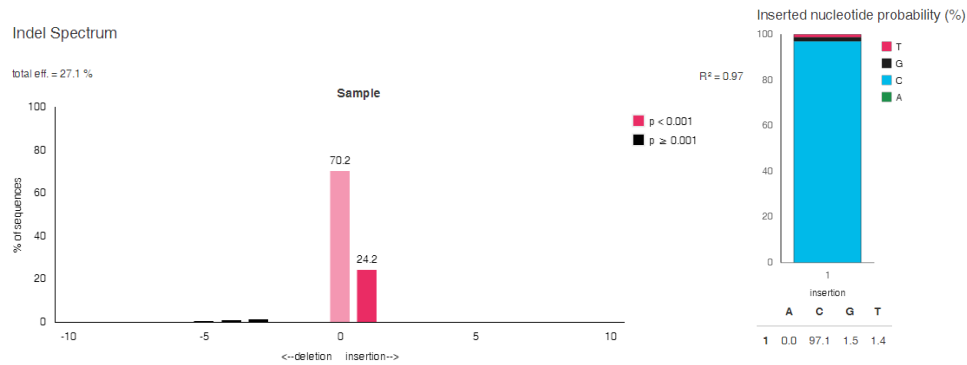
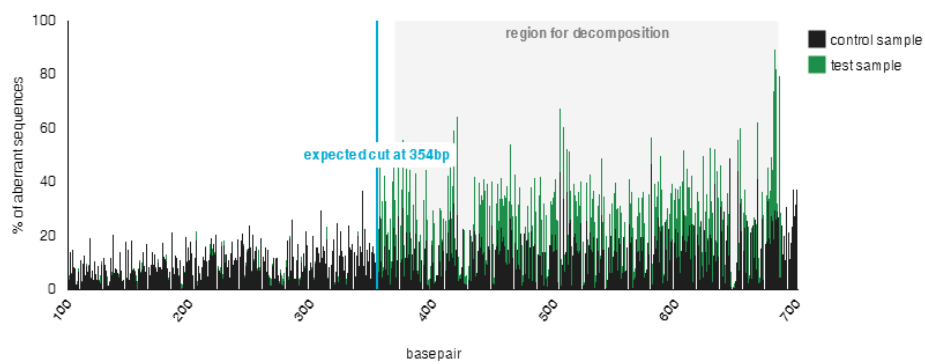


Supplementary Data:

gGGTA1 F2/R2



Quality control - Aberrant sequence signal



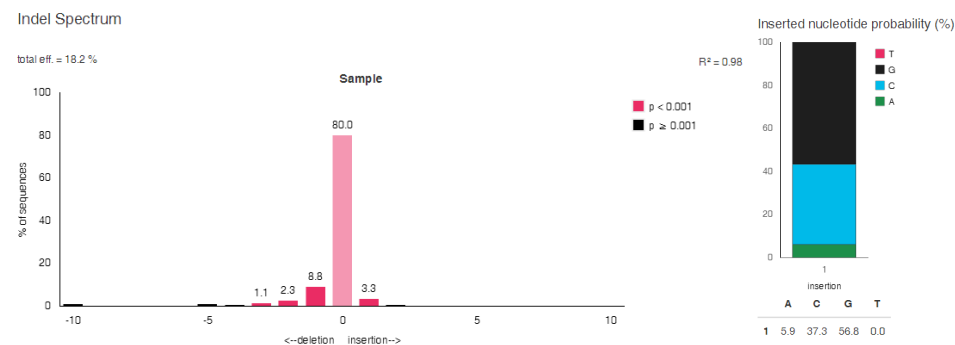
Alignment - local pairwise alignment score: 233.0

```
ctrl align: -----ATAGAGCTGGGTCCTCTGCGTTCTTTAAAGTGTTTGAGATCAAGTCCGAGAAGAGGTGGCAAGACATCAGCATGATGCGCATGAAGACCATC
GGGGAGCACATCCTGGCCACATCCAGCACGAGGTGGACTTCTCTTCTGCATGGACGTGGATCAGGTCTTCCAAAACAACTTGGGGTGGAGACCCTGGGCCAGTCGGTGGCTCAGC
TACAGGCCTGGTGGTACAAGGCACATCCTGACNAG

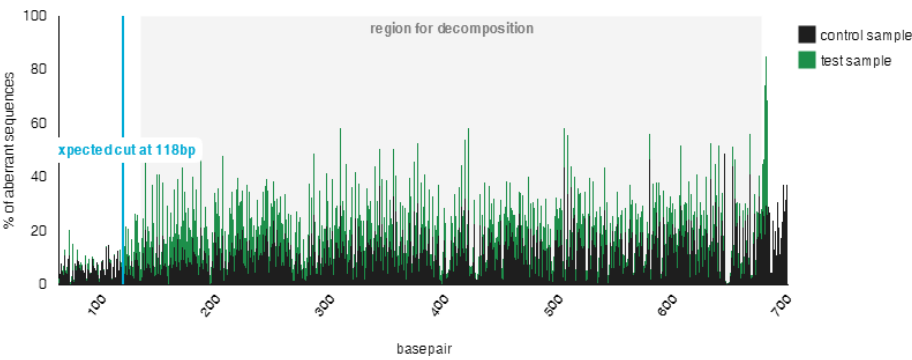
edit align:  CNGGATGCCTTTGATAGAGCTGGGTCCTCTGCGTTCTTTAAAGTGTTTGAGATCAAGTCCGAGAAGAGGTGGCAAGACATCAGCATGATGCGCATGAAGACCAT
CGGGGAGCACATCCTGGCCACATCCAGCACGAGGTGGACTTCTCTTCTGCATGGACGTGGATCAGGTCTTCCAAAACAACTTGGGGTGGAGACCCTGGGCCAGTCGGTGGCTCAG
CTACAGGCCTGGTGGTACAAGGC-----
```

