

**B**  
Indels% of liver gDNA from unedited hemophilia A mouse = 0.09% (background error)

Reference sequence:  
TAGATGCAAAAGACGCCTTAGCCTAAACACATCACAAACCAC  
sgRNA sequence:  
TAGATGCAAAAGACGCCTTAGCCTAAACACATCACAAACCAC

Indels% of edited HA mouse liver after injection of F8 donor plasmid only = 0.10% (background error)

Reference sequence:  
TAGATGCAAAAGACGCCTTAGCCTAAACACATCACAAACCAC  
sgRNA sequence:  
TAGATGCAAAAGACGCCTTAGCCTAAACACATCACAAACCAC

Indels% of edited HA mouse liver after injection with CRISPR plasmids only = 10.5%

Reference sequence:  
TAGATGCAAAAGACGCCTTAGCCTAAACACATCACAAACCAC  
sgRNA sequence:  
TAGATGCAAAAGACGCCTTAGCCTAAACACATCACAAACCAC  
TAGATGCAAAAGACGCCTTAAGCCTAAACACATCACAAACCAC-87.59% (24415 reads)  
TAGATGCAAAAGACGCCTTA-CCTAAACACATCACAAACCAC-2.24% (625 reads)  
TAGATGCAAAAGACGCCTTAAGCCTAAACACATCACAAACCAC-1.73% (481 reads)  
TAGATGCAAAAGACGCCTTA-CCTAAACACATCACAAACCAC-1.47% (411 reads)  
TAGATGCAAAAGACGCCTTAAGCCTAAACACATCACAAACCAC-0.76% (212 reads)  
TAGATGCAAAAGACGCCTTAAGCCTAAACACATCACAAACCAC-0.60% (168 reads)  
TAGATGCAAAAGACGCCTTAAGCCTAAACACATCACAAACCAC-0.46% (129 reads)  
TAGATGCAAAAGACGCCTTAAGCCTAAACACATCACAAACCAC-0.30% (85 reads)  
TAGATGCAAAAGACGCCTTAAGCCTAAACACATCACAAACCAC-0.25% (71 reads)  
TAGATGCAAAAGACGCCTTAAGCCTAAACACATCACAAACCAC-0.21% (59 reads)  
TAGATGCAAAAGACGCC- - - - - AAGACATCACAAACCAC-0.21% (58 reads)

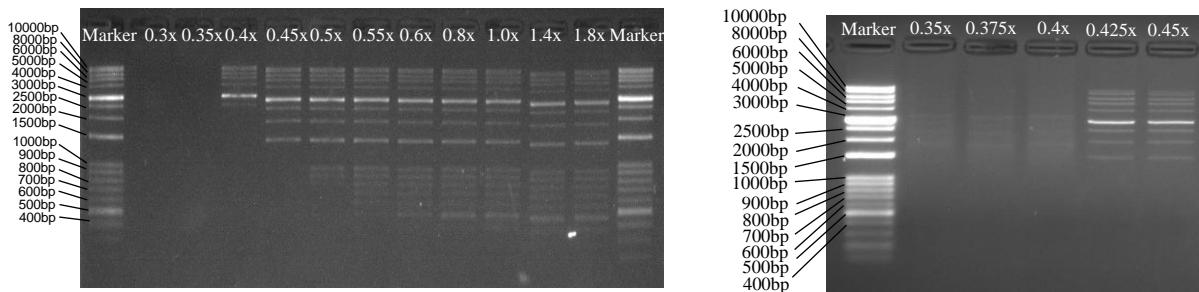
Indels% of edited HA mouse liver after injection of CRISPR and F8 donor plasmids = 11.53%

Reference sequence:  
TAGATGCAAAAGACGCCTTAGCCTAAACACATCACAAACCAC  
sgRNA sequence:  
TAGATGCAAAAGACGCCTTAAGCCTAAACACATCACAAACCAC  
TAGATGCAAAAGACGCCTTAAGCCTAAACACATCACAAACCAC-86.48% (38092 reads)  
TAGATGCAAAAGACGCCTTAAGCCTAAACACATCACAAACCAC-2.03% (894 reads)  
TAGATGCAAAAGACGCCTTAAGCCTAAACACATCACAAACCAC-1.93% (849 reads)  
TAGATGCAAAAGACGCCTTAAGCCTAAACACATCACAAACCAC-1.64% (723 reads)  
TAGATGCAAAAGACGCCTTAAGCCTAAACACATCACAAACCAC-0.92% (404 reads)  
TAGATGCAAAAGACGCCTTAAGCCTAAACACATCACAAACCAC-0.84% (372 reads)  
TAGATGCAAAAGACGCCTTAAGCCTAAACACATCACAAACCAC-0.53% (232 reads)  
TAGATGCAAAAGACGCCTTAAGCCTAAACACATCACAAACCAC-0.34% (149 reads)  
TAGATGCAAAAGACGCCTTAAGCCTAAACACATCACAAACCAC-0.27% (117 reads)  
TAGATGCAAAAGACGCCTTAAGCCTAAACACATCACAAACCAC-0.24% (106 reads)  
TAGATGCAAAAGACGCCTTAAGCCTAAACACATCACAAACCAC-0.21% (93 reads)  
TAGATGCAAAAGACGCCTTAAGCCTAAACACATCACAAACCAC-0.21% (91 reads)

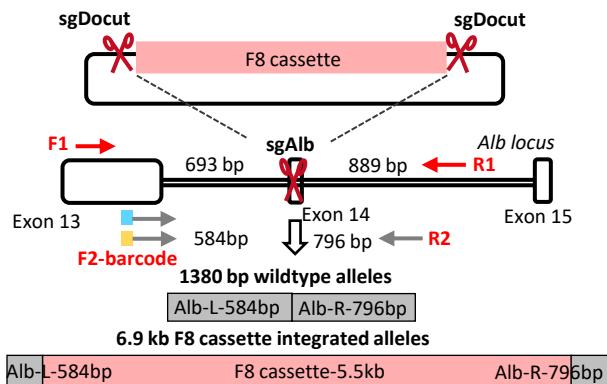
**Figure S1. sgRNA Design and Indel Frequencies at the Alb Locus.** (A) An sgRNA (sgAlb-E14) was designed to target the sequence surrounding the stop codon TAA (shown in red, reverse complement) in Exon 14 of the Alb gene. The red scissor icon indicates the anticipated Cas9 cleavage site, with "PAM" denoting the protospacer-adjacent motif (PAM) for SpCas9, recognized as NGG. (B) Frequencies of indels observed at the Alb locus following *in vivo* editing in the liver of hemophilia A mice. One week after the injection of editing plasmids, the sequence adjacent to the editing site was amplified from liver genomic DNA and subsequently analyzed using next-generation sequencing (NGS) and CRISPResso2.

A

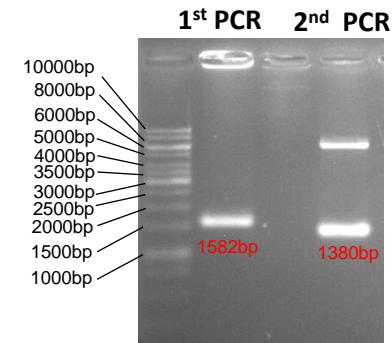
### Magbeads selection



B

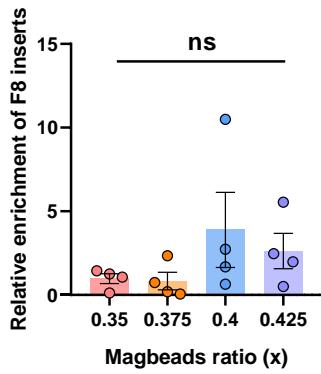


C



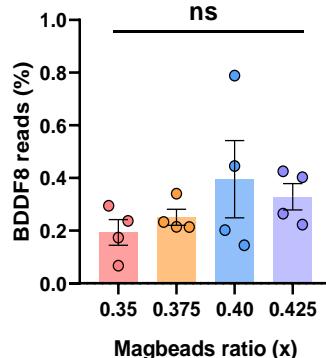
D

### qPCR

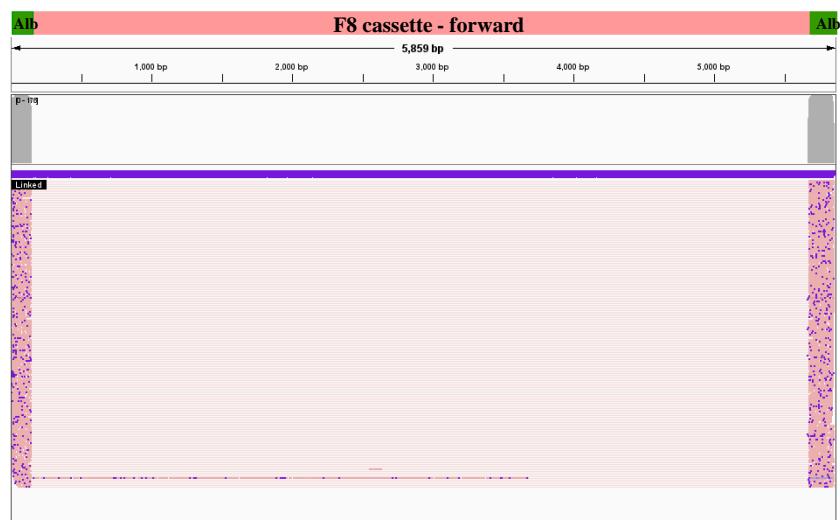
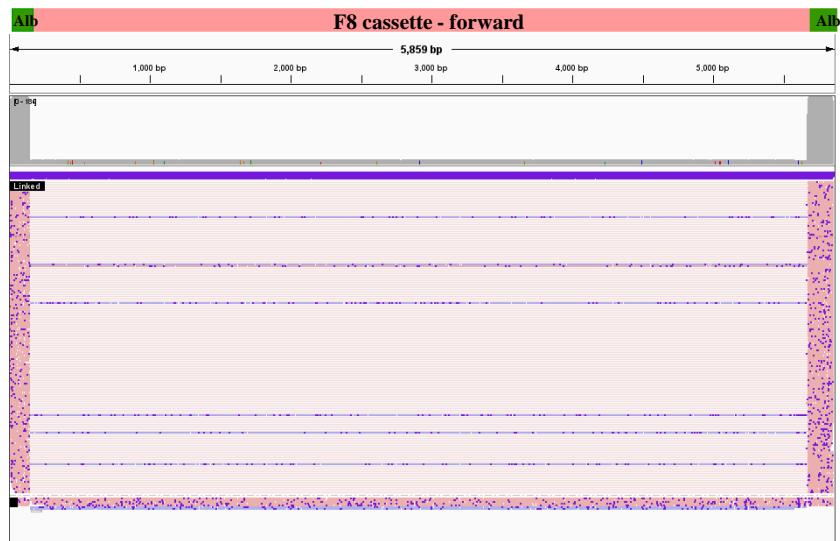


E

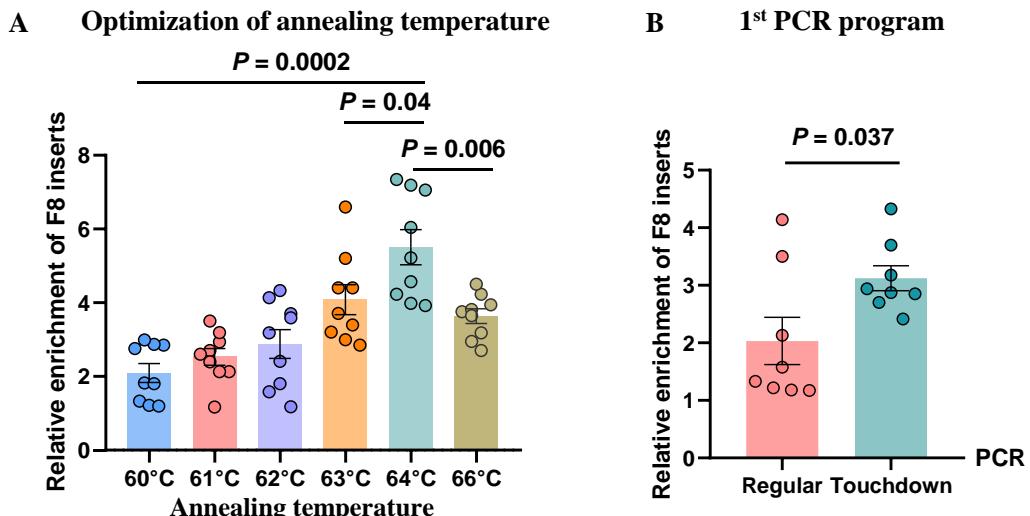
### Nanopore-seq



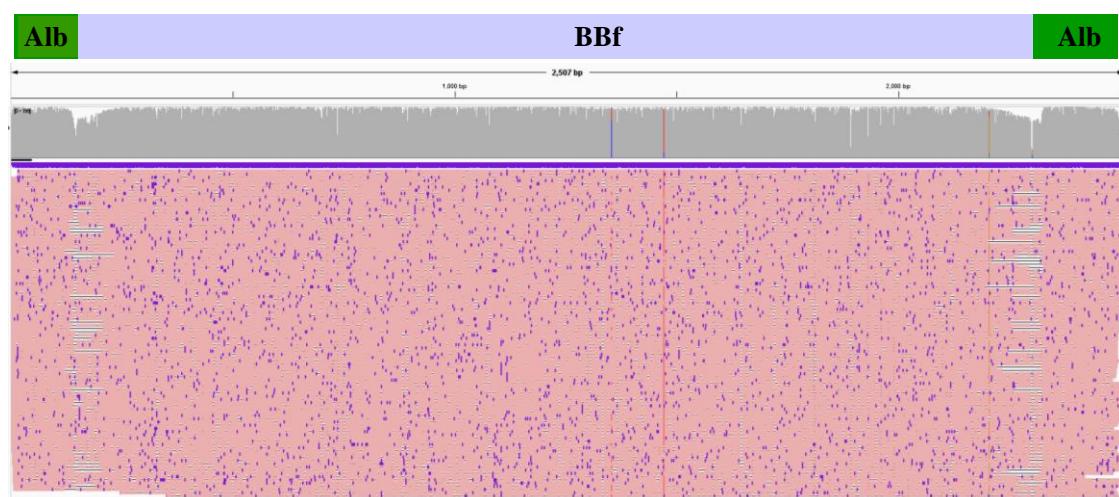
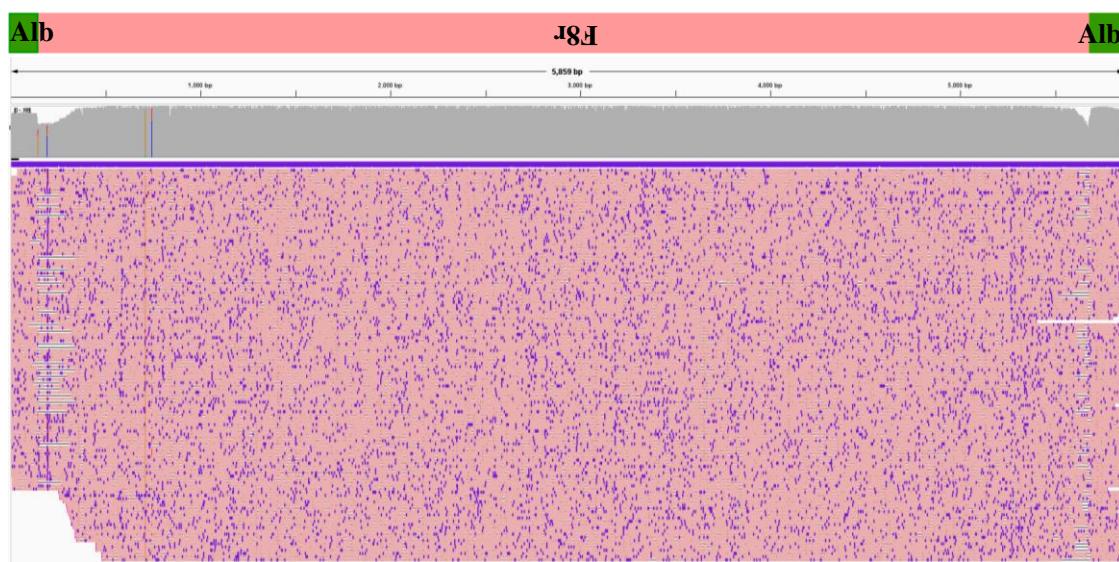
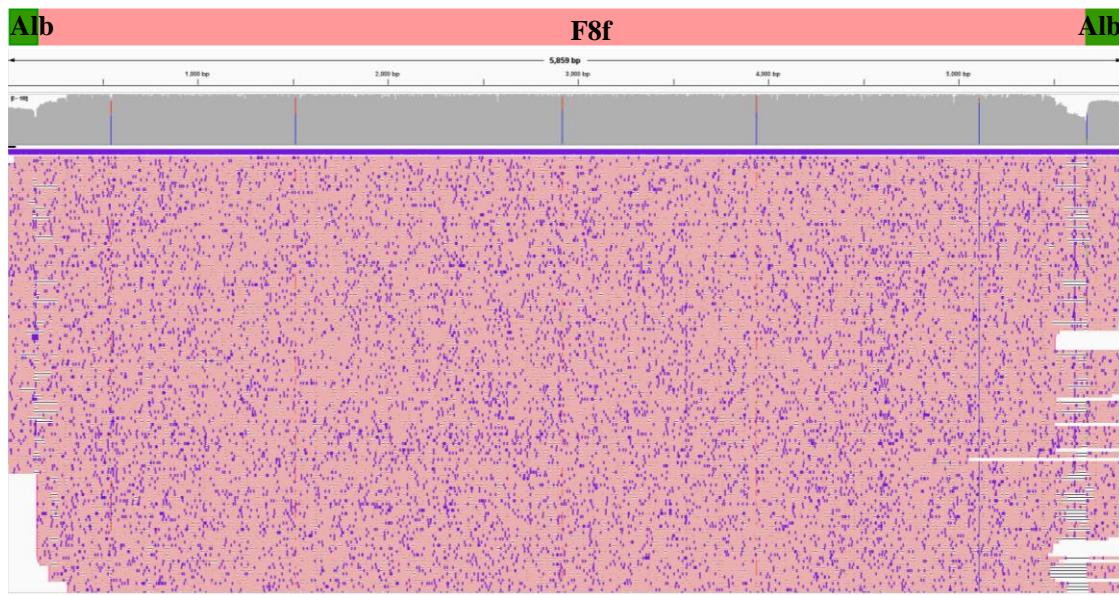
**Figure S2. Optimizing Magnetic Beads for the Enrichment of F8-Integrated Alleles.** (A) Evaluation of size selection efficiency using various ratios of magnetic beads (0.3x-1.8x). (B) Primer design for nested PCR, depicting expected PCR products, including the 1380bp wildtype alleles and the approximately 6.9kb F8 cassette-integrated alleles. (C) Representative results of gel electrophoresis for the 1st PCR products and the 2nd PCR products, which were amplified from the 1st PCR products after size selection using a beads ratio of 0.4x. The bands corresponding to alleles lacking donor insertion in the 1st and 2nd PCR products were 1586bp and 1380bp, respectively. (D) Relative enrichment of F8 inserts determined by qPCR after size selection using magnetic beads at various ratios. Error bars represent the mean  $\pm$  SEM, n = 4, and paired two-sided Student's t-tests were performed. (E) Determination of the percentage of both forward and reverse F8 inserts by nanopore sequencing (F8 reads %) in the 2nd PCR products following size selection of the purified 1st PCR products using different ratios of magnetic beads. Error bars represent the mean  $\pm$  SEM, n = 4, and paired two-sided Student's t-tests were conducted.

