

György B et al. Allele-specific gene editing prevents deafness in a model of dominant progressive hearing loss

Supplementary Data Set Files

Supplementary Data Set 1. TIDE analysis of all Sanger sequencing samples from Extended Data Fig. 1. SpCas9 only (GFP) was used as a control for analysis (pages 1-96).

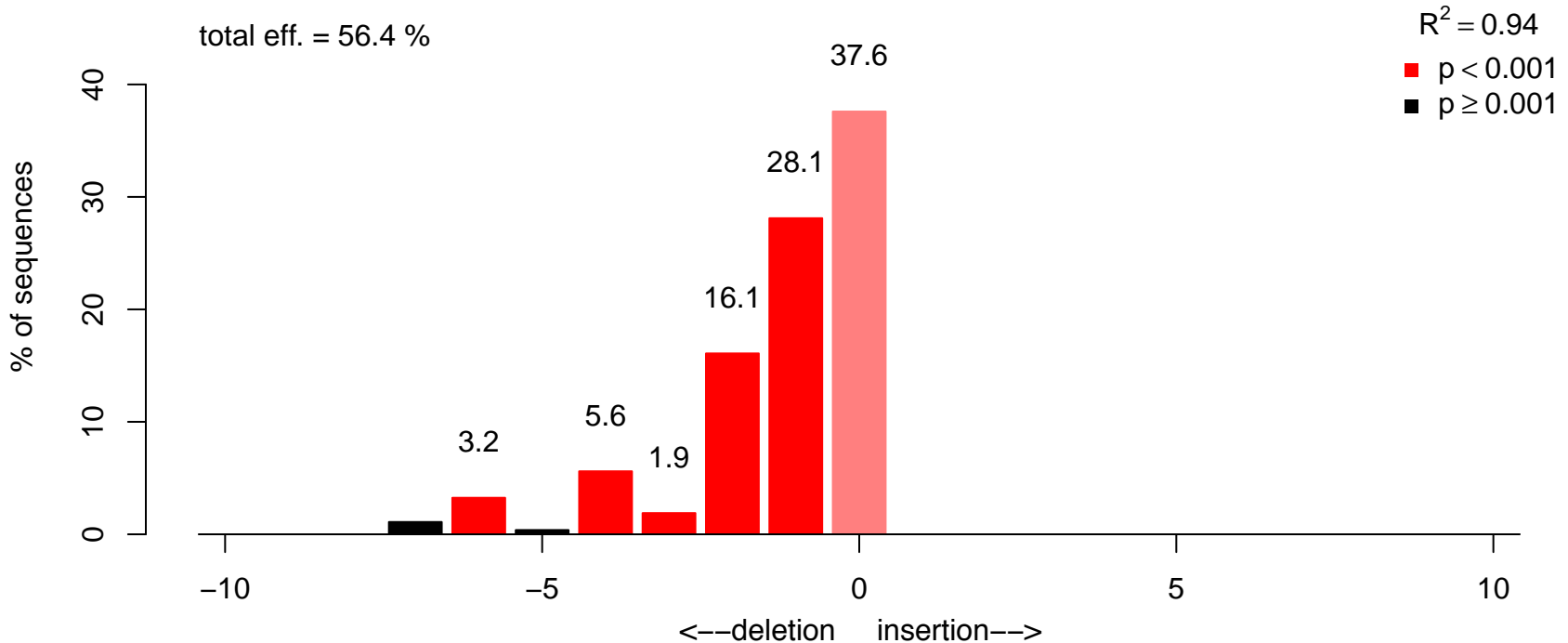
Supplementary Data Set 2. CRISPResso analysis on all samples from Extended Data Fig. 1e. In the case of *Tmc1Bth/WT* samples, reads were segregated to Bth and WT before CRISPResso analysis (pages 97-111).

Supplementary Data Set 3. CRISPResso analysis on all samples from Fig. 1b. In the case of *Tmc1Bth/WT* samples, reads were segregated to Bth and WT before CRISPResso analysis (pages 112-141).

Supplementary Data Set 4. Sequencing result from pBG201 empty vector (pAAVCMV-NLS(SV40)-SaCas9(E782K/N968K/R1015H)-NLS(nucleoplasmin)-3xHA-bGHpA0-U6-BsaI-sgRNA). Plasmid DNA was sequenced by next-generation sequencing using the Plasmid Sequencing Service of the MGH DNA Core (Cambridge, MA, USA) (pages 142-144).

sample: WT/WT cell line, WT gRNA, reverse
guide: GGGTGGGACAGAACATCCCC

total eff. = 56.4 %

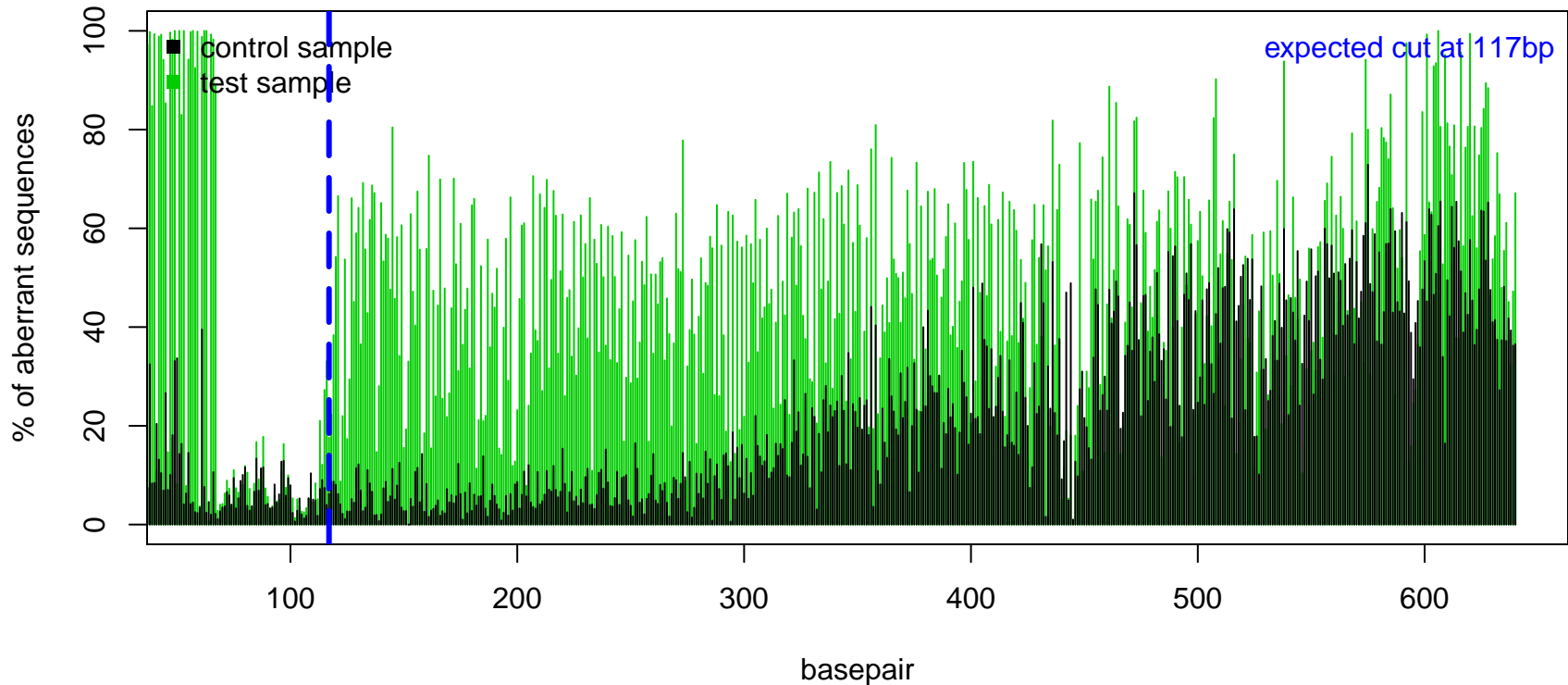


Warning: the spacing between the nucleotides in (one of) sanger sequence file(s) is not constant.

This might indicate for wrongly unannotated or wrongly additional annotated nucleotides.
Decomposition window lower and check the chromatogram for abnormalities.

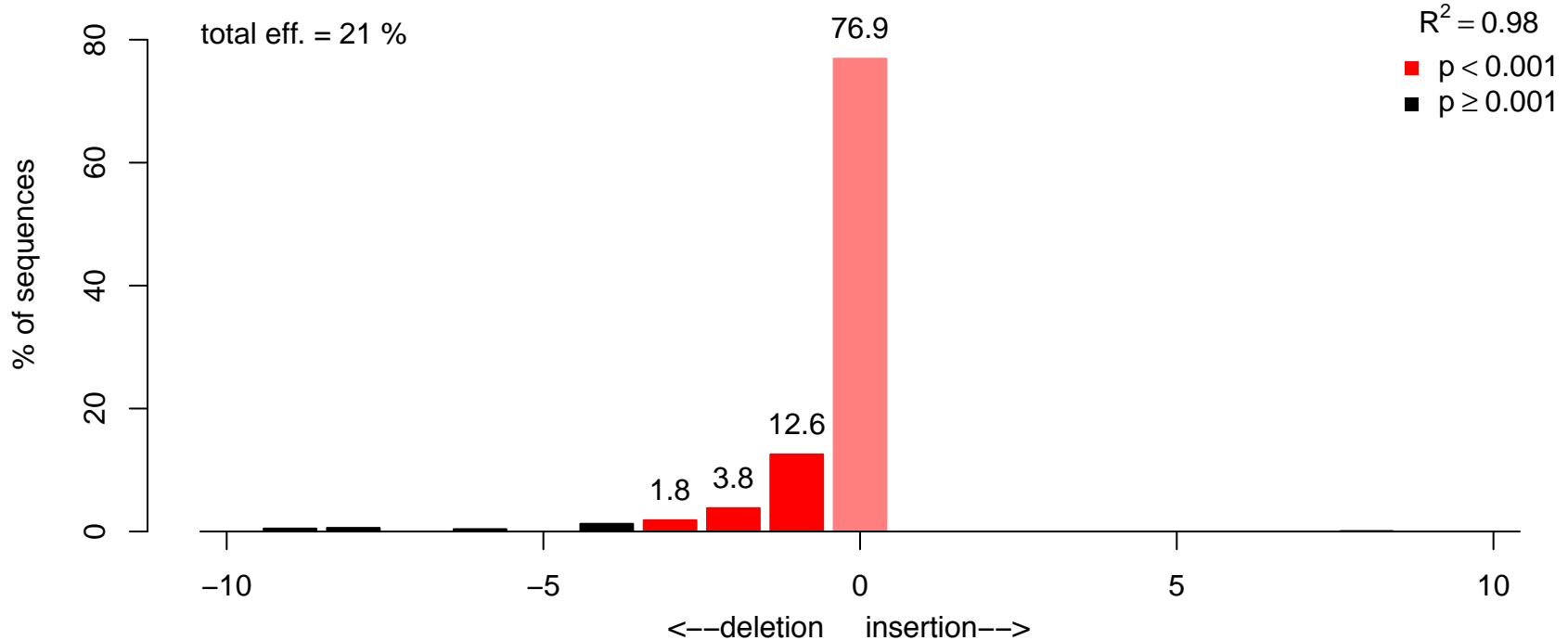
sample: WT/WT cell line, WT gRNA, reverse
guide: GGGTGGGACAGAACATCCCC

region for decomposition



Warning: left boundary of decomposition window was adjusted 132 . It must be at least 5bp plus the maximum indel size downstream of the expected break site

sample: WT/WT cell line, gRNA 1.1, reverse
guide: GGGTGGGACAGAACATCCCC

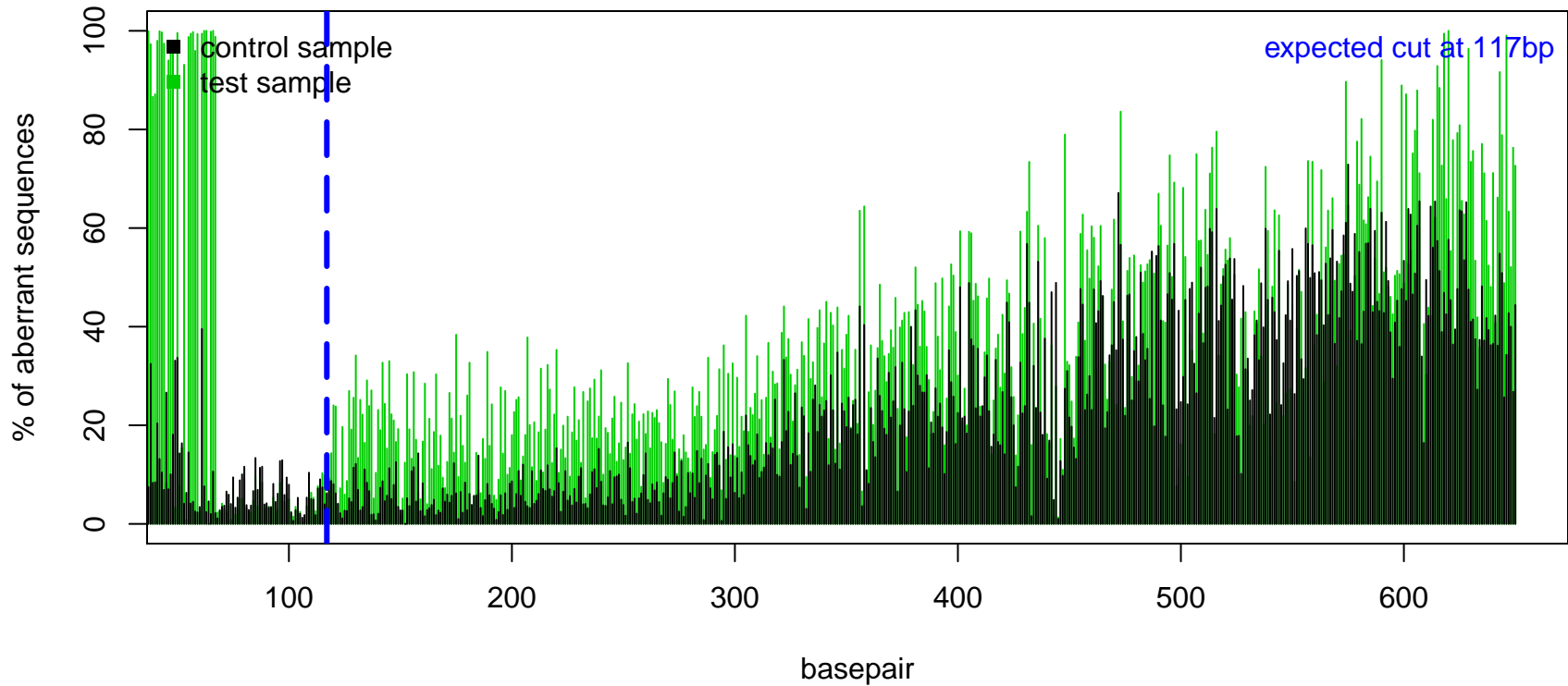


Warning: the spacing between the nucleotides in (one of) sanger sequence file(s) is not constant.

This might indicate for wrongly unannotated or wrongly additional annotated nucleotides.
Decomposition window lower and check the chromatogram for abnormalities.

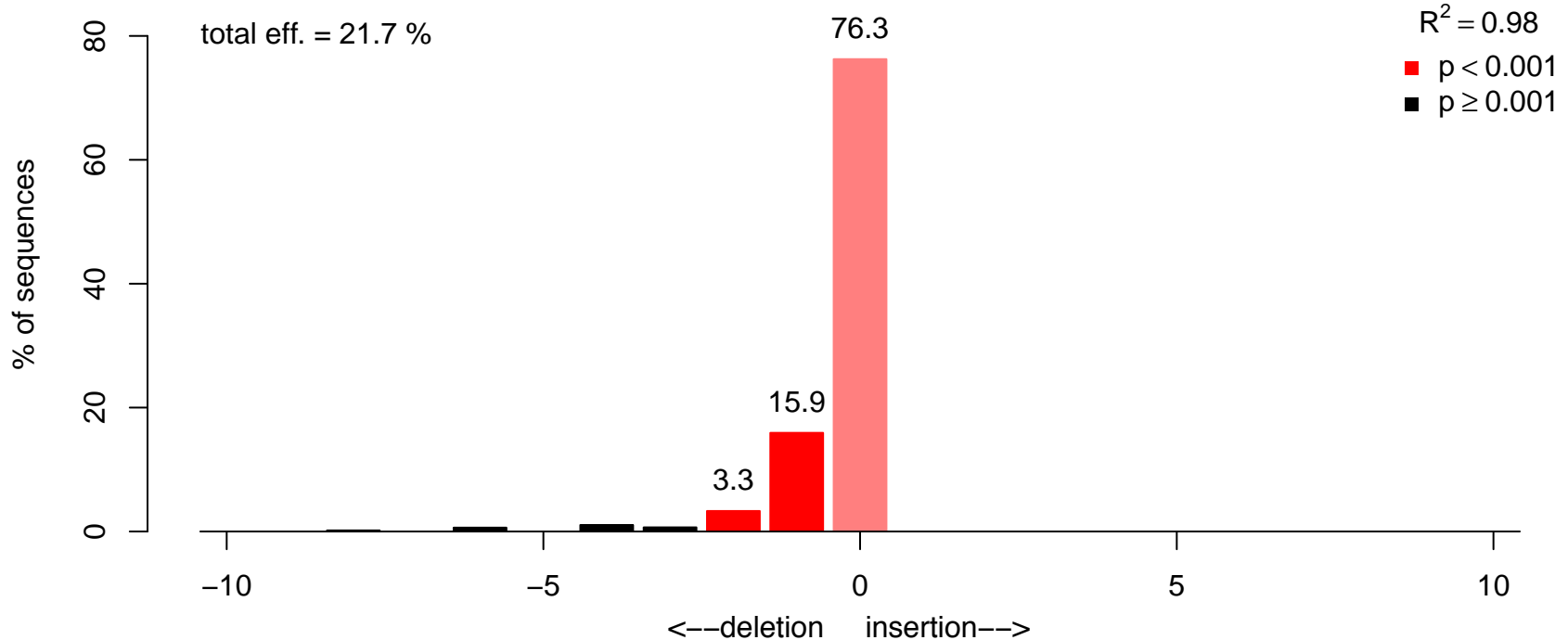
sample: WT/WT cell line, gRNA 1.1, reverse
guide: GGGTGGGACAGAACATCCCC

region for decomposition



Warning: left boundary of decomposition window was adjusted 132 . It must be at least 5bp plus the maximum indel size downstream of the expected break site