(a)

gGGTA1 F3/R3



Quality control - Aberrant sequence signal

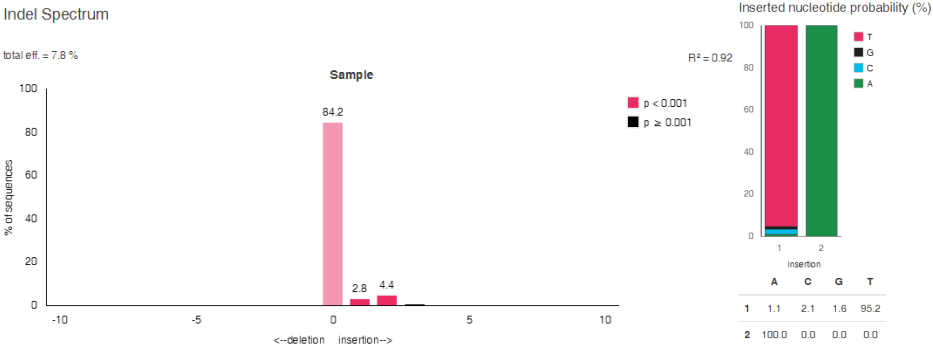


Alignment - local pairwise alignment score: 33.0

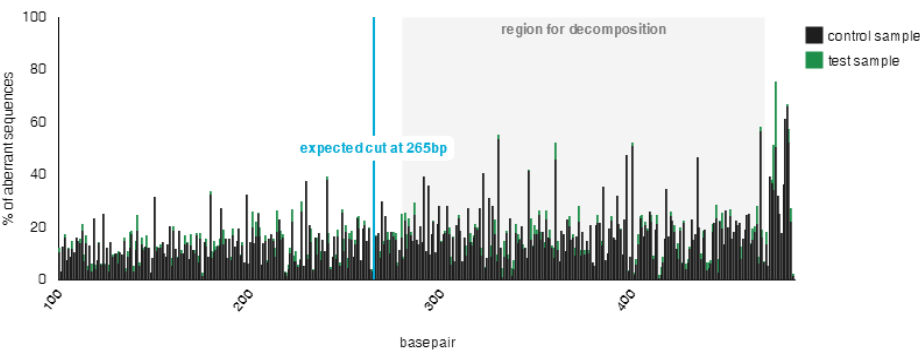
```
ctrl align: -----TTTTACATCATGGTGGATGATATCTCCAGGATGCCTTTGATAGAGCTGG
edit align: TGGCCACAAAGTCATCTTTTACATCATGGTGGATGATATCTCCAGGATG-----
```

(b)

gCMAH F1/R1



Quality control - Aberrant sequence signal

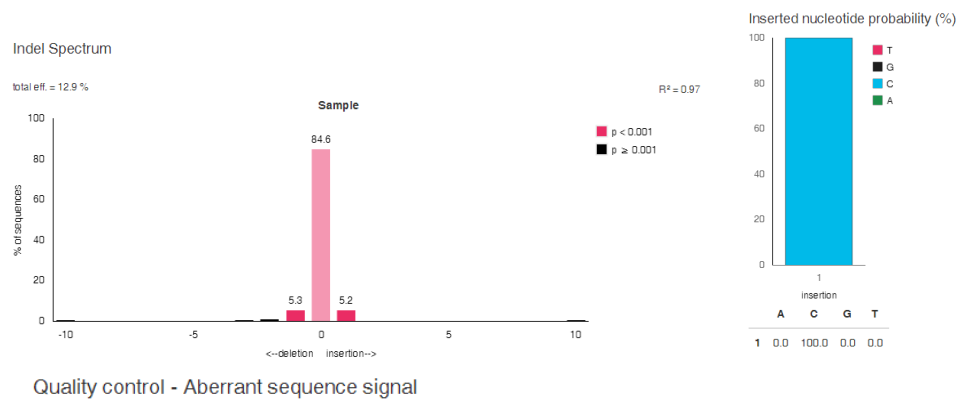


Alignment - local pairwise alignment score: 151.0

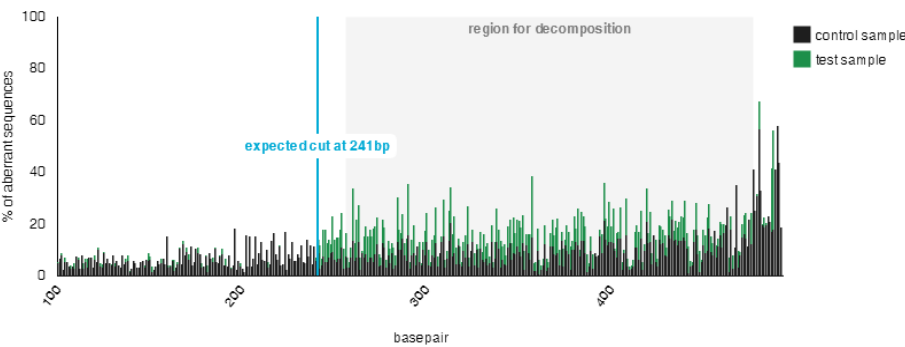
```
ctrl align: -GGCTTGCTGCTAACCAGCCAGTTCCTTNTTCTGGCTGGTAATGATCCGATCATCTGAATCTCACTGTCTTCCAACAGATCACGTACCTTACTCACGCCNGC
ATGGACCTCAAGCTGGGNNACAAGAGNATGGTGTTCGANCCTTGGTTAATCG
edit align: TGGCTTGCTGCTAACCAGCCAGTTCCTTNTTCTGGCTGGTAATGATCCGATCATCTGAATCTCACTGTCTTCCAACANATCACGTACCTTACTCACGCCCTG
CATGGACCTCAAGCTGGGNNACAANAGNATGGTGTTCGANCCTTGGTTAATC-
```

(c)

