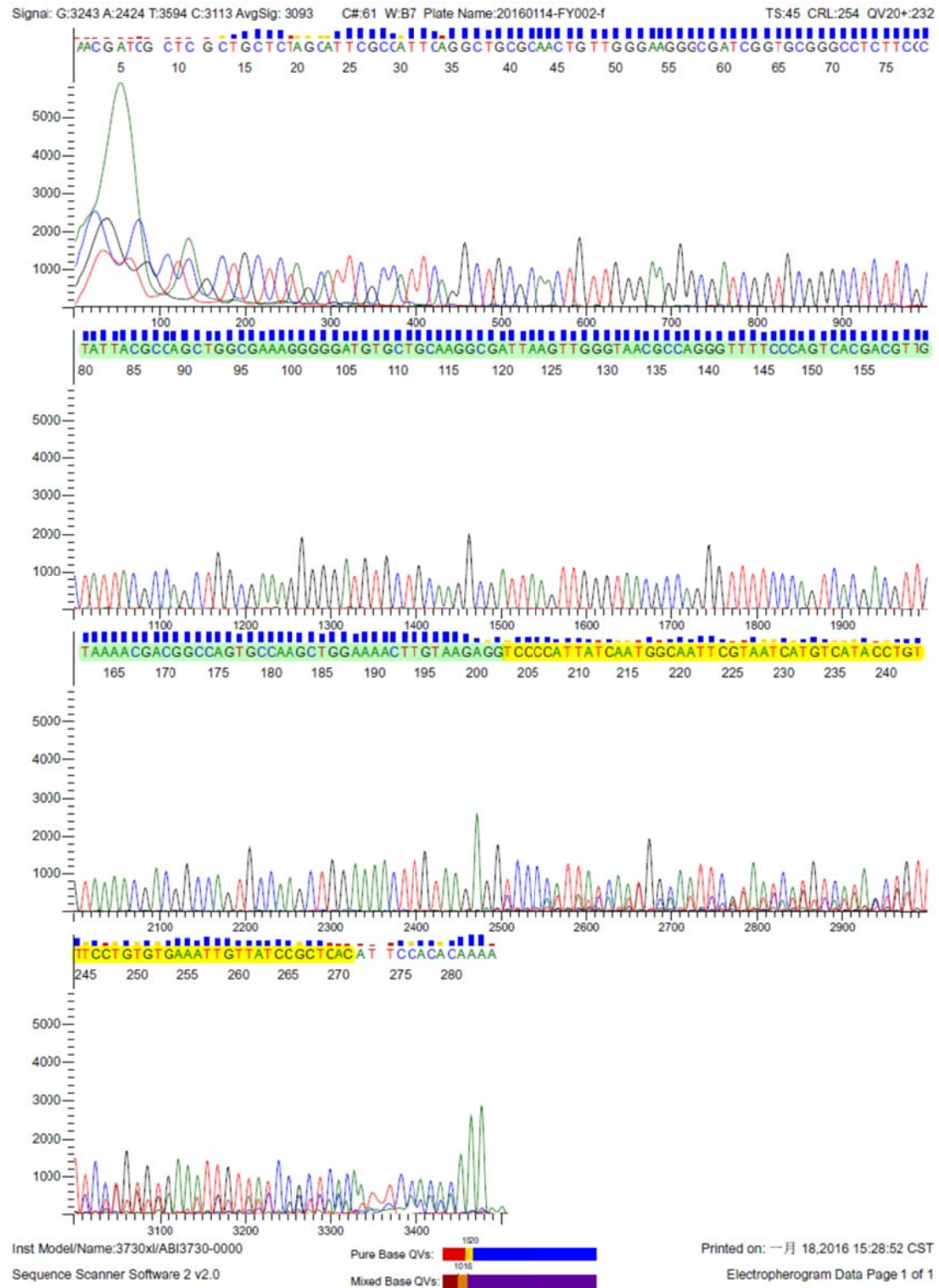
TS:49 CRL:788 QV20+:838



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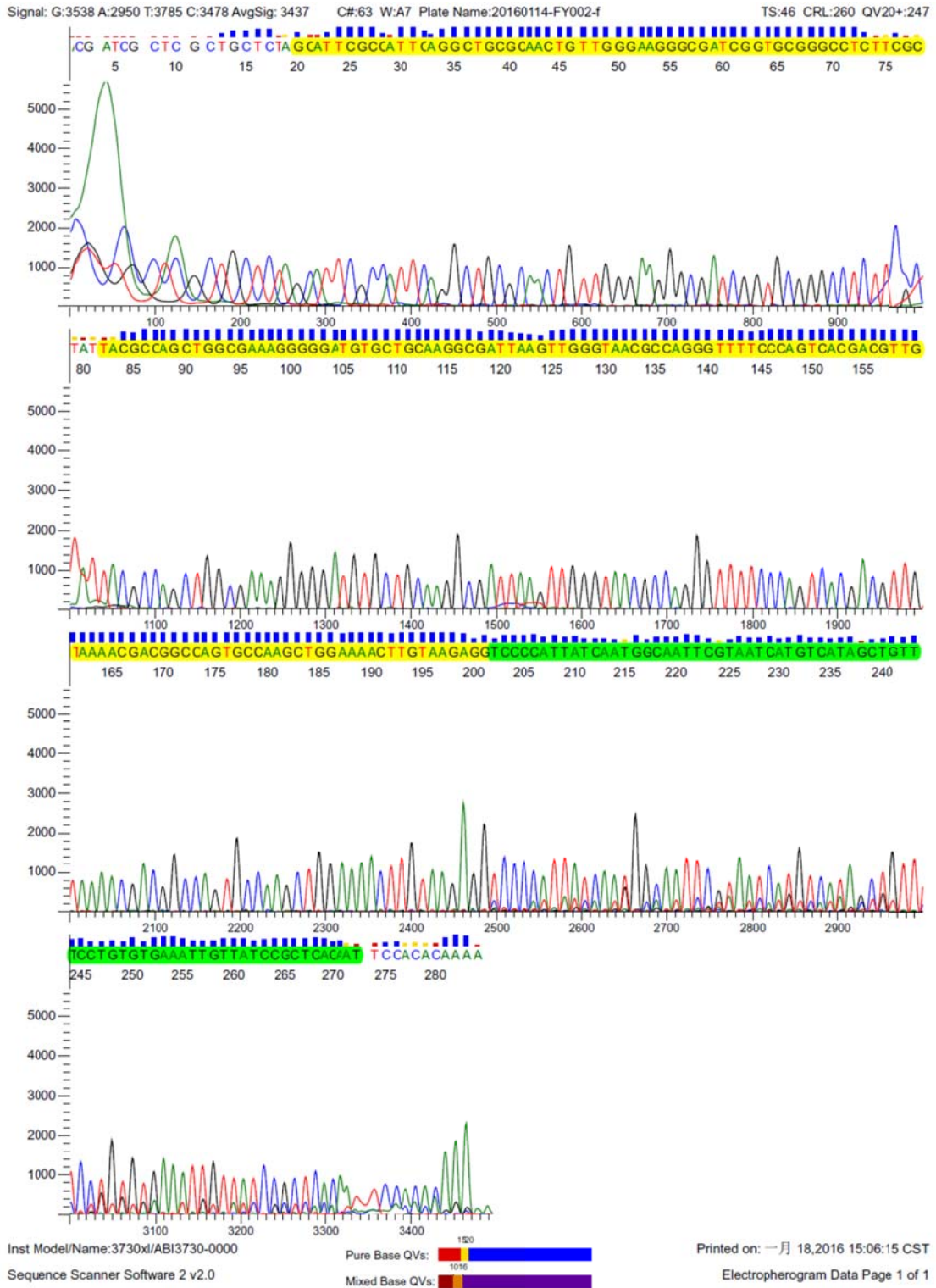
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