sample: WT/WT cell line, gRNA 1.2, reverse
guide: GGGTGGGACAGAACATCCCC

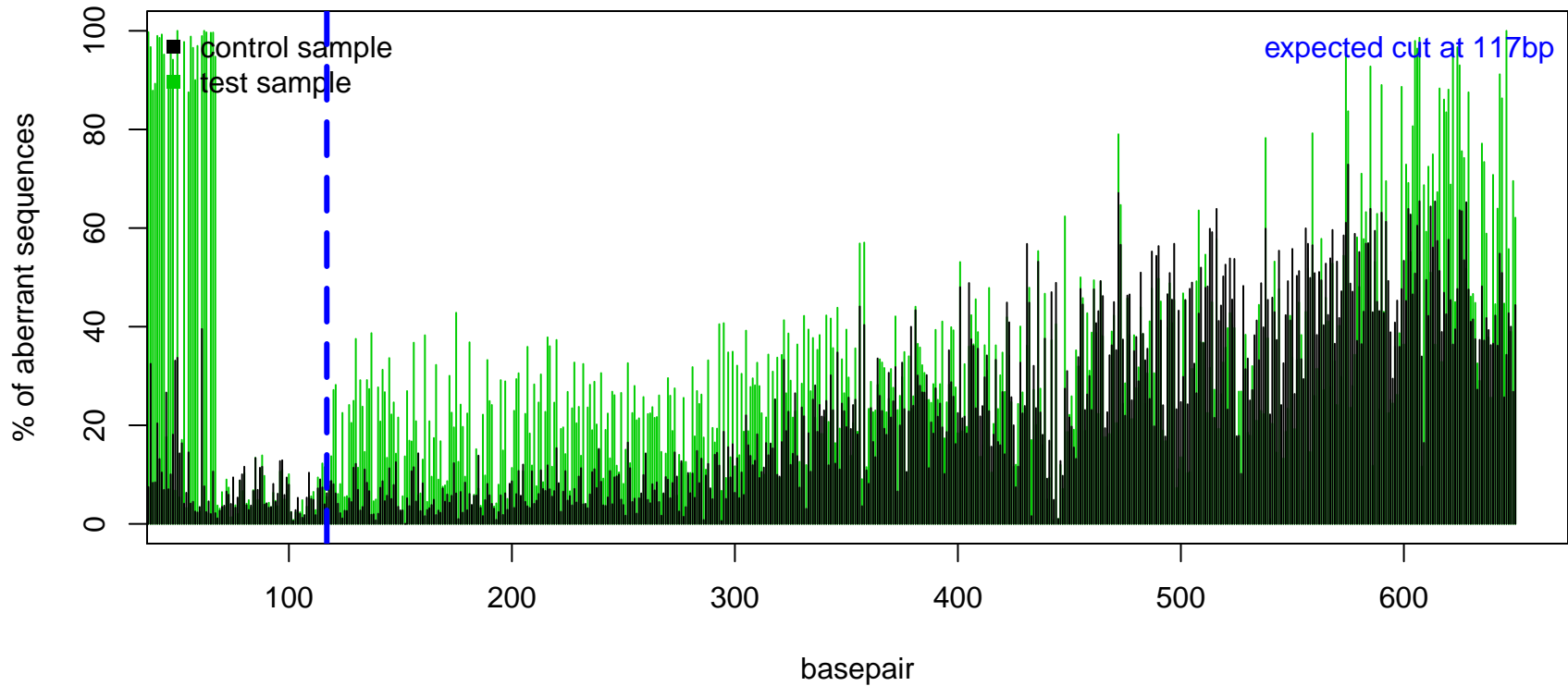


Warning: the spacing between the nucleotides in (one of) sanger sequence file(s) is not constant.

This might indicate for wrongly unannotated or wrongly additional annotated nucleotides.
Decomposition window lower and check the chromatogram for abnormalities.

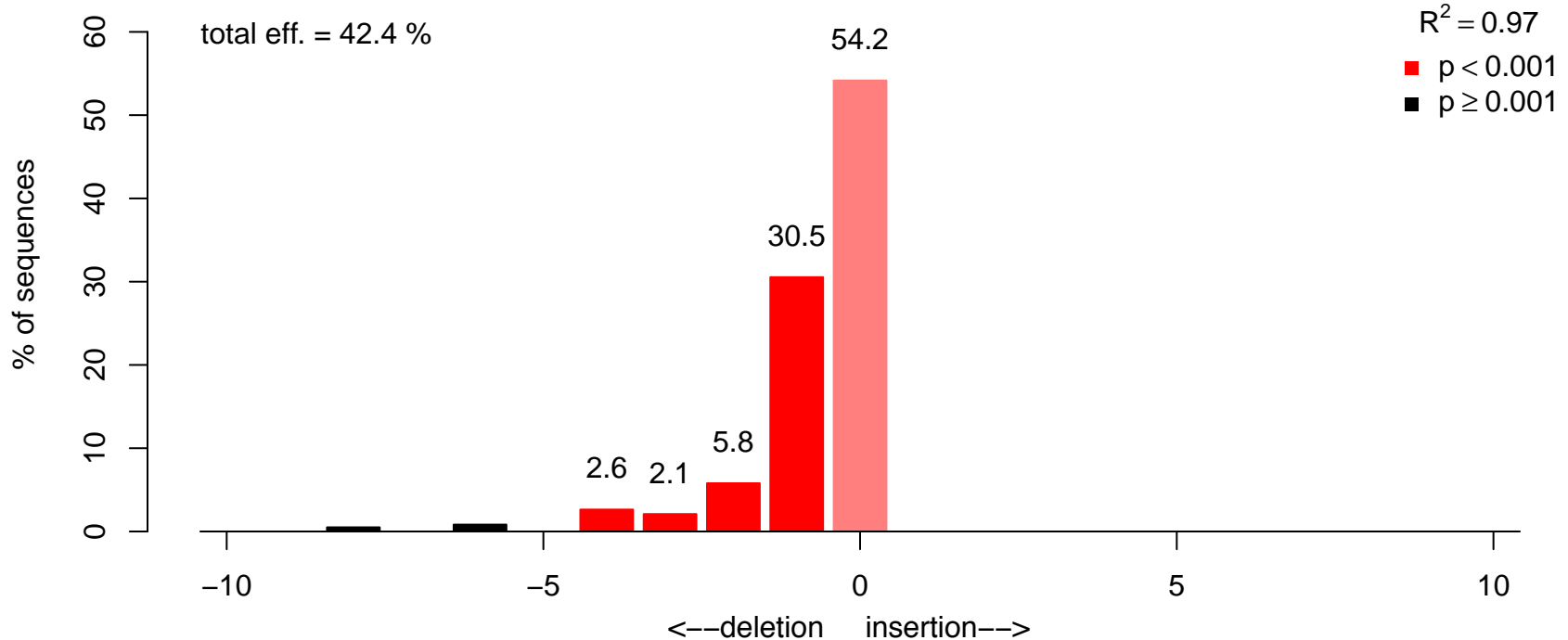
sample: WT/WT cell line, gRNA 1.2, reverse
guide: GGGTGGGACAGAACATCCCC

region for decomposition



Warning: left boundary of decomposition window was adjusted 132 . It must be at least 5bp plus the maximum indel size downstream of the expected break site

sample: WT/WT cell line, gRNA 1.3, reverse
guide: GGGTGGGACAGAACATCCCC

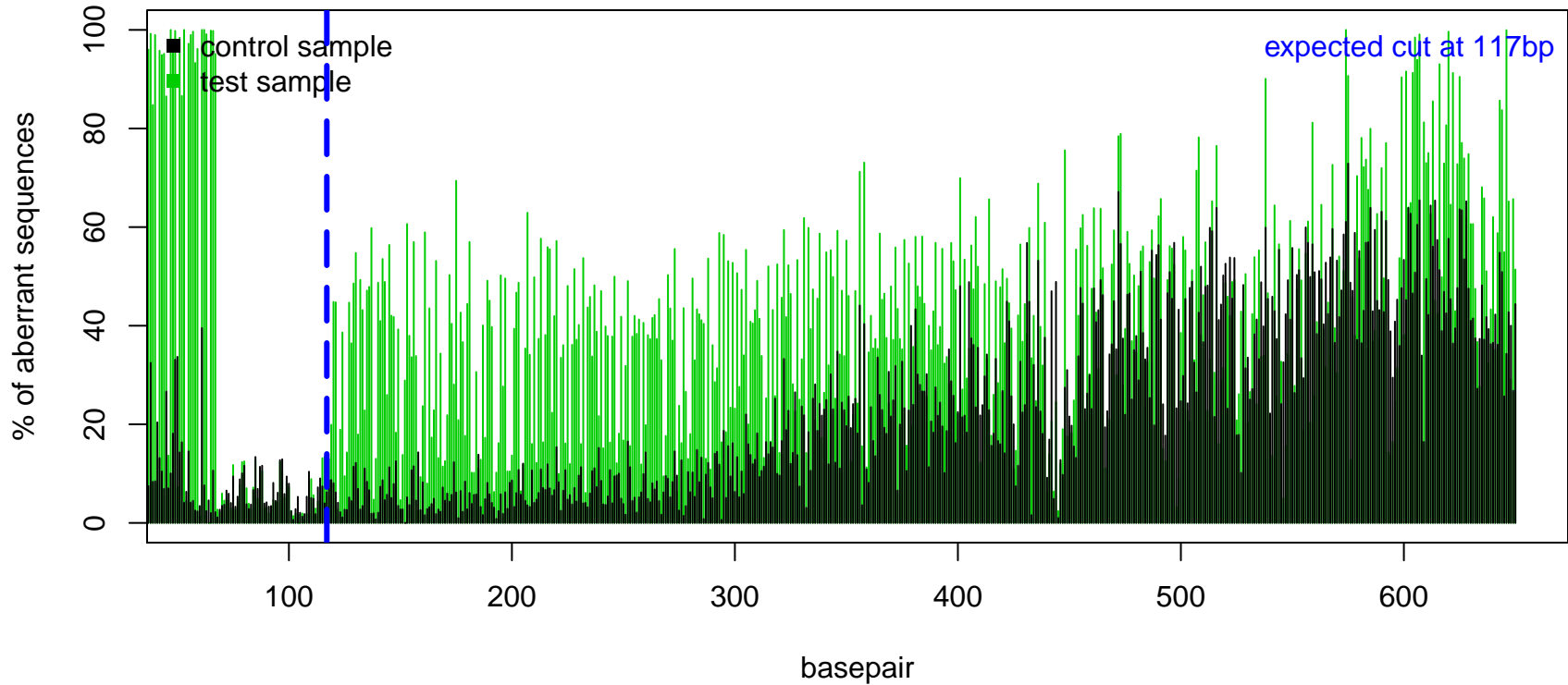


Warning: the spacing between the nucleotides in (one of) sanger sequence file(s) is not constant.

This might indicate for wrongly unannotated or wrongly additional annotated nucleotides.
Decomposition window lower and check the chromatogram for abnormalities.

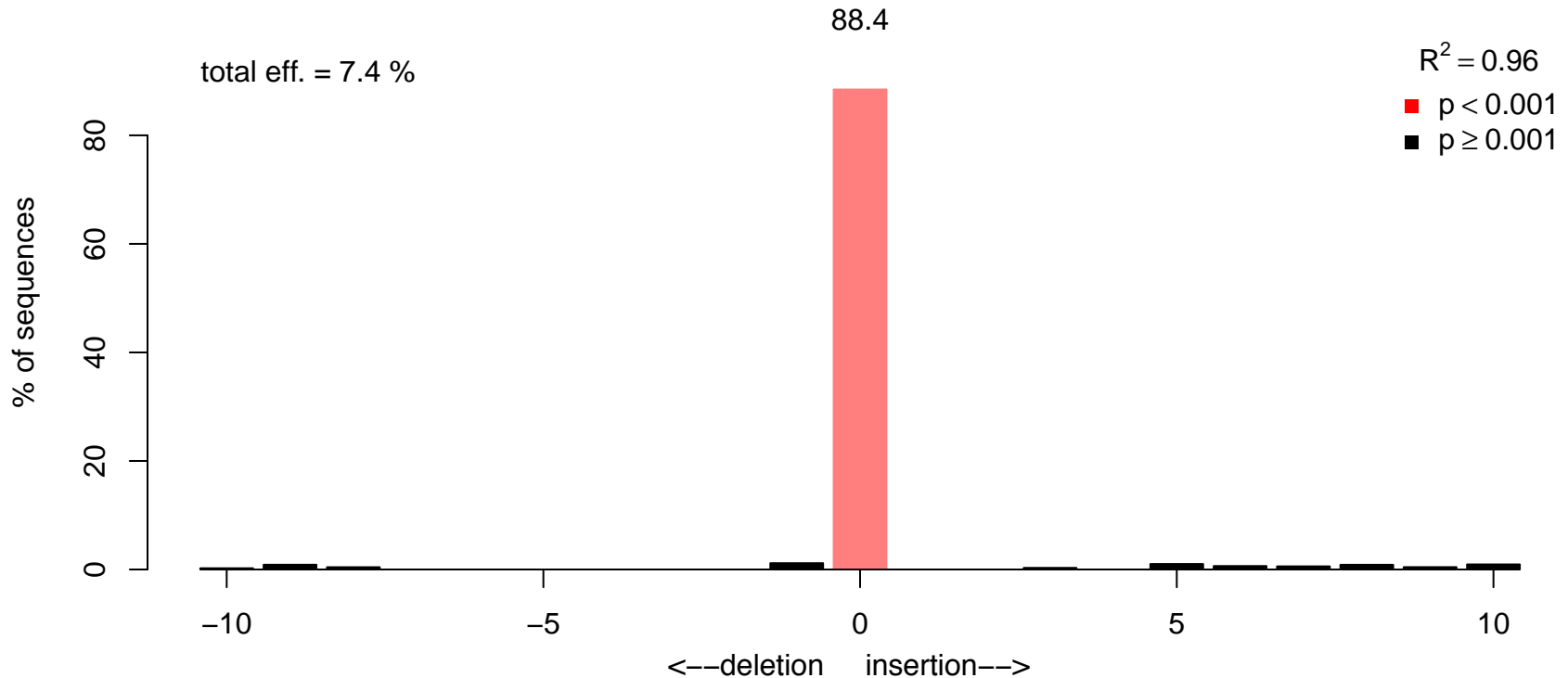
sample: WT/WT cell line, gRNA 1.3, reverse
guide: GGGTGGGACAGAACATCCCC

region for decomposition



Warning: left boundary of decomposition window was adjusted 132 . It must be at least 5bp plus the maximum indel size downstream of the expected break site

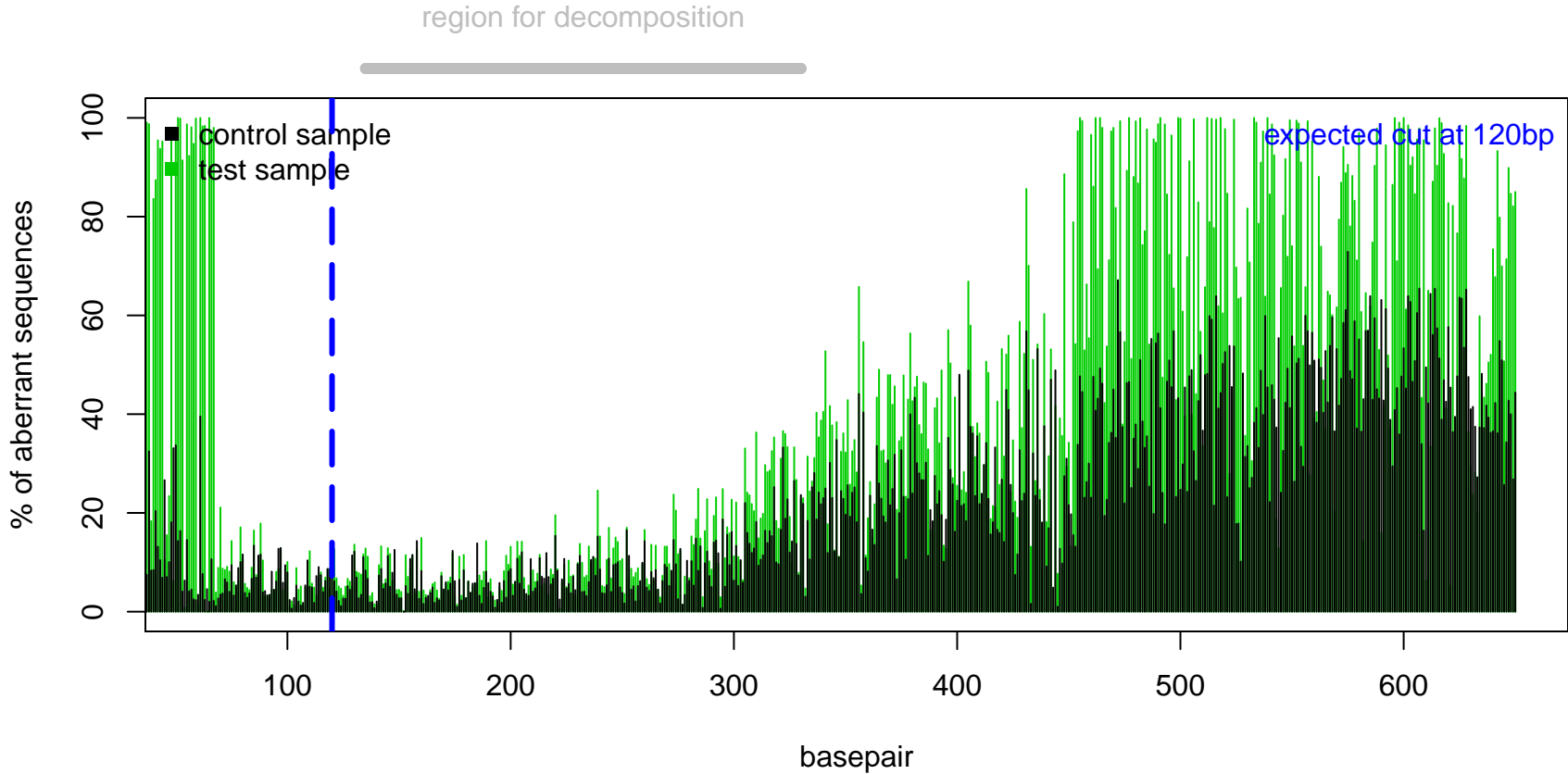
sample: WT/WT cell line, gRNA 1.4, reverse
guide: TGGGACAGAACATCCCCAGG



Warning: the spacing between the nucleotides in (one of) sanger sequence file(s) is not constant.