gCMAH F2/R2



Quality control - Aberrant sequence signal



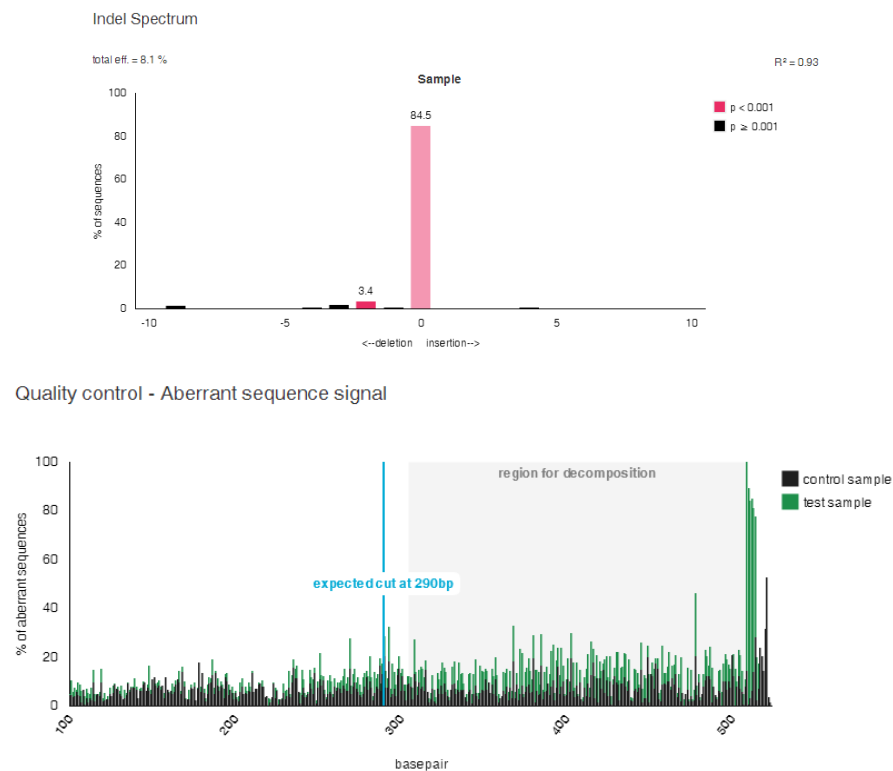
Alignment - local pairwise alignment score: 132.0

```
ctrl align: -TCCTGTTGTGCCTCTCACCTGCCGAAGCTGCCAATCTCAAGGAAGGAATCAATTTTGTTCGAAATAAGAGCACTGGCAAGGATTACATCTTATTTAAGAATAA
GAGCCGCCTGAAGGCATGTAAGAACATGTG

edit align: ATCCTGTTGTGCCTCTCACCTGCCGAAGCTGCCAATCTCAAGGAAGGAATCAATTTTGTTCGAAATAAGAGCACTGGCAAGGATTACATCTTATTTAAGAATA
AGAGCCGCCTGAAGGCATGTAAGAACATGT-
```

(d)

gβ4GalNT2 F1/R1



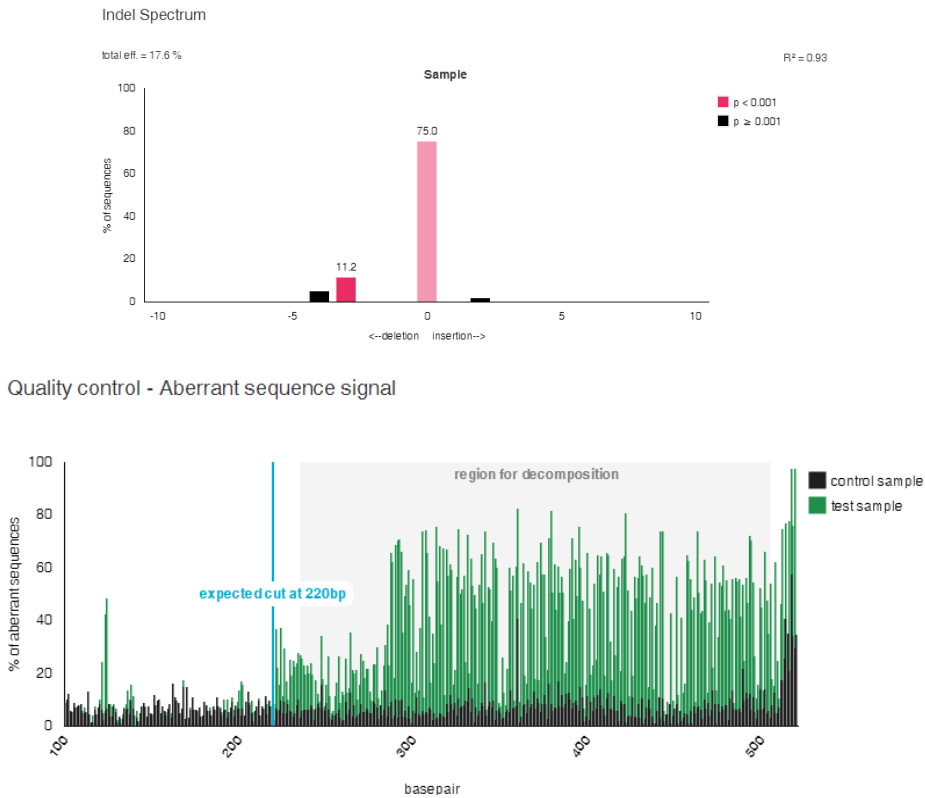
Alignment - local pairwise alignment score: 209.0

ctrl align: --ATCAATTTTGATACGTAGTGTACNAAACAGGTTTGACTTGCATTTTGTCTCAAGTTGCTATTCCCATCTATGTCGCACAATGAAATCTTTTAAACATACTC
AGAAAAGATTTTAACAGCGTTTGCTCTCTTGTGTCCCAACAGCCCTAGATGTCTGTGATCCTCAAGATATNGATGGTGCTTTTGGTCTGAGCGTTGGACTCTTTATG

edit align: AAATCAATTTTGATACGTAGTGTACNAAACAGGTTTGACTTGCATTTTGTCTCAAGTTGCTATTCCCATCTATGTCGCACAATGAAATCTTTTAAACATACT
CAGAAAAGATTTTAACAGCGTTTGCTCTCTTGTGTCCCAACAGCCCTAGATGTCTGTGATCCTCAAGATATNGATGGTGCTTTTGGTCTGAGCGTTGGACTCTTTA--

(e)

gβ4GalNT2 F2/R2



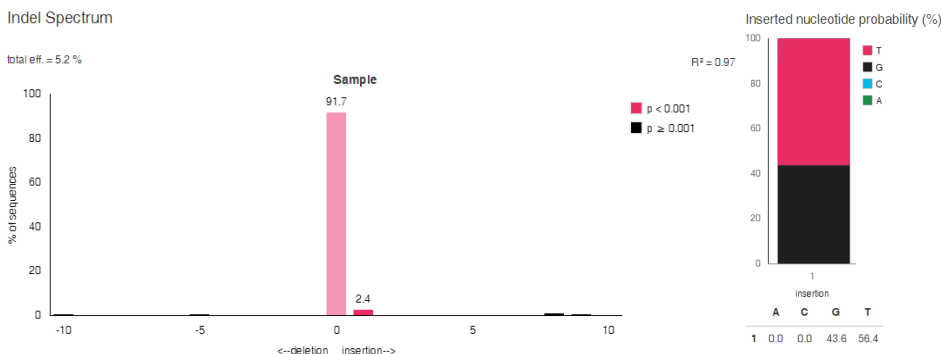
Alignment - local pairwise alignment score: 111.0

ctrl align: CACGGATCTACTGAGTTTACAGTCATCCATTTGTAGACTTTTGCTACACCACCAAAGTATAGCATCTGAGATTAAATATTAATCTCCAAACCTTAGGCCCCC
TCACTTGC-