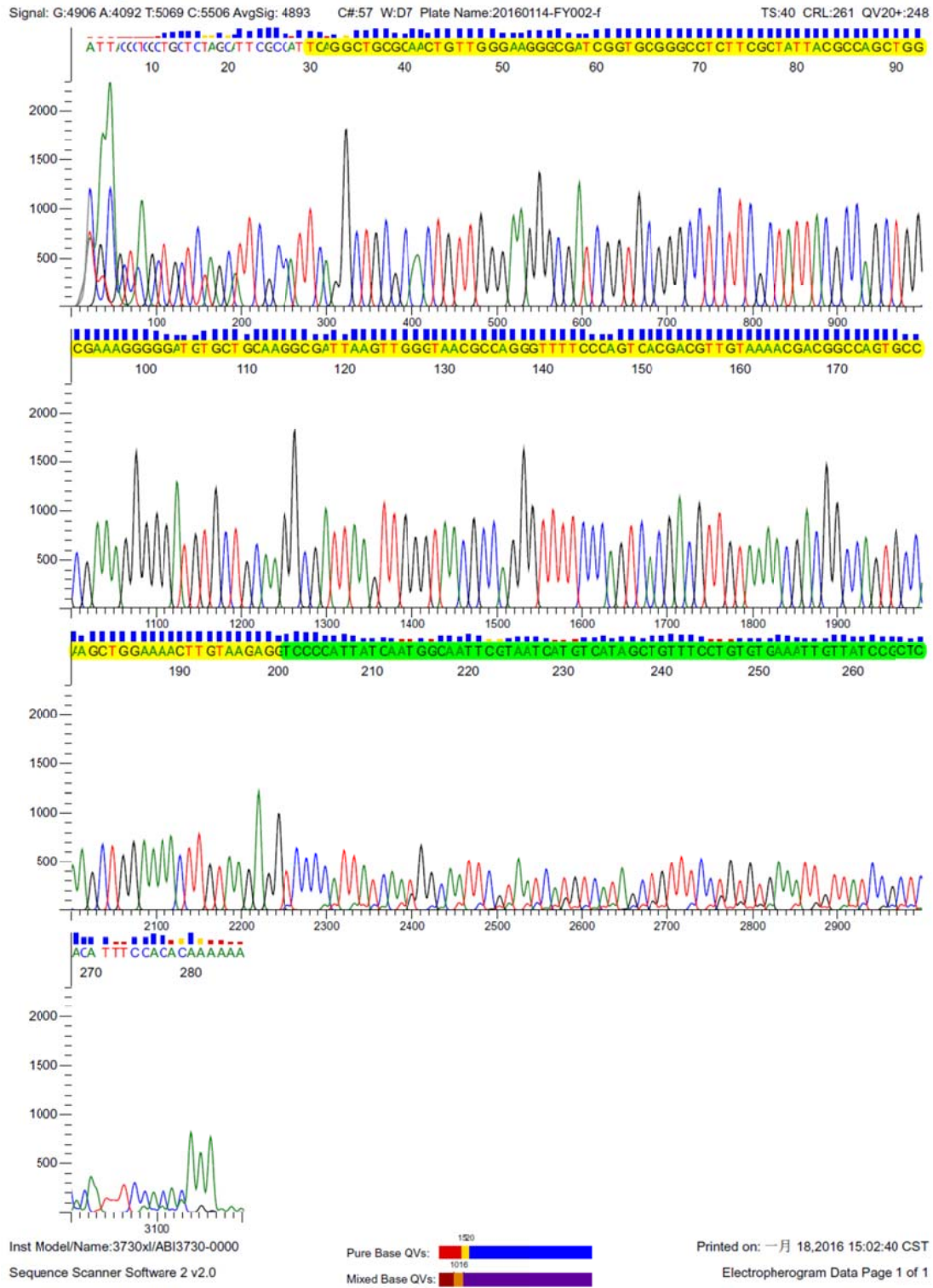
**Supplementary File 7.** One more biological replicates of the sequencing evidence for harboring re-joining junction site after DNA donor had been target deleted in plants.