**Size selection-None****Size selection-Once****Size selection-Twice**

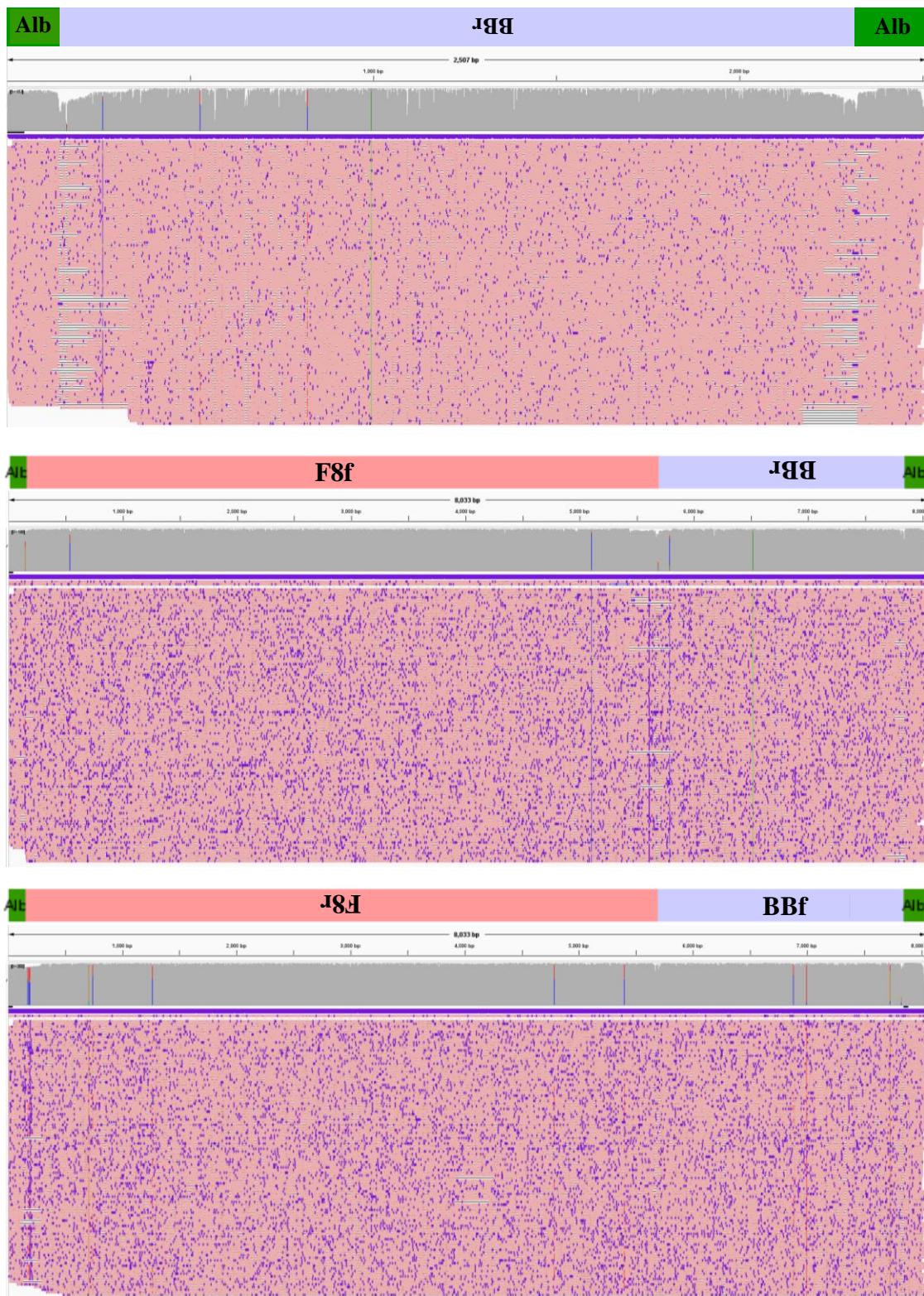
**Figure S3. Visualization of Sequencing Results for 2nd PCR Amplicons after Magnetic Beads Size Selection.** The reference sequence of the F8 cassette is flanked by 332bp of the Alb genomic sequence. Representative Integrated Genome Viewer (IGV) images display nanopore sequencing results after size selection of the 1st PCR products using magnetic beads 0 (above), 1 (middle), or 2 (bottom) times.



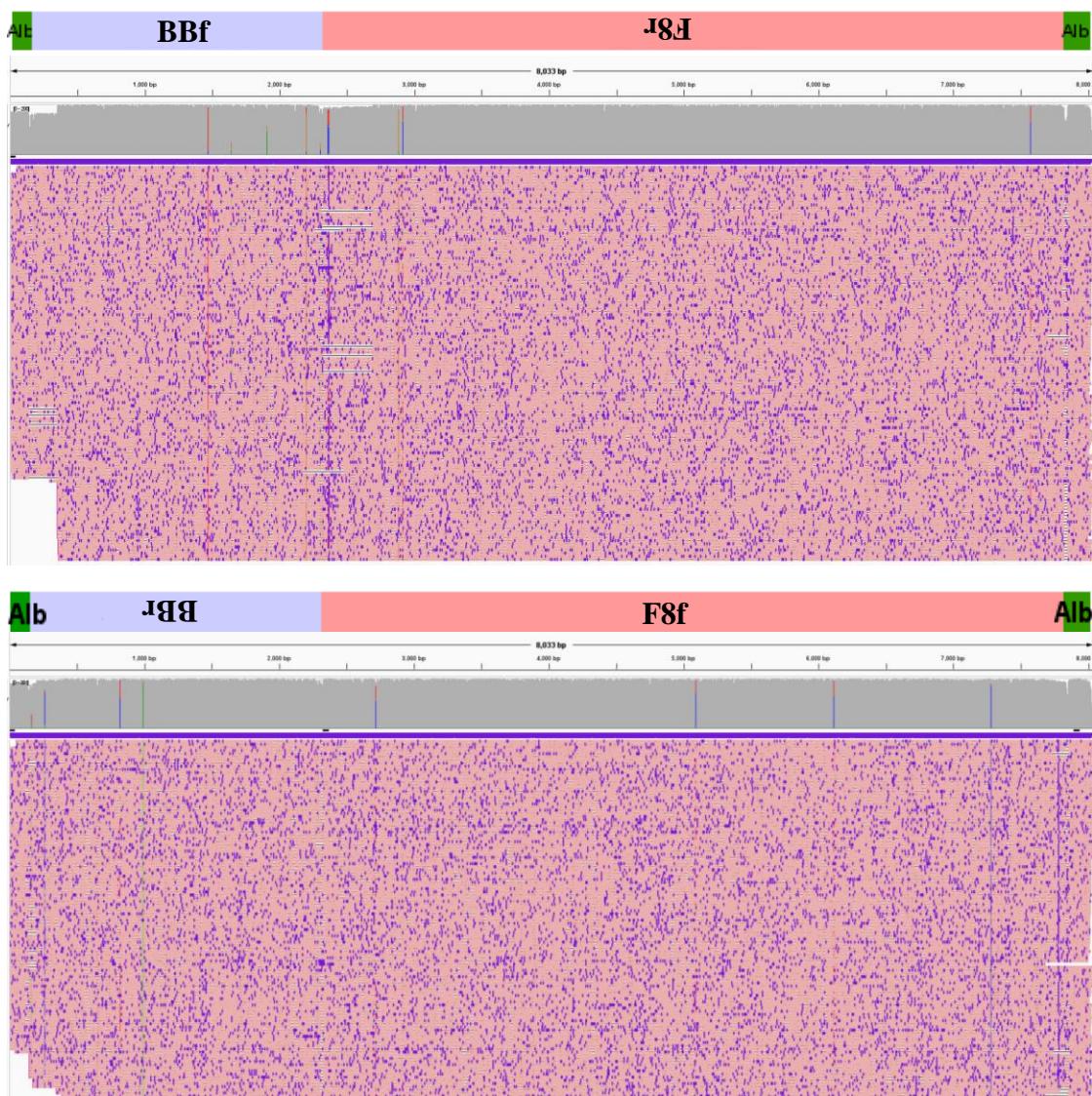
**Figure S4. PCR Conditions Optimization for Enhanced Amplification of F8 Inserts.** (A) Optimization of annealing temperature in the 1st PCR to improve the amplification of F8 inserts. The relative enrichment of amplicons with F8 inserts was determined using qPCR. Error bars represent the mean  $\pm$  SEM, n = 9, and paired two-sided Student's t-tests were performed. (B) Employment of a touchdown PCR program in the 1st PCR to increase the amplification of F8 inserts. The touchdown PCR program used was 6 cycles of [98°C for 10s, 68°C (-1°C/cycle) for 15s, 68°C for 6.5min]; followed by 25 cycles of [98°C for 10s, 62°C for 15s, 68°C for 6.5min]. Error bars indicate the mean  $\pm$  SEM, n = 8, and paired two-sided Student's t-tests were conducted.



**Figure S5.** Random 200 reads in the visualization of eight representative insertion patterns of the donor template in Figure 5E. The F8 cassette is abbreviated as F8, and the plasmid backbone is abbreviated as BB. Forward insertions are abbreviated as f, and reverse insertions are abbreviated as r. (continued).

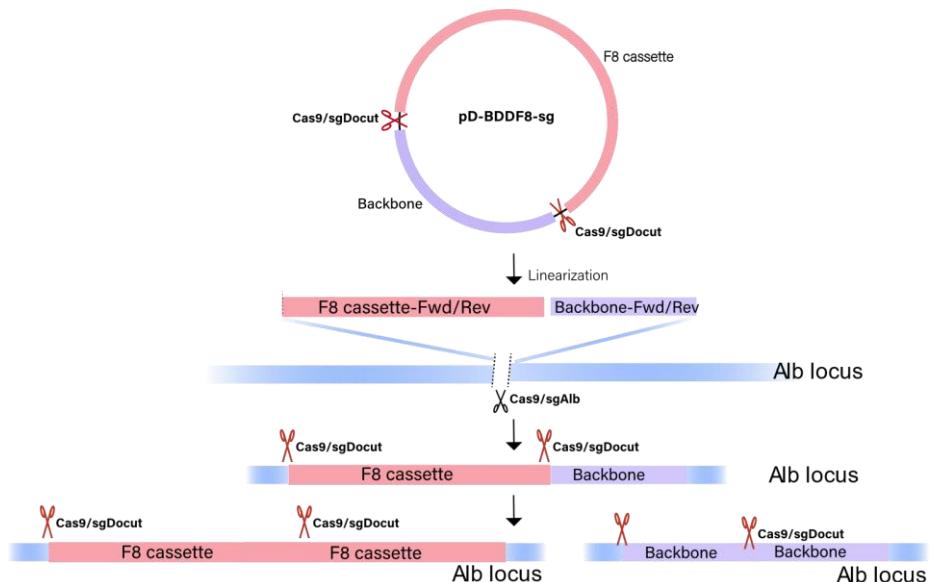


**Figure S5. Visualization of Insertion Patterns:** This figure presents the visualization of 200 randomly selected reads showcasing eight representative insertion patterns of the donor template, as depicted in Figure 5E. The insertions include components from the F8 cassette (abbreviated as F8) and the plasmid backbone (abbreviated as BB). The orientation of these insertions is also indicated, with forward insertions abbreviated as 'f' and reverse insertions as 'r'. This visualization aids in understanding the diversity and orientation of the insertions at the targeted genomic site. (Continued)



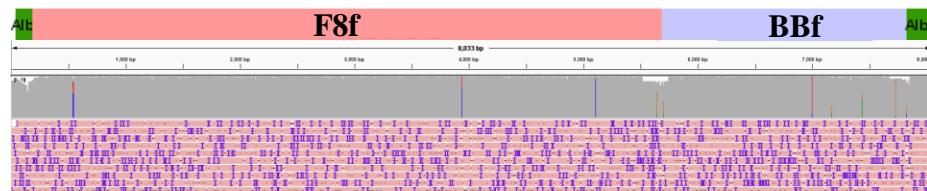
**Figure S5. Visualization of Insertion Patterns:** This figure presents the visualization of 200 randomly selected reads showcasing eight representative insertion patterns of the donor template, as depicted in Figure 5E. The insertions include components from the F8 cassette (abbreviated as F8) and the plasmid backbone (abbreviated as BB). The orientation of these insertions is also indicated, with forward insertions abbreviated as 'f' and reverse insertions as 'r'. This visualization aids in understanding the diversity and orientation of the insertions at the targeted genomic site.

## A Schematic of insertions of multiple double-cut donor fragments

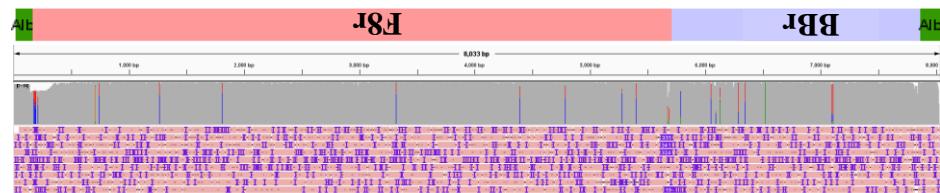


## B Additional two-fragment integrations

**F8fBBf inserts = 0.35%. Shows 10 out of 79 reads.**



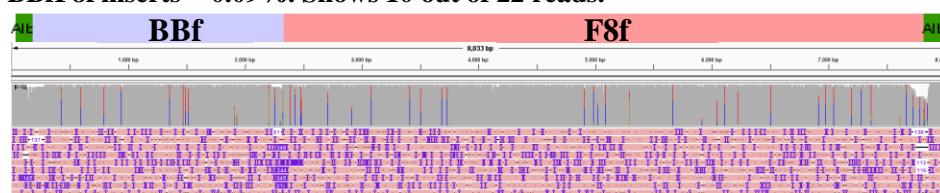
**F8rBBr inserts = 0.24%. Shows 10 out of 54 reads.**



**BBrF8r inserts = 0.22%. Shows 10 out of 51 reads.**

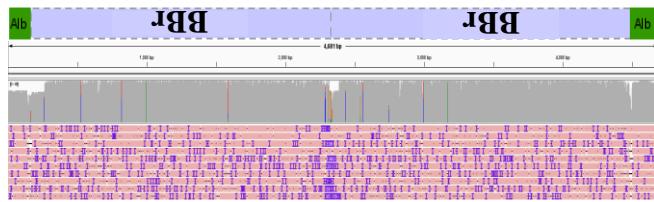


**BBfF8f inserts = 0.09%. Shows 10 out of 22 reads.**

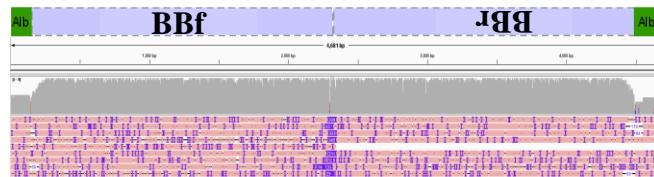


**Figure S6. Characterization of Multi-Fragment Insertions from Double-Cut Donor Plasmid Following Cas9-sgRNA Linearization.** The orientation of these insertions is indicated, with forward insertions abbreviated as 'f' and reverse insertions as 'r'. (A) Schematic representation of multi-fragment insertions resulting from the linearization of the double-cut donor plasmid. Following linearization, multiple fragments can integrate, albeit at lower frequencies. (B) Visualization of additional two-fragment integrations not shown in Figure 5, including four patterns of F8 and BB insertions in both orientations.

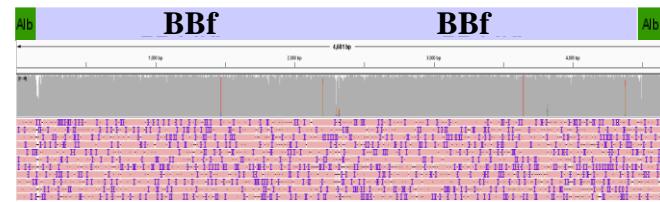
**BBrBBr** inserts = 0.22%. Shows 10 out of 49 reads.



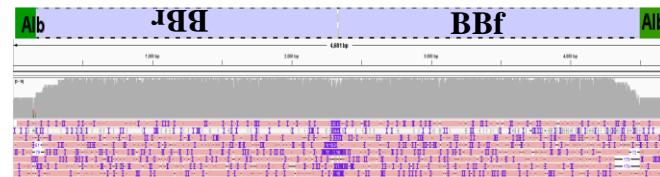
**BBfBBr** inserts = 0.04%. Shows 9 out of 9 reads.



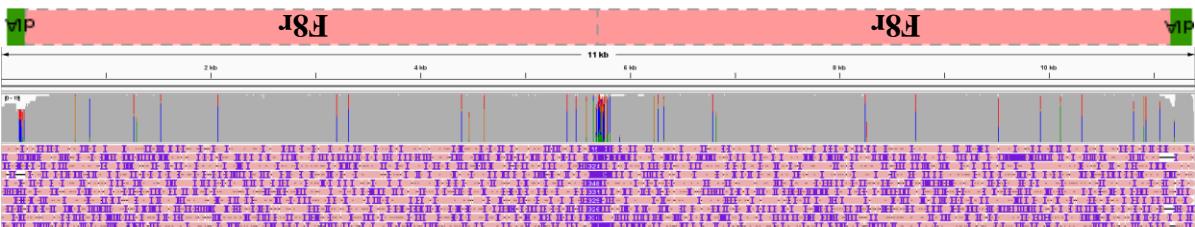
**BBfBBf** inserts = 0.20%. Shows 10 out of 46 reads.



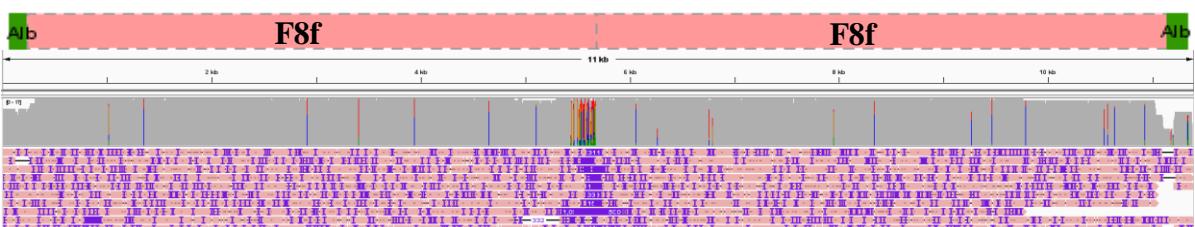
**BBrBBf** inserts = 0.04%. Shows 8 out of 8 reads.



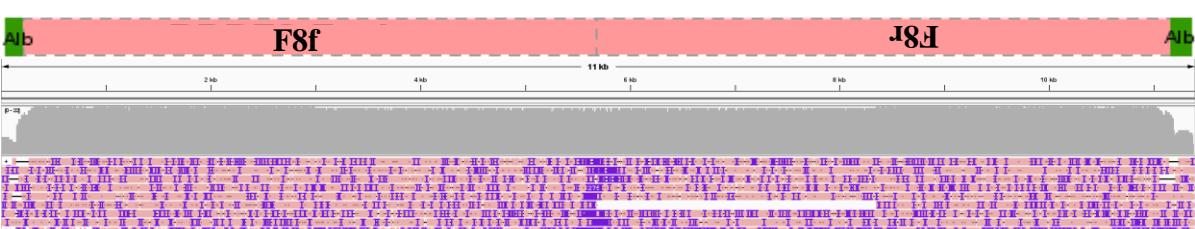
**F8rF8r** inserts = 0.08%. Shows 10 out of 19 reads.



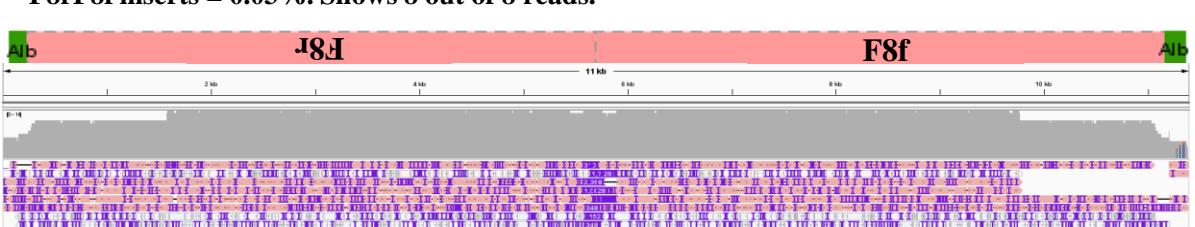
**F8fF8f** inserts = 0.08%. Shows 10 out of 17 reads.



**F8fF8r** inserts = 0.05%. Shows 10 out of 11 reads.



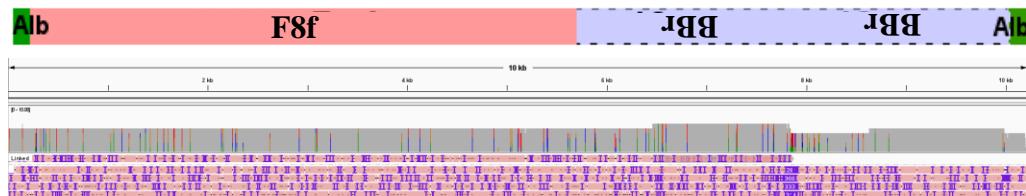
**F8rF8f** inserts = 0.03%. Shows 8 out of 8 reads.