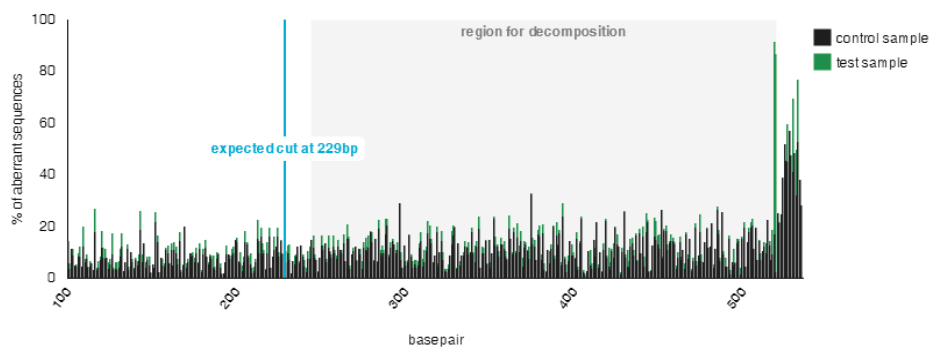
edit align: -ACGGATCTACTGAGTTTACAGTCATCCATTTGTAGACTTTTGCTACACCACCAAAGTATAGCATCTGAGATTAAATATTAATCTCCAAACCTTAGGCCCCC
CTCACTTGCA

(f)

gvWF F1/R1



Quality control - Aberrant sequence signal



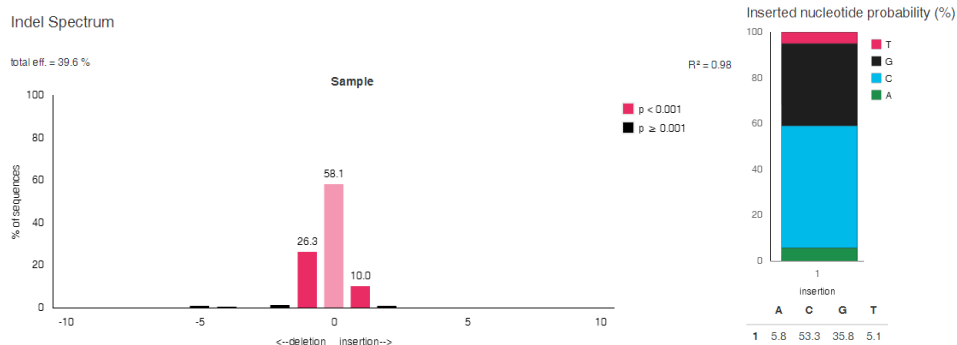
Alignment - local pairwise alignment score: 120.0

```
ctrl align: -AGAGTGCCCTCGGTGTTGCGCCGCTGCCACCCCTGGTGGACCCGAGCCTTTCGTGGCCCTGTGTGAGAAGATGCTGTGTCCATGTGCCAGGGGCTGCAGTG
CCCGTGCCCCGCGCTCCT

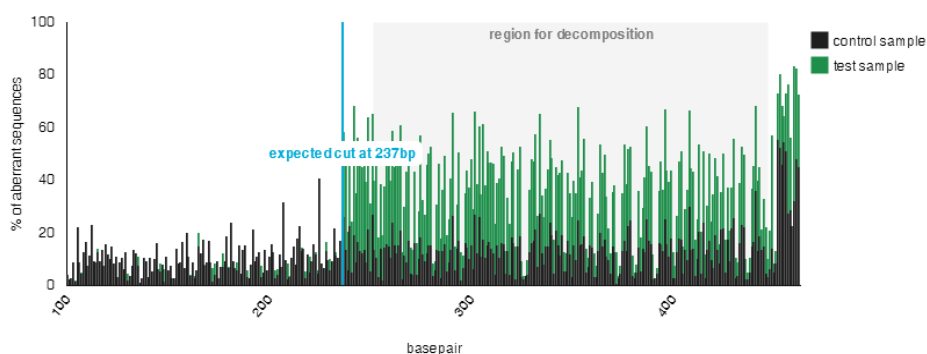
edit align: AAGAGTGCCCTCGGTGTTGCGCCGCTGCCACCCCTGGTGGACCCGAGCCTTTCGTGGCCCTGTGTGAGAAGATGCTGTGTCCATGTGCCAGGGGCTGCAGT
GCCCGTGCCCCGCGCTCC-
```

(g)

gvWF F3/R3



Quality control - Aberrant sequence signal



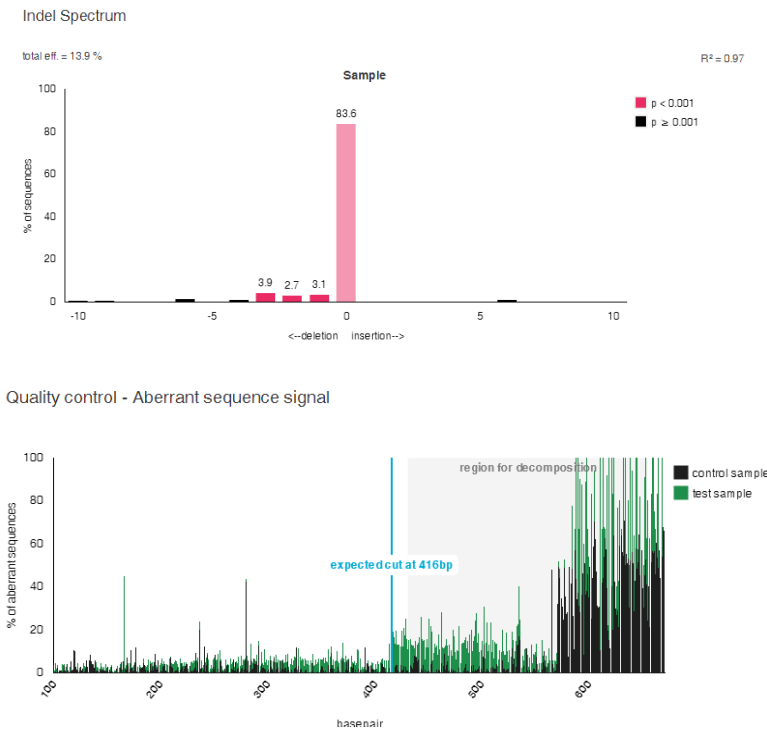
Alignment- local pairwise alignment score: 123.0

```
ctrl align: CTTTTGCAAGACGTGCTGAGCTGATGGTCACCCACGGGGATTCTGAGGTTATGGGATGAGTAAGGCTGATGACAAGGTTGAGTCTTGGCTTTGATGCCCTTGA
CCCANAGGGACAGCTCCTTGACNAC----

edit align: ----TCGCAAGACGTGCTGAGCTGATGGTCACCCACGGGGATTCTGAGGTTATGGGATGAGTAAGGCTGATGACAAGGTTGAGTCTTGGCTTTGATGCCCTTG
ACCCAGAGGGACAGCTCCTTGACGACGGCC
```