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**Supplementary File 8.** One more biological replicates of the sequencing evidence for harboring re-joining junction site after DNA donor had been target deleted in plants.

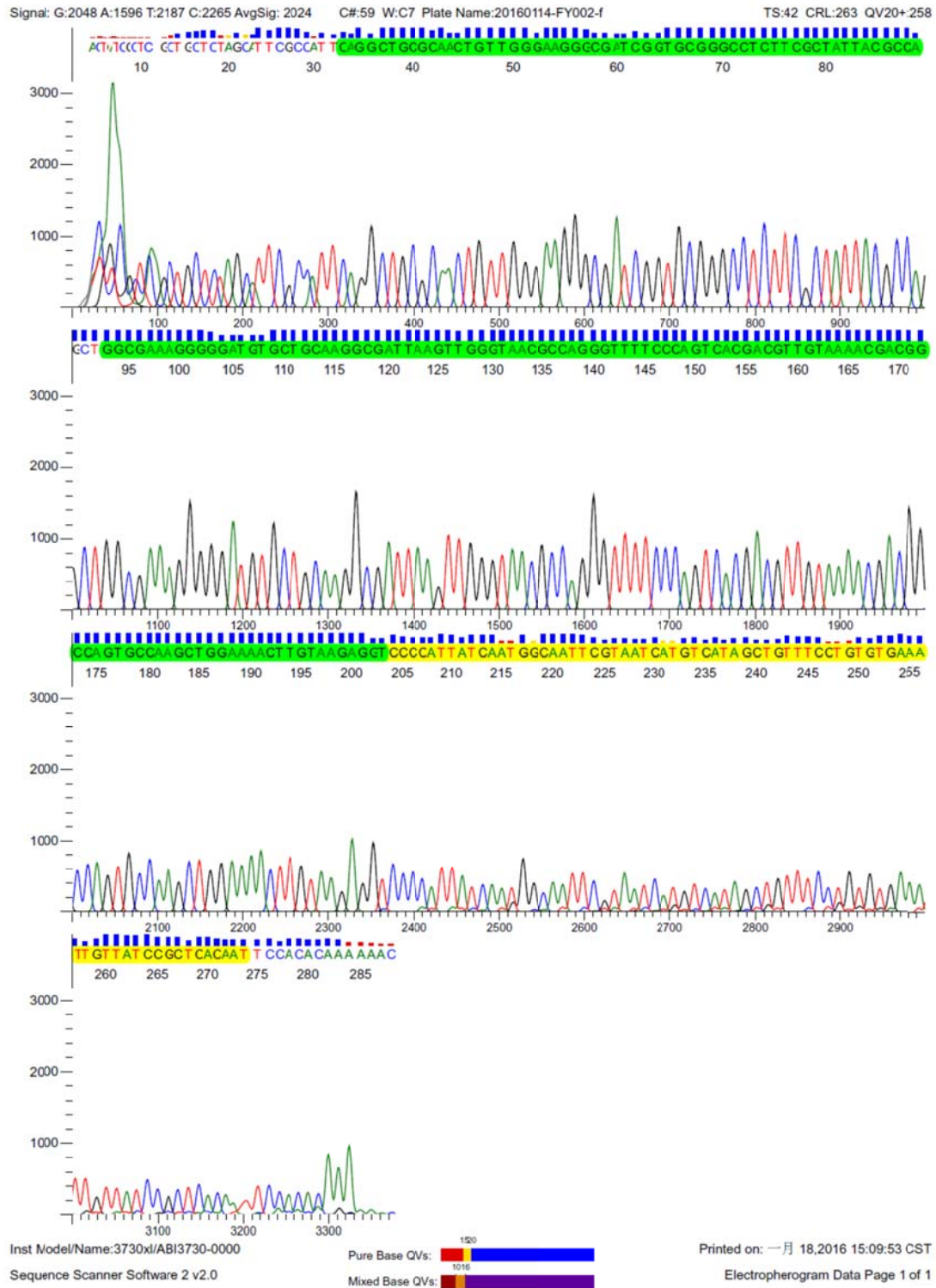




Title : An alternative strategy for targeted gene replacement in plants using a dual-sgRNA/Cas9 design

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**Supplementary File 9.** One more biological replicates of the sequencing evidence for harboring re-joining junction site after DNA donor had been target deleted in plants.



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Authors: Zhao Y., Zhang C., Liu W., Gao W., Liu C., Song G., Li W-X, Mao L., Chen B., Xu Y., Li X., Xie C.