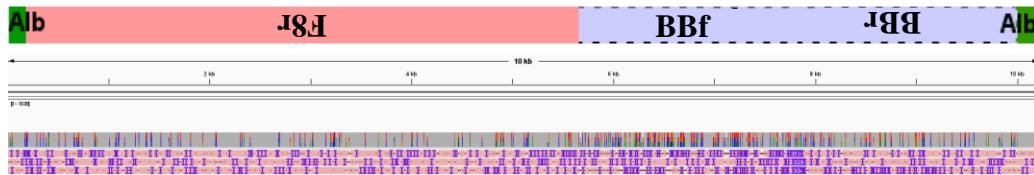
**Figure S6B.** Visualization of additional two-fragment integrations not shown in Figure 5, including four patterns of F8 and BB insertions in both orientations (continued).

### C Three-fragment insertions: BB+BB+F8

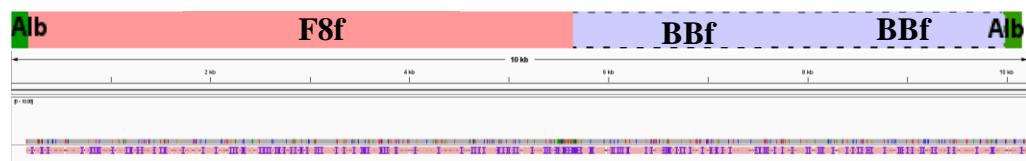
F8fBBrBBr inserts = 0.02%. Shows 5 out of 5 reads.



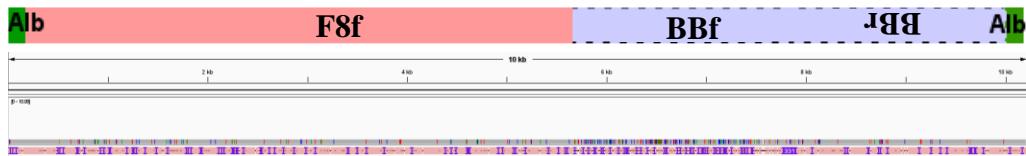
F8rBBfBBr inserts = 0.01%. Shows 3 out of 3 reads.



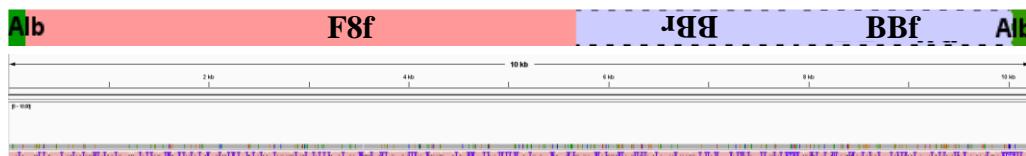
F8fBBfBBf = 0.004%. Shows 1 out of 1 read.



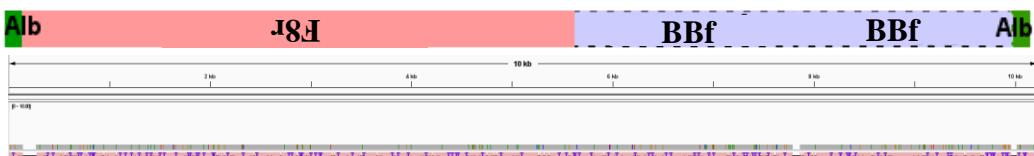
F8fBBfBBr = 0.004%. Shows 1 out of 1 read.



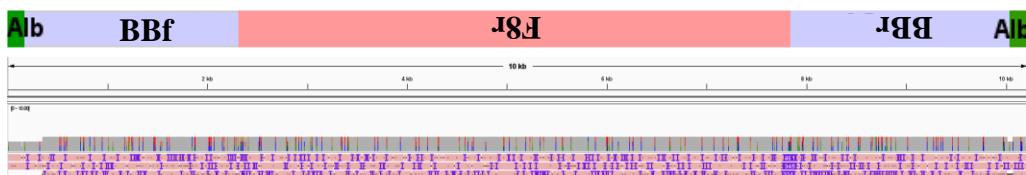
F8fBBrBBf = 0.004%. Shows 1 out of 1 read.



F8rBBfBBf = 0.004%. Shows 1 out of 1 read.



BBfF8rBBr inserts = 0.01%. Shows 3 out of 3 reads.



BBrF8fBBf = 0.004%. Shows 1 out of 1 read.

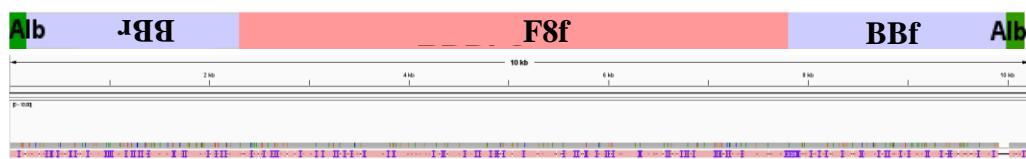
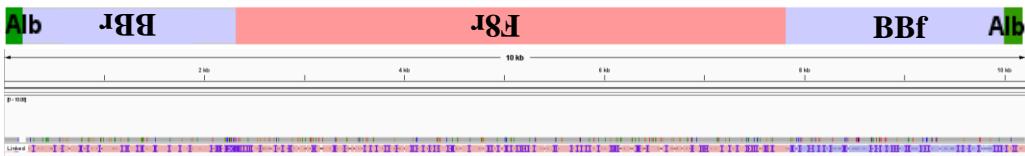
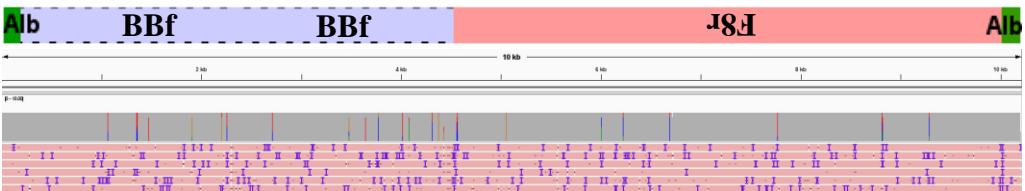


Figure S6C. Visualization of three-fragment insertions, specifically the insertion of two plasmid backbone fragments and one F8 fragment.

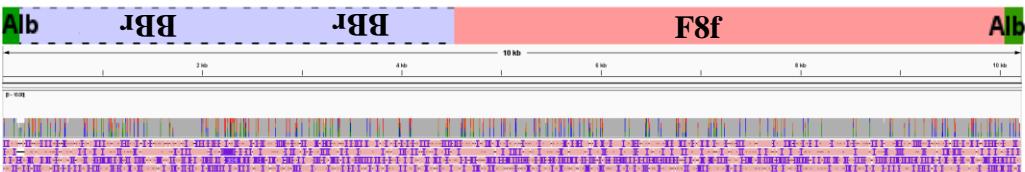
**BBrF8rBBf = 0.004%. Shows 1 out of 1 reads.**



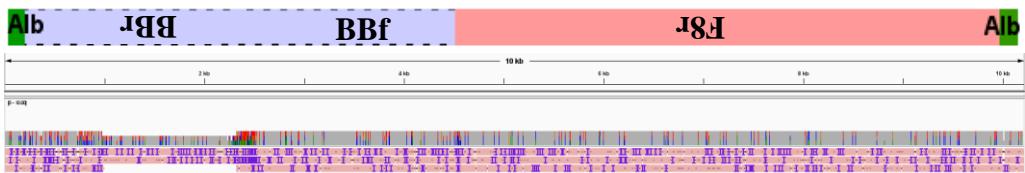
**BBfBBfF8r inserts = 0.03%. Shows 6 out of 6 reads.**



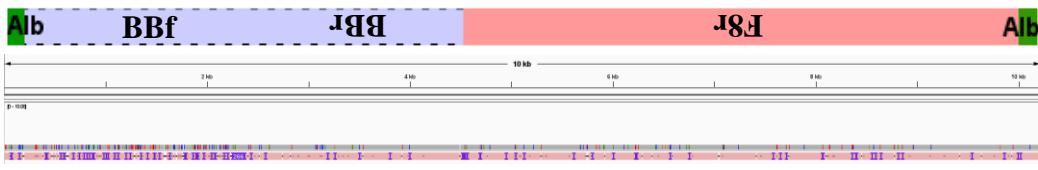
**BBrBBrF8f inserts = 0.02%. Shows 4 out of 4 reads.**



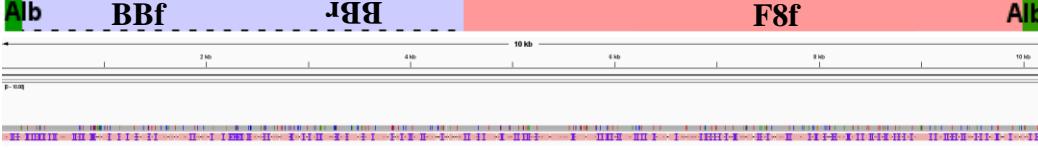
**BBrBBfF8r inserts = 0.01%. Shows 3 out of 3 reads.**



**BBfBBrF8r inserts = 0.004%. Shows 1 out of 1 reads.**



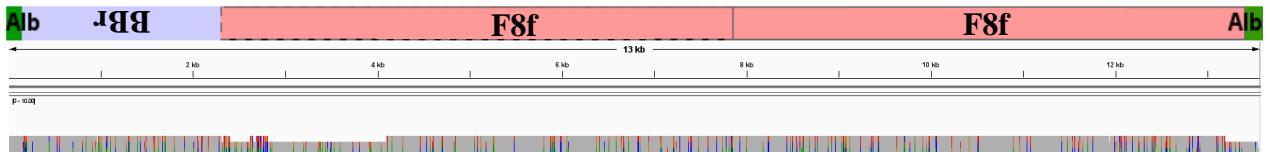
**BBfBBfF8f inserts = 0.004%. Shows 1 out of 1 reads.**



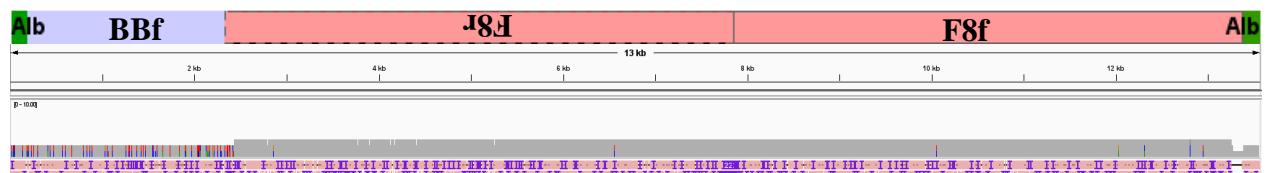
**Figure S6C. Visualization of three-fragment insertions, specifically the insertion of two plasmid backbone fragments and one F8 fragment (continued).**

## D Three-fragment insertions: BB+F8+f8

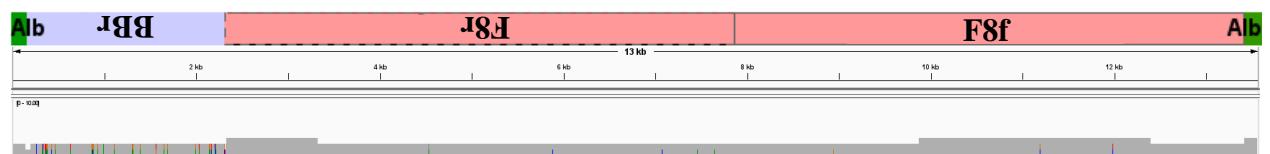
**BBrF8ff8f inserts = 0.01%. Shows 3 out of 3 reads.**



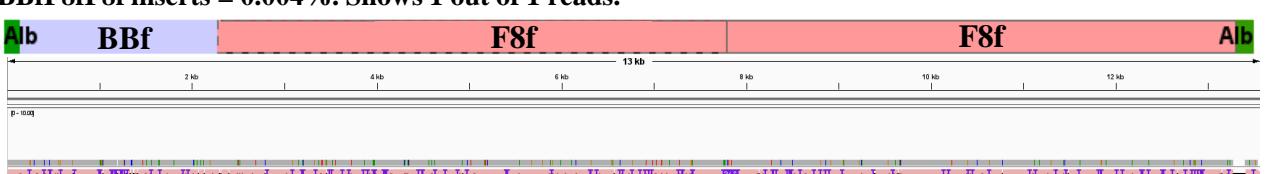
**BBfF8frF8f inserts = 0.01%. Shows 2 out of 2 reads.**



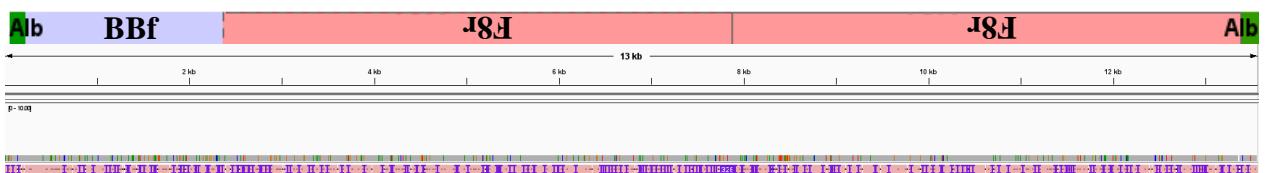
**BBrF8rf8f inserts = 0.01%. Shows 2 out of 2 reads.**



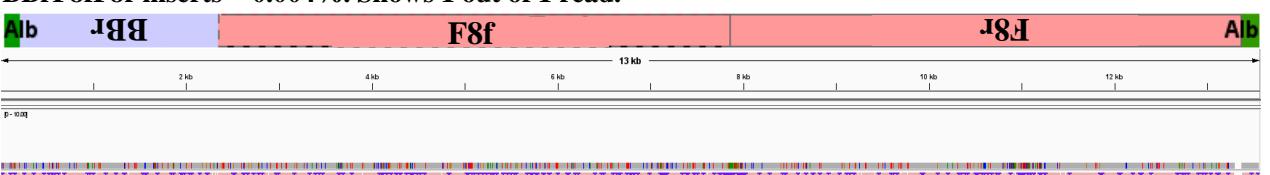
**BBfF8ff8f inserts = 0.004%. Shows 1 out of 1 reads.**



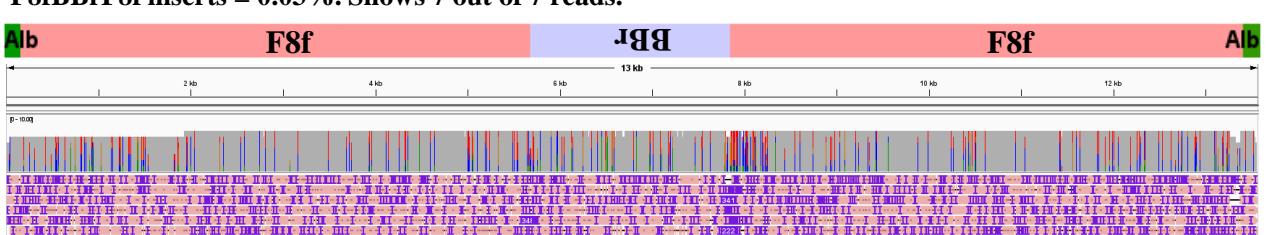
**BBfF8rf8r inserts = 0.004%. Shows 1 out of 1 read.**



**BBrF8ff8r inserts = 0.004%. Shows 1 out of 1 read.**



**F8fBBrF8f inserts = 0.03%. Shows 7 out of 7 reads.**



**F8fBBrF8r inserts = 0.03%. Shows 6 out of 6 reads.**

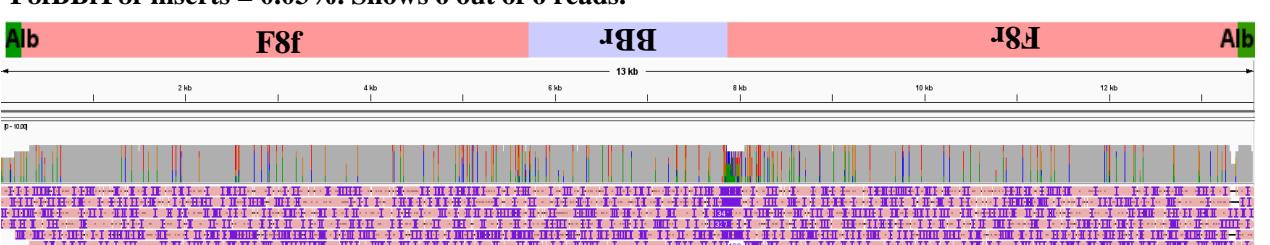
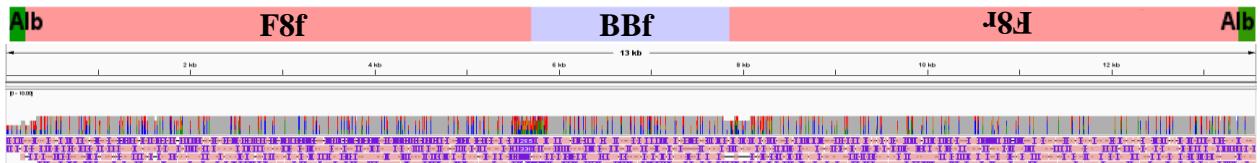
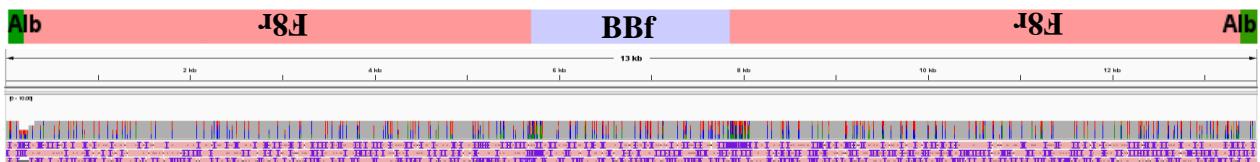


Figure S6D. Visualization of three-fragment insertions, specifically the insertion of one plasmid backbone fragment and two F8 fragments.

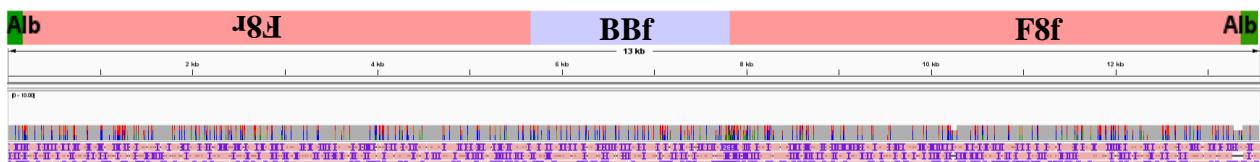
F8fBBfF8r inserts = 0.02%. Shows 4 out of 4 reads.



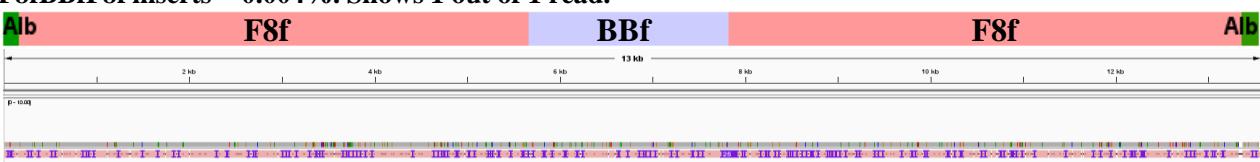
F8rBBfF8r inserts = 0.02%. Shows 4 out of 4 reads.



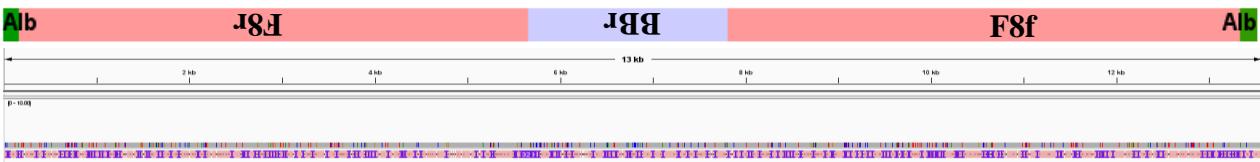
F8rBBfF8f inserts = 0.01%. Shows 3 out of 3 reads.