(h)

gASGR1 F1/R1



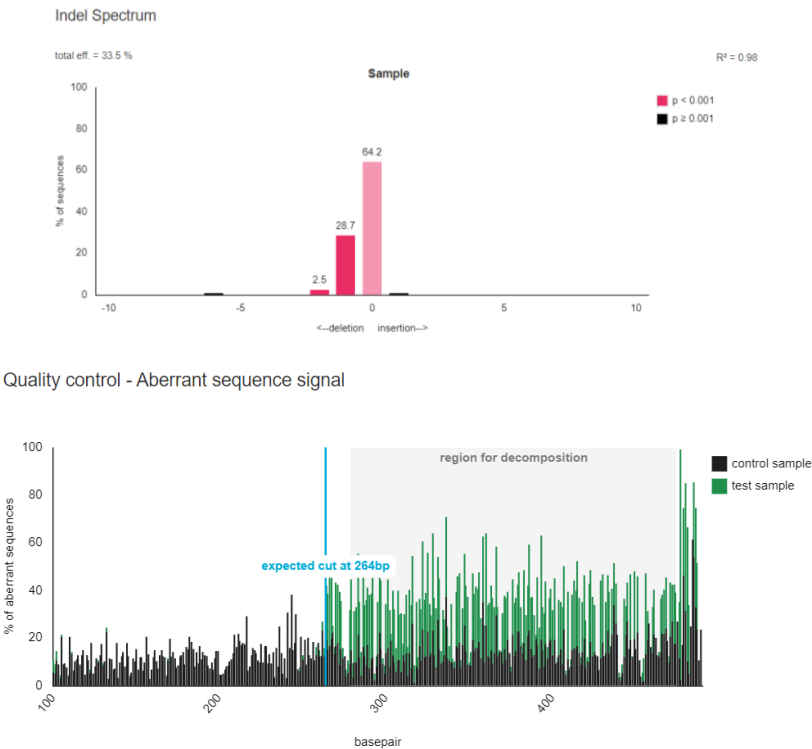
Alignment - local pairwise alignment score: 306.0

ctrl align: --GTGCTTTTCCTTCTTCTTTCCTTCCCTTCTCTCCCTCCCTCCTTCTTTTGGCTGTGTCTACATGCAGAAATCTTGGGCTAGGGATTGAA
CCCTTGCCATGGCAATGCTGGCTCTTTAACCCACCGAGCCACCAGGGAATCCCATGTTTCTTAATCTATAAGGTTCTGCTCGTCTACAAGAGGAGGCCAGGATGCTCTCTCTCA
GGACCCAGAGCTGCCCTGCCCAGGTCCCCTCTGTCCCTGAGGGCGTGACGCCCTCTCTCTTGACAGGGCCACCTCTCAACAGTCA

edit align: TCGTGCTTTTCCTTCTTCTTTCCTTCCCTTCTCTCCCTCCCTCCTTCTTTTGGCTGTGTCTACATGCAGAAATCTTGGGCTAGGGATTGA
ACCCTTGCCATGGCAATGCTGGCTCTTTAACCCACCGAGCCACCAGGGAATCCCATGTTTCTTAATCTATAAGGTTCTGCTCGTCTACAAGAGGAGGCCAGGATGCTCTCTCTCT
AGGACCCAGAGCTGCCCTGCCCAGGTCCCCTCTGTCCCTGAGGGCGTGACGCCCTCTCTCTTGACAGGGCCACCTCTCAACAGT --

(i)

gASGR1 F2/R2



Alignment - local pairwise alignment score: 154.0

```
ctrl align: --TGC GGC G C C C C G T G G C T C T G C C C C T C C A A C T G C G C C C C T C C C C A G T G G G C G G G T C C A G G G T G C C C A G G C T G C T C C C C T G G C T G A G G C T C T G G C C C C T G G G C C C C G T C C G T C T G T C T C T T T A G G A A C T G G A G A C C C G A N C A G C C G G A T G A
```

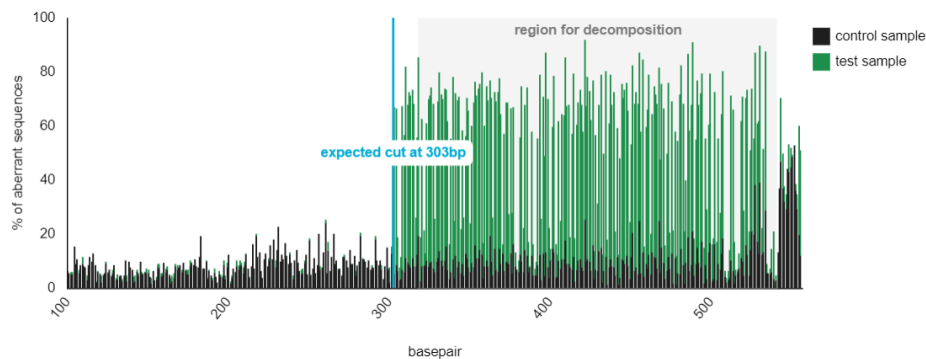
```
edit align: T G T G C G G C G C C C C G T G G C T C T G C C C C T C C A A C T G C G C C C C T C C C C A G T G G G C G G G T C C A G G G T G C C C A G G C T G C T C C C C T G G C T G A G G C T C T G G C C C C C T G G G C C C C G T C C G T C T G T C T C T T A G G A A C T G G A G A C C C G A N C A G C C G G A T --
```

(j)

Figure S1. The indel spectrum and inserted nucleotide probability results, alignment and decomposition quality controls for the other CRISPR/Cas9 genetic constructs containing gRNA tested for disruption of the porcine genes. Results obtained after use the plasmids with: (a) gGGTA1 F2/R2; (b) gGGTA1 F3/R3; (c) gCMAH F1/R1; (d) gCMAH F2/R2; (e) gβ4GalNT2 F1/R1; (f) gβ4GalNT2 F2/R2; (g) gvWF F1/R1; (h) gvWF F3/R3; (i) gASGR1 F1/R1; (j) gASGR1 F2/R2.