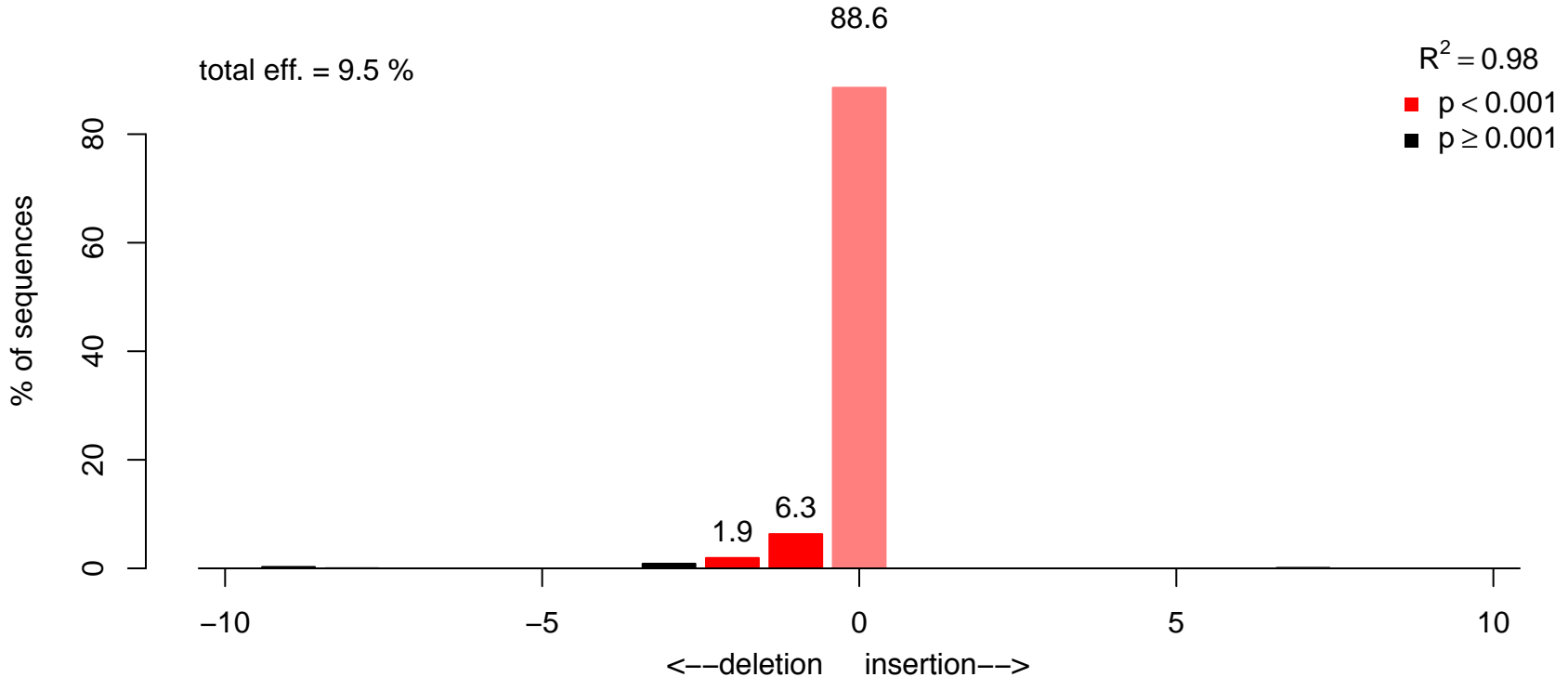
This might indicate for wrongly unannotated or wrongly additional annotated nucleotides.
Decomposition window lower and check the chromatogram for abnormalities.

sample: WT/WT cell line, gRNA 1.4, reverse
guide: TGGGACAGAACATCCCCAGG



Warning: left boundary of decomposition window was adjusted 135 . It must be at least 5bp plus the maximum indel size downstream of the expected break site

sample: WT/WT cell line, gRNA 2.1, reverse
guide: TGGGACAGAACATCCCCAGG

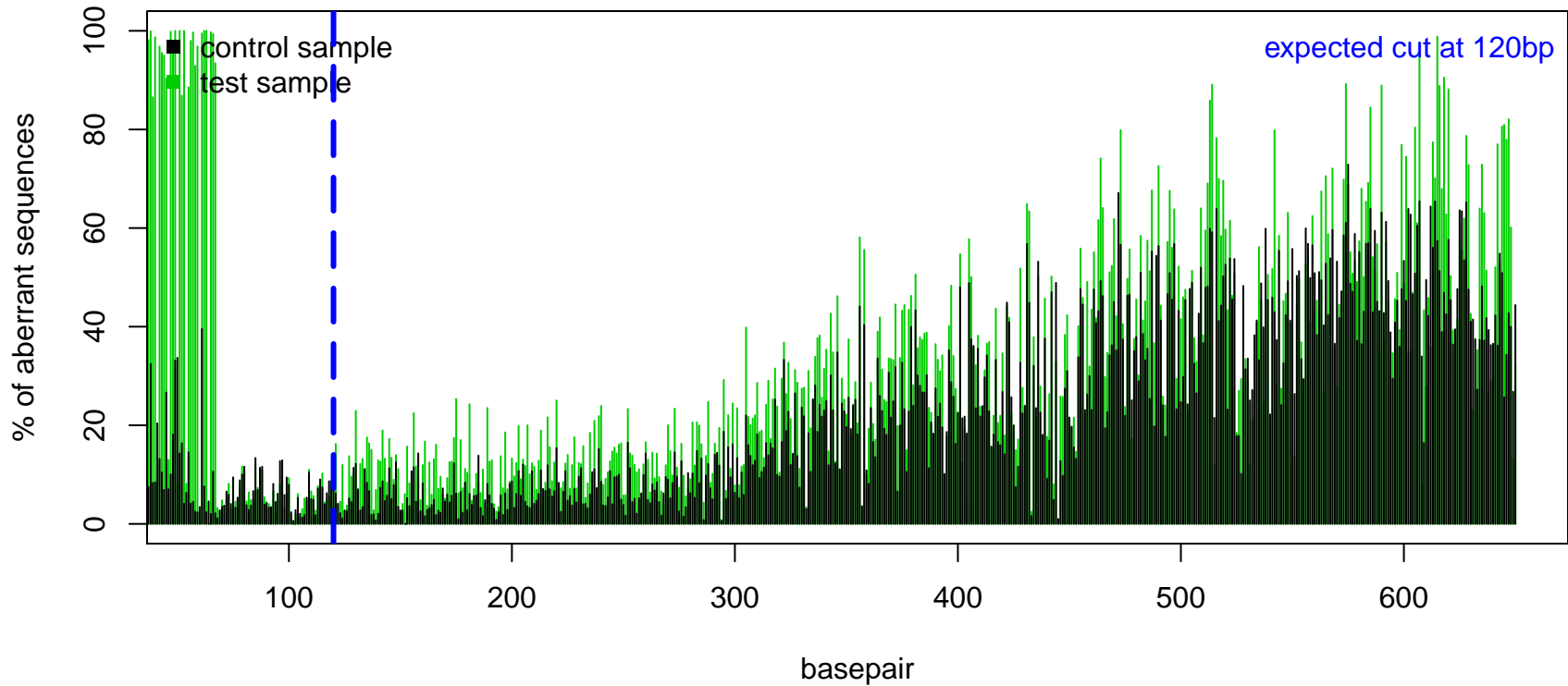


Warning: the spacing between the nucleotides in (one of) sanger sequence file(s) is not constant.

This might indicate for wrongly unannotated or wrongly additional annotated nucleotides.
Decomposition window lower and check the chromatogram for abnormalities.

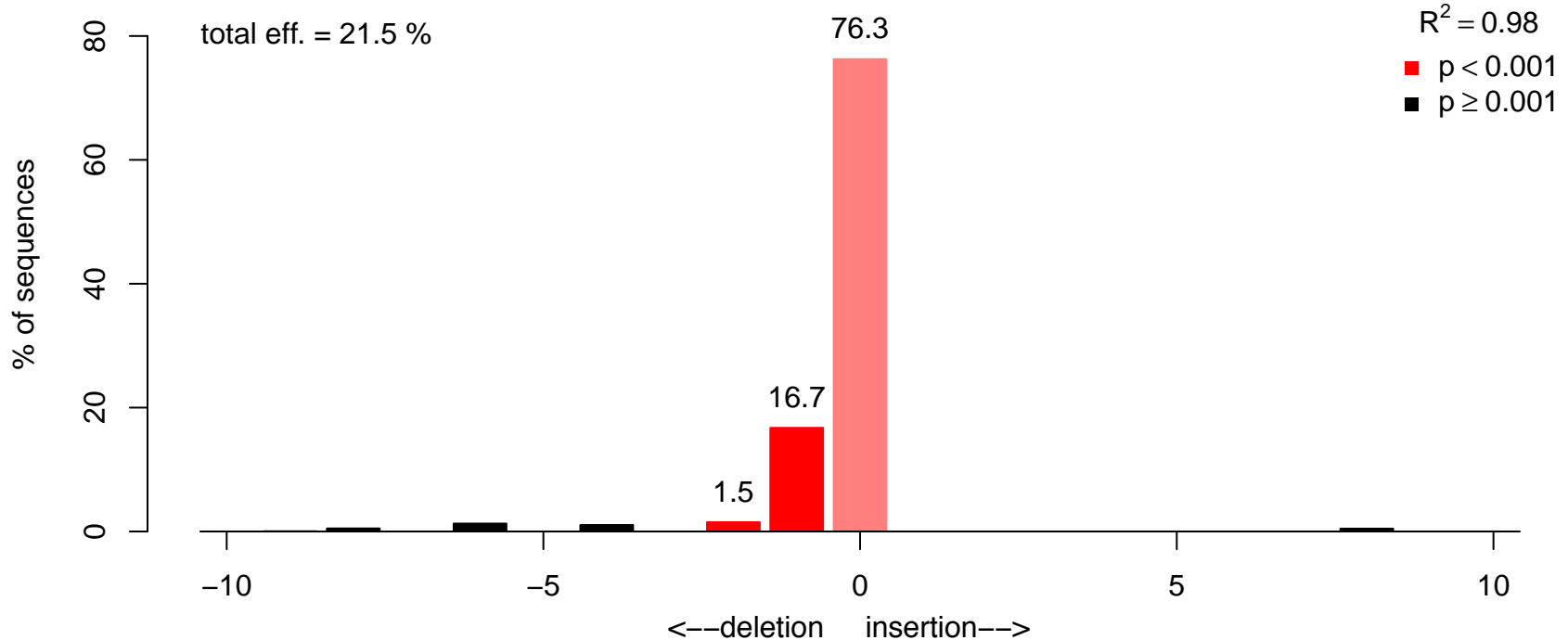
sample: WT/WT cell line, gRNA 2.1, reverse
guide: TGGGACAGAACATCCCCAGG

region for decomposition



Warning: left boundary of decomposition window was adjusted 135 . It must be at least 5bp plus the maximum indel size downstream of the expected break site

sample: WT/WT cell line, gRNA 2.2, reverse
guide: TGGGACAGAACATCCCCAGG

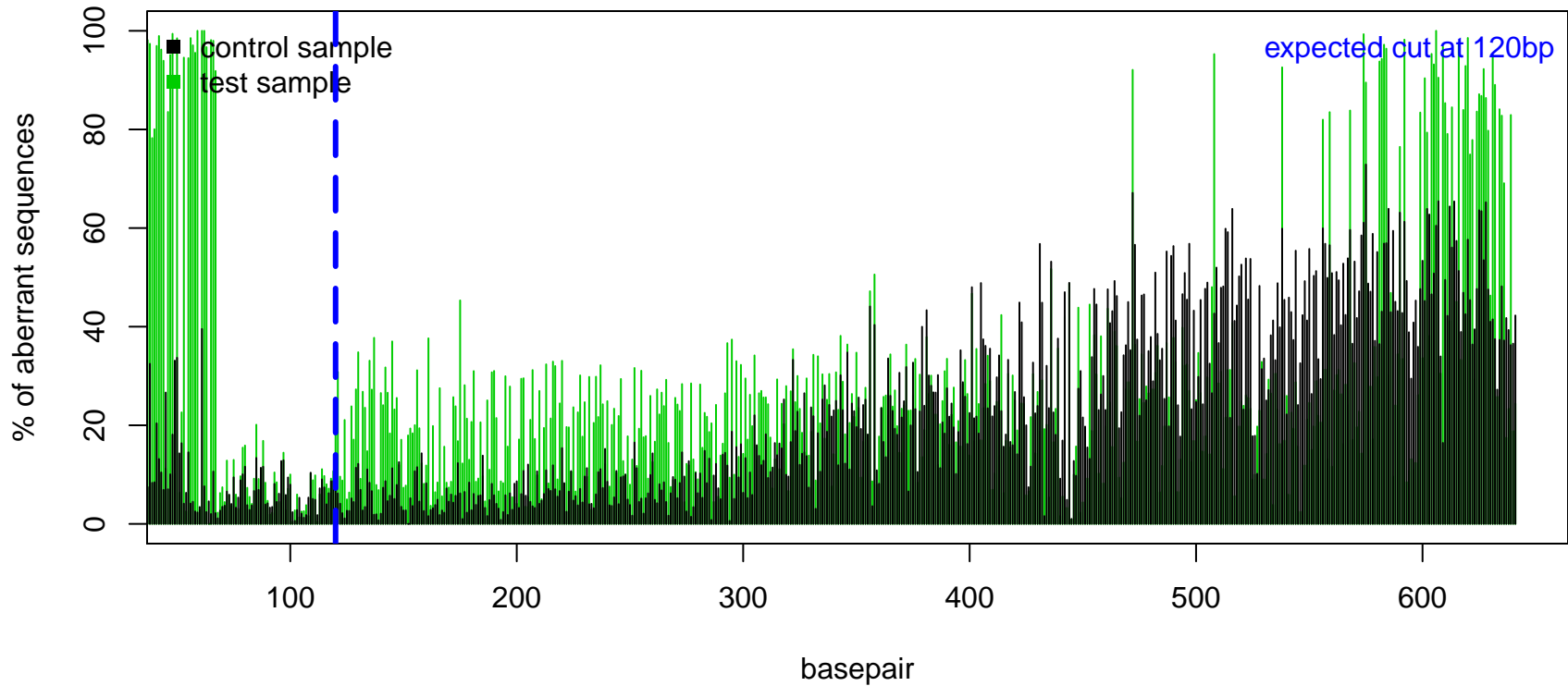


Warning: the spacing between the nucleotides in (one of) sanger sequence file(s) is not constant.

This might indicate for wrongly unannotated or wrongly additional annotated nucleotides.
Decomposition window lower and check the chromatogram for abnormalities.

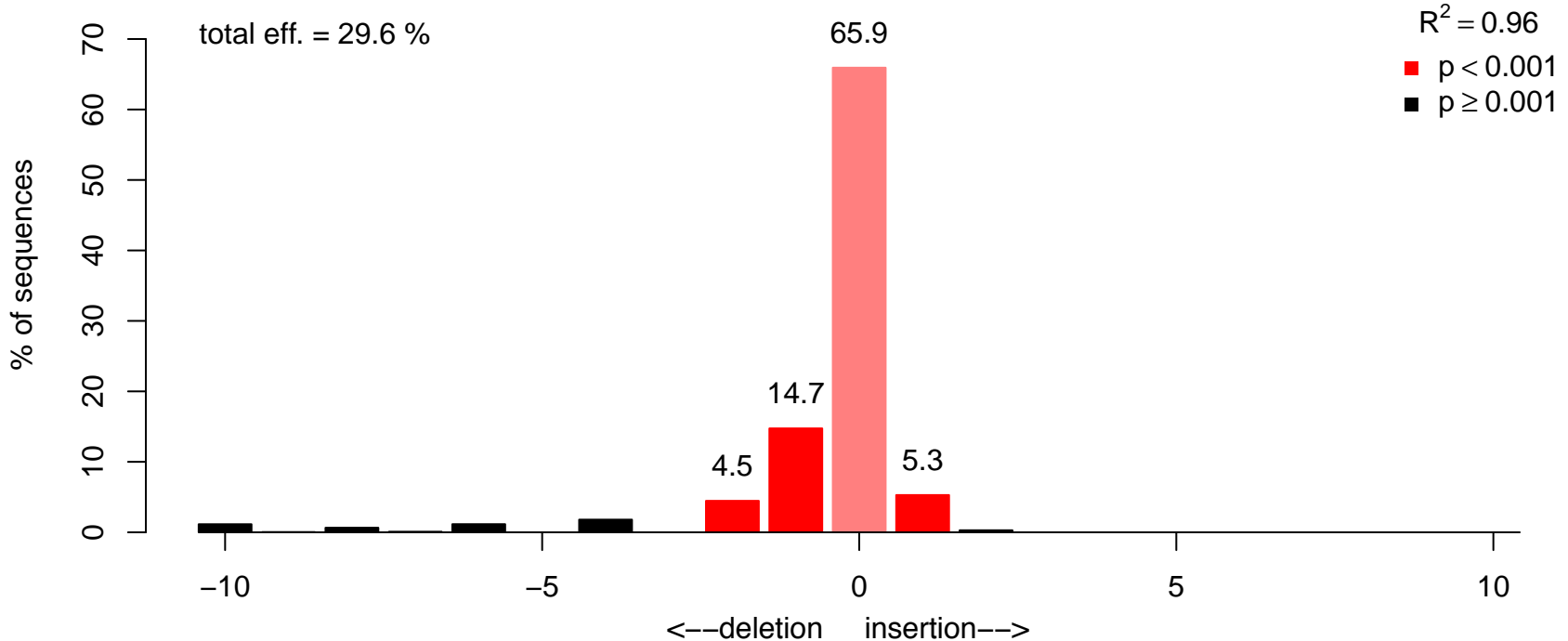
sample: WT/WT cell line, gRNA 2.2, reverse
guide: TGGGACAGAACATCCCCAGG

region for decomposition



Warning: left boundary of decomposition window was adjusted 135 . It must be at least 5bp plus the maximum indel size downstream of the expected break site

sample: WT/WT cell line, gRNA 2.3, reverse
guide: TGGGACAGAACATCCCCAGG

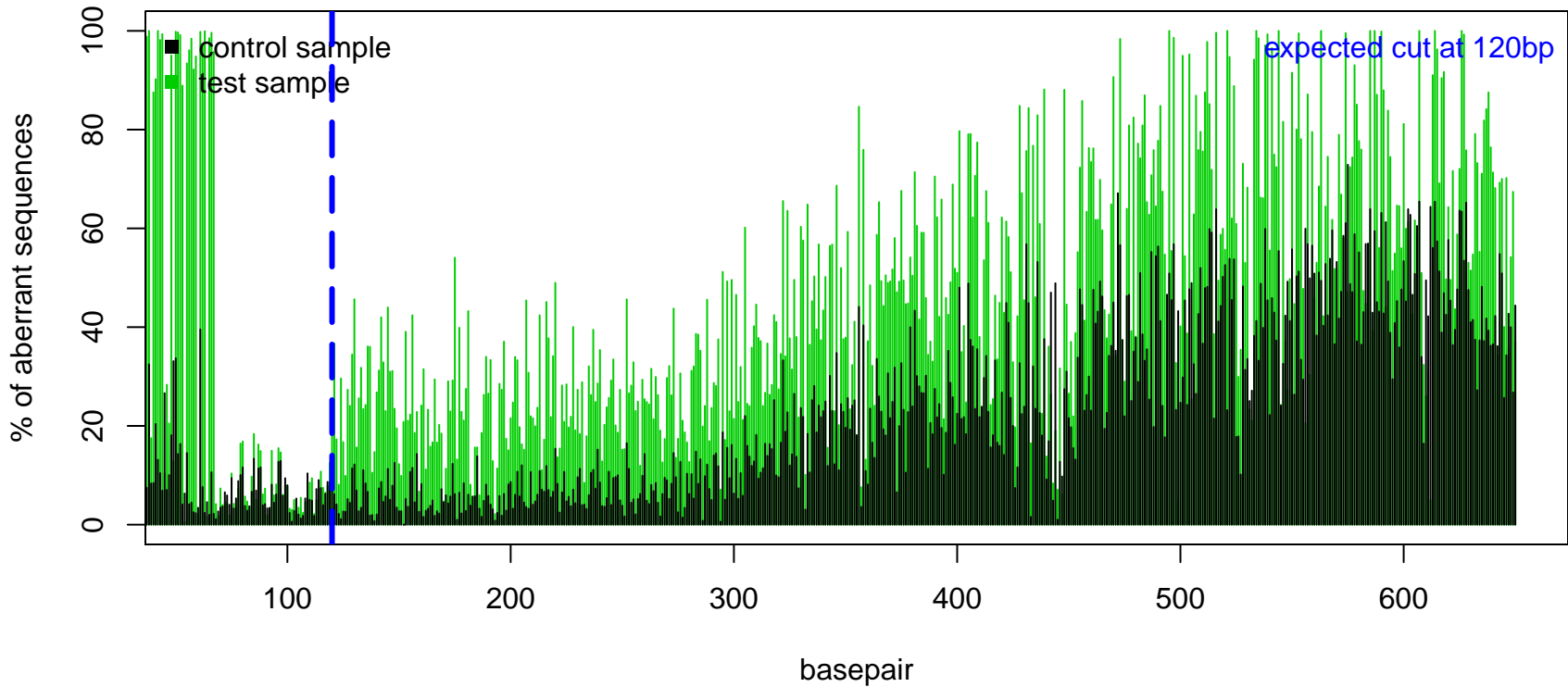


Warning: the spacing between the nucleotides in (one of) sanger sequence file(s) is not constant.