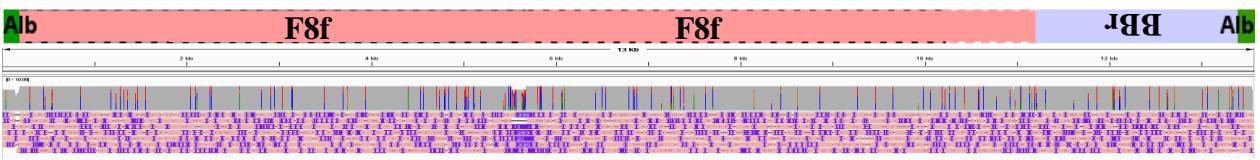
F8fBBfF8f inserts = 0.004%. Shows 1 out of 1 read.



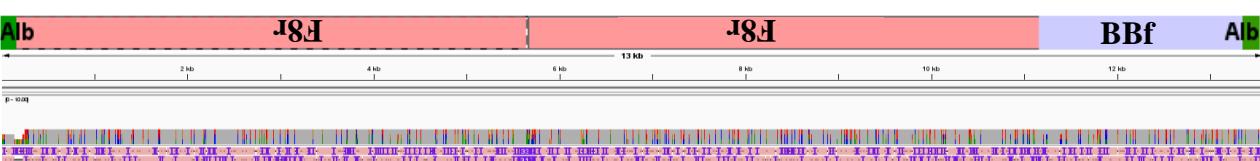
F8rBBBrF8f inserts = 0.004%. Shows 1 out of 1 read.



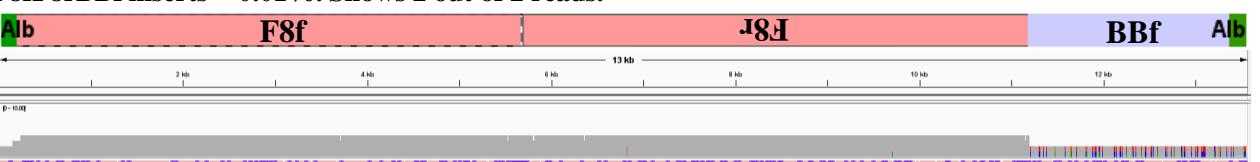
F8fF8fBBr inserts = 0.03%. Shows 7 out of 7 reads.



F8rF8rBBf inserts = 0.01%. Shows 3 out of 3 reads.



F8fF8rBBf inserts = 0.01%. Shows 2 out of 2 reads.



F8rF8fBBr inserts = 0.004%. Shows 1 out of 1 read.

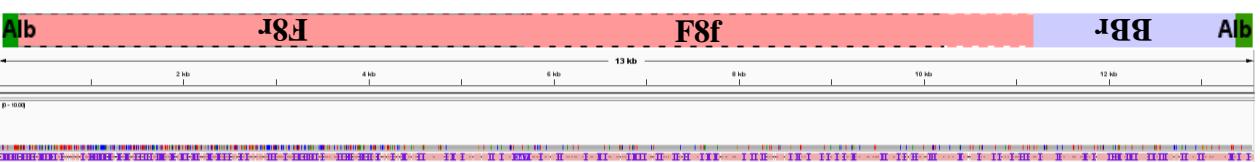
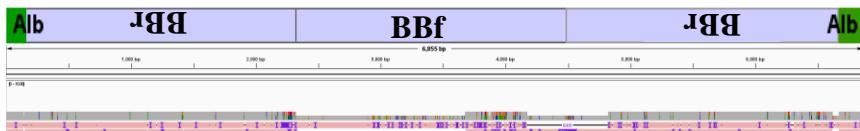


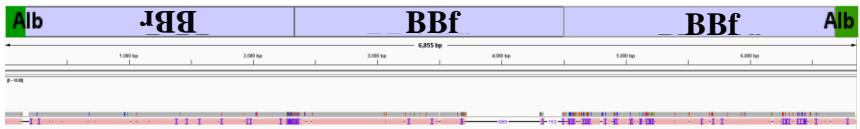
Figure S6D. Visualization of three-fragment insertions, specifically the insertion of one plasmid backbone fragment and two F8 fragments (continued).

## E Three-fragment insertions: BB+BB+BB

BBrBBfBBr inserts = 0.01%. Shows 2 out of 2 reads.



BBrBBfBBf inserts = 0.004%. Shows 1 out of 1 read.



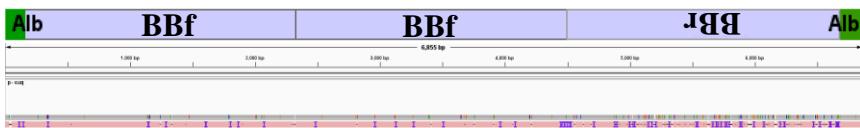
BBrBBBrBBr inserts = 0.004%. Shows 1 out of 1 read.



BfBBfBBf inserts = 0.004%. Shows 1 out of 1 read.

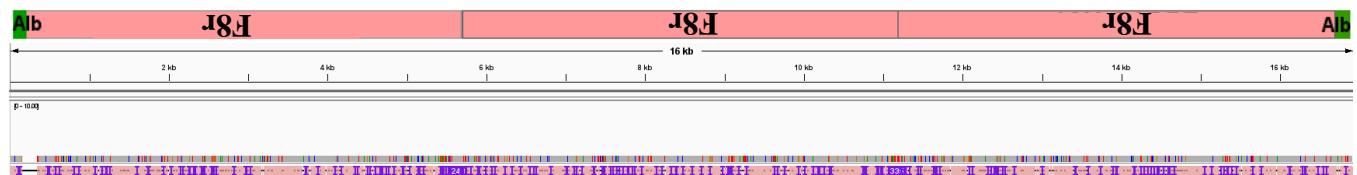


BBfBBfBBr inserts = 0.004%. Shows 1 out of 1 reads.



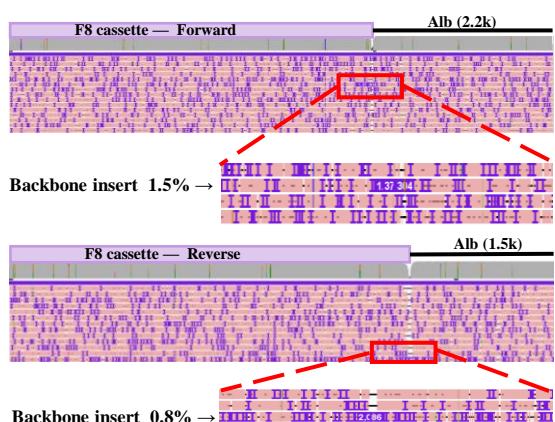
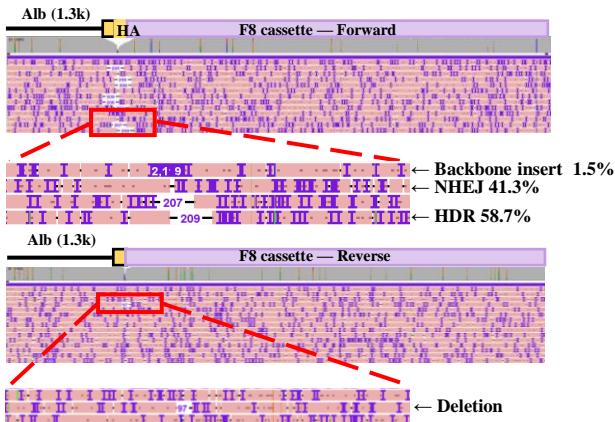
## F Three-fragment insertions: F8+F8+F8

F8rF8rF8r inserts = 0.004%. Shows 1 out of 1 read.

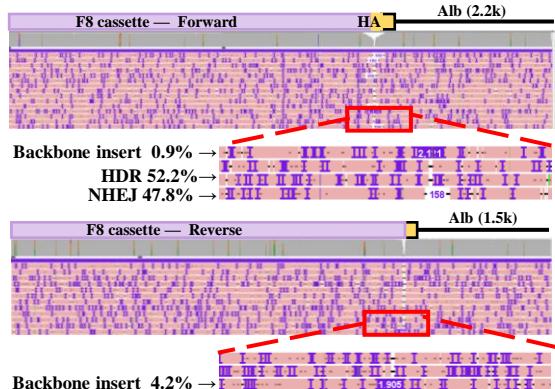
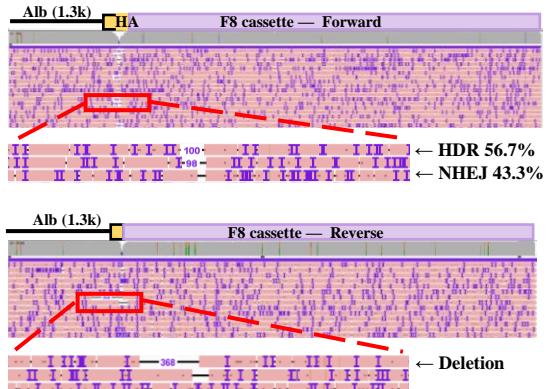


**Figure S6EF.** The visualization of three-fragment insertions, specifically the insertion of three plasmid backbone fragments (E), and three F8 fragments (F).

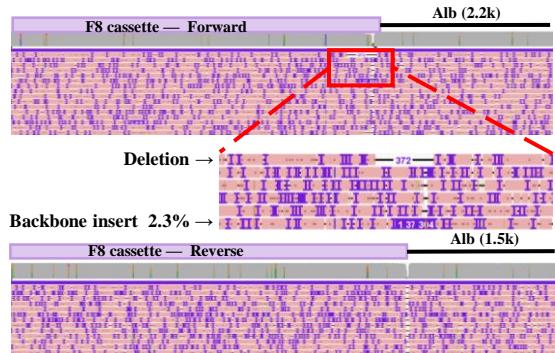
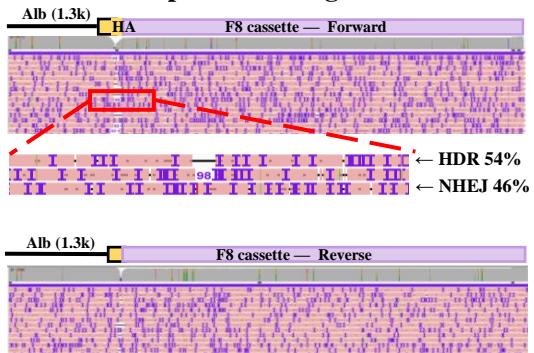
### Insertion of pD-BDDF8-sg with HA190-0



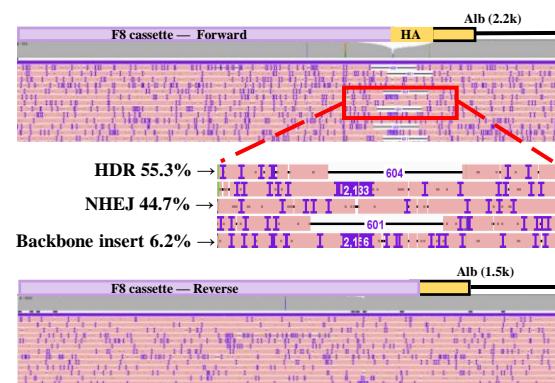
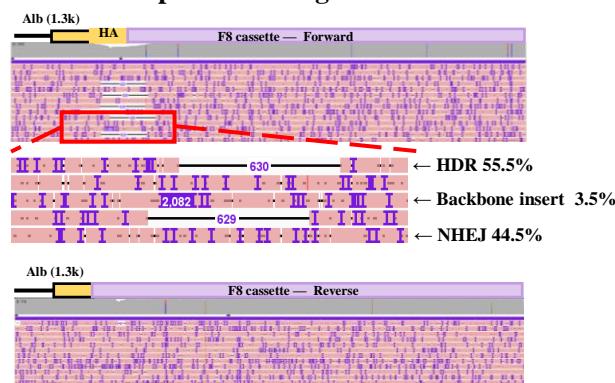
### Insertion of pD-BDDF8-sg with HA85-130



### Insertion of pD-BDDF8-sg with HA85-0

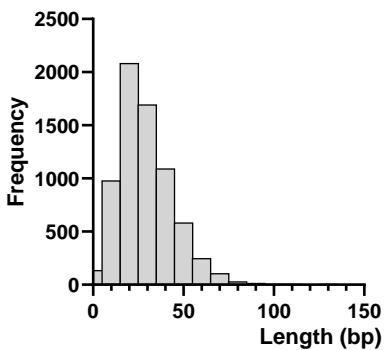


### Insertion of pD-BDDF8-sg with HA600-600

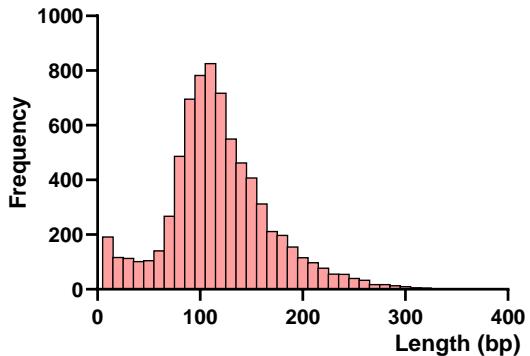


**Figure S7. Visualization of PCR Products from Mouse Liver Edited with Donor Plasmids Featuring Various Homology Arm Lengths.** Integrated Genomics Viewer (IGV) was employed to display the PCR products derived from mouse liver that had been edited using donor plasmids with different lengths of homology arms, specifically HA190-0, HA85-130, HA85-0, and HA600-600. The figure presents alignments of 15 randomly selected reads for each homology arm length.

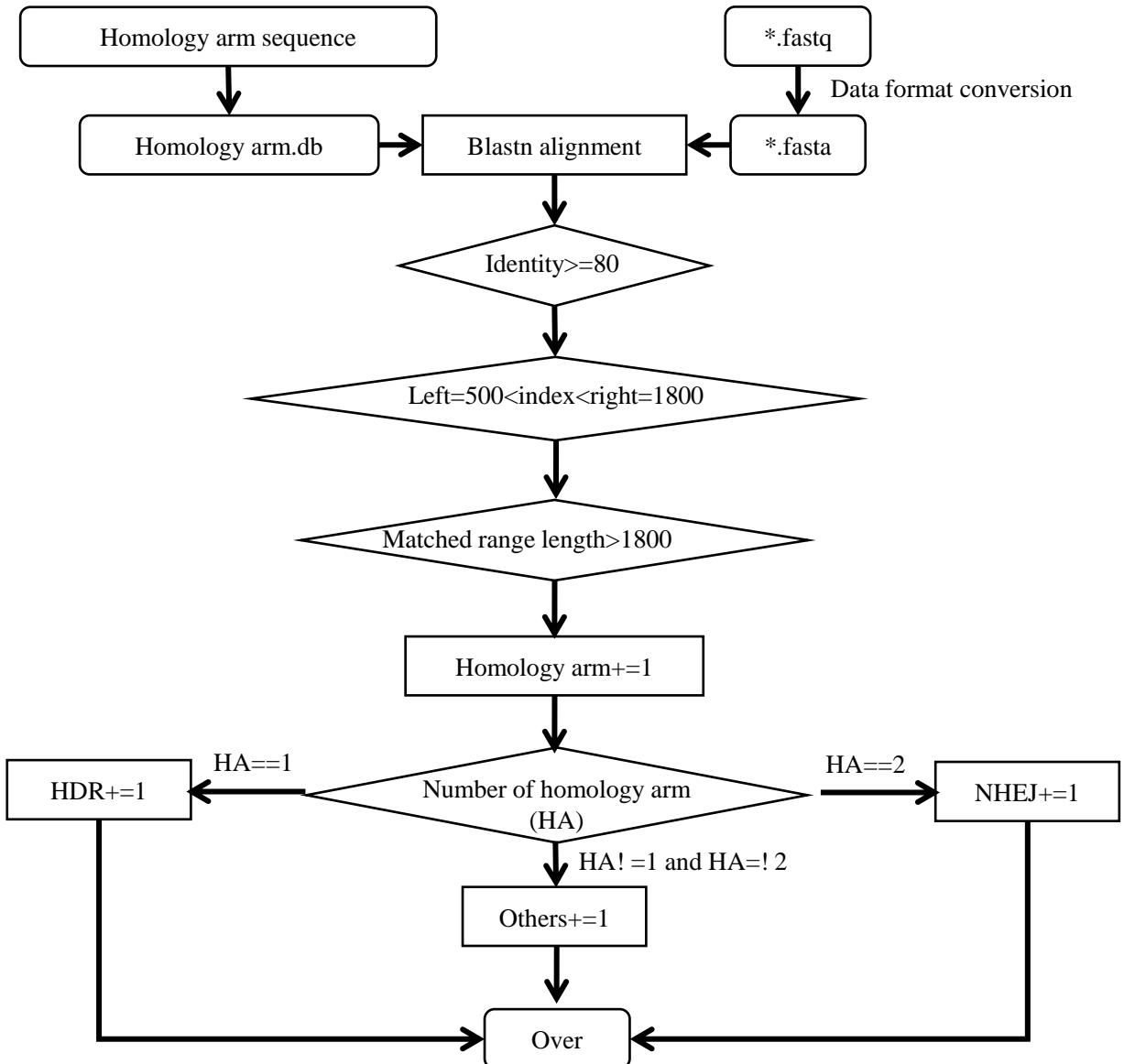
**A Length Distribution of Deleted Alb Fragments**



**B Length Distribution of Deleted F8 Fragments**



**Figure S8. Analysis of Deletion Length Distribution in Junction PCR of pD-BDDF8-sg Inserts with Homology Arm HA85-0.** (A) Length Distribution of Deleted Alb Fragments: This section presents the distribution of deletion lengths observed in the Alb fragments within the junction PCR of F8 donor inserts that utilized the HA85-0 homology arm. (B) Length Distribution of Deleted F8 Fragments: Here, the focus is on the distribution of deletion lengths found in the F8 fragments within the same junction PCR of F8 donor inserts, again using the HA85-0 homology arm.

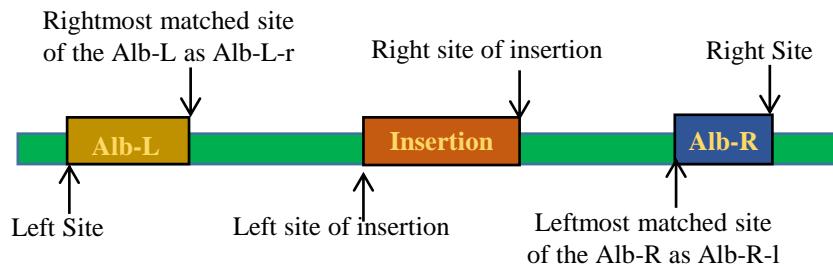


**Figure S9. Workflow for Distinguishing Non-Homologous End Joining (NHEJ) and Homology-Directed Repair (HDR) in Donor Insert Analysis.** This flow chart outlines the data processing steps used to differentiate between NHEJ and HDR events, with a focus on a donor with 600bp homology arms as a case example. The analysis employs the Basic Local Alignment Search Tool (BLAST) to search for corresponding arm sequences and determine the proportion of inserts mediated by each repair pathway. The steps include:

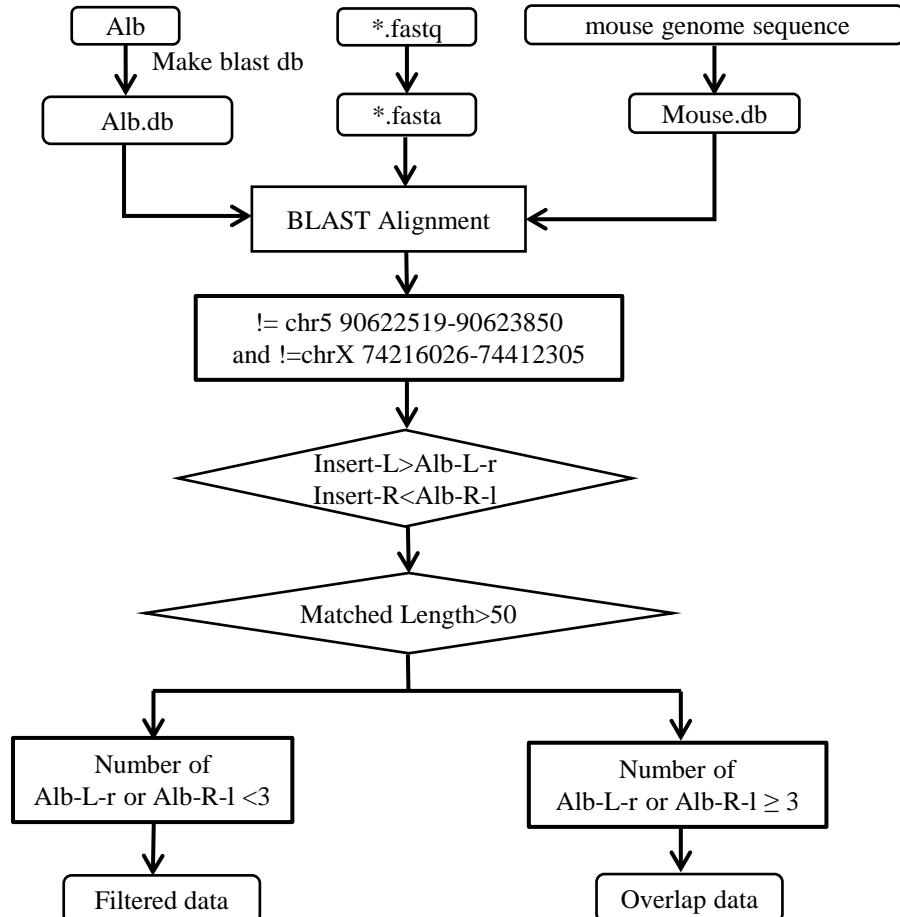
1. Aligning the homology arm sequences with the sequencing file and selecting reads with an identity score of 80 or more.
2. Restricting the range of alignment to ensure the homology arms are located near the target site.
3. Limiting the length of screened reads to exclude artifacts caused by incomplete Nanopore sequencing.
4. Classifying reads that match up to two copies of homology arms as 'NHEJ' and those matching only one homologous arm as 'HDR'. Reads not meeting either condition are categorized as 'Others'.