gGGTA1 F1/R1

Quality control - Aberrant sequence signal



Alignment - local pairwise alignment score: 195.0

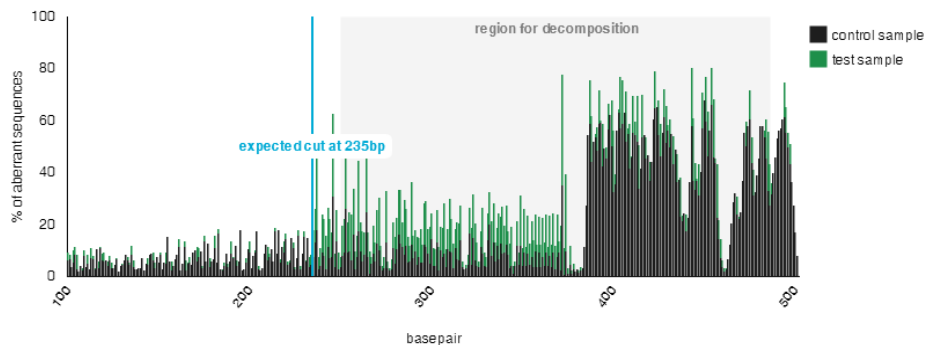
```
ctrl align: G A T A C A T T G A G C A T T A C T T G G A G G A G T T C T T A A T A T C T G C A A A T A C A T C T T C A T G G T T G G C C A C A A A G T C A T C T T T T A C A T C A T G G T G G A T G A T A T C C A G G A T G C C T T T G A T A G A G C T G G G T C C T G C G T T C C T T T A A A G T G T T T G A G A T C A A G T C C G A G A A G A G G T G G C A A G A C A T C A G C A T G A T G C G C A
```

```
edit align: G A T A C A T T G A G C A T T A C T T G G A G G A G T T C T T A A T A T C T G C A A A T A C A T C T T C A T G G T T G G C C A C A A A G T C A T C T T T T A C A T C A T G G T G G A T G A T A T C C A G A T G C C T T T G A T A G A G C T G G G T C C T G C G T T C C T T T A A A G T G T T T G A G A T C A A G T C C G A G A A G A G G T G G C A A G A C A T C A G C A T G A T G C G C A
```

(a)

gCMAH F3/R3

Quality control - Aberrant sequence signal



Alignment - local pairwise alignment score: 123.0

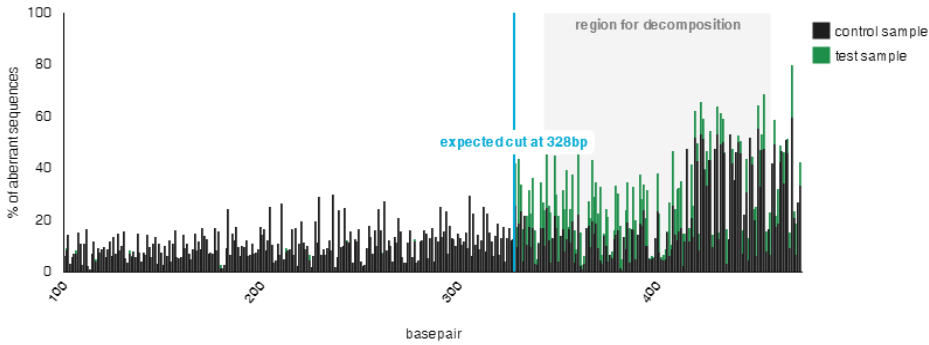
```
ctrl align: ---CATGCATTTCTGTCTTAGCGATGCTTTTAAAAAGTCATTTTTGGTTGATTATCCAGATTTGTCCACCTTTGCTTCTAGTTGTAGAAAAGGATGAAGAAAATGGAGTTTGTCTTAGAACTAAATC
```

edit align: GAGCCATGCATTTCTGTCTTAGCGATGCTTTTTAAAGTCATTTTTTGGTTGATTATCCAGATTGTCCACCTTTGCTTCTAGTTGTAGAAAAGGATGAAGAA
AATGGAGTTTTGCTTCTAGAACTA----

(b)

gβ4GalNT2 F3/R3

Quality control - Aberrant sequence signal



Alignment - local pairwise alignment score: 212.0

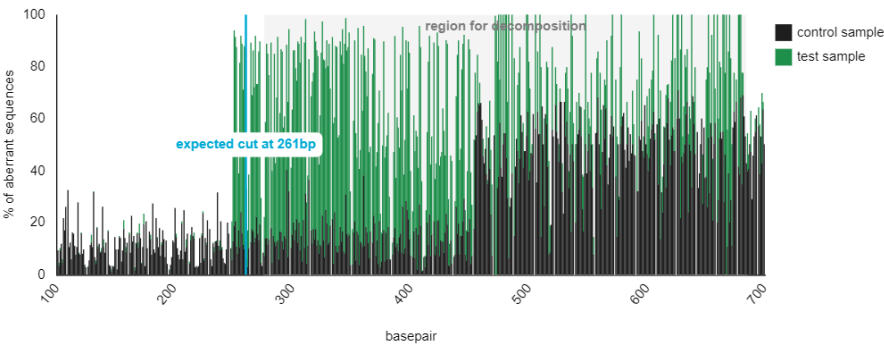
ctrl align: TGCTGGCCGTCCTGGGTATGTGCCTCTCTGCATTTAGGCTTTCTACCTCCTTTATCCTAGGTCACCTGACAGCTTCTCTGGGGACACTGAACACCCTTGCTGA
CGTCCCAGACAATGTGGTGAAGGGCANAGGCCAGAAGCAGCTGAACATTTTGACCAGTAGCCGGGAGCTTTTGAATTTTCATCTCCAGCATGTGACATACACGAGCACAGAGTACC --

edit align: -----GTCCTGGGTATGTGCCTCTCTGCATTTAGGCTTTCTACCTCCTTTATCCTAGGTCACCTGACAGCTTCTCTGGGGACACTGAACACCCTTGCTG
ACGTCCCAGACAATGTGGTGAAGGGCANAGGCCAGAAGCAGCTGAACATTTTGACCAGTAGCCGGGAGCTTTTGAATTTTCATCTCCAGCATGTGACATACACGAGCACAGAGTACCA
CCTCCAC