This might indicate for wrongly unannotated or wrongly additional annotated nucleotides.
Decomposition window lower and check the chromatogram for abnormalities.

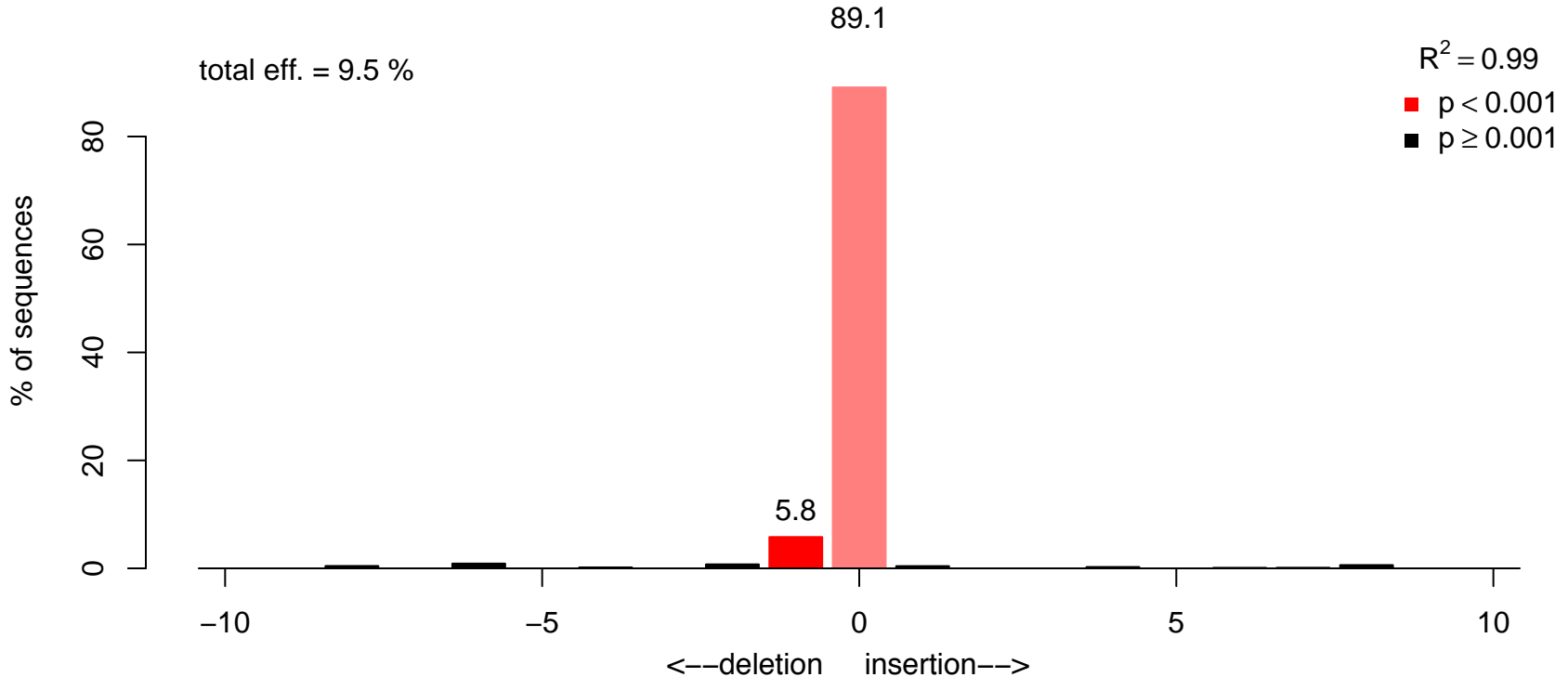
sample: WT/WT cell line, gRNA 2.3, reverse
guide: TGGGACAGAACATCCCCAGG

region for decomposition



Warning: left boundary of decomposition window was adjusted 135 . It must be at least 5bp plus the maximum indel size downstream of the expected break site

sample: WT/WT cell line, gRNA 2.4, reverse
guide: TGGTAATGTCCCTCCTGGGG

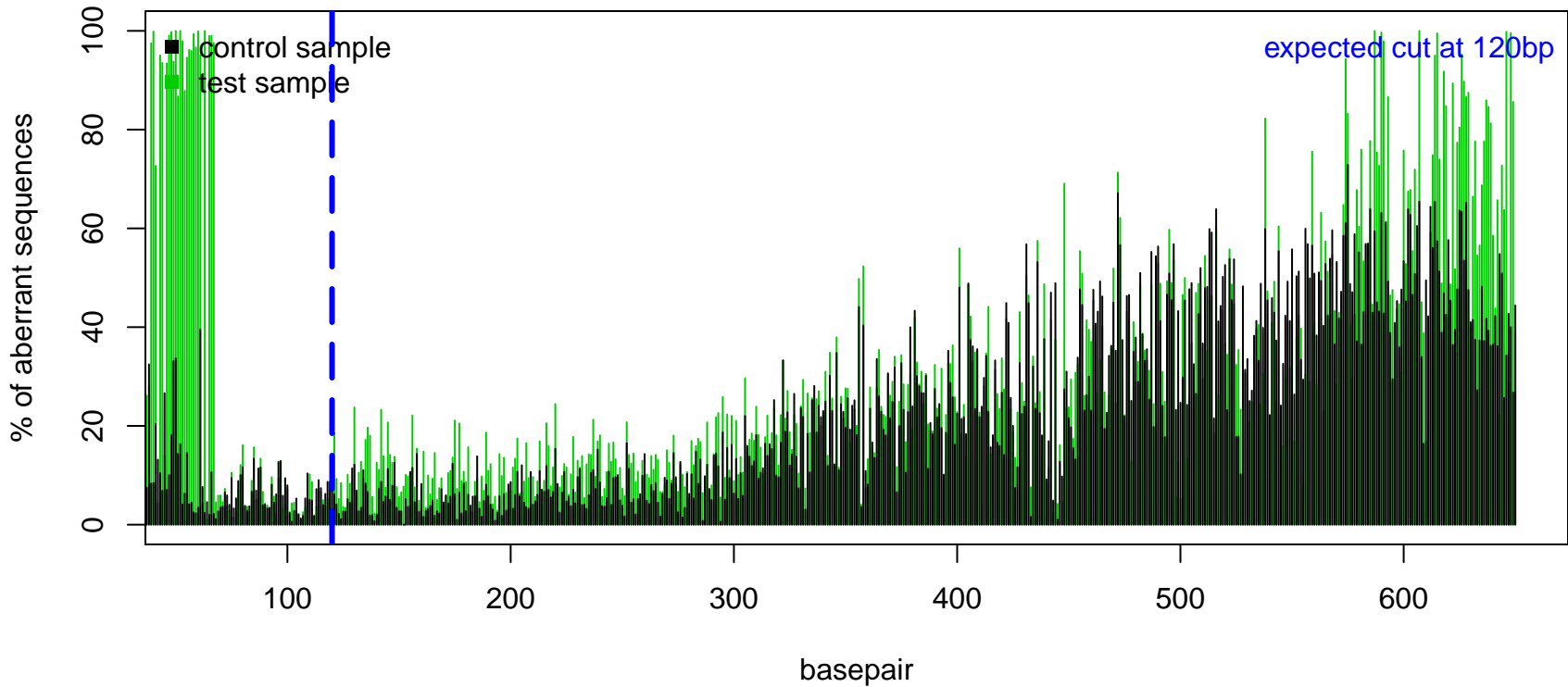


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This might indicate for wrongly unannotated or wrongly additional annotated nucleotides.
Decomposition window lower and check the chromatogram for abnormalities.

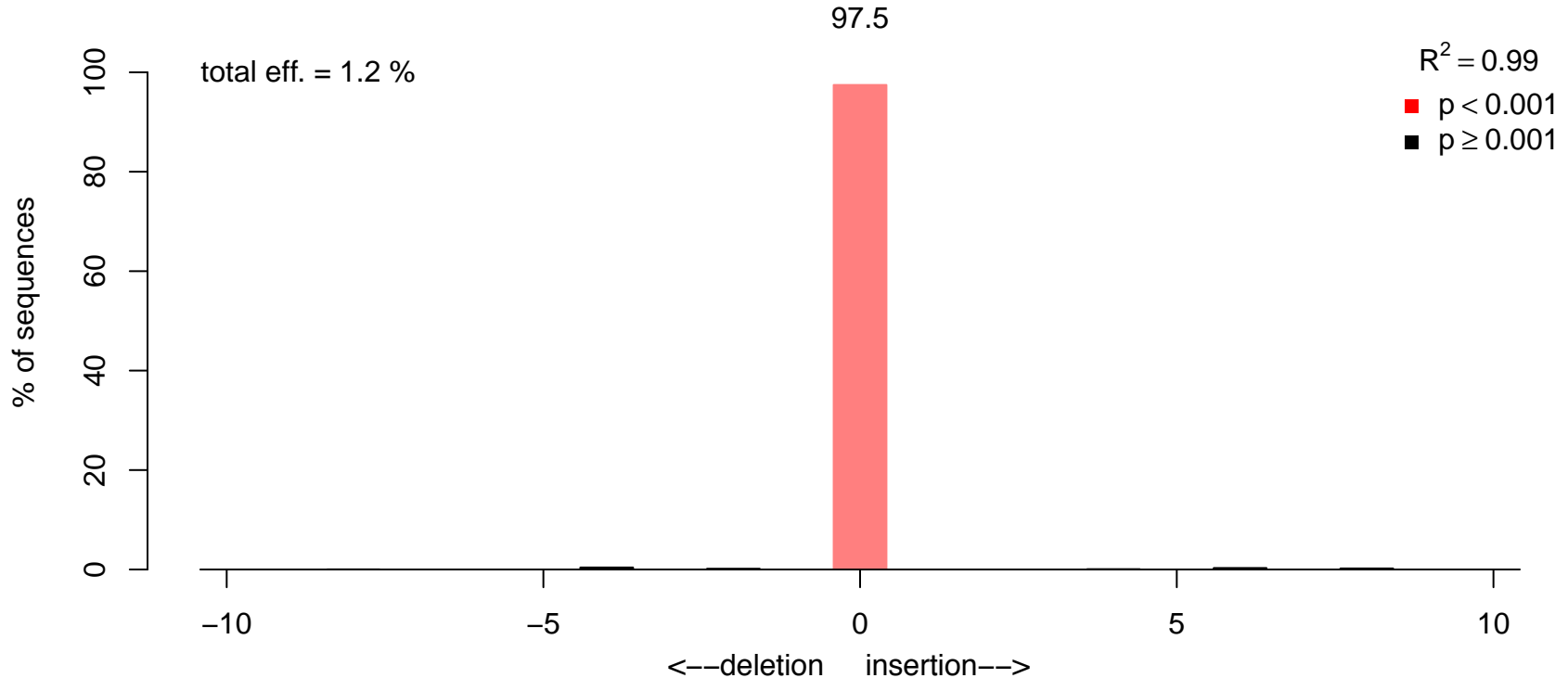
sample: WT/WT cell line, gRNA 2.4, reverse
guide: TGGTAATGTCCCTCCTGGGG

region for decomposition



Warning: left boundary of decomposition window was adjusted 135 . It must be at least 5bp plus the maximum indel size downstream of the expected break site

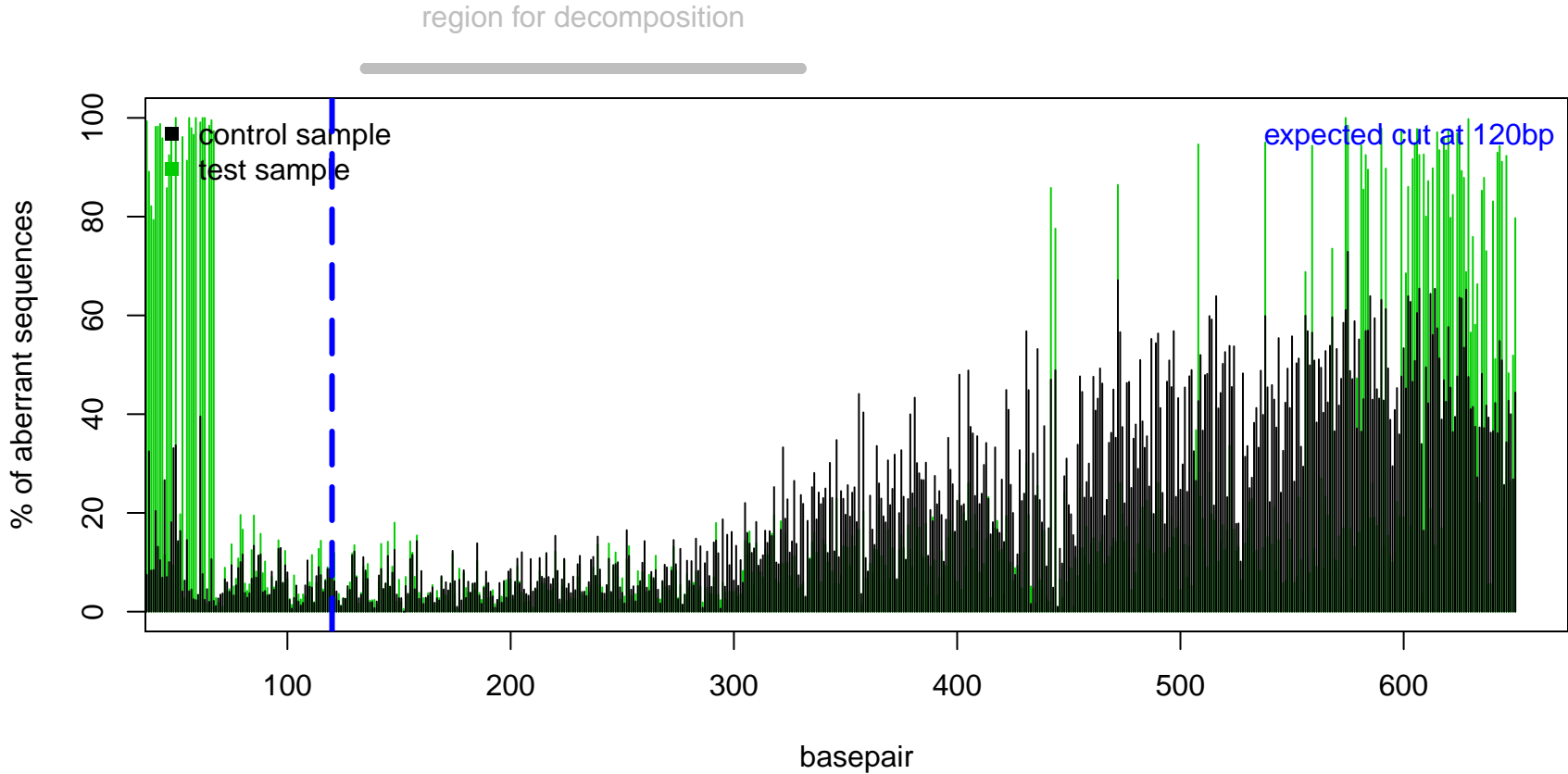
sample: WT/WT cell line, gRNA 3.1, reverse
guide: TGGTAATGTCCCTCCTGGGG



Warning: the spacing between the nucleotides in (one of) sanger sequence file(s) is not constant.

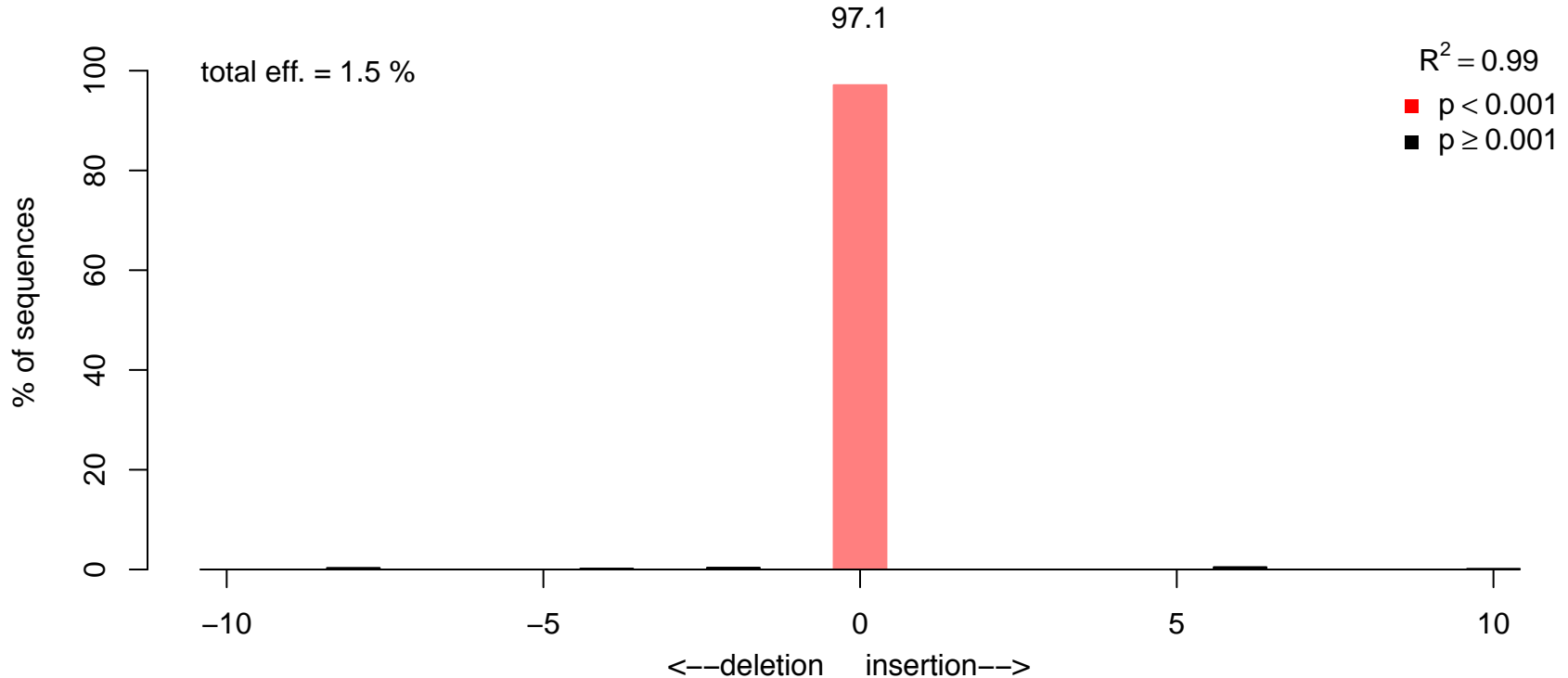
This might indicate for wrongly unannotated or wrongly additional annotated nucleotides.
Decomposition window lower and check the chromatogram for abnormalities.