The reference sequence used in this analysis was generated by directly inserting the donor with homology arms into the cleaved genomic sequence.

## A. Schematic definition of terms used in the data processing



## B. The flow chart for processing data to analyze endogenous genomic DNA insertion



**Figure S10. Data Processing Workflow for Analyzing Endogenous DNA Insertion.** This flow chart describes the steps for processing data to analyze the insertion of endogenous DNA. It includes the following key components:

### A. Definition of Terms:

Alb-L: The upstream homology arm near the cut site.

Alb-R: The downstream homology arm.

Alb-L-r: The rightmost matched site of Alb-L.

Alb-R-l: The leftmost matched site of Alb-R.

### B. Steps for Data Processing:

Generation of database files containing the 332bp homology arm sequence (denoted as Alb), the mouse genome sequence, and the LINE-1 sequence.

Conversion of sequencing data format from \*.fastq to \*.fasta.

Alignment of the sequencing file with the homologous arm sequences and the mouse genome sequence (or the LINE-1 sequence).

Elimination of sequences matching the Alb gene range on chromosome 5 and the F8 gene range on chromosome X.

Limitation of insertions between Alb-L-r and Alb-R-l to ensure endogenous DNA fragments integrate at the target site.

Removal of indexes matched with a length of less than 50bp.

Consideration of occurrences where the number of Alb-L-r or Alb-R-l is greater than three as derived from the same amplicon, counting them as the same type of insertion.

Read #1 Alb-chr1-Alb

CGCTTACACAGCAATGCAACGGCACCTAGCTTACTATGTCATTGCTTATGGCTAGAAGTCATAATCCTGCTAACTTTCTAACATCATCAATTCTCTTGTGTCAGGGTCCAAACCTTGTCAGTATGCAAAGACGCCCTT  
AAAAGACTCTAGGGGGTAGCAGGGGGCTGTGACTCTCTAAATACCAGGACCTGACTGTGCCCAGCACTCATCTGGTCAGATGGTTCTATGGTGTGGCTGGACAAATGACAGGAAAGGTGATATGCTCTAAACACATCA  
CAACACAAACCTTCTCAGGTAACTATCTGGGACTTAAACATAATCATATCTTTCTAAACGATCAAGACTGATAACCTTGCACAGAGGCCATACAGACAACGCACTGTCGGACTCTTGAAGCTTCAAGGTATGGTCAGT  
TTGGTGTCCATTGATAGATAAGAAC

Read #2 Alb-chr1-Alb

GTGACCAAGCAAATCGAACGGCACCTAGGTTTACTATGTCATGCCATTGGCTATGGCTAGGTCAGGAACTTCAACAGTCTGCATAACTTCTTCTAATCAGCTCATTTCTTCTTCAGGTCACACCCCTAGGGAGCCAGAGGAGA  
TGGGGCTCTCTGAGTCAGGCCAGCGCTGGTCTACAGGTTAGAATTCGAGAACACAGGCGCTACCCAAAACAGTGTCTCACAAAACCCAAAAAAAAGAAAAAGAAAAAGAGAGAGAGAGAGAGAGGGTG  
GAGGGCTCTAAACAGCTAGTTTACTAGCAGGAAAAAAACAGTCCTCAAAATTTTTTTAACCTCTGGAAACTTCTTCTAAATTAAAGTAAATTACATGACACTCATGAGTCCTGGCTGGGCTGGGGAAATGTGAAA  
AGACCTAAACACATCATCACAGGAAACCCCTCTCAGGTAACTACTTGGGACTTAAACATAATCATATCTTCTCAAACAGCTACAAGACTGATAACCATTGACAGGCCATACAGACAGGCCACCTGGCACTTGGGTCT  
TCAGTATGGTCATCAGTTGGGTTCAATTGCGAGATAAGAAC

Read #3 Alb-chr2-Alb

## Read #4 Alb-chr2-Alb

AATGCAAGGCCCTACGGTTTACTATGTACCGTTTATGCCATGAAGTCAGAACCTCTAACAGCTCCGTAACTTCTAACATCATATTCTTGTTTCAGGGTCCAAACCTCTGTCATGTCAGAACAGGCCTTCAGTTCTCCCA  
TATTCTGCATCATTATACTTCTTCAGGGTATTTCAGTTCTGCCATAATCCAGGTCTTCAGTGTGTCATTCTCATTTCTTTCAGTGTGATTCTCTGTCATTTCAGTCATCTTCAGTGTGGATGTTCATTTCTCA  
TTATTCTGCATCTTCTGTCACATCACACACCAACTCTCTCAGGTAACATATATTGGGACTTAAAAAACATAATCATATTCTTCCTAAACAGTCAGACTGATAACCATTGACAAGAGCTACAGATGCCACCGACTGGACTCT  
TAGGCTCTICAGTGTGTCATCAGTTGGGCTATTGAGA

## Read #5 Alb-chr2-Alb

CGACCCGCGGCCATGCAAGGGCACGTCTGGTAACTATGTCATGGCTATGGCTATGGAATACCTGCTAGCAACTTCTAACATCCATTCTGTTTCAGGGTCCAAACCTGTGACTAATATGCAAGAC  
GCCTCTAGCTCTAACTGGTGAATTTCTCATTTTGTCTGGTTTCTAGCTTCTCCGATATTCCAGGTCCTAGTGCTGATTCTCATTTTCACTGTTAGTGTGATTGGGATTTCGAAGTGTGATGTTCTCATTTTCCATG  
ATTTCTAGTCTTTCGGCCATATTCAGGCTCTACAGTGGCATTAAATTCTTCCACCTTCTAACACACAACCTCTCAGGTAATCTAGTGGGACTAAACATAATCTAACATCTTCTAACCATCAAGACTCA  
TAACATTGAGTAGAGCCATACAGACAAGCACCGCTGGACTCTAGGCTTCACTGATGGTCATCATGTTGGGTCTTCTAGTGTAGATAAGAGA**TCAT**

## Read #6 Alb-chr2-Alb

## Read #7 Alb-chr2-Alb

GGAGCAATCGAACGCCGCTACTGTTTACATGTCTATGGCTATGGCTATGAAGTCGAACTCTAACAGTCGCTAATACTTTCTAACATCCATCATTTCTTGTTTCAGGGTCAAACCTGTCACTAGATGCAAAGACGCTTGCAGG  
CCTATGACGAACTGTTGCTCTCTGTAAATGCAGACGCCATCTAACAGTCGAGCACAAAGGCCATTAAAGCAGACTAATCTGAAGACTGATCTGATCTTACATGCCAACAGTCAGGTTCAGACAGCTGAGATGAGATAAGAGAACTCA  
TGGAGGAACCTCCAGACAACAAAGATGCTAGAAGGTAAGACGACTCCAGGGAGTTCAGGAAAGCTGCGAGGACGCCATTAAAGGGAAAGAGAATCTATGTTGTTAGGTGCCATCTGAGTGAACACATCACAACCCAAACCTTCTCAGGT  
AATACTATGGGACTAAAAAACATAATCATATACTTCTCAAAACGATAGTTCAAGACTGATAACCATTTGACAAGGCCATACAGAACAGCACAGCTGGACTCTTAGGTCTCAGCTATGGTCATCGTTCTGAGT  
GTAGAT

## Read #8 Alb-chr2-Alb

AGCACCTACGCCCGT AGCAATGCGAACGCGACTGGTACTATGCTATGCCATTGCTATGAAATTACCAAATCTAACAGCTCGTAATACTTTCTAACATCCATCATTCTTGTTTCAGGGTCAACCTGTCACTAGATGC  
AAAAGCGCCCTAGTTTCTCCGGCATATTTCAGCTGTAATGTTCTGTTTCTGATTTTCAGGGATTTTCTCAACCATATTCCAGTCCCTGACTGCAATTTCAGCTTTAGTGTATTCCGTT  
TCTCAACACATCTCCAAACACAAACCTTCAGGTAATATACTGGGACTAAAAACATAATCATATCATTCTTCAAAAGCATCAAGACTGATAACCATTGACAAGAGGCCATACAGACAAGCAGCGTGCCTCTAGGT  
CTTCAGGTATGGTCACTAGTTGGAGTTCATTGT

## Read #9 Alb-chr2-Alb

GCACCTCTGACTAGACCGATAATGCAAGGCACGTACGGTTACTGCGTATGGCTCGGGCTATGAAGTGTAACTCAGTCCTGCTAATATTCTAACATCATTCCTTGTTCAGGCTCAAACCTGTCACTAGATGCC  
AAAGGACGCTTAAGTGGAAAATTGAAATGCTTACGGACGGCTGAAATGTCGAAACAAACTGAAATCATGAAAATGAGAACCCATCTGACCACTTGAAATGACCAAATCCTAAAACGCTGAAACGAGAAATGCAACACC  
GAAGGACCTGGTAAATGGCCTTAAACACACCAACCCCTGCAAGTAACTACTGGACTATACTGGACTATAACACATAATCTAACATCATTCCTAACGATCAAGACTGATAAACCATTCAGGCTCTATAAGATGGCACCGCTG  
GGAAAAAAATTGAGGTCTCACGTATGGTCAACGTTGGTCTTCTTGTAGATAAGAAAAC

## Read #10 Alb-chr2-Alb

AGGACACCGT AGCAAATGCAAGGTACTTCAGCTTACTATGTCATTGGCTATGGCTAAGTGCAAATCTAACAGTCGCTGATAATACTTTCTAACATCCACTGCTCTCTGTTTCAGGGTCAAACCTGTCACTAGATGCAAGACGCCCTCTCTGGCTCTGAGGCATCTAGTCAGACTGAGGTCCAAAACACCAGGCTACACAGAGAAACCTGTCCTAACATGAACAAAACACAGACTAACAAAACAAAGCTTAGAAAAGCTTAATGCCTAAACACATCACACACCAAAGTCAGGTTACATACTATGGGCTTAAACATATACTATTTCTCTAACACGATCAAGCTGATAACCTTGACAAGAGGCCATACAGACAAGCACCAGTGCACITCTAGGGCTCTCTCATGTATGGTCATCGTTGGTTCCTTGTAGATAAGAAC

Read #11 Alb-chr2-Alb

GAGCAATGCAAGGGACGTACGTTACTATGCTATTGGCATATGGAAGTGCACAACTCTAAGCTCGCTAACTTCTTCAACATCCATCATTCTTGTTCAGGGTCAAACCTTGTGCCTACGAATCACTAAAAAACGTCGAG  
AAAAATGAAATGCAACTGAAAGGGACTGGAAATATGGCGAGAAAACCGGAAATCACACTTGTAGGACTGAAATATAGCGGAAGATGCCAGAAAAGTGGAAAATTAGAAATGTGCACTGTAGGACTGGAATAT  
GGCGCAAAACTGAAAATCAGGGAAATACGAAAATAGGAATACACACTTGTAGGACTGTAATATGGCGAGAAAAGTGGGAAAATTAGGAATATGTCAGTGTAGGACTTGTAGGAGCAGAAAATGGAACATT  
CATCTTGAGCAGTGTAAAATGAAATCATAAAATACGTAAGGAAATGCAACACTGAGGACCTGGAAATATGCGAAAATCATGGAATAGGAAATACACTTGTAGGACCTGACATCACACCAACACTTGTGG  
AAGTAACACTTGGACTTAAACACATAACTAATCTGTTCTAAACGATCAGACTGATAACCATGACAAGGCCATCACAGAACGACCACTGGCAGCTCTAGGTCTTCAAGGGCTTGGTACATGTGGTCCATTGTA**TT**

Read #12 Alb-chr3-Alb

Read #13 Alb-chr3-Alb

**Figure S11. Representative Sequences Illustrating Various Insertion Patterns at the Alb Site.** (A) Single Genomic DNA Fragment Insertion: The displayed read sequences show the insertion of a single piece of genomic DNA fragment at the Alb site. 19

## Read #14 Alb-chr3-Alb

Read #15 Alb-chr4-Alb

ACACACACAGCAATCGAACGGACTGTACCTTAACTATGTCATGGCTATGCCATGAGCTGCAAATCTCTAACAGCTCGTAATACTTTAACATCATATTCTTGTTCAGGGTCCAAAACCTTGTCACTAGTGAGCATGCTTAG  
ACAGACAGACAGAGAGAAGGGAACTAGAGGGCAGTCTGGACACATGGAGTGGAGAGAGAAGGGAGACAGAGAAAGGGAGCAAGGTAAGCACAAGAAAATAAGGGTTAGAGTGTTGGGGAGGCCTAACACATCACACCCACACCTT  
CTCAGGTAACATACTTGGGACTTAAAAAACATAATCATATCTTCTTAAACGATCAAGACTGATAACCATTGACAGGCCATACAGACAGTACTAGCTGGCACTTAGGCTTCAGCTGTGGTCATCGTTGGGTTCCATTGTA  
GATAAGAACACT

## Read #16 Alb-chr4-Alb

AATGCAAGGCACGTACGGTTATATGCTATTGCTATGGCTATGAGTCAGTCAAATCTAACAGTCCTGCTAAATCTCTCTAACATCCATTTCTTCTGAGGTCACAAACCTTGTCACTAGATGCAAGAGGCCAGTGTGCAATTTCATTTCCAGTGTGTTTGGAGAAACATCCTACCTTACCTTGTAGTGTCTTCTGCTTCCCATATTTCATGTCACAAACCGTGTGTTGTCCTATTTTCATGTTCTGTTCTGTTCTGCTTCCATTTCAGGTCCTAAATTCACATTTCATTTTCACCTTACGGTCTTCTGAGGCTTACAAACACCAACACCAACACCAACCTGAGTAAACTATGGGACTAAAAAACATAATCATACATTTCTAAAGCATGCAAGACTGATAAAACATTGACAAGAGGCCATACATGACAAGCAACAGCTGACACTTACGGTCTTCTGAGTGTGCTACGTTGGCTCCATTGTAGAT

## Read #17 Alb-chr5-Alb

## Read #18 Alb-chr6-Alb

AGGCTCTAGCAATGCAAGGACGTAGTCAGATTGGCATACGGGTTTATGGCTGGAAGTCATAACAGTCCTGTAATACTTTCTAACATCCATCTTCTTGTGTCAGGCGAAAG  
ACGCTTCTCTAGCTGTGATCATCAATCTAAGGTATGTTAATCTAGTGTGGAAAAGCCTACCTGCCTTAAAGAGTAGGTGTTCTCAGTTTGATCTATAGTGGAGACAGCTGACTTCGATGCCTGAGTAT  
AGCATCATATTAGTGGAAAACAAGCTAACAGGACATGCTTAAAGACATGAACTCACAAACCTCACAGTAACTACCTGGGACTTAAAAATACAATCATCTTCCAAAAGCATAAGGACTGAAAA  
TCATTGACAGGCCATACAGATGCTGTCAGCTGGCAACTTGGCTCTACGTTGATGTCATCAGTTGGTCATTTGTCATAGTATGAGTATGAAAC

Read #19 Alb-chr6-Alb

AGGCTCTTA GCAAGGCAATCATTTACTATGTCATTGCCATGGCTATAGAAAGTACAATCTAACAGCTCTGCTAATACTTCTAACATCCATTGTTCTTTTTTTTTAGAACACCGAGTACCCCTTGACACTTGCGCTCTGCC  
CTTCTATCAATCTAGGCTATGCTTAATAATGAAGGCTCACCCTGACCTTAACTGGTTGTCTCTCTGTTGATCTCATCTAGGGTTGAACAGAACGACACGACATCACCTCCAATGATAGTACTCATATTAGTGAAACAA  
ATAAGAACCGAGATAAAATAGATACTAACACATCTAACACAAACCTCTGGGTTAACTACTTGGACTTAAAGGCTTATAATCATACATTTCTAACAGCTAACAGTACTGATAACCATTGACAAAGGCCATACA  
GACAAGACCGAGCTTGCACTCTAGCTTCACTGTTCTAACCTGTTCTGTTGATGAGTAAAGAAC

## Read #20 Alb-chr6-Alb

ATGCAAGGCACGGTAACTGGTTACTATGTCATGGCTATGGCTAGGTAAGTGAATCTAACAGCTCTCGCAGAATCTCTAACATCCATCATTCITGTTTCCAGGGTCGTCAGTGTCACTAGTGCAGAACAGCCTTAGCGTGACAGGGTCAGTCATAITGGAGCTGAATGTCATAAAGTCACATTAACCCAAAATCTATCCTCAAATTGATAACCTTATAAGAAAAAATTAGTTTACTCCATGTATTCTGAGTGAAGGCCCCAACAAATTCTCACGCAAAATGGACATCTAACACAAACAGGAGTGGAGTAGCCATTATATTGGATAATCTACTTCCACCCAAAGTTATCCTACAAAAGACAAGGGGACACTCTCATACTCATCAAAGTGAACACTCTCCAGGGAAACTCTCAATTCTCAAACACATCACAACCACAAACCTTCTCAGTAACTACTTACTGGACTAAACATAATCATACATTCTTCTAAACCATCAAAGACTGATAACCATTGACAAGGCCATACAGACAGTACCGCTGGTACTCTTGGCTTCAGTGTATGGTCATGTTGGGGTCCATTGTAGATAAGAAACTG

Read #21 Alb-chr6-Alb

CAATGCAAGGCACGTACGTTACTATGTCATTGGCTGGCATGGGCAAATCCCAACAGTCATAAATCTTCTAATCCTCATTTCTGTTTCAGGTCAAACCTGTCACTAGATGCAAAAGGCCCTTAGCTCTCACAGGCCTCAGGCCACCTGAAGGGCTAGCCCTGGGCTGGGAAACAGTCTATCTCTCTCTAGGTGGCTCAGACAGTGTGAGGCTCTCTGCCACTGCTCAGAGTACTCTGTAATACCGCATTCGAACAGGGGCAAGGGTTATTCTGGCCAGTGTCAAGAGCTCAGGGTCAAGTGGGCTAGTGGGCAAGGAAGTGTGGCAGGCCAAATTAAAGCTCTCTGGGTCAGGACCAAAGTGTGGGCTAGGAAGGCCAGTTCCTCTGGTCAAGGACCCAGTTCCTCTGGTCACTCTCTGGGCTAGTGGGCAAGGAGCTCAGGGCTCAGACAGGCTCTGGGCTAGGAGCCTGTCAGAATGGGCTCTGGGCTAGGAGCTTCAACCTAACACCCCTACACAGGCCAGTGGCGAGCTTCAACACCATCACACACCAACACCAACACCTCTCAGGTAACTATTCTGGGATAAAAAAAACATAACTATTCTCTAAGCATCAAGACTGATAACCTTCTGACAGAGCTTACACAGACAAGGCCAGCT

**Figure S11A. Single Genomic DNA Fragment Insertion:** The displayed read sequences show the insertion of a single genomic fragment into a DNA sequence at a particular location (arrowhead).