(c)

gvWF F2/R2

Quality control - Aberrant sequence signal



Alignment - local pairwise alignment score: 150.0

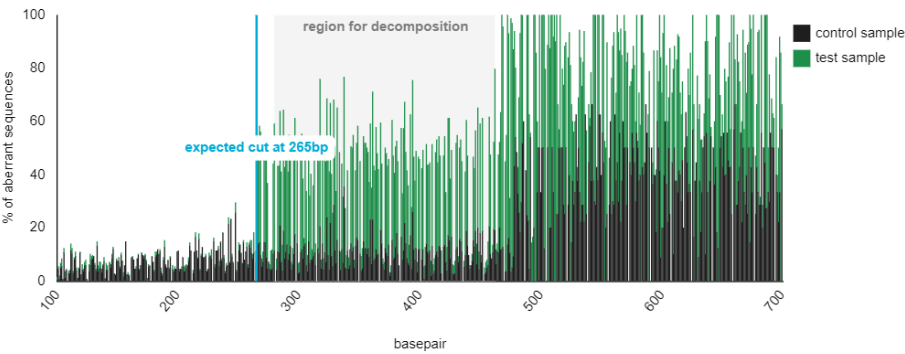
ctrl align: -TGGCCTCTGGGAACCTGAAGATGAGGGGGGAGACACTCAGCGGTGGGGGGAGGCAGGCTCTGAGCACCACATGGCTTGTGAGATGCTGCCTGAAGGGGGCGC
TGGGGAGACTCCTGATTTTTTCATTGCAGGGCCANACTGCCCGCGGGCA

edit align: ATGGCCTCTGGGAACCTGAAGATGAGGGGGGAGACACTCAGCGGTGGGGGGAGGCAGGCTCTGAGCACCACATGGCTTGTGAGATGCTGCCTGAAGGGGGCG
CTGGGGAGACTCCTGATTTTTTCATTGCAGGGCCAGACTGCCCGCGGGN-

(d)

gASGR1 F3/R3

Quality control - Aberrant sequence signal



Alignment - local pairwise alignment score: 155.0

```
ctrl align: GTGCGGCGCCCCGTGGCTCTGCCCTCCAACCTGCGCCCCCTCCCAAGTGGGCGGGTCCAGGGGTGCCAGGCTGCTCCCTCGGCTGAGGCTCTGGCCCCCTGG
GGCCCCCGTCCGTCTGGTCTCTTTAGGAAGTGGAGACCCGAGCAGCCGGATGA--
```

```
edit align: --GCGGCGCCCCGTGGCTCTGCCCTCCAACCTGCGCCCCCTCCCAAGTGGGCGGGTCCAGGGGTGCCAGGCTGCTCCCTCGGCTGAGGCTCTGGCCCCCTG
GGGCCCCCGTCCGTCTGGTCTCTTTAGGAAGTGGAGACCCGAGCAGCCGGATGACT
```

(e)

Figure S2. The alignment and decomposition quality controls for the CRISPR/Cas9 genetic constructs containing gRNA chosen as the best for the disruption of the porcine genes. Results obtained after use the plasmids with: (a) gGGTA1 F1/R1; (b) gCMAH F3/R3; (c) gβ4GalNT2 F3/R3; (d) gVWF F2/R2; (e) gASGR1 F3/R3.

Detailed results of the insertions and deletions obtained at potential off-target sites. Figure S3 shows the results for the genetic construct containing gGGTA1 F1/R1 excluding site No. 1 are shown in Figure 3.

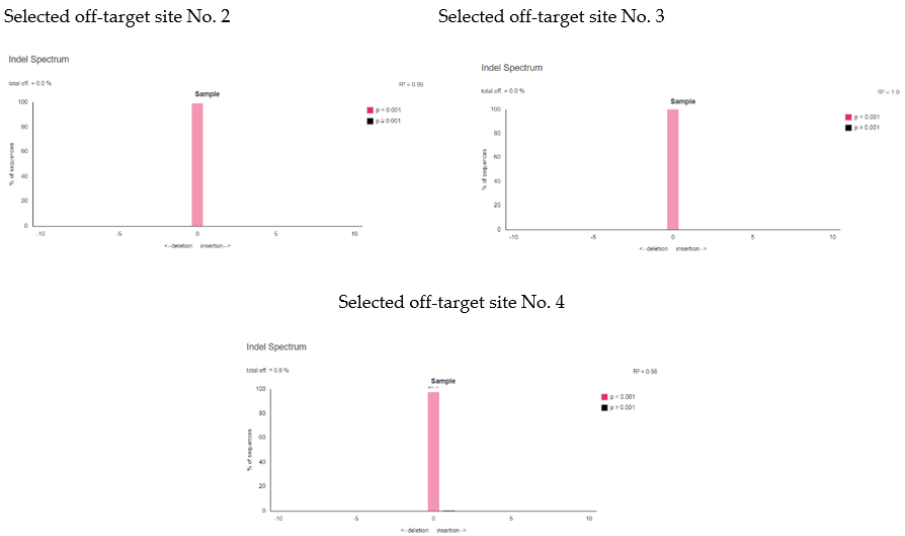
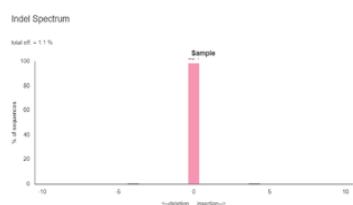


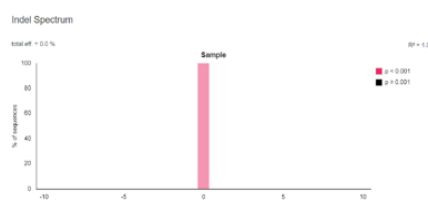
Figure S3. The indel spectrum for the numbers 2–4 off-target loci after the use of CRISPR/Cas9 genetic construct containing gGGTA1 F1/R1 chosen as the best for disruption of porcine *GGTA1* gene.

Figure S4 shows the indel spectrum results for the potential off-target sites for genetic construct containing gCMAH F3/R3.