**Supplementary file 10. The sequence of the mentioned key elements of CRISPR/Cas9 expression cassette in this study.**

>*hspCas9* sequence

```
ATGGACTATAAGGACCACGACGGAGACTACAAGGATCATGATATTGATTACAAAGACGATGACGATAAGATGGCCCC
AAAGAAGAAGCGGAAGGTCGGTATCCACGGAGTCCCAGCAGCCGACAAGAAGTACAGCATCGGCCTGGACATCGG
CACCAACTCTGTGGGCTGGGCCGTGATCACCGACGAGTACAAGGTGCCAGCAAGAAATTCAAGGTGCTGGGCAA
CACCGACCGGCACAGCATCAAGAAGAACCTGATCGGAGCCCTGCTGTTTCGACAGCGGGCAACAGCCGAGGCCAC
CCGGCTGAAGAGAACCGCCAGAAGAAGATACACCAGACGGAAGAACCGGATCTGCTATCTGCAAGAGATCTTCAG
CAACGAGATGGCCAAGGTGGACGACAGCTTCTCCACAGACTGGAAGAGTCCTTCCTGGTGGAAAGAGGATAAGAA
GCACGAGCGGCACCCCATCTTCGGCAACATCGTGGACGAGGTGGCCTACCACGAGAAGTACCCACCATCTACCAC
CTGAGAAAAGAACTGGTGGACAGCACCGACAAGGCCGACCTGCGGCTGATCTATCTGGCCCTGGCCACATGATCA
AGTTCCGGGGCCACTTCCTGATCGAGGGCGACCTGAACCCCGACAACAGCGACGTGGACAAGCTGTTTCATCCAGCT
GGTGCAGACTACAACCAGCTGTTTCGAGGAAAACCCCATCAACGCCAGCGGCGTGGACGCCAAGGCCATCTGTC
TGCCAGACTGAGCAAGAGCAGACGGCTGGAATACTGATCGCCAGCTGCCCGGCGAGAAGAAGATGGCCTGTT
CGGAAACCTGATTGCCCTGAGCCTGGCCCTGACCCCAACTTCAAGAGCAACTTCGACCTGGCCGAGGATGCCAAA
CTGCAGCTGAGCAAGGACACCTACGACGACGACCTGGACAACCTGCTGGCCAGATCGGCGACCAAGTACGCCGAC
CTGTTTCTGGCCGCAAGAACCTGTCCGACGCCATCTGCTGAGCGACATCTGAGAGTGAACACCGAGATCACCA
AGGCCCCCTGAGCGCCTCTATGATCAAGAGATACGACGAGCACCACCAGGACCTGACCCTGCTGAAAGCTCTCGT
GCGGCAGCAGCTGCCTGAGAAGTACAAAGAGATTTTCTTCGACCAGAGCAAGAACGGCTACGCCGGCTACATTGAC
GGCGGAGCCAGCCAGGAAGAGTTCTACAAGTTCATCAAGCCCATCTGGAAAAGATGGACGGCACCGAGGAAGT
CTCGTGAAGCTGAACAGAGAGGACCTGCTGCGGAAGCAGCGGACCTTCGACAACGGCAGCATCCCCACCAGATC
CACCTGGGAGAGCTGCACGCCATTCTGCGGCGCAGGAAGATTTTTACCCATTCTGAAGGACAACCGGGAAAAGA
TCGAGAAGATCCTGACCTTCCGCATCCCTACTACGTGGGCCCTCTGGCCAGGGGAAACAGCAGATTCGCCTGGAT
GACCAGAAAGAGCGAGGAAACCATCACCCCTGGAACCTTCGAGGAAGTGGTGGACAAGGGCGCTTCCGCCGAGA
GCTTCATCGAGCGGATGACCAACTTCGATAAGAACCTGCCAACGAGAAGGTGCTGCCAAGCACAGCCTGCTGTA
CGAGTACTTACCGTGTATAACGAGCTGACCAAAGTGAAATACGTGACCGAGGGAATGAGAAAAGCCCGCCTTCCTG
AGCGGCGAGCAGAAAAAGCCATCGTGGACCTGCTGTTCAAGACCAACCGGAAAAGTGACCGTGAAGCAGCTGAA
AGAGGACTACTTCAAGAAAATCGAGTGCTTCGACTCCGTGGAAATCTCCGGCGTGGAAAGATCGGTTCAACGCCTCC
CTGGGCACATACCAGATCTGCTGAAAATTATCAAGGACAAGGACTTCTGGACAATGAGGAAAACGAGGACATTC
TGGAAGATATCGTGCTGACCCTGACACTGTTTGAGGACAGAGAGATGATCGAGGAACGGCTGAAAACCTATGCCCA
CCTGTTTCGACGACAAAAGTGATGAAGCAGCTGAAGCGGCGGAGATACACCGGCTGGGGCAGGCTGAGCCGGAAGCT
GATCAACGGCATCCGGGACAAGCAGTCCGGCAAGACAATCCTGGATTTCTGAAGTCCGACGGCTTCGCCAACAGA
AACTTCATGCAGCTGATCCACGACGACAGCCTGACCTTAAAGAGGACATCCAGAAAAGCCAGGTGCCGGCCAGG
GCGATAGCCTGCACGAGCACATTGCCAATCTGGCCGGCAGCCCCGCCATTAAGAAGGGCATCTGCAGACAGTGAA
GGTGGTGGACGAGCTCGTGAAGTGATGGGCCGGCACAAGCCCCGAGAACATCGTGATCGAAAATGGCCAGAGAGAA
CCAGACCACCCAGAAGGGACAGAAGAAGCCGCGAGAGAATGAAGCGGATCGAAGAGGGGCATCAAAGAGCTGG
GCAGCCAGATCCTGAAAGAACACCCCGTGGAAAACACCCAGCTGCAGAACGAGAAGCTGTACCTGTACTACCTGC
AGAATGGGCGGGATATGTACGTGGACCAGGAACTGGACATCAACCGGCTGTCCGACTACGATGTGGACCATATCGTG
CCTCAGAGCTTTCTGAAGGACGACTCCATCGACAACAAGGTGCTGACCAGAAGCGACAAGAACCGGGGCAAGAGC
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GACAACGTGCCCTCCGAAGAGGTCGTGAAGAAGATGAAGAATACTGGCGGCAGCTGCTGAACGCCAAGCTGATT  
ACCCAGAGAAAGTTCGACAATCTGACCAAGGCCGAGAGAGGCGGCTGAGCGAACTGGATAAGGCCGGCTTCATC  