Read #22 Alb-**chr6**-Alb

AGCACCTCCAGGCTT AGCAATGCAAGGCACGTACGTTACATATGCTATGGCTATGAAGTCACGCCAAGTATAACTTTCTAACATCCATCATTCTTGTGTTTCAAGGGTCAAACCTTGTCACTAGATG  
GCAAAAGGCGGAAAGGTTACACTCTCTATCCCCAAACATTCTGGGTATTCTCTATCTAAAGGCTGTACAAATCTGTCCTAAAATTGAGTTCTAGTTAGAAGATGACAACACTGTGTACGTTACGCTAAACACATCAACACAAACCT  
TCTCAGGTAACCATCTGGGATTTAAACATACTAAATCATCTTCTAAAGCATGCAAGACTGTAAACCATTTGACAAGGCCATACAGACAAGGCCAGCTGGACCTTCTTAGGTCITCAGCTATGGTCATCAGTTGGTTCCA  
TTGTAGATAAGAACCTG **GTC**

## Read #23 Alb-chr7-Alb

GTGACCAAGCAATGCAAGCAGTCAGCTTAACTATGTCATGGTTATGGCTATGAAAGTCATAACGCTCTGTAATACTTCTAACATCATTCATTCTCTGTCAGGGTCAAACCTGTCACTAGATGCTATTTAACCA  
GAGATAGACTCAAGATGTTCAAGGGGAAGGGAAAGACCTCTAATTATAGGACATCACTATGCCAGGTATAAAAGAACCTGTCAAAGTAGGGCTAGGGGTTCAGGCTCATAGAACGCCCTAAACACATCACAAAATCCACAAACCTTCAGG  
TAACTACTCTGGGACTTAAACATATAATCATTAATCATTTCTAACAGATCAAGACTGATAACCATTGACAAGAGCCATACAGACAAGTACCAAGCAGTCAGGACTCTTCAGTCTCTGTATGGTCAGTGCGGTTCCATTGTGAGATAAGGAA  
C

## Read #24 Alb-chr7-Alb

## Read #25 Alb-chr7-Alb

**AGTCATAGCAATGCAAGGCACTATGTTACTAGGTCTTGCATGGCTATGGCTATGAGTCGAACATCCAACTGGCTCTGTAATACTTTAACATCATTATTCCTTCTCAGGGTCAAACCTAGCTGGATATAAAATTAACTCAAACA  
AGTCATGGCTTCTCTACACAAAAGATAACAGGTGACAAAGAAAATTAGGAAACAAATCCCTCTCAATAGGTCTACAAATAATAAAACCTTGGGTGACTCTAAGA** CCTAAACACATCACAAACCCACAAACCTCTCAGGTAAC  
ATACTTGGGACTTAAACATAATCATCGATTTCCTAAATGATCAGAACCTCATAAACCATCTACAGAGGCCATACAGAACGACCAGCTGGCAACTCAGGTTCTCATGCACTGGTCATCAGTTGGGTTCTATTGAGAAATAAG  
AAAC

## Read #26 Alb-chr8-Alb

CACTGACAGACGAAATCGAACGAGTCAGTTACTCGGTGTCATTGGCTATGGCTATGAAGTGCAAATCAAATAGTCTGGCAGGTACTTCTAACATCCATCATTCTTTGTTTCAGGGTATTGTCAGGGCAGCGGCACATAATTATTA  
TGAATGTTATTTAGAAAATAACAAATAAGGGGTTCCGGCAGCGCATGGTGCAGGAGCAGGCTGAGAGGCTCACATCTAACCTGTCAGGGCAGGTGAGAGGCGAACATGCACTTGGCATGGCTTCTAACCTCAAAGGCCACTCA  
CACTGAGCAACACCCTTGGCAGGCCAGGCTCTAACAAACCAACCAACATACAACTTGGCAGGTACTTGGACTTCAAAACATATCATATTCATTTCTAAACGATGACAGTACAACCCATTGACAAGGCCATA  
GACAGACAACCCATTGGCAGGCCAGGCTCTAACAAACCAACCAACATACAACTTGGCAGGTACTTGGACTTCAAAACATATCATATTCATTTCTAAACGATGACAGTACAACCCATTGACAAGGCCATA

## Read #27 Alh-chr8-Alh

## Read #28 Alh-chr8-Alh

## Read #29 Alb-chr9-Alb

CCTCCAGGCTTCAATGCAAGGACCGTAGCTTACTATGTCATTGGCTATGGCTATGAAGTAATCTTCAACAGCTCTGCTAATACTTTCTAACATCCATCATTCTTGTTCAGGTCAAACCTGTCAGTAGATGCAAAGGCC  
TTATAAACACAGGCTGACTGGTTGTCACCTAGATCTCTGCTGCTCTCTGCTCTCTGATGATAATCTGATTTAAATTCAGTTTACCATACATGTCGAAACATTTTATGACATCTGTTTTGAA  
AGATTTGACTCTTCTGTCAGGCTTAAACACATCACACACCAACCTTCTGAGTAACATACTTGGAACCTAAACATAATCATATCTTCTAAACGATCAAGACTGATAACCATTGACAAGAGCCATACAGAAC  
ACAGCTGGCACTCTGACTGTCACCTGGTCACCTGGTTCTCTTGTAGATAAGAAC

### Read #30 Alb-chr9-Alb

KGCAATGCAAGGCCAGCTACGGTTACTATGTCATGGCTCGGAAGTGCAAATCCAAACAGTCTCTAACTACCTTAACTACATCCATCATTCTTGTGTTGGGTCACAAACCTGTCACTAGATGCAAAGATTTAGGGCTGAATC  
CAGGGCACCTTGCATCAGGGATGGGATCATACAGGCTCATCTCTACAGCAGGGTTAAACCTTAACTACCTGGGACCCCTTAAATACAGTCTCCATATITGTGTGACCCCCAACATAAAATTAACCTGTCACTTCAACTTTAAT  
TTGTCAGTGTATGATGATAATGATATCTGATAGATAACATCTGGGGGTATAACCAACAGGATGACACAACCTTGTGACGACTACCTGGGACTAAACATATACTTCAACTTCAACTTTAAT  
AAAGCATCAAGAGCTGATAACCTTGTGCAAGAGCTTACAGACAAGCTTGTGTTAATTGGGGTCTCAATGTGGTCATCAGTTGGGCTTACCTGGTAGAC

## Read #31 Alb-chr9-Alb

### Read #32 Alb-chr9-Alb

Read 157 C1H 319 151  
GACCTCCACTAGACCGAGTAGGGCACTGGTCTTACTATGCTGTACCTACACCGCTGTAATTCTGAAATCCTAACAGTCCTGTAATACCTTCTAACATCCTCATCTCTTTAGGGTCAAACCTTGTCAGTATGCC  
AAGGCAACACGAGCTGGAAATTATGAAATGTGTTACTGTAGGCAGAAATATGCAAGAAAATCTGAAATGAGAACCTTCACTGACGGAGAAAATGAGAAATCTAAACATGAAAAATAGAAATACACACTGA  
GACCTGAAATGAGGCGCTTACACACAACCCTCTGAAATCTACTTGGGACTTAAACATAATCATTAATCTTCTAACAGCATGAACTGATAACCGTGTACAAGACCATGACAGCAAGCACCGCTGCTC  
TTGAGTCCTGCTGTCGTCATGAGTTGCTGTTGATCTGTTGAAATGAAAGAACAGCTGGTC

### Read #33 Alb-chr9-Alb

REGULATORY ELEMENTS  
REG1 CTCF CH1 K15  
GCACCTCCAGGCTCTTCAAGATCGAACGGCACGTACCTTTACTATGTCATTGGCTATGGCTATGGCATAGTGCAAATCTAAATAACAGCCTCCTACAGCTCTCTCTAACATCCATTCTTCTTCAAGGGTCCAACCTTGTCACTAGA  
TGCAAAGATGCTCTTAGCACAGAAAATGCAACTGAGGACCTGGAAATATGGCGAGAAAAAACTGAAAATCAGCTAAATGAGAAATACACCTTCTAGGACTGAAATATGAAGGAGAAAATCTGCTGAAATTAGAAATGTCATC  
AGTACAGATGGAAATATGCAAGAAAATCAGGAAAATCCTCACTTGACACTGCTGAAATGACAATTAACCTAAACGCTGAAAACGAGAAAATGCCACTGAAGACCTGGAATATGCCGAGAAAATCTGAAATAA  
CAGAAAATGAGAAATACACCTTCTAGGAACTATGGCTAACTATGGGACTTAAACACCTAATCATATCTTCTCTAAACGATCAAGACTGATAACCCATTGACAAGGAGCCGAAGTACAGACAAGGCCACCGCTGGCACTCTTGG  
CTCTTCCCTAAATACGACTTGTCTGGCTGCAATTAGTCAACTGAGCTTC

### Read #34 Alb-chr9-Alb

**Figure S11A. Single Genomic DNA Fragment Insertion:** The displayed read sequences show the insertion of a single piece of genomic DNA fragment at the Alb site (continued).

## Read #35 Alb-chr11-Alb

GACACGCTAGCATGCAAGCCACTGCGTACTGCTATGTTATGTGCAACTCTAACAGTCGTAATACTTTCTAACATCATTCTTGTGTTCTGGTCAAACCTTGTCACTAGATGCAAGCGT  
GACGCCAACATGCAAGCCAGGTGGAGAATCTAACATAAAGGAGCTTGTGAGTGGCACATCTTGTGTCAGGAGCAGACTCAGGGAGCAGAACGAGCTGGAATCTGAGTTGAGACCAATCTGGTCTATTTAAC  
AAGTTCCAGACGGCCAACTGATCTAGTGTGCTAACACATCACAACCAACACTTCTCAGGTAATCTTGGAACCTAAACATAATCATATTTCTCTAACAGTCAAGACTGATAACCATTGACAAGAGCCATACAG  
GACAAGCACCAGCTGGCACTCTAGGTCTCAGCTATGGTCATCAGTTGGTCTCATTGTGAGATAAGAAC

Read #36 Alb-chr11-Alb

```

CCGGTACACAAGCATGCAAGGCACGTACGTAAGTTTTGGCATTATGCTATGGCTATGAACTTCCAAACAGTCCTGCTAATCTTCTAACATCATCATTCTTGTTTCAGGGTCAACCTTTGTCAGTAGTC
AAGGGACAGACCTGGCTCTGGCCTGGGGCTGGTTTATTTTTTTTTTTTTTTGGTTTTCGAGACAGGGTTCTCTGTGAGGCCCTGAGTGTCTGGGTTAAAGGCATACCTACTCTCTGGTCTGAACCTTTTTTCT
TTTAAACATGCTTCAACACATCACAAACCAAACTCTCGTAACATACTACTGGGACTTAAAACATAATCATATCATTCTCAAACGATCAAGGGTGTAAACATTGACAAGGGCATACAGAACGACAGCTGGACT
CTTGGGTCTTCACTGATGGTCACTAGTTGGGTCATTGTTAGATAAGAAC

```

Read #37 Alb-**chr12**-Alb

AGTCATGACCAATCGAACGGCACCTACATTACTATGTCTTGCCTATGGCTATGAGTACCAAATCTTAACTACGTCCTGCTAAATTTCTTCATTCCTCATTCCTTCTTCAGGGTCCAAAACCTTGTCTAGATGCCAAGAGCCCTTC  
CTCTGAGGAACTGGCTGTGAGGAAAGTCTGACCCTATGCTGCTTCTCCTGCTGAGGTGGGGCCGACCCCCCTGGCCCTTCAAAACACATGAGGAGAGAGAGATTTTCTTAAACACATCAACACACACCTCTCCAGGTAACTATACTTGGGAC  
TAAAAACATAATCTAAATCTTCTTCAAAACATGAAGATATAACCTTTGAGAACAGGCTACAGACAGGACCCAGCTGACTCTCTAGGTCTTCAAGTGGGTCCTAACATGAGATAAGAACAGA

## Read #38 Alb-chr14-Alb

CAATGCAAGGCACGTATTGTTACTATGCTATGGCTATGGCATGAAGTCAACTCTAACAGTCTGCTAATCTTCTAATATCCATCGTATTCTTCTTCAGGTCACAACTCTGTCAGTAGATGCAAAGAGGCCCTAGCTGG  
AATCCCTGCTTCTCAGCCCCATTCAGCAGCTTAAAGCTAACCGAGGTCAGGTCAGCTGACAGAAAGTAAGGATTCAAGGCCACAGGCCCTCTGAAAGGACTTACCCAGAAAGGCCAACTCTGTGCCCTAAACACATCACAA  
CACACCTCTAGGTTACTATCTGGGACTTAAACATAATCATAAATCTTCTAACAGATCAAGCTGATAACCATTGAGAGGCCATACAGACAAGCAGCAGCTGGACTCTCTGAGGTCAGTTGTCATCAGTTGG  
GTTCCATTTGAGAT

## Read #39 Alb-chr15-Alb

GCACCTGCAACAGAGGAGCAATACGAAGGACCGTACGGTTACTATGTCAGAGCTGTATATGAAACATGAAAGTCAGGAACTTCAAACAGTCTGTAAATACCTTCTAGCATCCATTCTTGTGTCAGGGTCACAACTCTGTCAGTAGA  
TGCAGAAAGCCTCCGCTACTCTTGTTACTGTTGTTGTCATTTCATCACCTGTTGGATGCTTCTGTTTCTTAAAGGACTCTACGTGTTGATGTTGTTCTCTTAAAGGACTGTAACCTGTCATGTTGTCAGGGTCAACCTGTCAGTAGA  
CATACAGAACACAACATGTTGACTATCTGGACTAAGAAAACATAATCATACATTCTTCCATAAACAGATCAAGACTGATAACCATTGACAAGGCCATACAGAACGACCCAGCTGGACTCTTGGTCATGTTGTCAGGGTCAACCTGTCAGTAGA  
ATCTGGTTGGGTTCTTGTAGATAAGAAAAGTGGTC

Read #40 Alb-**chr16-Alb**

ACTAGACGAGCAATGCAAGGCACGTACGGTTACTATGTCATGCCATTGCTATGAAGTGCCTAACTCCTAACAGCTCTGCTAACTATTTCTAATCCATCATTTCTTGTTCAAGGCTTGTCACTAGATGCAAAGACGCCCTG  
GATCAAGTCTCTGCGAGGATTAGCTCATCTCTCCATATTCCAGACAAAGGCGGCCCTCTGTCATGTGTCGCGCTTCTGTCAGCTTATATGCTCTTGTGTTGCTCATCTCTGAAATTCCCAAGGACTCAGGTAGTTGCTA  
TGGTCATCAGTTGAGCTTCCATTGAGATAAGAACATAACGTCATCTTGTGACTTAATCTGACTAAACATAATCATATTCTCAAACGATCAAGACTGATAACCATTGACAAGAGGCCATACAGACAAGGCCAGCTGGACTCTTAGGTCTCAGGT  
TGGTCATCAGTTGAGCTTCCATTGAGATAAGAACATAACGTCATCTTGTGACTTAATCTGACTAAACATAATCATATTCTCAAACGATCAAGACTGATAACCATTGACAAGAGGCCATACAGACAAGGCCAGCTGGACTCTTAGGTCTCAGGT

## Read #41 Alb-chrX-Alb

**Figure S11A. Single Genomic DNA Fragment Insertion:** The displayed read sequences show the insertion of a single piece of genomic DNA fragment at the Alb site (continued).

Read #42 Alb-**chr10**-chr3-Alb

CCAAATGCAAGCATGCAAGGCCACGTCTGGTTACTATGTCATTGCGTGTGGCTGTGAAGTGCAAACTCTAACAGCTCTGCTAATCTTCTAACATCCATCTTCTTGTGTCAGGTTCCAACCTTGTCACTAGATGCAAAAGCCTT  
AGCATCTCCGCTGACCATCTTGAAGACTCAGATAATCACGCCAGGTACTCTCAGGTTCTCTCTCTCCATCCAGTGTGCGCAGTTGATGCGAAAAGGTGGAGTCATAACAGCAAAAGGGAGGATCATACCAACTGTAGTCCTCCAGGATT  
AGGCTTGAACCTTGAACAAAAAAACACAATTAATTGTAATAACTAATGGATGTTAGCAGGGACCTAGATGCACAGAGGGGGAGTGTCTGGGTGCAAGGCATAATATCTCTAGATGAGATTCTACCTAGCAGAAGGGACTCTAAACC  
ACAACACAAACCTCTCAGGTAACATACTTGGGACTTAAAAACATAATCATATACTTCTTCTAAACGATCAAGCTGTAAACCTTGTACAGAAAGCCATACAGACAAGCAGCCTGCGACTCTTGGAGTCCTCAGTATGGTCA  
CAGTTGGGTCTCATTTGTA

## Read #43 Alb-**chr2**-chr9-**chr13**-Alb

Read #44 Alb-**chr5**-chr1-chr2-chr8-Alb

**Figure S11B. Multiple Genomic DNA Fragments Insertion:** The illustrated read sequences demonstrate the insertion of multiple pieces of genomic DNA fragments at the Alb site.

## Read #45 Alb-BB-chr9-Alb

## Read #46 Alb-chr1-BB-Alb

## Read #47 Alb-chr3-BB-Alb

## Read #48 Alb-chr13-BB-Alb

**Figure S11C. Plasmid Backbone and Genomic DNA Fragments Insertion:** The presented read sequences reveal the insertion of both plasmid backbone and genomic DNA fragments at the Alb site.

## Read #49 Alb-F8-chr7-Alb

**Figure S11D. F8 and Genomic DNA Fragments Insertion:** The depicted read sequence showcases the insertion of both F8 and genomic DNA fragments at the Alb site.