sample: WT/WT cell line, gRNA 3.1, reverse
guide: TGGTAATGTCCCTCCTGGGG



Warning: left boundary of decomposition window was adjusted 135 . It must be at least 5bp plus the maximum indel size downstream of the expected break site

sample: WT/WT cell line, gRNA 3.2, reverse
guide: TGGTAATGTCCCTCCTGGGG

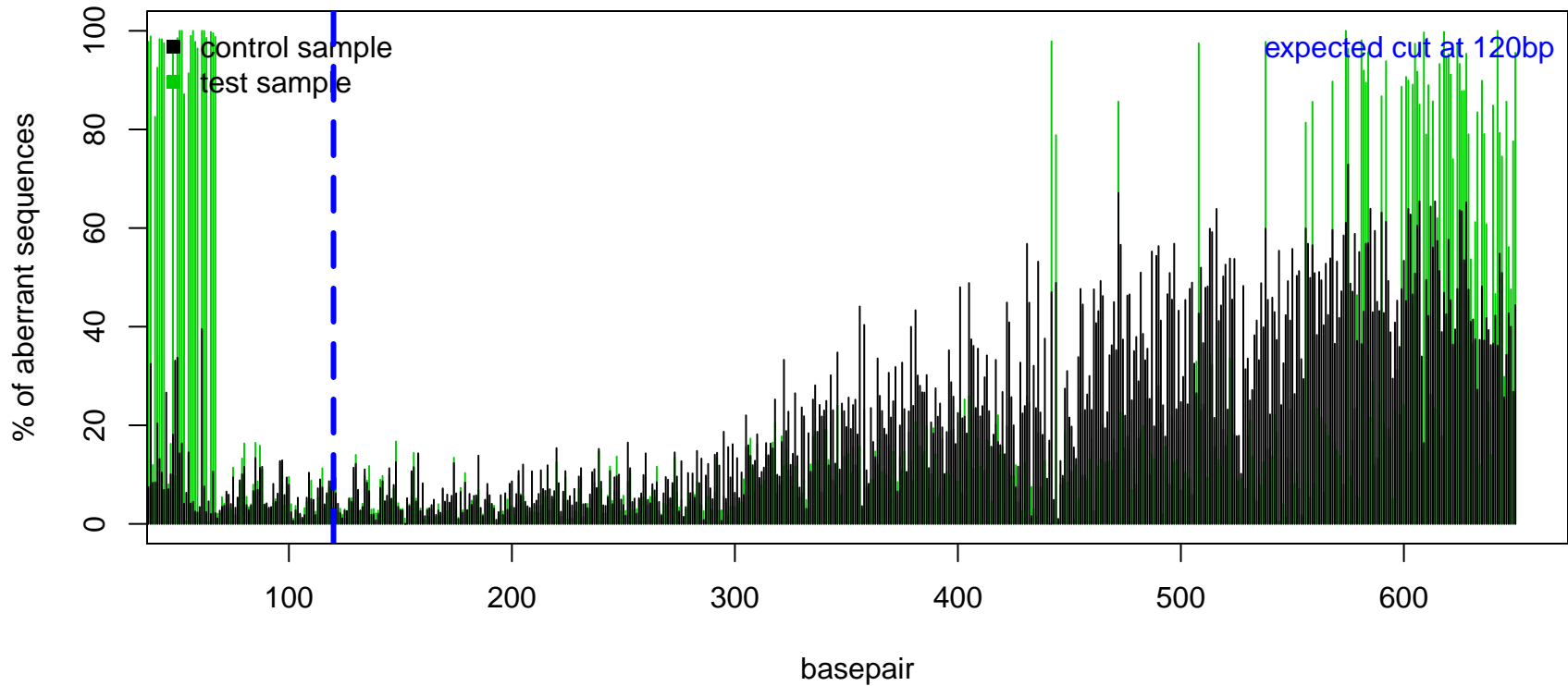


Warning: the spacing between the nucleotides in (one of) sanger sequence file(s) is not constant.

This might indicate for wrongly unannotated or wrongly additional annotated nucleotides.
Decomposition window lower and check the chromatogram for abnormalities.

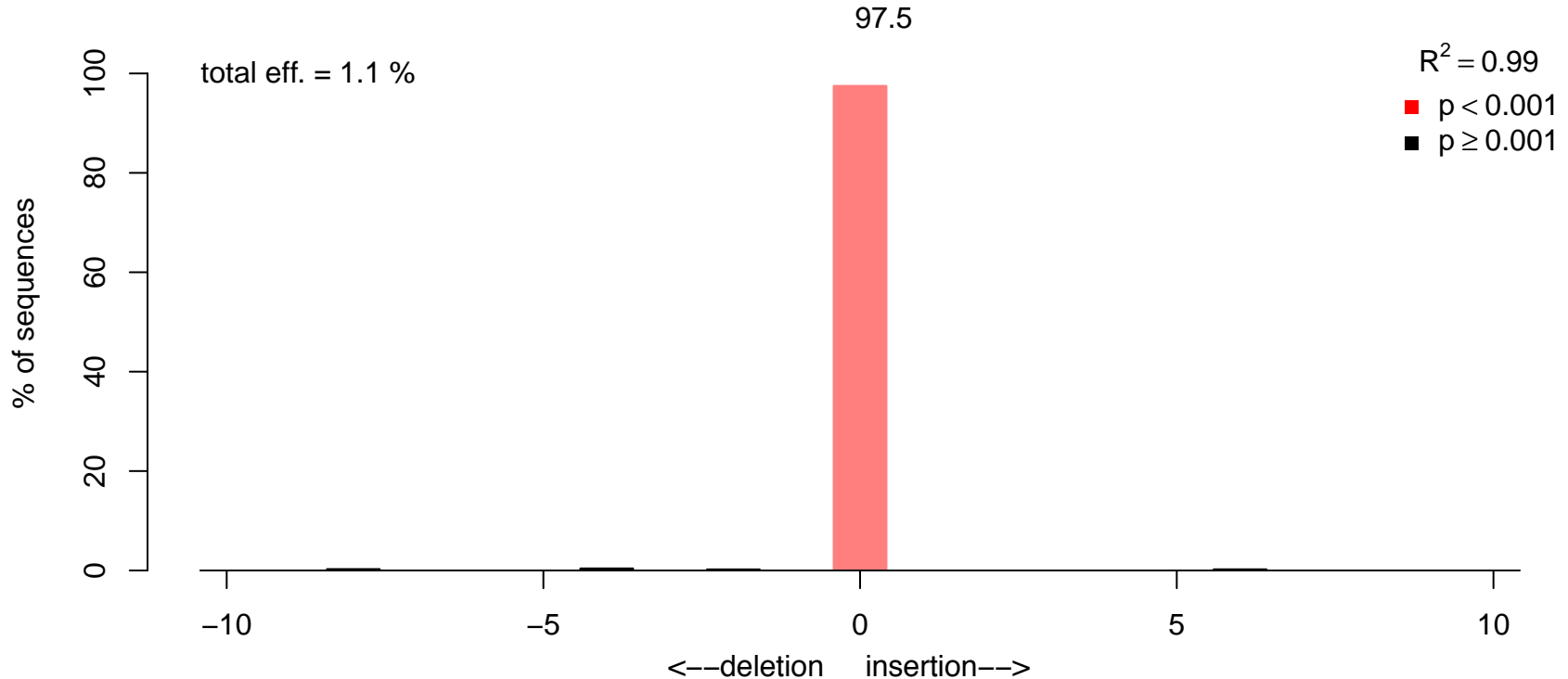
sample: WT/WT cell line, gRNA 3.2, reverse
guide: TGGTAATGTCCCTCCTGGGG

region for decomposition



Warning: left boundary of decomposition window was adjusted 135 . It must be at least 5bp plus the maximum indel size downstream of the expected break site

sample: WT/WT cell line, gRNA 3.3, reverse
guide: GGGTGGGACAGAACATCCCC

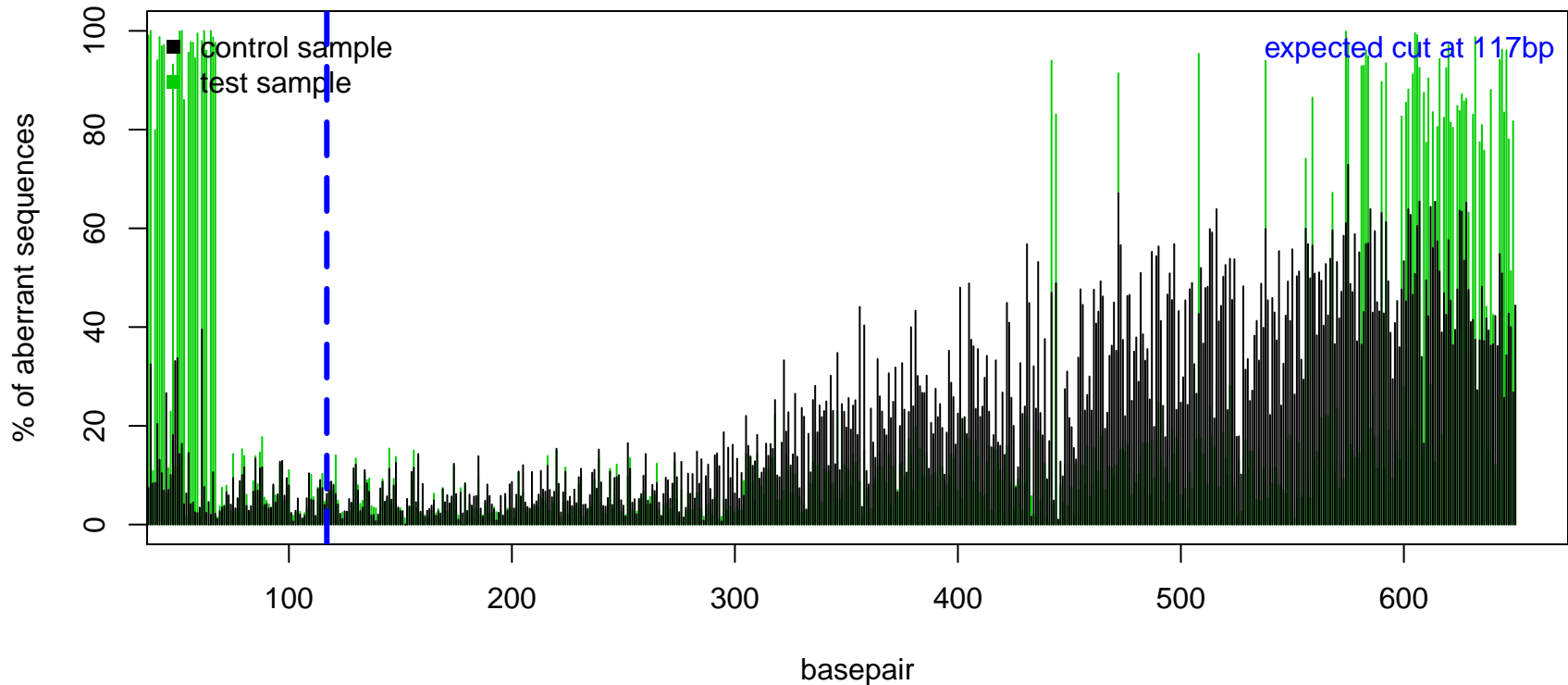


Warning: the spacing between the nucleotides in (one of) sanger sequence file(s) is not constant.

This might indicate for wrongly unannotated or wrongly additional annotated nucleotides.
Decomposition window lower and check the chromatogram for abnormalities.

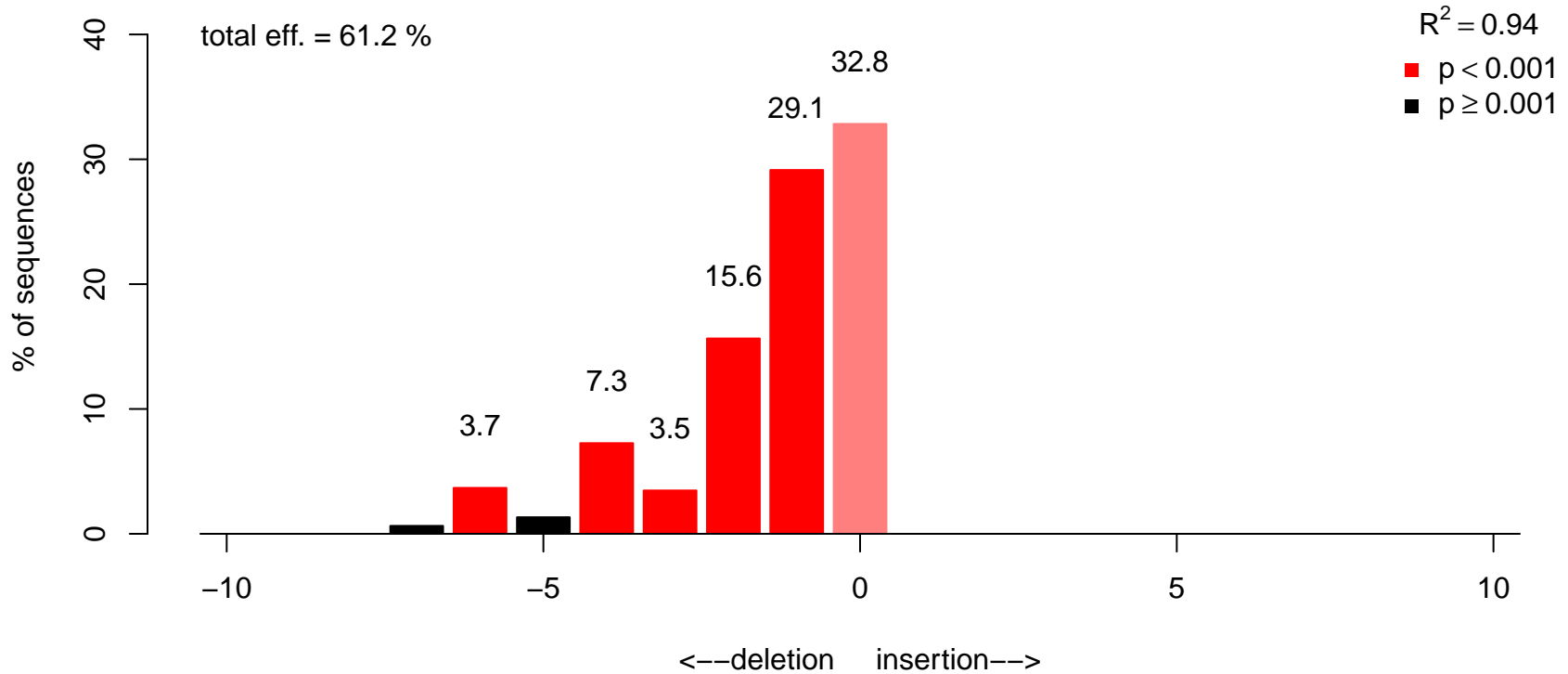
sample: WT/WT cell line, gRNA 3.3, reverse
guide: GGGTGGGACAGAACATCCCC

region for decomposition

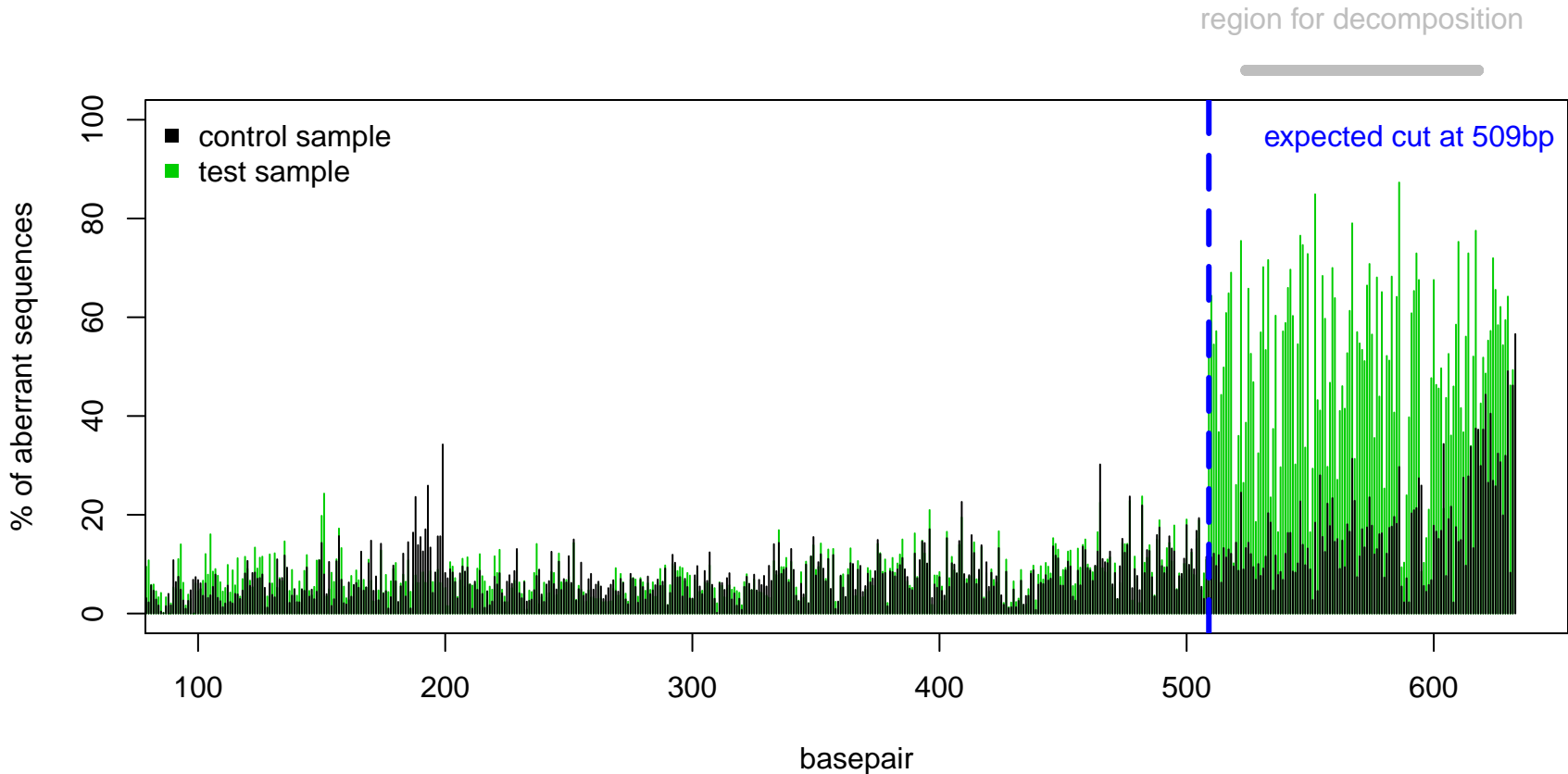


Warning: left boundary of decomposition window was adjusted 132 . It must be at least 5bp plus the maximum indel size downstream of the expected break site