AAGAGACAGCTGGTGGAAACCCGGCAGATCACAAAGCACGTGGCACAGATCCTGGACTCCCGGATGAACACTAAG  
TACGACGAGAATGACAAGCTGATCCGGGAAGTGAAGTGATCACCTGAAGTCCAAGCTGGTGTCCGATTTCCGGA  
AGGATTTCCAGTTTTACAAAGTGC GCGAGATCAACAATACTACCACCAGCCCACGACGCCTACCTGAACGCCGTCGT  
GGGAACCGCCTGATCAAAAAGTACCCTAAGCTGGAAAGCGAGTTCGTGTACGGCGACTACAAGGTGTACGACGT  
GCGGAAGATGATCGCCAAGAGCGAGCAGGAAATCGGCAAGGCTACCGCCAAGTACTTCTTCTACAGCAACATCATG  
AACTTTTTCAAGACCGAGATTACCCTGGCCAACGGCGAGATCCGGAAGCGGCCTCTGATCGAGACAAACGGCGAA  
ACCGGGGAGATCGTGTGGGATAAGGGCCGGGATTTTGCACCGTGC GGAAAGTGCTGAGCATGCCCCAAGTGAATA  
TCGTGAAAAAGACCGAGGTGCAGACAGGCGGCTTCAGCAAAGAGTCTATCCTGCCAAGAGGAACAGCGATAAGC  
TGATCGCCAGAAAGAAGGACTGGGACCCTAAGAAGTACGGCGGCTTCGACAGCCCCACCGTGGCCTATTCTGTGCT  
GGTGGTGGCCAAAGTGAAAAGGGCAAGTCCAAGAACTGAAGAGTGTGAAAGAGCTGCTGGGGATCACCATCAT  
GGAAAGAAGCAGCTTCGAGAAGAATCCCATCGACTTTCTGGAAGCCAAGGGCTACAAAGAAGTGAAAAAGGACCT  
GATCATCAAGCTGCCTAAGTACTCCCTGTTTCGAGCTGGAAAACGGCCGGAAGAGAATGCTGGCCTCTGCCGGCGAA  
CTGCAGAAGGAAACGAACTGGCCCTGCCCTCCAAATATGTGAACTTCTGTACCTGGCCAGCCACTATGAGAAGC  
TGAAGGGTCCCCGAGGATAATGAGCAGAAACAGCTGTTTGTGGAACAGCACAAGCACTACCTGGACGAGATCAT  
CGAGCAGATCAGCGAGTTCTCCAAGAGAGTGATCCTGGCCGACGTAATCTGGACAAAGTGCTGTCCGCCTACAAC  
AAGCACGGGATAAGCCCATCAGAGAGCAGGCCGAGAATATCATCCACCTGTTTACCCTGACCAATCTGGGAGCCC  
CTGCCGCTTCAAGTACTTTGACACCACCATCGACCGAAAGAGGTACACCAGCACCAAAGAGGTGCTGGACGCCA  
CCCTGATCCACCAGAGCATCACCGGCCTGTACGAGACACGGATCGACCTGTCTCAGCTGGGAGGGCAGAAAAGGC  
CGGCGGCCACGAAAAGGCCGGCCAGGCAAAAAAGAAAAAGTAA

#### >AtU6-26 Sequence

CATTCGGAGTTTTTGTATCTGTTTCATAGTTTGTCCCAGGATTAGAATGATTAGGCATCGAACCTTCAAGAATTTGAT  
TGAATAAAACATCTTCATTCTTAAGATATGAAGATAATCTTCAAAAGGCCCTGGGAATCTGAAAGAAGAGAAGCAG  
GCCATTTATATGGGAAAGAACAATAGTATTTCTTATATAGGCCCATTTAAGTTGAAAACAATCTTCAAAAGTCCCAC  
ATCGCTTAGATAAGAAAACGAAGCTGAGTTTATATACAGCTAGAGTCGAAGTAGTGATT

#### > Enhanced CaMV35S promoter

CCTGCAGGTCAACATGGTGGAGCAGCAGACACTTGTCTACTCCAAAAATATCAAAGATACAGTCTCAGAAGACCAA  
AGGGCAATTGAGACTTTTCAACAAAGGGTAATATCCGGAACCTCCTCGGATTCCATTGCCAGCTATCTGTCACTTT  
ATTGTGAAGATAGTGAAAAGGAAGGTGGCTCCTACAAATGCCATCATTGCGATAAAGGAAAGGCCATCGTTGAAG  
ATGCCCTCTGCCGACAGTGGTCCCAAAGATGGACCCCCACCCACGAGGAGCATCGTGGAAAAAGAAGACGTTCCAA  
CCACGTCTTCAAAGCAAGTGGATTGATGTGATAACATGGTGGAGCAGCAGACACTTGTCTACTCCAAAAATATCAA  
GATACAGTCTCAGAAGACCAAAGGGCAATTGAGACTTTTCAACAAAGGGTAATATCCGGAACCTCCTCGGATTCC  
ATTGCCAGCTATCTGTCACTTTATTGTGAAGATAGTGAAAAGGAAGGTGGCTCCTACAAATGCCATCATTGCGATA  
AAGGAAAGGCCATCGTTGAAGATGCCTCTGCCGACAGTGGTCCCAAAGATGGACCCCCACCCACGAGGAGCATCG  
TGGA AAAAGAAGACGTTCCAACCAGTCTTCAAAGCAAGTGGATTGATGTGATATCTCACTGACGTAAGGGATGA  
CGCACAATCCCACTATCCTTCGCAAGACCCTCCTCTATATAAGGAAGTTCATTTCAATTTGGAGAGGACCTCGACCTC  
AACACAACATATAAAAACAAACGAATCTCAAGCAATCAAGCATTCTACTTCTATTGCAGCAATTTAAATCATTCTT  
TTAAAGCAAAAAGCAATTTTCTGAAAATTTTACCATTACGAACGATA

#### > SV40 NLS sequence

ATGGCCCCAAAGAAGAAGCGGAAGGTCGGTATCCACGGAGTCCCAGCAGCC

> Nucleoplasmin NLS sequence

AAAAGGCCGGCGGCCACGAAAAAGGCCGGCCAGGCAAAAAAGAAAAAG

> Universal sgRNA sequence

GTTTGTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCT  
TTTTTT

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**Supplementary File 11. The list of primers used in this study.**