Read #50 Alb-F8-chr3-BB-Alb

**Figure S11E. F8, Plasmid Backbone, and Genomic DNA Fragments Insertion:** The exhibited read sequence displays the insertion of F8, plasmid backbone, and genomic DNA fragments at the Alb site

**Figure S12.** The consensus sequence of L1MdA\_I in the LINE-1 family.

Read #1 Alb-L1-Alb @6054e536-fd9d-4ce6-bf33-b065bed95978

Read #2 Alb-L1-Alb @88a19c42-27f1-4911-b00a-1e132a1b9c61

ACATGAGGAGCAATGCAAGGCACACTTTGTTACTATGCTATTGACTATGGCTATGAAGTCATAACAGTCTGTAAATCTTCTAATCCATCATTCTTGTTAGGGTCAAACCTT  
GTCCACTAGATGCAAAGAACGCCCTTATAGCTCTTTCTATTGGGATCTTAAAGGATACTGTCTCTGTGCCCTAGTTAGCTGGTAAGGGTTTATCTATCTTGTTATTTCTCAA  
TGTACCAAAACCATCACCAACCAACTTCAGGAAACTATACITGGGATCTTAAAACATAATCATTTCTAAACGATCAAGACTGTAGCAAATTGACAAGAGGCCATACAGACAAGC  
ACCAGCTAACTCTTAGGTTCTCACCTGTGTCATGTTGGGGTCATTGTAGATAAGAAC

Read #3 Alb-L1-Alb @d5a82961-5d4f-4c2e-b8e2-232b26dbf4d8

TTACCTGATTACCTCAGCAATGCAAGGCCAGCTACGTTACTATGTCATTGGCTATGGCAACTACAGTCTGGTAATACTTTCTAACATCATTCATTCTTGTGTCAGGGTC  
AAACACTTGTGCTAGCTGCAAAGGCCCTTAGAAACACTTGCTAGTGTAGCTGGTGTAGCTGGAACTGGTATAGGATCCCGAGATAAGCAGTCTCTAGATGGTCATCCCTTCTGTC  
CAGCTCAACATTCTGTCCTAACTTACAAACACATCACAAAGCCAACCTTCTGGCTAGTACTGGAACTTAAACATAATCACCTGGTGTAGGAGTCCCTAAACGATCAAGACTGATAACCATTT  
GACAAGGCCATACAGACATAAGGCCAGCTGGCATAACAGACTCTTCAAGCTATGGTCAATGTTGGAGTCCCTTGTAGATAAGA GCTGAGGTGC

Read #4 Alb-L1-Alb @0d0a64cb-40d1-46c7-bbae-5601d14b962e\_R

CGTTACGTGCAAGCAAATGCAAGGCACGTAAGCTTACTATGTCATGGCTATGGCTAAAGAAGTGCATAATCCAGTCAGTCCTGCTAATACCTTCTAACATCCTCATATTCTCTGTTCTGTTAGGTCCA  
ATTTCTGTCATAACAGAGGAGCTGATAAACTGCTAGGTACTGTATAGAGCACAGTGAGACAGTCAGGAACTTGAAGCTCCAAAGTCAAGATCCAGAAATGAAACCCACACSCATGTCACTGTGATC  
ATTCGACACCTAAACATCACACCAACCCCTTCCTCTGCTAGCTAATACTATGTCAGGACTTAAAGAAAACATAATCATTCATTCTCTAAACGATCAAGACTGATAACCATTGAGCAGAGCTT  
TTCATACAGAGAGACAAGCACCAGCTGGCACCCTTCTAGGTCTCAGTATGGTCATCAGTTGGGTTCCATTGAGATAAGAAC

Read #5 Alb-L1-Alb @845b268b-2288-4aa5-b915-53780c9fa804\_R

AGTCATGAGCAATGCAAGGACTACGGTTACTAGGTCTATGCCATTGGCTATGAAGTCAACGCTTAACTTAACTCCATTATTCCTTCTTCAGGGTCAAACCTTGTGCA  
CTGATGCAAAAGGCTTAAAGCTGGATATAAAAATTAACAACTAACATGGCTTCTTCAACAAAAGAATAACCGCTGCACAAAGAAATTAAGGAAACAATACCCCTCTCAATAGCTCACAATAA  
TATAAAATACATGCTGACTCATTAACAGCTAACACATCACACCAACCTCTCAAGTAACTACTTGTTGGATAAAAAACATAATCATACGATTTCTCTAAATGATCAAGAACCTCATACCC  
CTACAAAGGCCATACAGACACACCAGCTGGCAACTCAGGTCTCATGCTACTGGTCTTGGTCCATTGTGAGATAAGAAC

Read #6 Alb-L1-Alb @9aca963b-8fb1-4709-905c-f0ba2759f766

GAGCCATAGGAATGCAAGGGCGTAGCTGGTTTACTATGTCTTGCTATGGCTATGAACTGCAAATCTAACAGCTCGTAATACTTTCTAACATCAAAGCCTTCTTTCAGGGTCAAACGTCAC  
TAGATGCAAGGACCCCTGGGAAGTACAGACAAATAAAGAAAAACAAAAGCATGAGCACCCTGAGAATGAGAACCTAGGAAAGAGATCTAGAACCTAGATGCCGACCATCACCAACACAATACAGAAAATGG  
AGAGAAATCTAAGGTGCGAGAAGATTCTAGAGAACATCTAGCTGTTACATACAAACACAACTTCTCCAGGTAACACTACTTGGCTTAACAAAAGAAAACAATCTACTCTAACATTTCCATAAAAA  
CTGATCAAGACTGATAACCATTTGCAAGGACCATACAGCGCAACAGGACAGCTTGGCACTTCTGGACTCTTCAAGCTGTCTAGTGTCAAGTTGGGTCTTCTTGCATAGTTAGATAAGAAC

Read #7 Alb-L1-Alb @92f1ed7a-d649-470f-bc21-3215f61678e1

GGCTGACAGACAATACAAGGCACATTACAGTTACTATATGTACCTATGGCTATGAAGTGCACAACTCTAACAGTCCTGCTAATCTTCTCATCATTCTGTTTCAGGGCTCAAACCTG  
TCACATAGCTAAAGGCCATGTAGATATCTTAAATGGACTCTCCAAACCCCCAAAATCTCAAAAGGACAAGGAGACACTCTACATCTACATCCAAAGTTAAAATCTCCAGGAACTCTCCAATCTG  
AATATCTATGCTCAAAATGCAAGGGCAGGGCACATTCAAAAGAGACTTTTAGAAGCTCAAGGACACATTACCTCATACACAATAAATAGGAGACTTGCCTACTTTCATCAATGGATAGATCCTGG  
CAGAAAAGCTTAAACATCACAAACCAACCTCTCAGGTAATGAGGACTTAAACATAATCATCATTCTCTAAACGATCAAGACTGATAACCATTGACCAAGAGGCCATACAGACAG  
CACAACAACTCTGAGGCTTCACATGTGATCATCGTTGGGTTCTATTGTAGATAAGAAC

Read #8 Alb-L1-Alb @7a05acea-6e10-403a-bfd9-d05e5b25ef5c\_R

ACCACTATCAGAACATGCAAGGCACGTCAGTTACTATGTCATTGGCTATGGCTAGAAGTCACATCTAACAGTCCTGCTAACTCTTCTAACATCCATCTTCTGTTTCAGGGCTCAAACCTGTCAGTAGATGCCAAAGGACGCCCTAGTAAGTATGGATCACATTCTACATGATAACAACCAGTTGTGCCAGCACCATAATGTTGAAATGCTGCTTCTTCCACTGGATGTTGTTGCTCCCTGTTGAAGATCACTGGCATAGGTGTTGTCATTCTGTCATTCATCTTCTAATCCATTGGTCCACTTGTGTCCTATACCACTGGAGCTTCTTATACCAATTGCTCTGAGTAAAGCTTGGCTGGATAAACACATCACAAACCAACCTGGTCATTCAGGTAACATACATGGACTAAACAAACATAATCATATCTTCTAAACAGCATCAAGACTGATAACCATTTGACAAGAGCCATCACGAGCACAAAGCACCAGCTGGCACCTCTTAATGTCAGGTATGTCATCTGGGTTCTATGTTAGA

Read #9 Alb-L1-Alb @05d5093e-f9d6-4514-8d26-c3a74881845f

**Figure S13. (A) The representative read sequences display the insertion of a single LINE-1 fragment at Alb.**

Read #10 Alb-chrl-L1-Alb @450abd0c-3536-4496-b7d3-78d412798077\_R  
ATGCAAGGCACCGTAACTGGTTACTATGCTATTGCTATGGCTATGGCTATGAAGTGAATCCTAACAGTCCTCGCGAGAACTTCTAATCCATCATTTCTTGTCTTCCAGGGTGGTACCTTGTCACTAGATGCC  
AAAGACGCCCTAACGGTGCACAGGGTCAAGTCATTGGAGGTGAAGTGTCCATAAGGTCCAATCTAAACCAAAAATCTATCTCCAATTGATATAACCTTAAAGAAAATATTACTTACTCTAACATGAT  
TTCACTGAGTGAAGGGCAAAACAAATTCTTCCAAGCAAAAGTGGACTCAAGAACAGCTGGTGGACTGATTATTGATAAACTCTTCAACCCAAAGTCAAAAAAGACAAGGGAGGAGCACCTC  
ATACTCTAACAGTAAACTCTTCAAGAGGAACACTCTCAATTCTTCAACACATCAACACCAACCTCTCAGGTAACATACTTCTGGACTTAAACAAACATAATCTAAACTTCTTCTAACACATCA  
AAAGCTGATAAACCAATTCTTCAAGAACAGCCATACAGAACAGTACCCAGCTGGTACTCTTAGGCTTCACTGGTATGTCATCAGTCTGGTCTTCAATTGATAGATAAGAACCTG

Read #11 Alb-L1-chr15-Alb @c7c6b1ba-fd1e-4ca1-aded-92dd0734e698  
GCACCTGCAACAGAGGAAGCAATACGAAGGCACGTACGTTTACATGTCAGAGTCGATATGAAACATGCAAACTCTAACAGCTGCTAAATCTTCTAGGCATCCATCTTCTTGTTCA  
GGGTCACAACTCTGTCACTAGATGCAAAGCCTGCTACTCTCTTAAAGTCATGTAGTGTTCATTCCATCACCTGTTGGATGCTTCTCTGTTTCTTAAAGCATCTTACCGTGT  
TGATGTTGTTCTCTTCTTAAAGGACTGTAACCTAACACATCACAAACACTCTCGGTAACATACTGGGAAACAAACATATACTTCTGTTGGTCATCAGTTGGCTTCTTAAAGCATCAAGACTG  
ATAACATTGTCAGAAGGCCATACAGACAAGCACCAGTCGGCTACTTCTAGGTCATCATGGTCATCAGTTGGCTTCTTAAAGCATCAAGACTG

Read #13 Alb-L1-chr1-L1-Alb @d2d4a3f-5803-4c82-b0fc-7af9a078f5e7\_R  
CAACAACACTAGGAATCGAAGGCCAGCTTACGGTAACTATGCTATTGCTATGGCTATAACTTTCTAACAGTCTGTAACTTCTTCTGAGGTCACAAACCTGTCACTAGATGCAAAGAGGCC  
TTGATTCTATCTTCTCTCTGTAAACAGCTAACAGACTCCACATAAAAACAGAGAGACTTATAGAGGAGAAAGCTGGTCTGATATGGGCACAGGGAAAATTCCTGAAACAGAACACT  
AGTGGCTTGTGCTGTAAAGGACATTAACAGGACCTTAACTTAAAGCTGTAAGAACAGAACAGGAAAGGGCAGTGTAAAGAACAGAACAGTGGAAAATTCCTAACCTAACAGGATAATTCCTAAC  
TATTACCAAGAACACTGAAAGTGGACTCTGAGAACCAAAATTAACCTTCTTAAATGGATCACAGAACAAAGACTCTAACAGGACTTACAGAACAAATGGTCTGAGGACCAAAATGGTCTAACATCTGTCATGGGAAAATG  
CAATCAAAACAAACCTGAGATTCACCTCACACCGTCAAGATGCTAAAGATCAAAACACTCAGGTGACAGCAGACACTGGCAAGAATGTAGAGAGGAGTACTCTCTCATGCTGGGATTGCAAGCTGTTACAAACACTCTGAAAATC  
TGTTGTTGTTGTCAGAAATTTGGTACAGTACTACATGAGGATTCAGGCAACTTACCTCTGGCTTCTGAGGATCTGCAAGCTGTTACAGGCTCCCTATTTTAAAGGCCAGGAGCTGGA  
GAGAGGCCCCAGATTCCTCTCACAGGGGTAGAGGAGGATCAGAGGATTTGCGCATTTCACATGTTGACTACATGAGCTTAAACAAATTTGGTCAATTGAGGATCTACATGTCATGGGATTC  
TCAATCACAAAAGAACACTCATGATATGCTTCACTGATAAGTGGATATTAGCCCAGTAGCTCGGAAATACCAAGATACGATTGCAAATATATGAAATTCAAAAGGAACCAAAGTGTAGTGTCTGATCTCTCATAGAAGGGGG  
GAGCAGGAAATTCATGGAGGAGTACTGAGGAGAACAGGAACTGAGCAGGAGACTGAAGAATGAGCATTGCGGACATGGGGGACATTCGGGCTAAACAAACCCAAAACAGGACACTATGAGCACCACAAAGGCTTGTGCG  
AGGACCTGTATGATCTCTCTGGACAGGCTCTGCAACTACTGACAAATGCTTACAGGAGTCTCACAGGAGACTTCAGGAGACTTACAGGAGCTTACAGGAGCTTACAGGAGACAAATTAAC  
AAGGACTCATGCTAACAGGCTCTGGGAAACTACCAATCAAGAACATATGCTAGGATTCTGTCATGTCATATGACATGAGTGGCTCTGAGGCTCTGAGGCTCTGGTCTGATGTTCTATGGCCAG  
TATAGGAAACTCTCAGGGCCAGGAATTGGGAGTGGGTAGGTGGGGAGCAGGGGAGATGGGGAAAGGGATAGGGGATTITGGTGTAGGAAAGACTAACATTGAAATGTTAAATAAGGAAATTA  
TGGGGTACAGGCTAACAAAGAACATTCATGGGAGGATCTAAACATGGCAAGAACCCATTAAGGGAAAGTGTCACTTGGGCTTCTGAGGAAACTCTGAGGAAAGGATTAACATTGAAATGTTAAATAAGGAA  
AAAACACTGGTGTACAGGAGCTGGGGAGGATCTGGGGAGATGGGAGGAGGGGGAGCTTCCATTGGGGGTTGGGTGAGGTTAACCTGAGGAAAGTGTCACTTGGGCTTCTGAGGACCTGAGGATGATGTC  
TGATCCAGTTACTACTCTCTGGGCAATACCCAGAGATGCTTCAACATGTAATAAGGACACATGCTCTACTATATCATCAGGCTTATTTATAATGCCAGAAGATGGAAAAGAACCCAGATGCTCTCACAGGAGATGGATACAG  
AAAATGTCGCACTCTCACAAACTAGACTACTCTGAGTTTTTTAAATGATGATTCTGAGGAAATTCCTGAGGAAACTGAAAAAATCATCTGCTGAGTGTAGGAGCTTACAGGAGACACATGATGCACTGATA  
AGTGGCTATGTTGCTAACACCTCAAAACCTCAAAAGATCACATGAGCACCACATGAGGAGCTTACAAACCAACAAACCTGCTTCTGAGGAAACTGAGGAAAGAACACATGATGCACTGATA  
GAGACTGATCTGAGTCTTACAGGAGCTTACAGGAGGACATGAGGAGCTGAGGACTCTAGGTCTCACAGGAGCTTACATGAGGAGCTTACAGGAGCTTACAGGAGCTTACAGGAGATGGATACAG  
AAAATGTCGCACTCTCACAAACTAGACTACTCTGAGTTTTTTAAATGATGATTCTGAGGAAATTCCTGAGGAAACTGAAAAAATCATCTGCTGAGTGTAGGAGCTTACAGGAGACACATGATGCACTGATA

**Figure S13. (B)** The representative read sequences display the insertion of LINE-1 and genomic DNA fragments at Alb.

Read #15 Alb-chr5-L1-chr5-L1-Alb @f4993ccf-89c0-4e58-85c8-03f07f708a2b\_R

**Figure S13. (B) The representative read sequences display the insertion of LINE-1 and genomic DNA fragments at Alb (continued).**

Read #17 Alb-BB-L1-Alb @f17a093d-ed82-46f9-95e2-ffbfd705893a

Read #18 Alb-BB-L1-Alb @3e9c16a4-5357-40ab-a0e4-94b9550244a9

**Figure S13. (C)** The representative read sequences illustrate the insertion of both the plasmid backbone and LINE-1 fragment at Alb.

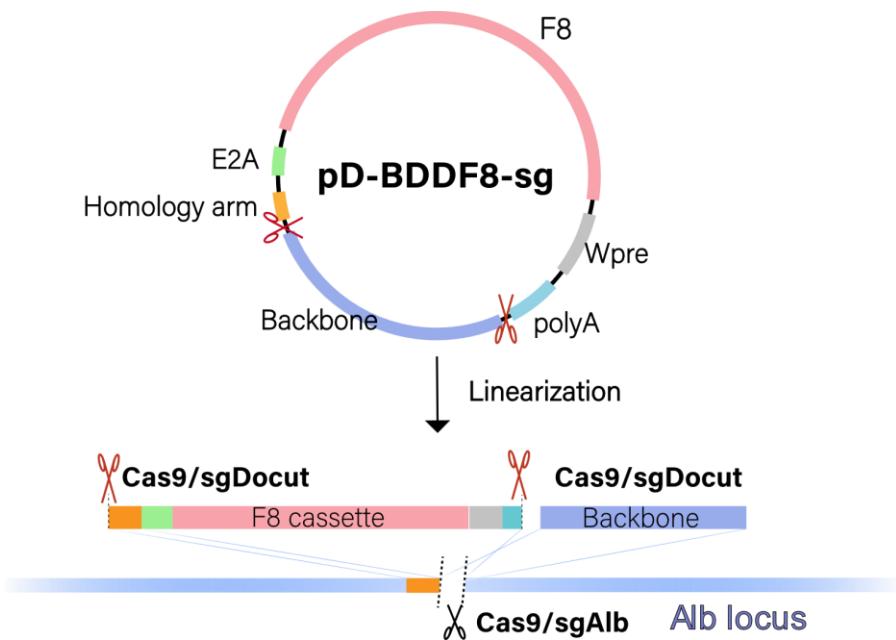
Read #19 Alb-Unknown sequence-L1-BB-Alb @7e188ad4-dbcd-4017-aadd-9336b25e1012

Read #20 Alb-BB-L1-chr5-BB-Alb @1955fd7b-f139-4c6d-9951-ffebbbf333b9\_R

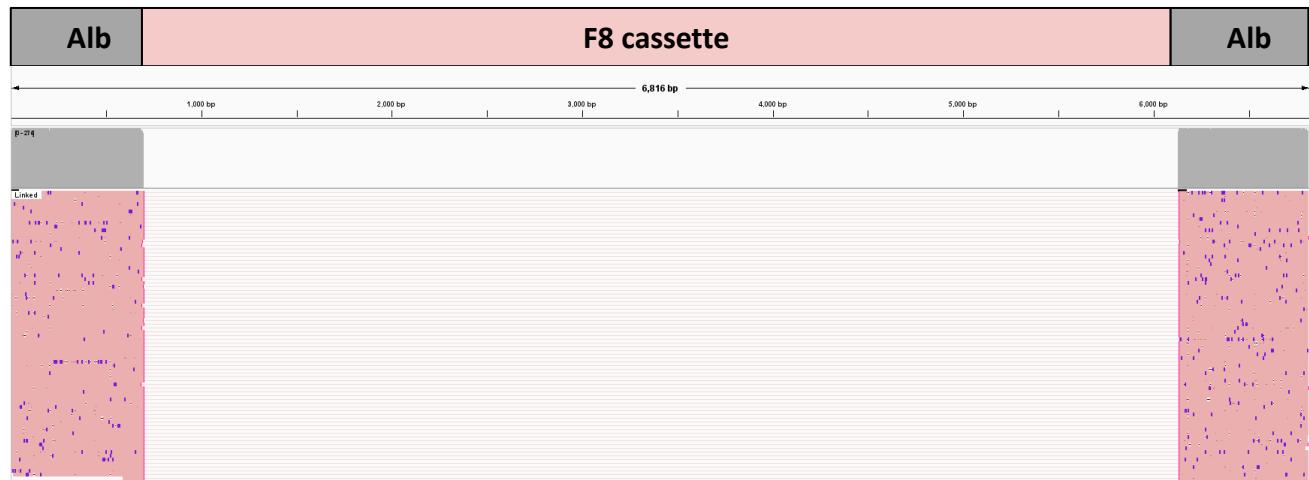
**Figure S13. (D) The representative read sequences show the insertion of the plasmid backbone, LINE-1, and genomic DNA fragment at Alb.**

pD-**sgDocut**-LA190-E2A-BDDF8-Wpre-PolyA-RA130-**sgDocut**-Backbone (**sgBB**)

**Figure S14.** The sequence of pD-BDDF8-sg vectors with HA190-130. The backbone used for the plasmids in our study is derived from pBR322, a well-known bacterial cloning vector.



**Figure S15. Linearization and Integration of Double-Cut Donor Plasmid:** This schematic illustrates the process where a double-cut donor plasmid is linearized into two distinct fragments within hepatocytes. Subsequently, these fragments integrate at the genomic site cleaved by sgAlb. The diagram provides a visual representation of the linearization and integration steps, highlighting the two resulting fragments and their integration at the targeted genomic location.



**Figure S16. Analysis of Circular Donor Plasmid Integration:** This figure analyzes the integration of a circular donor plasmid with HA600-600 homology arms, which lacks the sgDocut, into the target genomic site. The reference sequence used for alignment is based on the expected outcome of homology-directed repair (HDR) editing. This panel shows random 200 reads out of over 6000 aligned with the reference sequence. Nanopore sequencing of over 6,000 reads failed to reveal any F8 insertions. This lack of detection likely resulted from the preferential amplification of shorter background sequences (1.3 kb) without insertions, overshadowing potential longer insertions.