sample: WT/WT cell line, gRNA WT, forward
guide: GGGTGGGACAGAACATCCCC



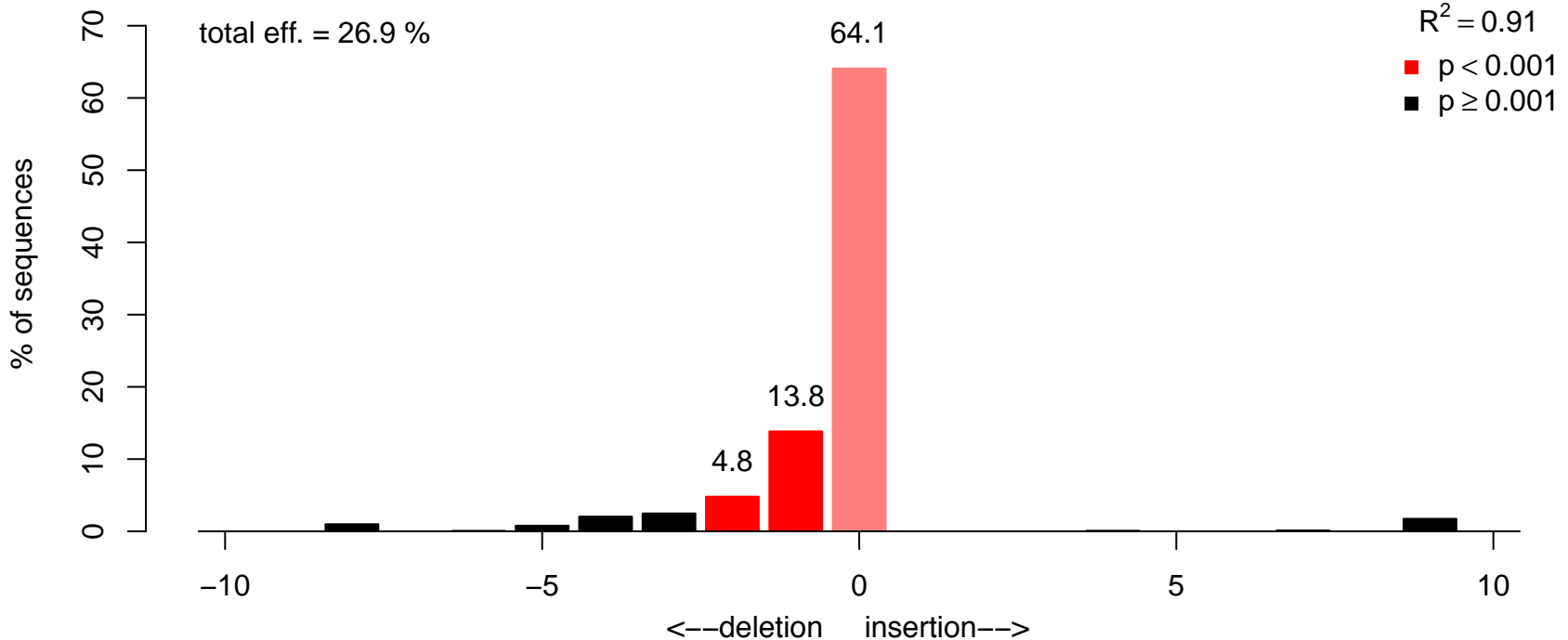
sample: WT/WT cell line, gRNA WT, forward
guide: GGGTGGGACAGAACATCCCC



Warning: left boundary of decomposition window was adjusted 524 . It must be at least 5bp plus the maximum indel size downstream of the expected break site

Warning: right boundary of decomposition window was adjusted to 618 . It must be at least 5bp plus the maximum indel size downstream of the expected break site

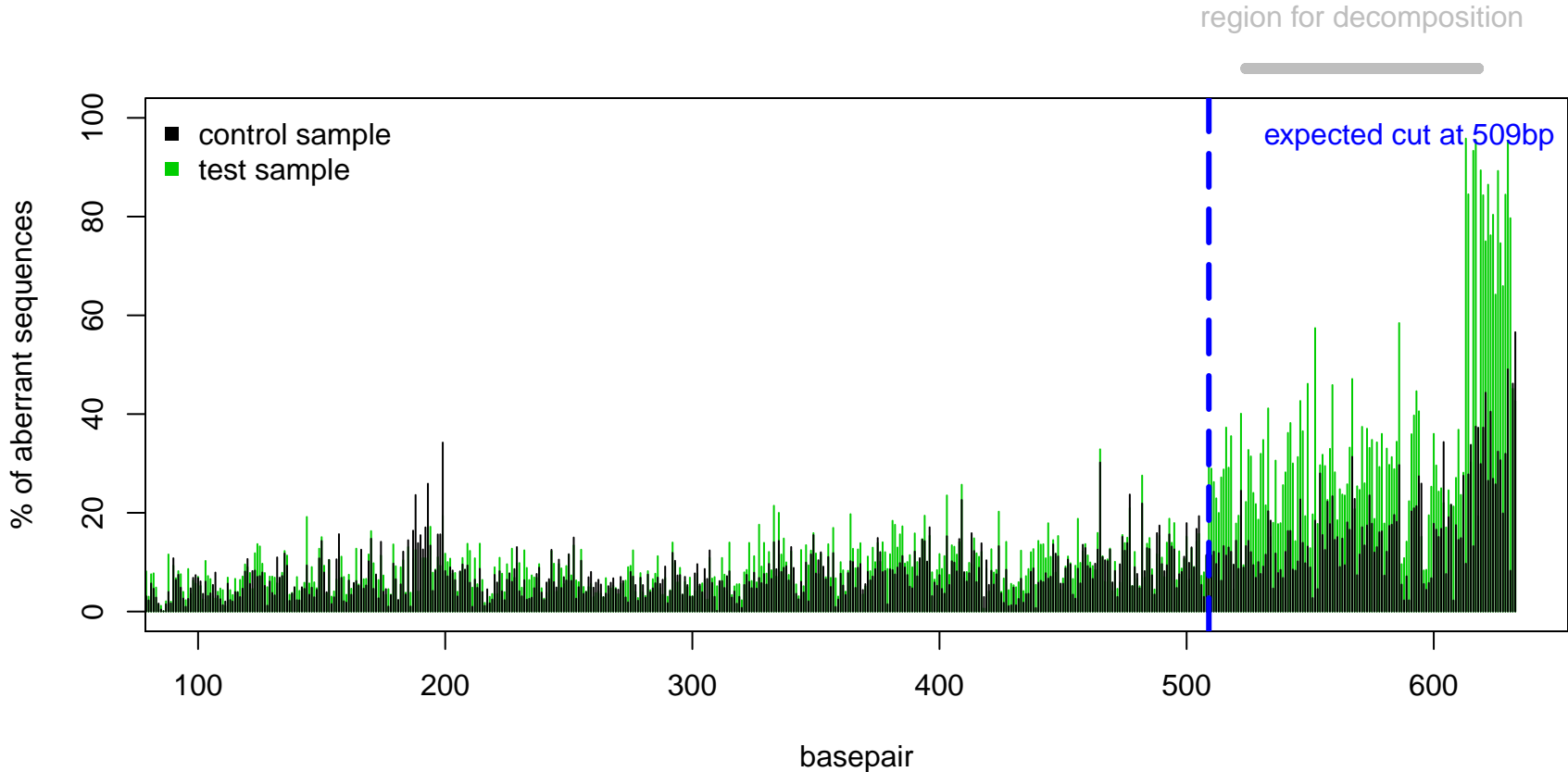
sample: WT/WT cell line, gRNA 1.1, forward
guide: GGGTGGGACAGAACATCCCC



Warning: the spacing between the nucleotides in (one of) sanger sequence file(s) is not constant.

This might indicate for wrongly unannotated or wrongly additional annotated nucleotides.
Decomposition window lower and check the chromatogram for abnormalities.

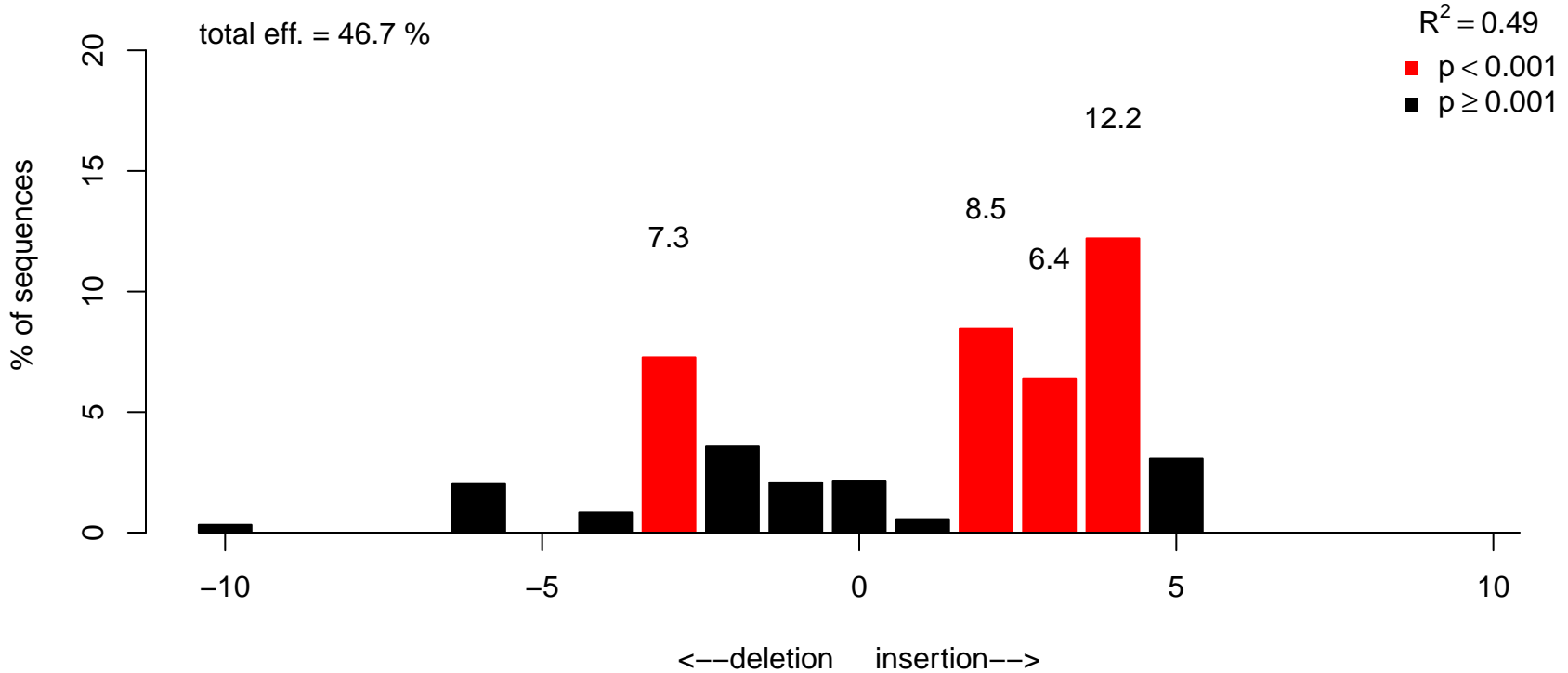
sample: WT/WT cell line, gRNA 1.1, forward
guide: GGGTGGGACAGAACATCCCC



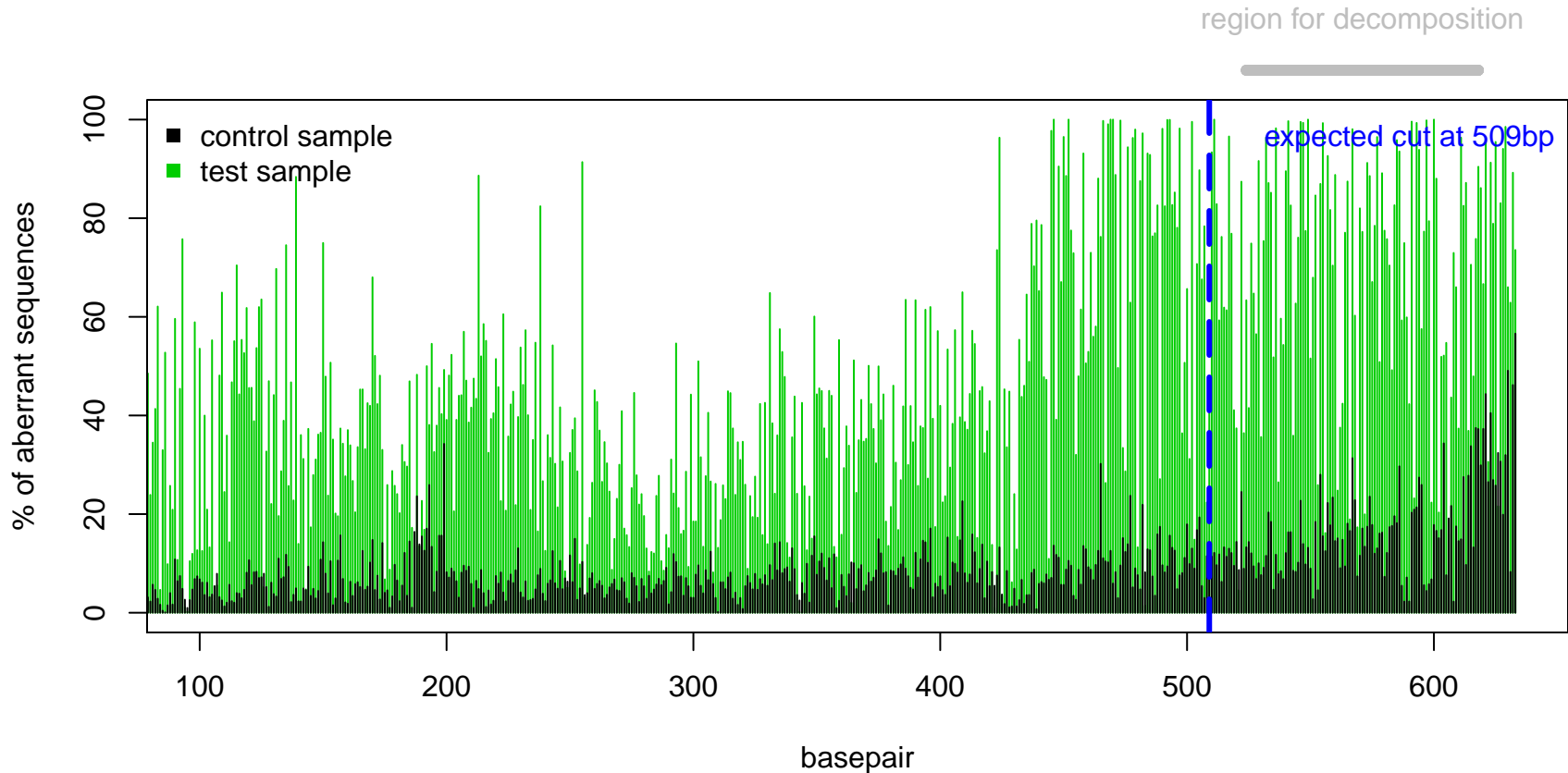
Warning: left boundary of decomposition window was adjusted 524 . It must be at least 5bp plus the maximum indel size downstream of the expected break site

Warning: right boundary of decomposition window was adjusted to 618 . It must be at least 5bp plus the maximum indel size downstream of the expected break site

sample: WT/WT cell line, gRNA 1.2, forward
guide: GGGTGGGACAGAACATCCCC



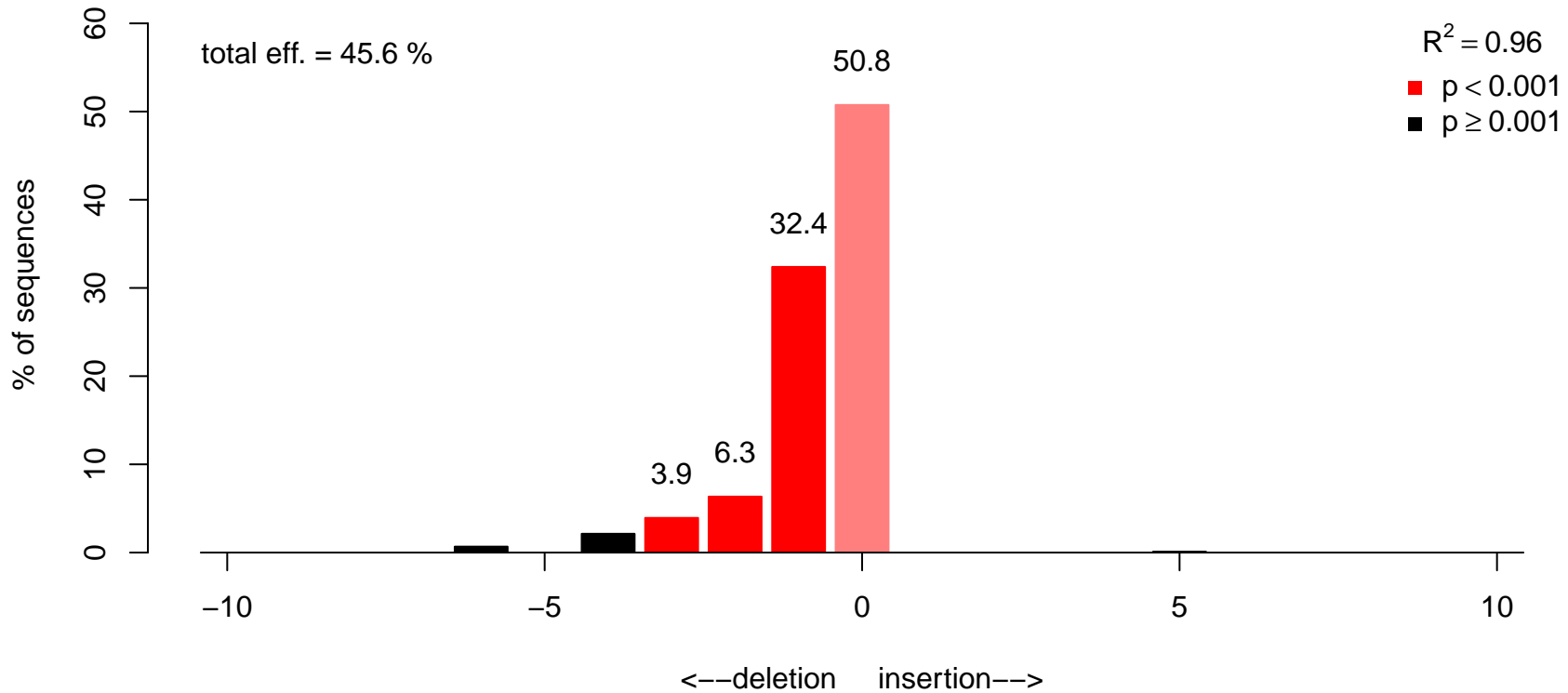
sample: WT/WT cell line, gRNA 1.2, forward
guide: GGGTGGGACAGAACATCCCC