Gene or target	Primer orientation	Sequence (5'-3')	Application
AtMIR169a	Forward	AGGATGGAGAAGCATGGAGG	PCR screening of deletion mutation
	Reverse	CTCATGGTTGGCAGCAGTTT	
AtMIR827a	Forward	CCTTTTTTCTGTAATCACCAGT	PCR screening of deletion mutation
	Reverse	AGCTTCAGAGGTTCCAAATACA	
AtU6-26	AtU6-26-1F	GCAGGCATGCAAGCTCATTCCGGAGTTTTGTATCTTGTT	To get sequence for vector construction
	AtU6-26-2F	GCTTTTTTTAAGCTCATTCCGGAGTTTTGTATCTTGTT	
	Reverse	AATCACTACTTCGACTCTAGCTGTATAT	
Enhanced CaMV35S promoter	Forward	GGCCAGTGCCAAGCTTGCATGCCTGCAGGTCAAC	To get sequence for vector construction
	Reverse	GATCGGGGAAATTCGAGCTCTATCGTTCGTAATGGTGAAAATT	
AtMIR169a sgRNA1 and sgRNA2	sgRNA1F	ATATACAGCTAGAGTCGAAGTAGTGATTGAGATTTTATGCCCCAAGA GTTTTAGAGCTAGAAATAGCAAGTT	In fusion PCR for vector construction
	sgRNA2F	ATATACAGCTAGAGTCGAAGTAGTGATTGAAATAGTTTCTAATTCTGG GTTTTAGAGCTAGAAATAGCAAGTT	
	UsgRNA-R	GGCCAGTGCCAAGCTTAAAAAAAAGCACCGACTCG	
AtMIR827a sgRNA1 and sgRNA2	sgRNA1F	ATATACAGCTAGAGTCGAAGTAGTGATTGGATCATCTATTGAAGGAAC GTTTTAGAGCTAGAAATAGCAAGTT	In fusion PCR for vector construction
	sgRNA2F	ATATACAGCTAGAGTCGAAGTAGTGATTGCAAATCGAAAAGCTTCTTA GTTTTAGAGCTAGAAATAGCAAGTT	
	UsgRNA-R	GGCCAGTGCCAAGCTTAAAAAAAAGCACCGACTCG	
U6: gRNA1: sgRNA	UgRNA1F	GCAGGCATGCAAGCTCATTCCGGAGTTTTGTATCTTGTT	Splicing overlap extention PCR for vector construction
	UsgRNA-R	GGCCAGTGCCAAGCTTAAAAAAAAGCACCGACTCG	
U6: gRNA2: sgRNA	UgRNA2F	GCTTTTTTTAAGCTCATTCCGGAGTTTTGTATCTTGTT	Splicing overlap extention PCR for vector construction
	UsgRNA-R	GGCCAGTGCCAAGCTTAAAAAAAAGCACCGACTCG	
AtTFL1	TFL1-F1	CTTTGTTTTTCATTTGGTTATCG	PCR screening of gene replacement and for TA clone of amplicons for sequencing.
	TFL1-R1	AGAGAAAGAGACGACCGAGACAT	
	TFL1-F2	ATGTCTCGGTCGTCTTTTCTCT	

	TFL1-R2	ATGGTGAGCAAGGGCGAGGAG	
	TFL1-F3	GCAGAGGCATCTTCAACGAT	
	TFL1-R3	CATGACCTGTTTTGCATTTTCG	
	TFL1-F4	CGAAATGCAAAACAGGTCATG	
	TFL1-R4	GTGACCTATCAAGCCATGTATGAG	
	F5 (BEcoRI-F)	TTGTGTGGAATTGTGAGCGG	PCR identification of DNA donor had been deleted and TA clone for sequencing validation.
	R5 (AHindIII-R)	AAACTGAAGGCGGGAAACG	
M13 R		CAGGAAACAGCTATGAC	Sequencing mutations in TA clone

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**Supplementary File 12. The sequence detail of DNA donor template before and after deletion to supply for HDR repair.**

Note:

- The DNA repair donor sequence should be the sequence between 1<sup>st</sup> and 2<sup>nd</sup> sgRNA target sites. This sequence would be deleted to supply as DNA repair donor
- The two ↓ indicating the expected cut sites induced by Cas9 nuclease.
- PAM (protospacer-adjacent motif) sequences had been underlined and indicated as “PAM”.
- This sequence harboring left region and right border (RB) sequence, eGFP expression cassette and both flanking homolog arms of TFL1.
- The text between the lines of the sequence were the captions.
- Detection primer pair (F5 and R5 pair were designed on the RE site of the *EcoRI* and *HindIII*, respectively.)  
F5 (BEcoRI-F): 5' TTGTGTGGAATTGTGAGCGG 3'  
R5 (AHindIII-R): 5' AAAGTGAAGCGGGAAACG 3'  
the blue shadow indicating the sequence regions.