Target site	sgRNA Sequence
sgAlb-E14	GTTGTGATGTGTTAGGCTA
sgDocut	GGTGGTGCAGATGAACTCCA
sgBB	AATAAACAGCCAGCCGGAA

**Table S1.** The target sequences of sgRNAs utilized in this study.

Primer	Sequence	Length
Alb-PE150-F-BC1	aacaaggATTGCCTATGGCTATGAAGTGC	242 bp
Alb-PE150-F-BC2	aacattccATTGCCTATGGCTATGAAGTGC	
Alb-PE150-F-BC3	aaccgtaaATTGCCTATGGCTATGAAGTGC	
Alb-PE150-F-BC4	aacgagaaATTGCCTATGGCTATGAAGTGC	
Alb-PE150-F-BC5	aacttggATTGCCTATGGCTATGAAGTGC	
Alb-PE150-F-BC6	aagaccaaATTGCCTATGGCTATGAAGTGC	
Alb-PE150-F-BC7	aaggtcatATTGCCTATGGCTATGAAGTGC	
Alb-PE150-F-BC8	aatagtggATTGCCTATGGCTATGAAGTGC	
Alb-PE150-F-BC9	aatgccttATTGCCTATGGCTATGAAGTGC	
Alb-PE150-F-BC10	acaatagcATTGCCTATGGCTATGAAGTGC	
Alb-PE150-F-BC11	acaggattATTGCCTATGGCTATGAAGTGC	
Alb-PE150-F-BC12	accgacctATTGCCTATGGCTATGAAGTGC	
Alb-PE150-F-BC13	acgagtccATTGCCTATGGCTATGAAGTGC	
Alb-PE150-F-BC14	acgcataaATTGCCTATGGCTATGAAGTGC	
Alb-PE150-F-BC15	acggacgaATTGCCTATGGCTATGAAGTGC	
Alb-PE150-F-BC16	acgtatggATTGCCTATGGCTATGAAGTGC	
Alb-PE150-F-BC17	actaaccaATTGCCTATGGCTATGAAGTGC	
Alb-PE150-F-BC18	actcaggtATTGCCTATGGCTATGAAGTGC	
Alb-PE150-F-BC19	acttgttgATTGCCTATGGCTATGAAGTGC	
Alb-PE150-F-BC20	agaagtacATTGCCTATGGCTATGAAGTGC	
Alb-PE150-F-BC21	agccactcATTGCCTATGGCTATGAAGTGC	
Alb-PE150-F-BC22	agctctaaATTGCCTATGGCTATGAAGTGC	
Alb-PE150-F-BC23	aggtgtctATTGCCTATGGCTATGAAGTGC	
Alb-PE150-F-BC24	agtccgttATTGCCTATGGCTATGAAGTGC	
Alb-PE150-R	TGCTTGCTGTATGGCTTTGT	

**Table S2.** The primers employed to determine the cleavage efficiencies of Cas9-sgRNA that targets Alb.

Primer	Sequence	Length
Alb-4.9kb-F-BC1	gccgggtggaaTGAGACCTTCACCTTCCACTCTG	4886 bp
Alb-4.9kb-F-BC2	ggtatacatggTGAGACCTTCACCTTCCACTCTG	
Alb-4.9kb-F-BC3	gtacttgttagTGAGACCTTCACCTTCCACTCTG	
Alb-4.9kb-F-BC4	taagctgcaagTGAGACCTTCACCTTCCACTCTG	
Alb-4.9kb-F-BC5	tgcctccatcTGAGACCTTCACCTTCCACTCTG	
Alb-4.9kb-F-BC6	ttagaatcacgTGAGACCTTCACCTTCCACTCTG	
Alb-4.9kb-F-BC7	ttcaggtttcTGAGACCTTCACCTTCCACTCTG	
Alb-4.9kb-F-BC8	ttctgcaccgcTGAGACCTTCACCTTCCACTCTG	
Alb-4.9kb-F-BC9	caatcttacagTGAGACCTTCACCTTCCACTCTG	
Alb-4.9kb-F-BC10	ccaggagggtTGAGACCTTCACCTTCCACTCTG	
Alb-4.9kb-F-BC11	cgagactattcTGAGACCTTCACCTTCCACTCTG	
Alb-4.9kb-F-BC12	gacctgacatcTGAGACCTTCACCTTCCACTCTG	
Alb-4.9kb-F-BC13	aacaacaacacTGAGACCTTCACCTTCCACTCTG	
Alb-4.9kb-F-BC14	aacatttgagccTGAGACCTTCACCTTCCACTCTG	
Alb-4.9kb-F-BC15	aagaccataggTGAGACCTTCACCTTCCACTCTG	
Alb-4.9kb-F-BC16	aatagtgtcggTGAGACCTTCACCTTCCACTCTG	
Alb-4.9kb-F-BC17	acaatgcgaatTGAGACCTTCACCTTCCACTCTG	
Alb-4.9kb-F-BC18	accgctatgccTGAGACCTTCACCTTCCACTCTG	
Alb-4.9kb-F-BC19	acgttaggataaTGAGACCTTCACCTTCCACTCTG	
Alb-4.9kb-F-BC20	actattactccTGAGACCTTCACCTTCCACTCTG	
Alb-4.9kb-F-BC21	agctcggacctTGAGACCTTCACCTTCCACTCTG	
Alb-4.9kb-F-BC22	agtctagcgttTGAGACCTTCACCTTCCACTCTG	
Alb-4.9kb-F-BC23	atggaggacggTGAGACCTTCACCTTCCACTCTG	
Alb-4.9kb-F-BC24	attgggtgcataTGAGACCTTCACCTTCCACTCTG	
Alb-4.9kb-R	TGGCTCGTTATTAGCCCAGTTGATAGC	

**Table S3.** The primers utilized to detect large deletions in Figure 1C.

Primer	Sequence	Length
Alb-4.7kb-F-BC1	aacaccttcttTGTGGGCAAAAACCACAGTA	4727 bp
Alb-4.7kb-F-BC2	aaccgtccaccTGTGGGCAAAAACCACAGTA	
Alb-4.7kb-F-BC3	aagcggtataTGTGGGCAAAAACCACAGTA	
Alb-4.7kb-F-BC4	aattccgcgctTGTGGGCAAAAACCACAGTA	
Alb-4.7kb-F-BC5	acctcctgtaaTGTGGGCAAAAACCACAGTA	
Alb-4.7kb-F-BC6	acggaaccagcTGTGGGCAAAAACCACAGTA	
Alb-4.7kb-F-BC7	agaagaagagaTGTGGGCAAAAACCACAGTA	
Alb-4.7kb-F-BC8	aggtagtgacttTGTGGGCAAAAACCACAGTA	
Alb-4.7kb-R	ACCTGGCTCGTTATTAGCCCCAGTTGATAG	

**Table S4.** The primers utilized for long-range PCR amplification in Figure 2A.

Primer	Sequence	Length
Alb-HA600-1.5kb-F1	GGAGCAACTGAAGACTGTATGGA	1586 bp
Alb-HA600-1.5kb-R1	AGTGTCAAAGTCAGGGGTCTCACC	
Alb-HA600-1.4kb-F2-BC1	aaacacttctcCGGAGCAACTGAAGACTGTCA	1380 bp
Alb-HA600-1.4kb-F2-BC2	ttaacgaaaccgCGGAGCAACTGAAGACTGTCA	
Alb-HA600-1.4kb-F2-BC3	aaactctgagaaCGGAGCAACTGAAGACTGTCA	
Alb-HA600-1.4kb-F2-BC4	tgtatcaaagacCGGAGCAACTGAAGACTGTCA	
Alb-HA600-1.4kb-F2-BC5	aacgtctccataCGGAGCAACTGAAGACTGTCA	
Alb-HA600-1.4kb-F2-BC6	tcgatttaactgaCGGAGCAACTGAAGACTGTCA	
Alb-HA600-1.4kb-F2-BC7	acaaggtaacccCGGAGCAACTGAAGACTGTCA	
Alb-HA600-1.4kb-F2-BC8	tagcgaacaaccCGGAGCAACTGAAGACTGTCA	
Alb-HA600-1.4kb-F2-BC9	acagcagtttgCGGAGCAACTGAAGACTGTCA	
Alb-HA600-1.4kb-F2-BC10	gttagagacatgtCGGAGCAACTGAAGACTGTCA	
Alb-HA600-1.4kb-F2-BC11	accatagctaagCGGAGCAACTGAAGACTGTCA	
Alb-HA600-1.4kb-F2-BC12	gcactaaccttCGGAGCAACTGAAGACTGTCA	
Alb-HA600-1.4kb-F2-BC13	atgcacgaacagCGGAGCAACTGAAGACTGTCA	
Alb-HA600-1.4kb-F2-BC14	gatatgatgttgcggAGCAACTGAAGACTGTCA	
Alb-HA600-1.4kb-F2-BC15	caaacacttccaCGGAGCAACTGAAGACTGTCA	
Alb-HA600-1.4kb-F2-BC16	cgttccaatacCGGAGCAACTGAAGACTGTCA	
Alb-HA600-1.4kb-R2	AGCCTTCATTATTGCCCTATT	

**Table S5.** The primers employed for nested PCR amplification of long genomic flanking regions in Supplementary Figure S2.

Primer	Sequence	Length
Alb-HA85-0.5kb-F1	Acaacagatgtcagagagccgtc	499 bp
Alb-HA85-0.5kb-R1	Cagggcttaactcccttgctctgg	
Alb-HA85-332bp-F2-BC1	acgccacgttAGCAATGCAAGGCACGTACG	332 bp
Alb-HA85-332bp-F2-BC2	cgactagaccAGCAATGCAAGGCACGTACG	
Alb-HA85-332bp-F2-BC3	cagtgaccagAGCAATGCAAGGCACGTACG	
Alb-HA85-332bp-F2-BC4	ccaggctttAGCAATGCAAGGCACGTACG	
Alb-HA85-332bp-F2-BC5	tgcgcacactAGCAATGCAAGGCACGTACG	
Alb-HA85-332bp-F2-BC6	agccgtcacaAGCAATGCAAGGCACGTACG	
Alb-HA85-332bp-F2-BC7	gtgcataatccAGCAATGCAAGGCACGTACG	
Alb-HA85-332bp-F2-BC8	accgagccatAGCAATGCAAGGCACGTACG	
Alb-HA85-332bp-F2-BC9	cactctcaggAGCAATGCAAGGCACGTACG	
Alb-HA85-332bp-F2-BC10	gtagtcaatgAGCAATGCAAGGCACGTACG	
Alb-HA85-332bp-F2-BC11	ccgtgtggtaAGCAATGCAAGGCACGTACG	
Alb-HA85-332bp-F2-BC12	gaatcggagacAGCAATGCAAGGCACGTACG	
Alb-HA85-332bp-F2-BC13	gacgcggtaaAGCAATGCAAGGCACGTACG	
Alb-HA85-332bp-F2-BC14	gaacaccacaAGCAATGCAAGGCACGTACG	
Alb-HA85-332bp-F2-BC15	caactcctgaAGCAATGCAAGGCACGTACG	
Alb-HA85-332bp-F2-BC16	cgattacctcAGCAATGCAAGGCACGTACG	
Alb-HA85-332bp-F2-BC17	gaccactatcAGCAATGCAAGGCACGTACG	
Alb-HA85-332bp-F2-BC18	gagacacgttAGCAATGCAAGGCACGTACG	
Alb-HA85-332bp-F2-BC19	gatatgcgttAGCAATGCAAGGCACGTACG	
Alb-HA85-332bp-F2-BC20	gcaacagaggAGCAATGCAAGGCACGTACG	
Alb-HA85-332bp-F2-BC21	gccagacaagAGCAATGCAAGGCACGTACG	
Alb-HA85-332bp-F2-BC22	gctaggatctAGCAATGCAAGGCACGTACG	
Alb-HA85-332bp-F2-BC23	ggagttaccgAGCAATGCAAGGCACGTACG	
Alb-HA85-332bp-F2-BC24	ggtacgtcaAGCAATGCAAGGCACGTACG	
Alb-HA85-332bp-F2-BC25	gtactgacaaAGCAATGCAAGGCACGTACG	
Alb-HA85-332bp-F2-BC26	taacatgaggAGCAATGCAAGGCACGTACG	
Alb-HA85-332bp-F2-BC27	tacaacggatAGCAATGCAAGGCACGTACG	
Alb-HA85-332bp-R2	TATCTACAAATGGAACCCAAACTGATGACC	

**Table S6.** The primers utilized for nested PCR amplification of short genomic flanking regions in **Figure 3.**

Primer	Sequence	Length
qPCR-BDDF8-FL-F	CACGTACGTTACTATGTCA	261bp
qPCR-BDDF8-FL-R	AGTATCTCTGGTGGCACTA	
qPCR-BDDF8-FR-F	CTGTAAGCGGATGCCGGGAG	249bp
qPCR-BDDF8-FR-R	GCTGGTGCTTGTCTGTATGG	
qPCR-BDDF8-RL-F	GCACGTACGTTACTATGTC	283bp
qPCR-BDDF8-RL-R	AAACCTCTGACACATGCAGC	
qPCR-BDDF8-RR-F	CCCAGGTAGTATCTTCTGGT	281bp
qPCR-BDDF8-RR-R	CCAGCTGGTGCCTGTCTGTA	
qPCR-BB-FL-F	CCTATGGCTATGAAGTGCAA	248bp
qPCR-BB-FL-R	GTTGAATACTCATACTCTTC	
qPCR-BB-FR-F	AAGCGGGCAGTGAGCGAAC	248bp
qPCR-BB-FR-R	GGCTCTGTCAAATGGTTAT	
qPCR-BB-RL-F	CACGTACGTTACTATGTCA	277bp
qPCR-BB-RL-R	ACGACAGGTTTCCGACTGG	
qPCR-BB-RR-F	CGCACATTCCCCGAAAAGT	285bp
qPCR-BB-RR-R	TCTCCCTGGTTGGTCTCCT	
qPCR-F8fBBr-junction-F	GCTTGTCTGTAAGCGGATGC	203bp
qPCR-F8fBBr-junction-R	CACTCATTAGGCACCCAGG	
qPCR-F8rBBf-junction-F	GCACAGAAAGAAGCAGGTGGA	227bp
qPCR-F8rBBf-junction-R	CATTTCCCCGAAAAGTGCCA	

**Table S7.** The primers employed for qPCR to correlate with the proportion of different insertion outcomes analyzed based on Nanopore sequencing data in Figure 5.

Primer	Sequence	Length
<b>Forward left junction</b>		
Alb-S516-FL-F-BC1	aacattgagccCGTCATGGGTGTGACTTTT	
Alb-S516-FL-F-BC2	aagtccatccCGTCATGGGTGTGACTTTT	
Alb-S516-FL-F-BC3	accacagattaCGTCATGGGTGTGACTTTT	
Alb-S516-FL-F-BC4	aacaccgttagCGTCATGGGTGTGACTTTT	
Alb-S516-FL-F-BC5	aaccactctaagCGTCATGGGTGTGACTTTT	
Alb-S516-FL-F-BC6	aaccgtatccgtCGTCATGGGTGTGACTTTT	
Alb-S516-FL-F-BC7	aaccttggatggCGTCATGGGTGTGACTTTT	
Alb-S516-FL-F-BC8	aactctctccCGTCATGGGTGTGACTTTT	
Alb-S516-FL-F-BC9	aagaaggtaacgCGTCATGGGTGTGACTTTT	
Alb-S516-FL-F-BC10	aagagtggaaagtCGTCATGGGTGTGACTTTT	
Alb-S516-FL-F-BC11	aaggatactctcCGTCATGGGTGTGACTTTT	
Alb-S516-FL-F-BC12	aagtcacacgccCGTCATGGGTGTGACTTTT	
Alb-S516-FL-HA85-190-R	AAACTCATCAATGTATCTTATCATGTCTG	5.3kb
Alb-S516-FL-HA600-R	CCCAGGGTTGCAGTCAAAC	4.9kb
<b>Forward right junction</b>		
Alb-S516-FR-F-BC1	acgttagataaCCTTGGAAATCTGCCAATA	
Alb-S516-FR-F-BC2	attaacatgccCCTTGGAAATCTGCCAATA	
Alb-S516-FR-F-BC3	catacgaccgcCCTTGGAAATCTGCCAATA	
Alb-S516-FR-F-BC4	aatagcaatcgGCCTTGGAAATCTGCCAATA	
Alb-S516-FR-F-BC5	aattacgagaggGCCTTGGAAATCTGCCAATA	
Alb-S516-FR-F-BC6	acaaccctcagcGCCTTGGAAATCTGCCAATA	
Alb-S516-FR-F-BC7	acaatgacaaggGCCTTGGAAATCTGCCAATA	
Alb-S516-FR-F-BC8	acaggtaataggGCCTTGGAAATCTGCCAATA	
Alb-S516-FR-F-BC9	accacaatgtatGCCTTGGAAATCTGCCAATA	
Alb-S516-FR-F-BC10	accgaacgcccGCCTTGGAAATCTGCCAATA	
Alb-S516-FR-F-BC11	acctccctcgaaGCCTTGGAAATCTGCCAATA	
Alb-S516-FR-F-BC12	acggccatacataGCCTTGGAAATCTGCCAATA	
Alb-S516-FR-HA85-190-R	actctgtcatgtgtatataagtgtg	
Alb-S516-FR-HA600-F-BC1	aaggaggaggtttgactgcaaaggctggg	
Alb-S516-FR-HA600-F-BC2	ctggaaaatgttgactgcaaaggctggg	
Alb-S516-FR-HA600-F-BC3	cttgtgggttgactgcaaaggctggg	
Alb-S516-FR-HA600-F-BC4	tatgcgtgtttgactgcaaaggctggg	
Alb-S516-FR-HA600-R	GTGGGCAGATGACACACTGA	4.1kb
<b>Reverse left junction</b>		
Alb-S516-RL-F-BC1	ccagagcacacCGTCATGGGTGTGACTTTT	
Alb-S516-RL-F-BC2	cgagactattcCGTCATGGGTGTGACTTTT	
Alb-S516-RL-F-BC3	cttgcacgttaaCGTCATGGGTGTGACTTTT	
Alb-S516-RL-F-BC4	acggttctaattcCGTCATGGGTGTGACTTTT	
Alb-S516-RL-F-BC5	actcagccggtaCGTCATGGGTGTGACTTTT	
Alb-S516-RL-F-BC6	actgaggtgagcCGTCATGGGTGTGACTTTT	
Alb-S516-RL-F-BC7	agagcataaggaaCGTCATGGGTGTGACTTTT	
Alb-S516-RL-F-BC8	aggaagagagagCGTCATGGGTGTGACTTTT	
Alb-S516-RL-F-BC9	aggtaaagcgtccCGTCATGGGTGTGACTTTT	
Alb-S516-RL-F-BC10	agtatctgttgcgttcCGTCATGGGTGTGACTTTT	
Alb-S516-RL-F-BC11	agtcttctatcCGTCATGGGTGTGACTTTT	
Alb-S516-RL-F-BC12	ataagactaccCGTCATGGGTGTGACTTTT	
Alb-S516-RL-R	ACACAGACCTTGACAAATTATACTACT	6.1kb
<b>Reverse right junction</b>		
Alb-S516-RR-F-BC1	gagtcgtgttAAATCACAGCCCCATCAACTCC	
Alb-S516-RR-F-BC2	ggcacccgttaAAATCACAGCCCCATCAACTCC	
Alb-S516-RR-F-BC3	gtcgtcatgtcAAATCACAGCCCCATCAACTCC	
Alb-S516-RR-F-BC4	atctccaaggtaAAATCACAGCCCCATCAACTCC	
Alb-S516-RR-F-BC5	atggagatgttAAATCACAGCCCCATCAACTCC	
Alb-S516-RR-F-BC6	attgagtcttccAAATCACAGCCCCATCAACTCC	
Alb-S516-RR-F-BC7	caacgttagtaagAAATCACAGCCCCATCAACTCC	
Alb-S516-RR-F-BC8	cacattcattggAAATCACAGCCCCATCAACTCC	
Alb-S516-RR-F-BC9	cacttcggactAAATCACAGCCCCATCAACTCC	
Alb-S516-RR-F-BC10	cagagcaaccatAAATCACAGCCCCATCAACTCC	
Alb-S516-RR-F-BC11	caggttgcgttAAATCACAGCCCCATCAACTCC	
Alb-S516-RR-F-BC12	catcaagaacggAAATCACAGCCCCATCAACTCC	
Alb-S516-RR-R	ATTCAAGAATTCTCGTAATGTTGAAGTATT	

**Table S8.** The primers utilized to distinguish NHEJ and HDR in Figure 6.

Primer	Sequence	Length
Alb-HA600-1.8kb-F1	CCTTAAACTGTGGCCTCACATTCC	1832 bp
Alb-HA600-1.8kb-R1	TAC TTGGTGGGCAGATGACACACT	
Alb-HA600-1.4kb-F2	GGAGCAACTGAAGACTGTCATGG	1384bp
Alb-HA600-1.4kb-R2	AAGCCTTCATTATTGCCCTATTT	

**Table S9.** The primers utilized to detect the insertion of donor plasmid at a circular stage (with no sgDocut).