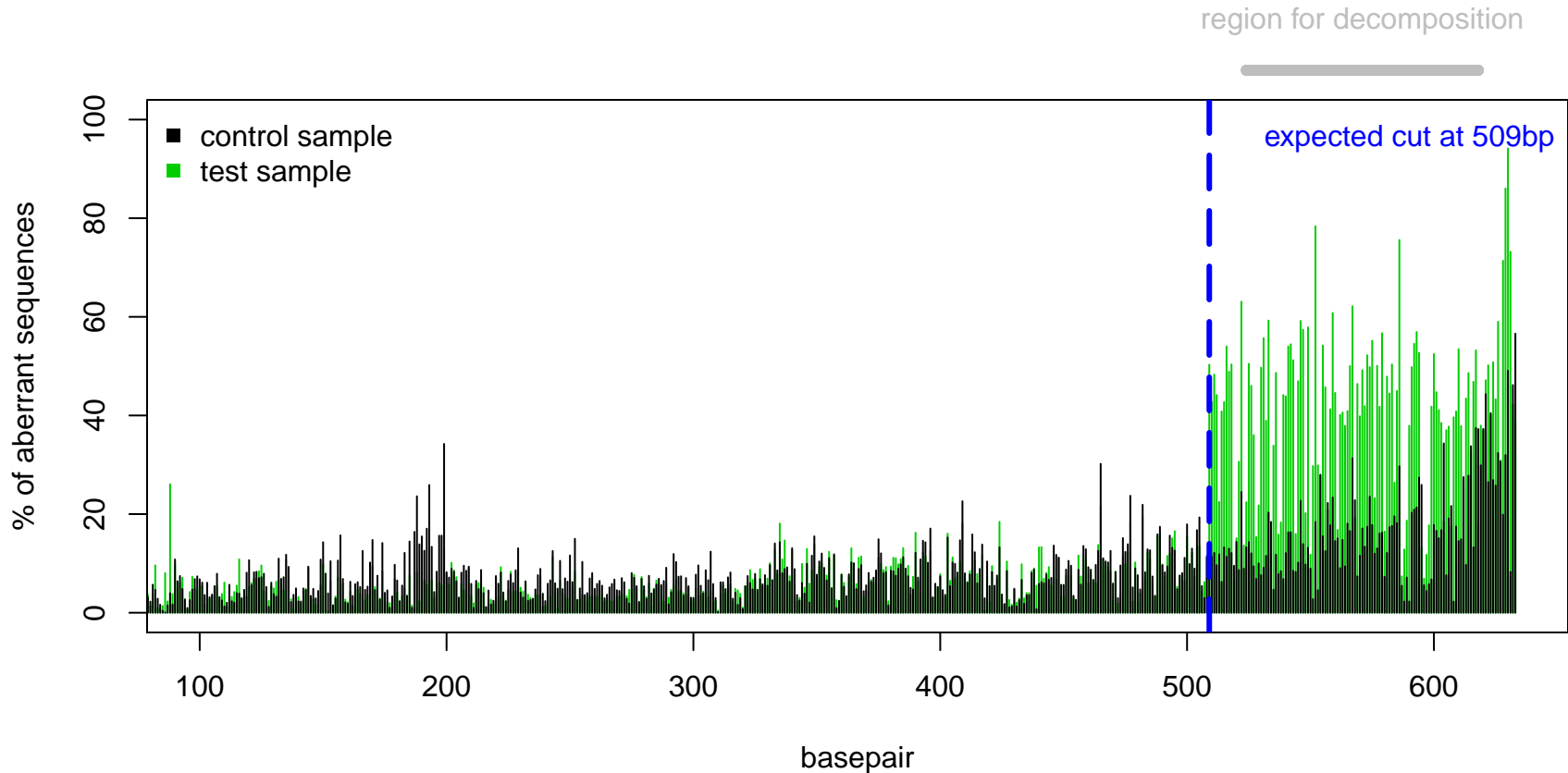
Warning: left boundary of decomposition window was adjusted 524 . It must be at least 5bp plus the maximum indel size downstream of the expected break site

Warning: right boundary of decomposition window was adjusted to 618 . It must be at least 5bp plus the maximum indel size downstream of the expected break site

sample: WT/WT cell line, gRNA 1.3, forward
guide: GGGTGGGACAGAACATCCCC



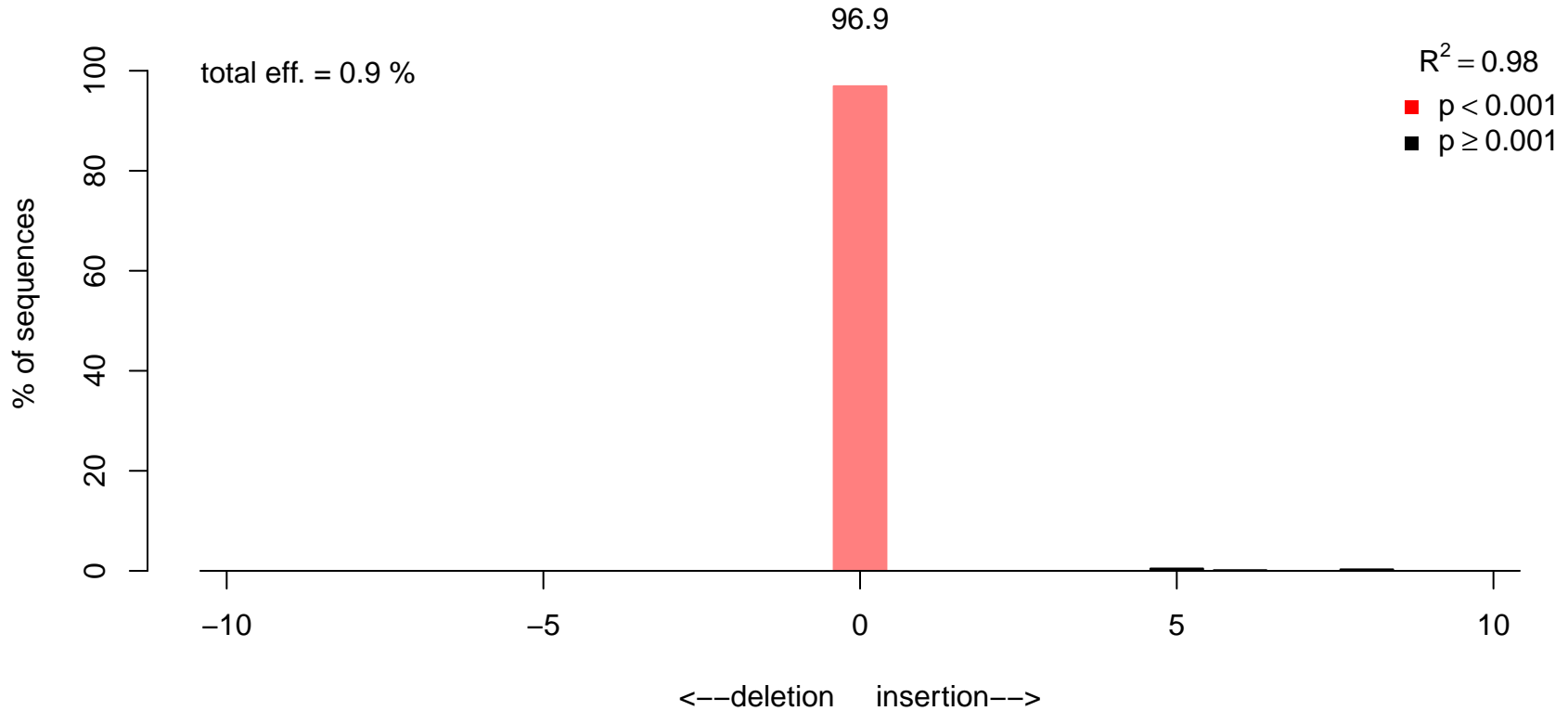
sample: WT/WT cell line, gRNA 1.3, forward
guide: GGGTGGGACAGAACATCCCC



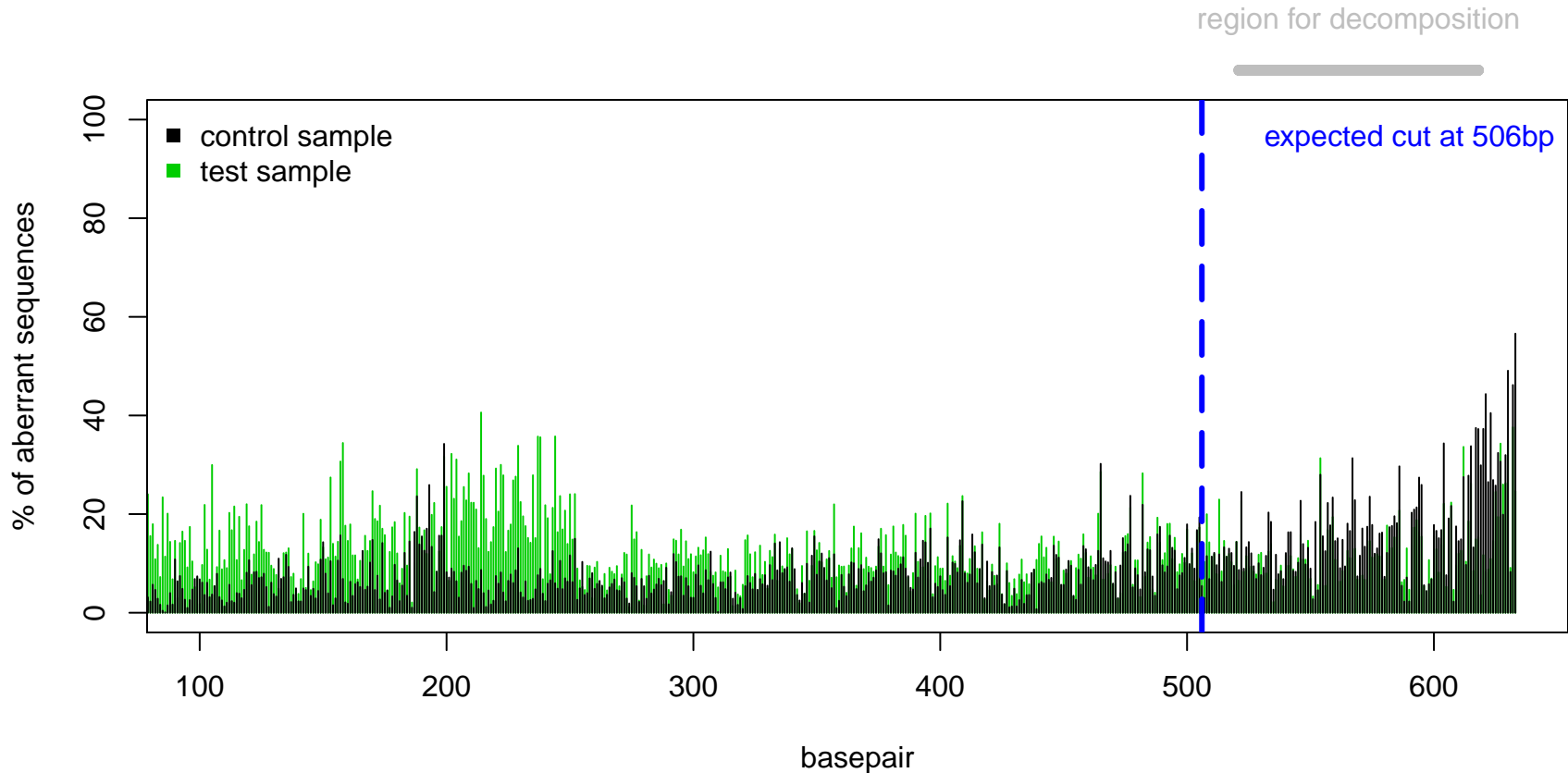
Warning: left boundary of decomposition window was adjusted 524 . It must be at least 5bp plus the maximum indel size downstream of the expected break site

Warning: right boundary of decomposition window was adjusted to 618 . It must be at least 5bp plus the maximum indel size downstream of the expected break site

sample: WT/WT cell line, gRNA 1.4, forward
guide: TGGGACAGAACATCCCCAGG



sample: WT/WT cell line, gRNA 1.4, forward
guide: TGGGACAGAACATCCCCAGG

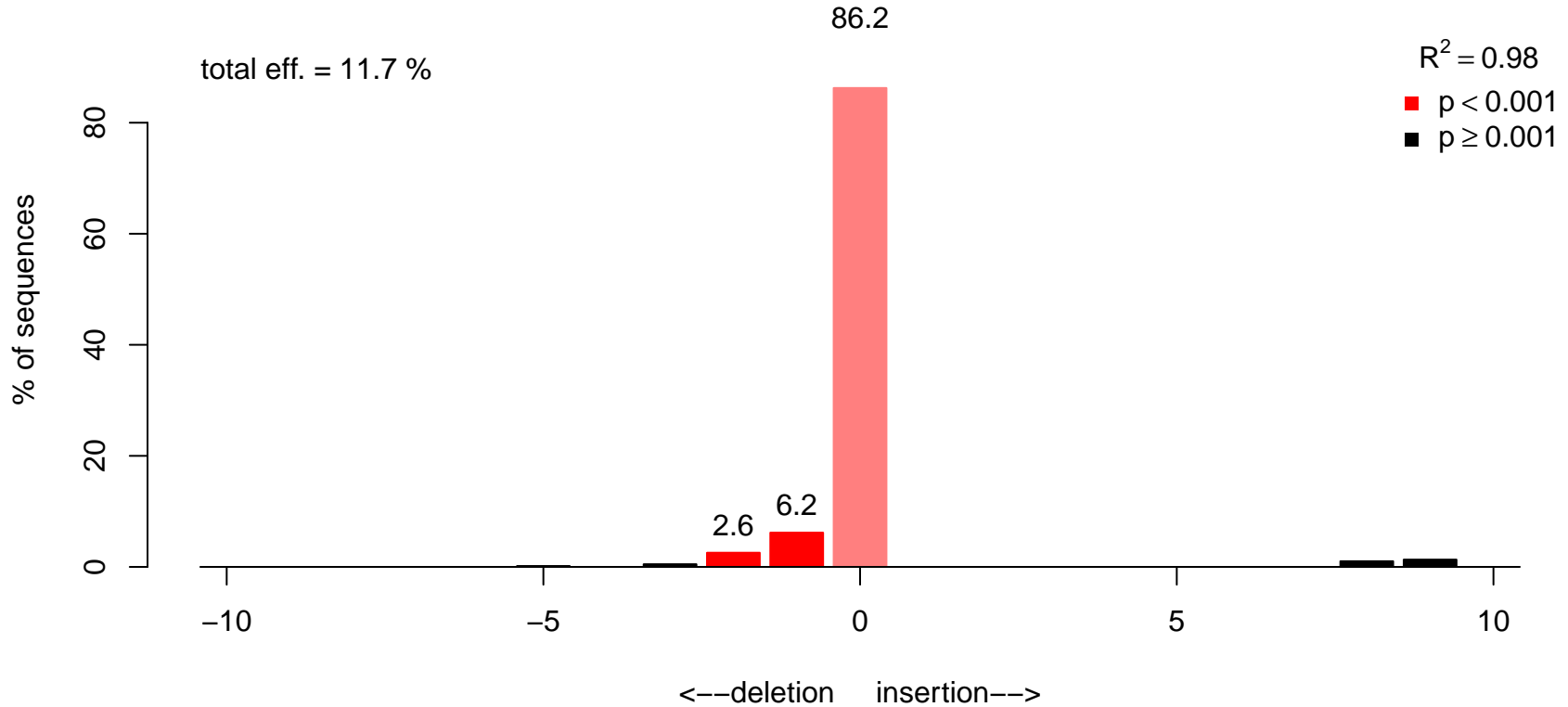


Warning: left boundary of decomposition window was adjusted 521 . It must be at least 5bp plus the maximum indel size downstream of the expected break site

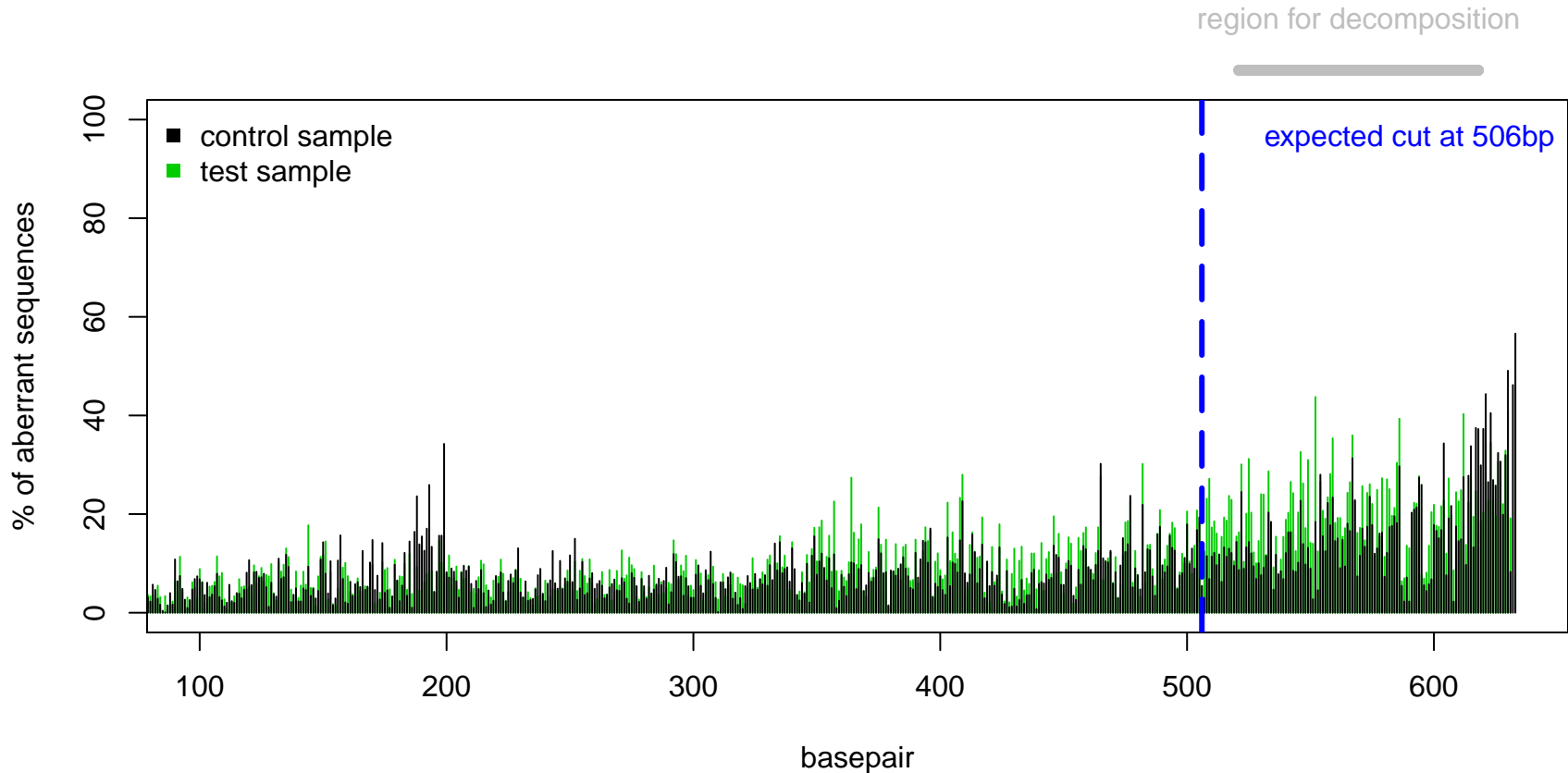
Warning: right boundary of decomposition window was adjusted to 618 . It must be at least 5bp plus the maximum indel size downstream of the expected break site