**I. Before deletion happened (total length 3902 bp)**

> left region outside repair donor (1-96 bp region)

Primer F5 (BEcoRI-F)

AGGCTTTACA CTTTATGCTT CCGGCTCGTA TGTTGTGTGG AATTGTGAGC GGATAACAATTTACACACAGG  
AAACAGCTAT GACATGATTA CGAATT

>TFL1 left homologous arm (97-897 bp region)

sgRNA target region PAM  
DCCATTGATA ATUGGGA ↓ GAG TGGTTAGCGG TTTTTTGCC CAGGCCTACT CTGAGCAATA  
ATTGTATCCG GAGTTGTAAT AGAATCAAAG TACGATGAGA GTGTTTTTAT GACAAATATC  
TTAATCTTGG CCAATTATAT GTTCTACTGA AATTCTTTT GAATTCATCG ACCAGTGAGA  
CTTAAAAATA GCTTTTTATT CGCCGAGGTA TATATAGCTA GGAATTTTGT CGAAATTTAG  
ACGTTAGTGG GTTTTGTTCT TCGTGACACA AAAGATATTC TATATATTA CGAAATCTAG  
CGATCGATAT GGTATTTATA TAAAGTCTTG GTCATAGATA GGGGTTGAAA CTTGAAACCA  
TGCATGATAT GCCAATGTTG CTGAAGCAGT CAATGTTGCT GAAGAAGTCA AACGTAATTA  
TATAGTGAAT ACCAAAAAAG TGATATTTCT TAATCAATT AAATATAATT ATAGTTTTAA  
ATCACCTAAA ATAAGTACT TATTAAAAACC CCCCAAATTT ACTTTAATAT AGTTGGTGA  
CATGTTTGG AAAGCAAACA AAAAGAAAAA GAAAAAGAAA AAAAAAAGAG AAAGAGGTTA  
GTACACATAA TTGGGAATTA ATGTCTATTG ATCTTTTAT CTTTCTCTCT CTCTCTAAGA  
CGGAAAACCC CTATAAATAG ATGTCTCGGT CGTCTCTTTG TCTCCCAAT CACTACAAAT  
CTCTCTTTC CTCTAAGTTA ACAAAGAAA ATGGAGAATA TGGGAAGTAG AGTGATAGAG  
CCATTGATAA TGGGGAAATT C

> Tnos-eGFP-E35Spromoter (898-2812 bp region, the expression cassette was placed on the minus strand)

CCGATCTAGT AACATAGATG ACACCGCGCG CGATAATTTA TCCTAGTTTG  
CGCGCTATAT TTTGTTTTCT ATCGCGTATT AAATGTATAA TTGCGGGACT  
CTAATCATAA AAACCATCT CATAAATAAC GTCATGCATT ACATGTTAAT  
TATTACATGC TTAACGTAAT TCAACAGAAA TTATATGATA ATCATCGCAA  
GACCGGCAAC AGGATTCAAT CTTAAGAAAC TTTATTGCCA AATGTTTGAA  
CGATCGGGGA AATTCGAGCT CGGTACCCGG GCGATCATA CTTTCTCTC  
TTCTTGGGAG AACCCCTTT GTACAGCTCG TCCATGCCGT GAGTGATCCC  
GGCGGCGGTC ACGAACTCCA GCAGGACCAT GTGATCGCGC TTCTCGTTGG  
GGTCTTTGCT CAGGGCGGAC TGGGTGCTCA GGTAGTGGTT GTCGGGCAGC  
AGCACGGGGC CGTCGCCGAT GGGGGTGTTC TGCTGGTAGT GGTGCGGAG  
CTGCACGCTG CCGTCTCGA TGTGTGGCG GATCTGAAG TTCACCTGA  
TGCCGTTCTT CTGCTTGTG GCCATGATAT AGACGTTGTG GCTGTTGTAG  
TTGTACTCA GCTTGTGCC CAGGATGTTG CCGTCTCT TGAAGTCGAT  
GCCCTTCAGC TCGATGCGGT TCACCAGGT GTCGCCCTCG AACTTCACCT  
CGGCGCGGGT CTTGTAGTTG CCGTCTCT TGAAGAAGAT GGTGCGCTCC  
TGGACGTAGC CTTGCGGCAT GGCAGCTTG AAGAAGTCGT GCTGCTCAT  
GTGGTCGGG TAGGCGCTGA AGCACTGCAC GCCGTAGTG AAGGTGGTCA  
CGAGGGTGGG CCAGGGCACG GGCAGCTTGC CGGTGGTGCA GATGAACCTC  
AGGGTCAGCT TGCCGTAGGT GGCATCGCC TCGCCCTCG CGGACACGCT  
GAACCTGTGG CCGTTACGT CGCCGTCCAG CTCGACCAGG ATGGGCACCA  
CCCCGGTGA CAGTCTCTCG CCCTTGCTCA CCATCCCGGG GATCCTCTAG  
AGTCCCCGT GTTCTCTCA AATGAAATGA ACTTCTTAT ATAGAGGAAG  
GGTCTGCGA AGGATAGTG GATTGTGCGT CATCCCTTAC GTCAGTGGAG  
ATATCACATC AATCCACTTG CTTTGAAGAC GTGGTTGGAA CGTCTTCTT  
TTCCACGATG CTCTCTGTG GTGGGGTCC ATCTTTGGGA CCACTGTCGG

CAGAGGCATC TTCAACGATG GCCTTTCCTT TATCGCAATG ATGGCATTG  
 TAGGAGCCAC CTTCCCTTTC CACTATCTTC ACAATAAAGT GACAGATAGC  
 TGGGCAATGG AATCCGAGGA GGTTCGGA TATTACCCTT TGTTGAAAAG  
 TCTCAATTGC CCTTTGGTCT TCTGAGACTG TATCTTTGAT ATTTTGGAG  
 TAGACAAAGT TGTCGTGCTC CACCATGTTG ACGAAGATTT TCTTCTGTG  