Selected off-target site No. 5



Selected off-target site No. 6



Selected off-target site No. 7

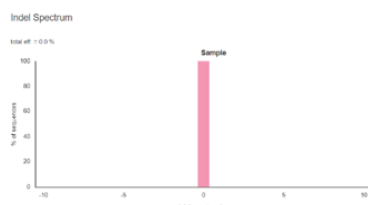
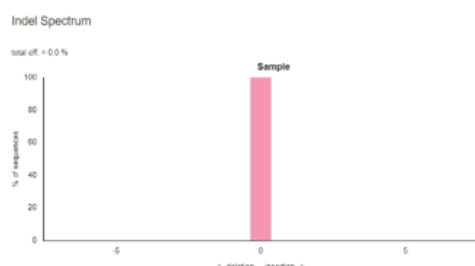


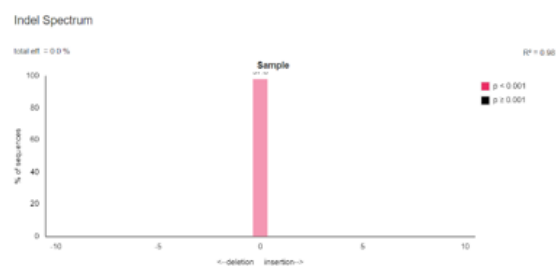
Figure S4. The indel spectrum for the numbers 5–7 off-target loci after the use of CRISPR/Cas9 genetic construct containing gCMAH F3/R3 chosen as the best for disruption of porcine *CMAH* gene.

Figure S5 shows the indel spectrum results for the potential off-target sites for genetic construct containing g β 4GalNT2 F3/R3.

Selected off-target site No. 8



Selected off-target site No. 9



Selected off-target site No. 10

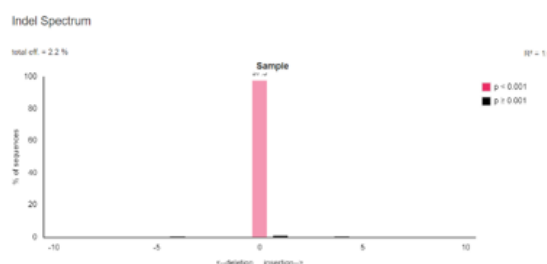
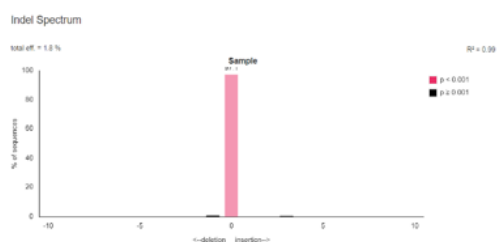


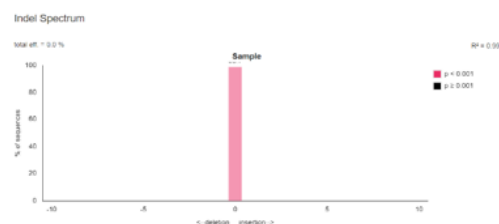
Figure S5. The indel spectrum for the number 8–10 off-target loci after the use of CRISPR/Cas9 genetic construct containing g β 4GalNT2 F3/R3 chosen as the best for disruption of porcine *β 4GalNT2* gene.

Figure S6 shows the indel spectrum results for the potential off-target sites for genetic construct containing gvWF F2/R2.

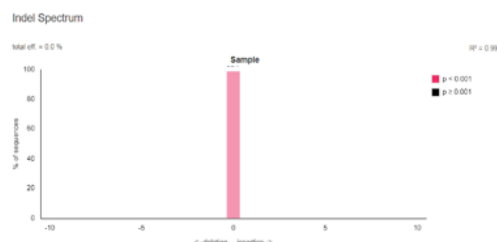
Selected off-target site No. 11



Selected off-target site No. 12



Selected off-target site No. 13



Selected off-target site No. 14

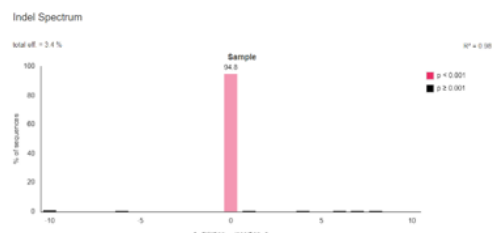
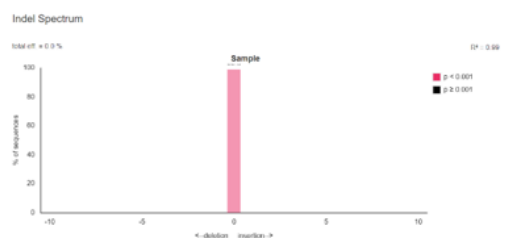


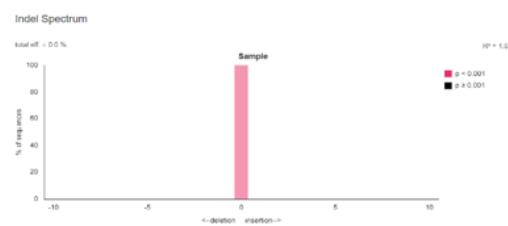
Figure S6. The indel spectrum for the numbers 11–14 off-target loci after the use of CRISPR/Cas9 genetic construct containing *gvWF* F2/R2 chosen as the best for disruption of porcine *vWF* gene.

Figure S7 shows the indel spectrum results for the potential off-target sites for genetic construct containing *gASGR1* F3/R3.

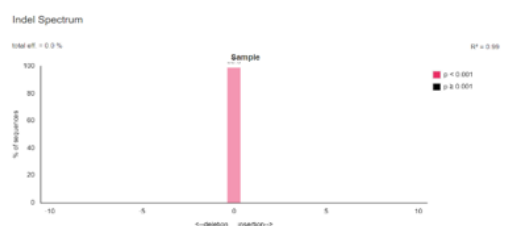
Selected off-target site No. 15



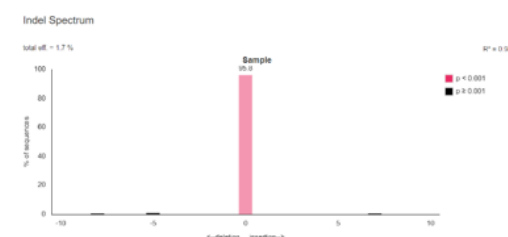
Selected off-target site No. 16



Selected off-target site No. 17



Selected off-target site No. 18



Selected off-target site No. 18

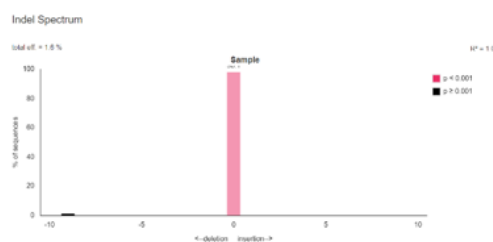


Figure S7. The indel spectrum for the numbers 15–19 off-target loci after the use of CRISPR/Cas9 genetic construct containing *gASGR1* F3/R3 chosen as the best for disruption of porcine *ASGR1* gene.