 ATTGAGTCGT AAGAGACTCT GTATGAACTG TFCGCCAGTC TTFACGGCGA  
 GTTCTGTTAG GTCCTCTATT TGAATCTTTG ACTCCATGGC CTTTGATTCA  
 GTGGAACTA CCTTTTAGA GACTCCAATC TCTATTACTT GCCTTGGTTT  
 GTGAAGCAAG CCTTGAATCG TCCATACTGG AATAGTACTT CTGATCTTGA  
 GAAATATATC TTTCTGTG TTCTTGATGC AGTTAGTCTT GAATCTTTG  
 ACTGCATCTT TAACCTTCTT GGGAAAGTAT TTGATTTCTT GGAGATTATT  
 GCTCGGGTAG ATCGTCTTGA TGAGACCTGC TCGTAAGCC TCTTAACCA  
 TCTGTGGGTT AGCATTCTTT CTGAAATTGA AAAGGCTAAT CTGGGGACCT  
 GCAGGCATGC AAGCT

> TFL1 right homologous arm (2813-3665 bp region)

CCTCTTACAA GTTTTCCATT TCTAACTCAA TAATCTTATA AATTGTAGCT TTAGTTTTTA  
 TCATTCCTTT TTCCAGTCTT TTTTITTTAA TGGTAAAAC CAACCGAAAT GCAAAAACAGG  
 TGATGATAGA CCCAGATGTT CCAGGTCCTA GTGACCCCTT TCTAAAAGAA CACCTGCACT  
 GGTACGTTA ATTTATTTAT TCTTCTTTT CATTITGGGC CCATATTCCA TATACATTGC  
 ATTTAAATCA TTTTCGTTATA ACCCTAATAA AGTTTTTTTT GGGTGTAAGT TATATACATT  
 TGAGTTGGTC AAAGATCTCC ATCGCCATGA GTTCTCAGAA CTTTTCTGT AAAGTAATAA  
 TATTAGTATT GTTGAATGTT TCAATAGGAT CGTTFACAAAC ATTCCCGGCA CAACAGATGC  
 TACGTTTGGT AAGGCCTCTT CATGAATCTT GTAATTTAAA TACTTATACA TATATCATGT  
 TATATAGAAA TAAAAATATT TGCATTGTAA TATAGGCAA GAGGTGGTGA GCTATGAATT  
 GCCAAGGCCA AGCATAGGGA TACATAGGTT TGTGTTTGT CTGTTCAGGC AGAAGCAAAG  
 ACGTGTATC TTTCTAATA TCCCTTCGAG AGATCACTTC AACACTCGTA AATTTGCGGT  
 CGAGTATGAT CTTGGTCTCC CTGTGCGGGC CGTCTCTT AACGCACAAA GAGAAACCGC  
 TGCACGCAA CGCTAGTTTC ATGATTGTCA TAACTGCAA AAATGAAAGA AGAAAATTG  
 CATGTAATCT CATGTTTATT TGTGTTCTGA ATTTCCGTAC TCTGACCTTT ↓ CCTCTTACA  
 PAM PAM sgRNA target region  
 AGTTTTCCAG CTT

> right border (3667-3902 bp region)

GGCACTG GCCGTGTTT TACAACGTCG TGACTGGGAA AACCTGGCG TTACCCAAT TAATCGCCTT  
 GCAGCACATC CCCCTTCGC CAGCTGGCGT AATAGCGAAG AGGCCCGCAC CGATCGCCCT TCCCAACAGT  
 TGCGCAGCCT GAATGGCGAA TGCTAGAGCA GCTTGAGCTT GGATCAGATT GTCGTTTCCC GCCTTCAGTT  
 TAAACTATCA GTGTTGACAG TAATTGGGGC R5 (A<sub>H</sub>indIII-R)

## II. After deletion happened to supply the DNA donor for HDR repair

1> The junction sequence after donor template has been cut to supply for HDR repair

TTGTGTGAA TTGTAGCGG ATAACAATT CACACAGGAA ACAGCTATGA CATGATTAG  
 AATTGCCATT GATAATGGGG ACCTCTTACA AGTTTTCCAG CTGGCACTG GCCGTCGTT  
 The junction site  
 TACAACGTCG TGACTGGGAA AACCTGGCG TTACCCAAT TAATCGCCTT GCAGCACATC  
 CCCCTTCGC CAGCTGGCGT AATAGCGAAG AGGCCCGCAC CGATCGCCCT TCCCAACAGT  
 TGCGCAGCCT GAATGGCGAA TGCTAGAGCA GCTTGAGCTT GGATCAGATT GTCGTTTCCC  
 GCCTTCAGTT T

2> Reverse complementary of the Junction sequence

AAACTGAAG CGGAAACGA CAATCTGATC CAAGCTCAAG CTGCTTAGC  
 ATTCCGATT CAGGCTGCG AACTGTTGG AAGGGCATC GGTGCGGGC  
 TCTTCGCTAT TACGCCAGCT GCGAAAAGG GGATGTGCTG CAAGGCGATT  
 AAGTTGGTA ACGCCAGGT TTTCCAGTC ACGACGTTG AAAACGACG  
 CCAGTGCAA GCTGAAAAC TTGTAAGAG TCCCATTAT CAATGGCAAT  
 The junction site  
 TCGTAATCAT GTCATAGCTG TTTCTGTG GAAATTGTA TCCGCTACA  
 ATTCCACACA A

Note: Our sequencing results confirmed by sequencing of reverse complementary sequence by using M13 R primer in TA clone of PCR amplicons.