sample: WT/WT cell line, gRNA 2.1, forward
guide: TGGGACAGAACATCCCCAGG

total eff. = 11.7 %



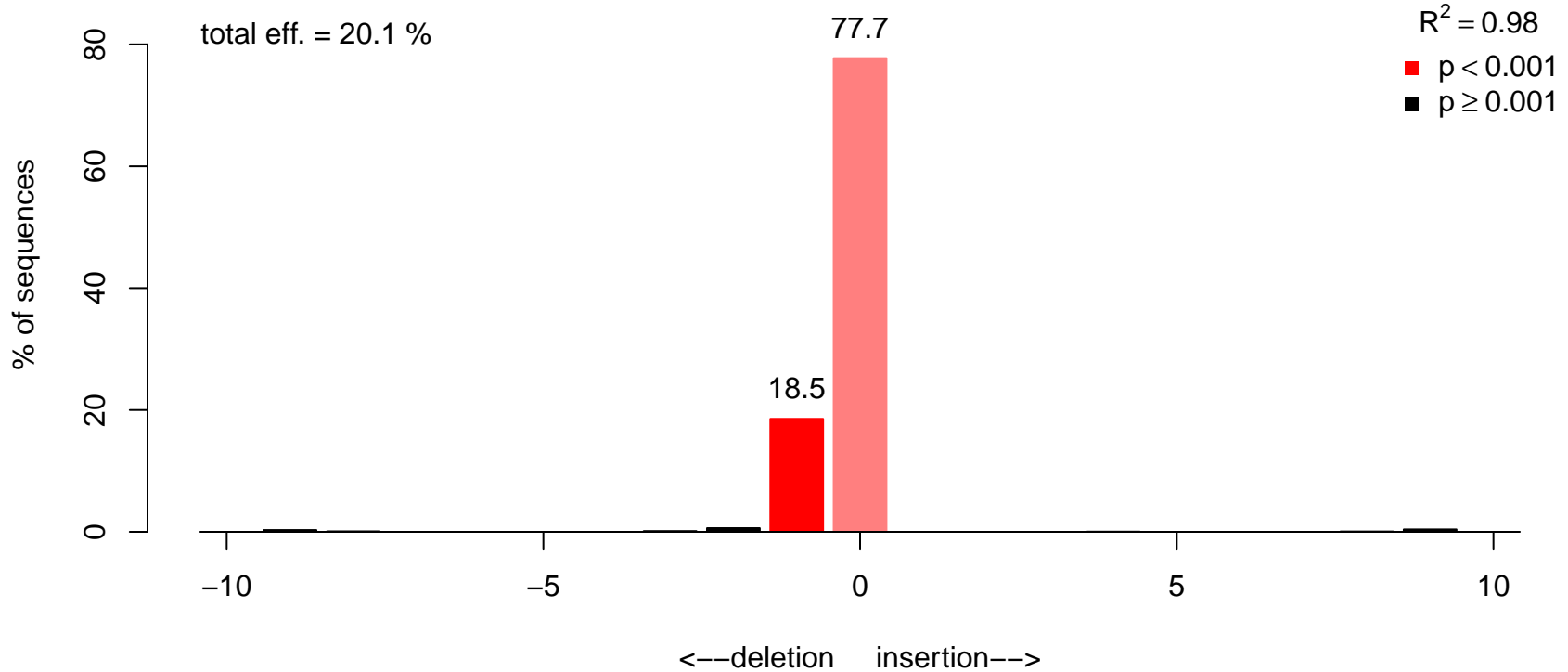
sample: WT/WT cell line, gRNA 2.1, forward
guide: TGGGACAGAACATCCCCAGG



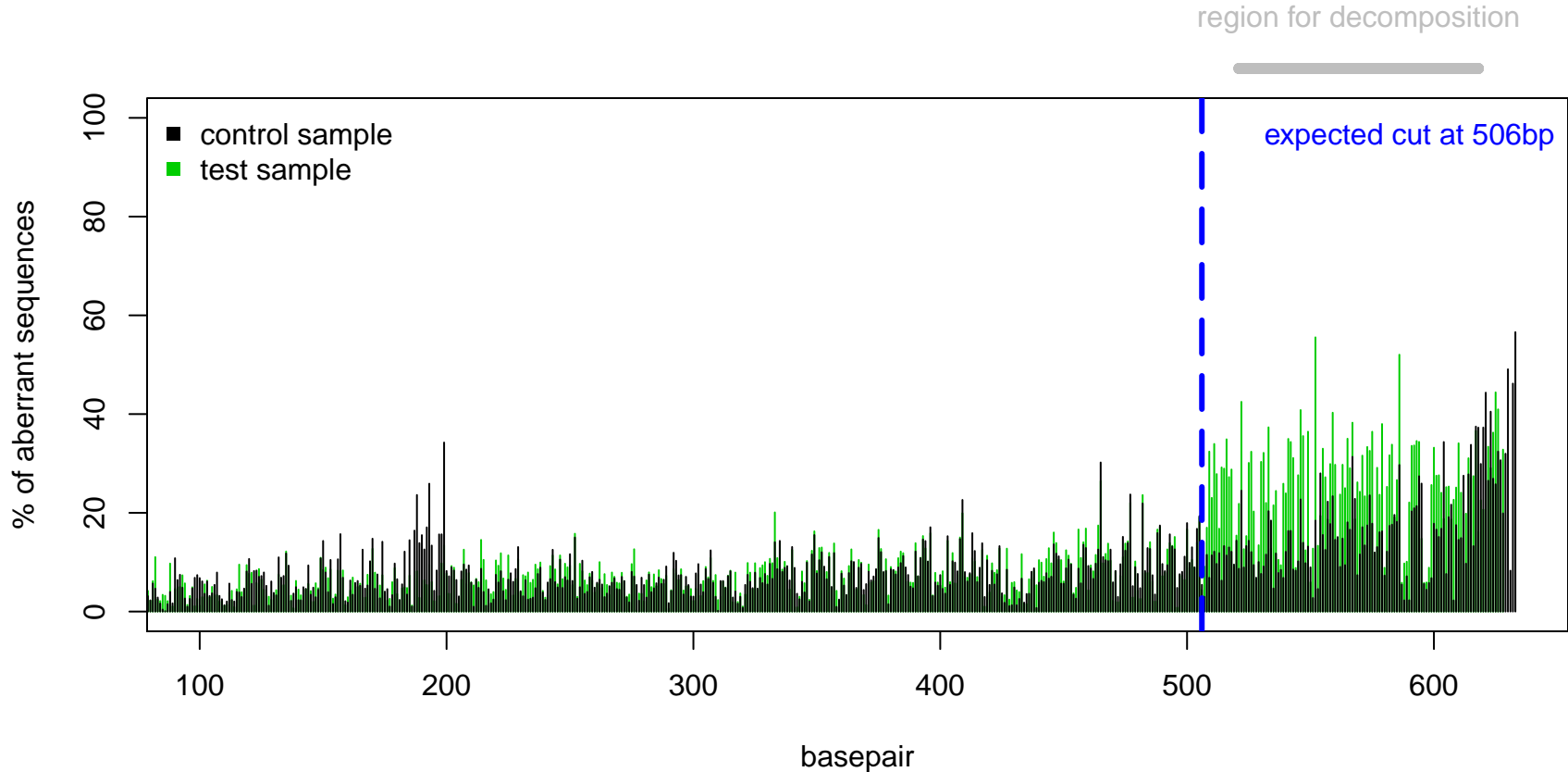
Warning: left boundary of decomposition window was adjusted 521 . It must be at least 5bp plus the maximum indel size downstream of the expected break site

Warning: right boundary of decomposition window was adjusted to 618 . It must be at least 5bp plus the maximum indel size downstream of the expected break site

sample: WT/WT cell line, gRNA 2.2, forward
guide: TGGGACAGAACATCCCCAGG



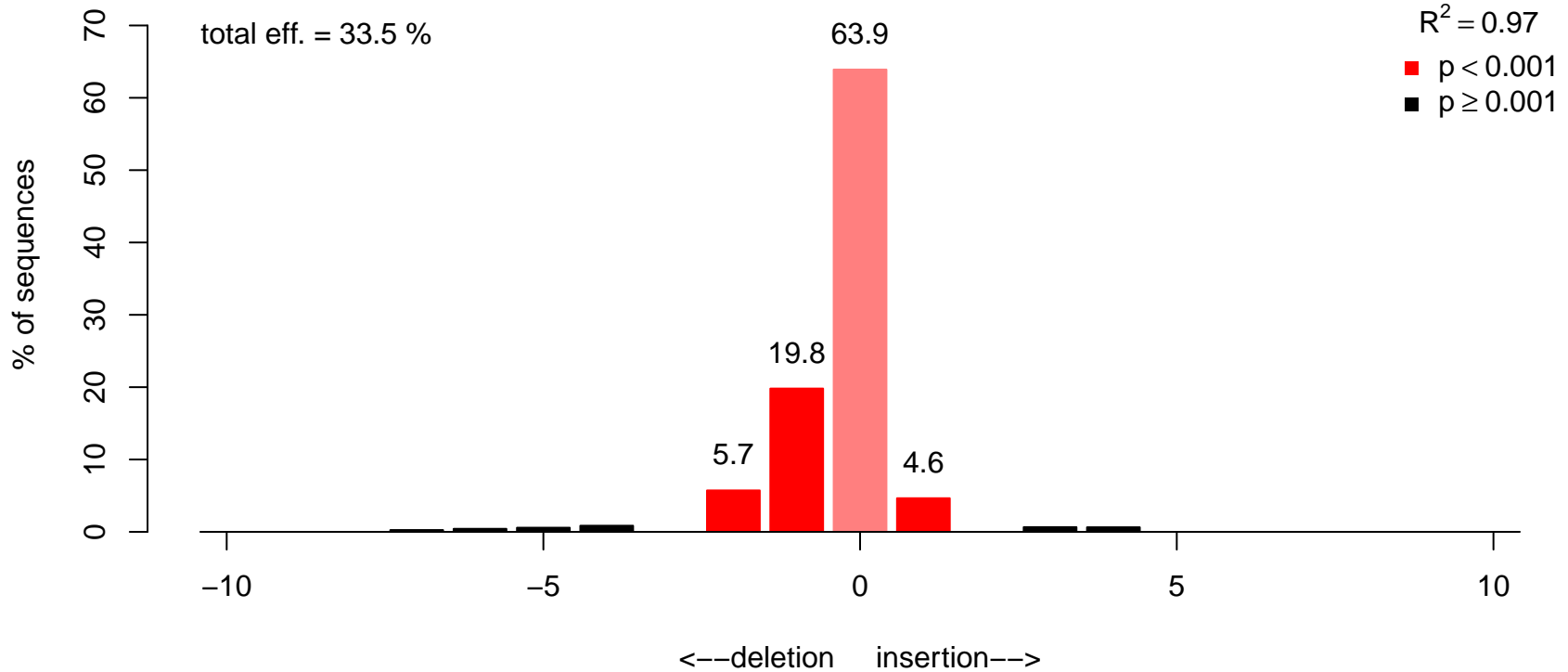
sample: WT/WT cell line, gRNA 2.2, forward
guide: TGGGACAGAACATCCCCAGG



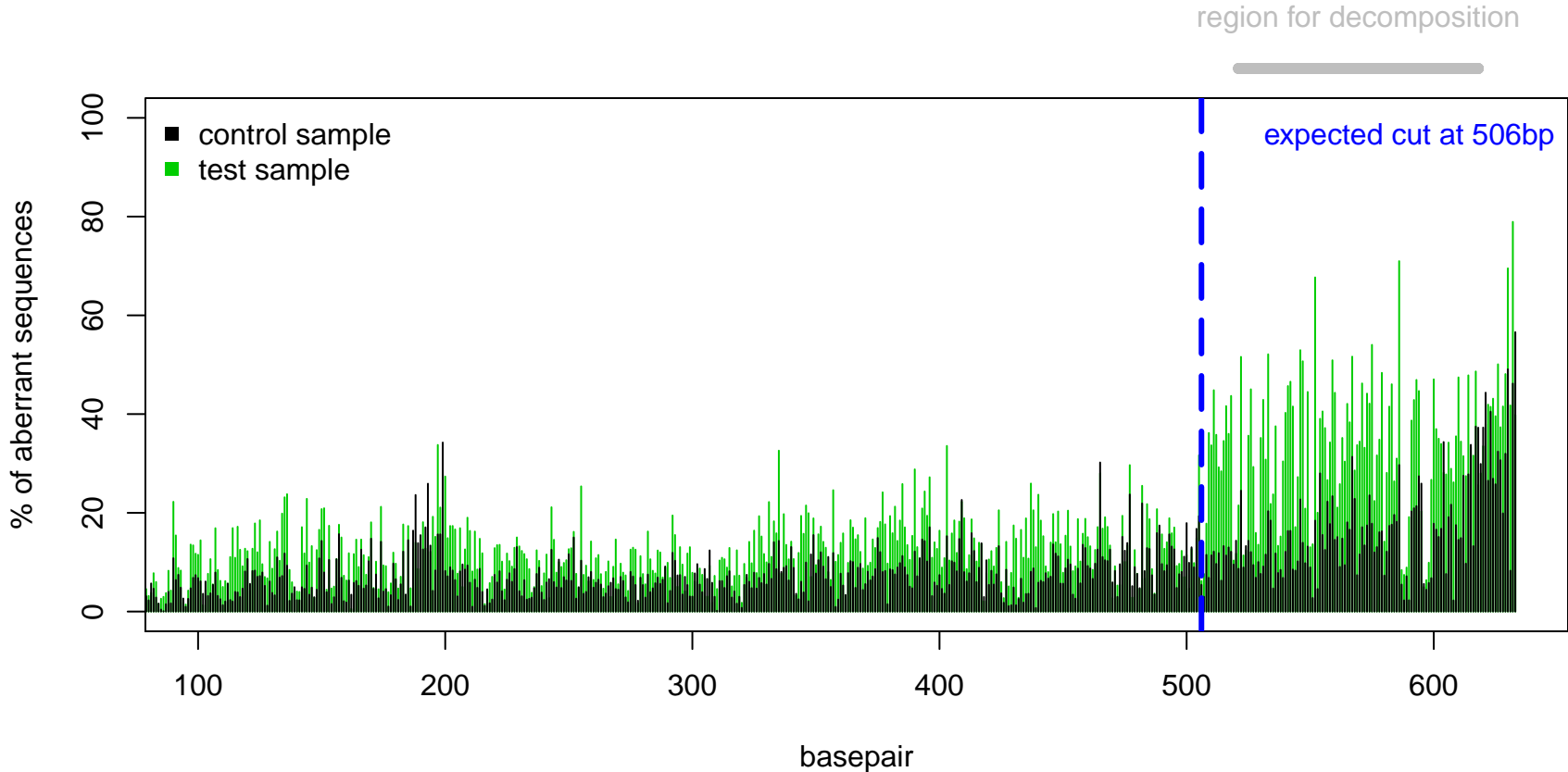
Warning: left boundary of decomposition window was adjusted 521 . It must be at least 5bp plus the maximum indel size downstream of the expected break site

Warning: right boundary of decomposition window was adjusted to 618 . It must be at least 5bp plus the maximum indel size downstream of the expected break site

sample: WT/WT cell line, gRNA 2.3, forward
guide: TGGGACAGAACATCCCCAGG



sample: WT/WT cell line, gRNA 2.3, forward
guide: TGGGACAGAACATCCCCAGG

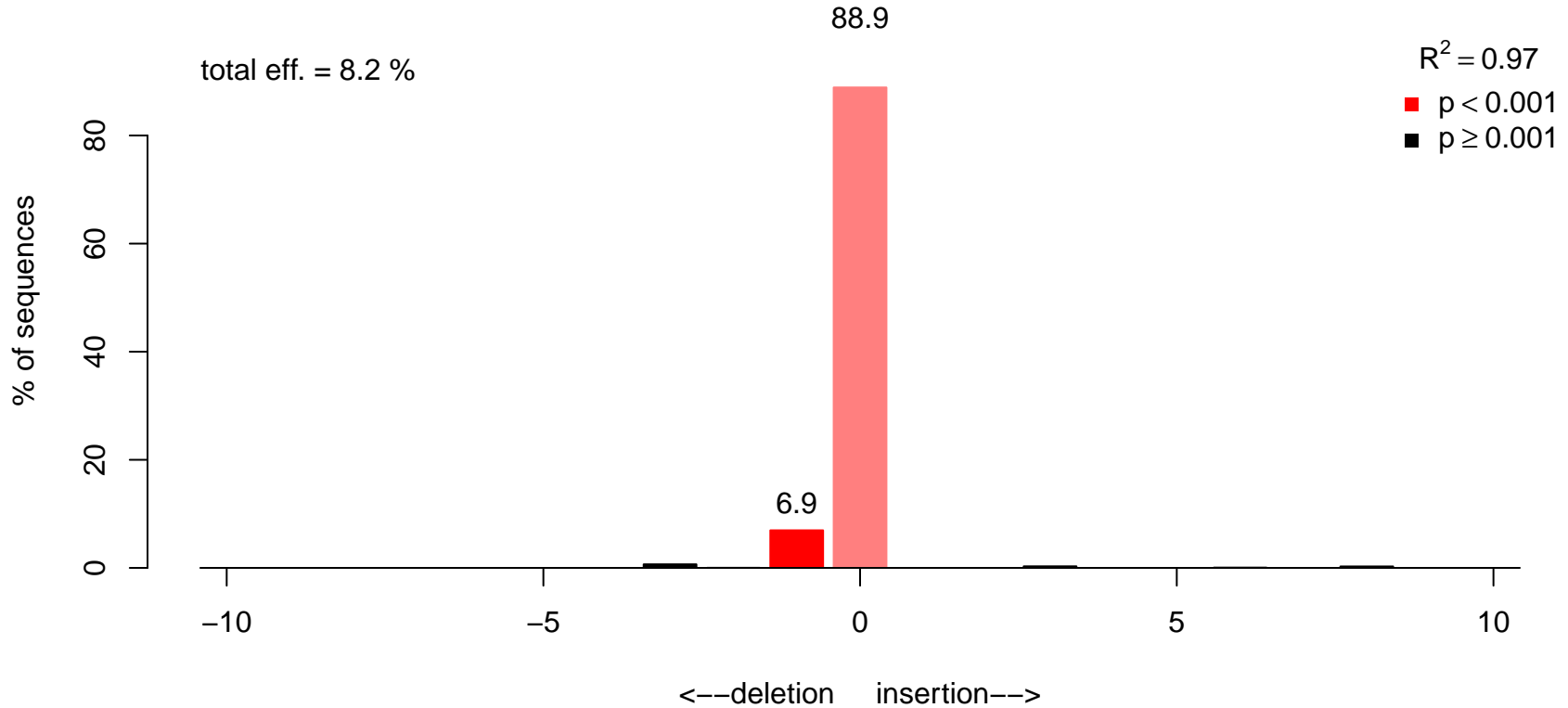


Warning: left boundary of decomposition window was adjusted 521 . It must be at least 5bp plus the maximum indel size downstream of the expected break site

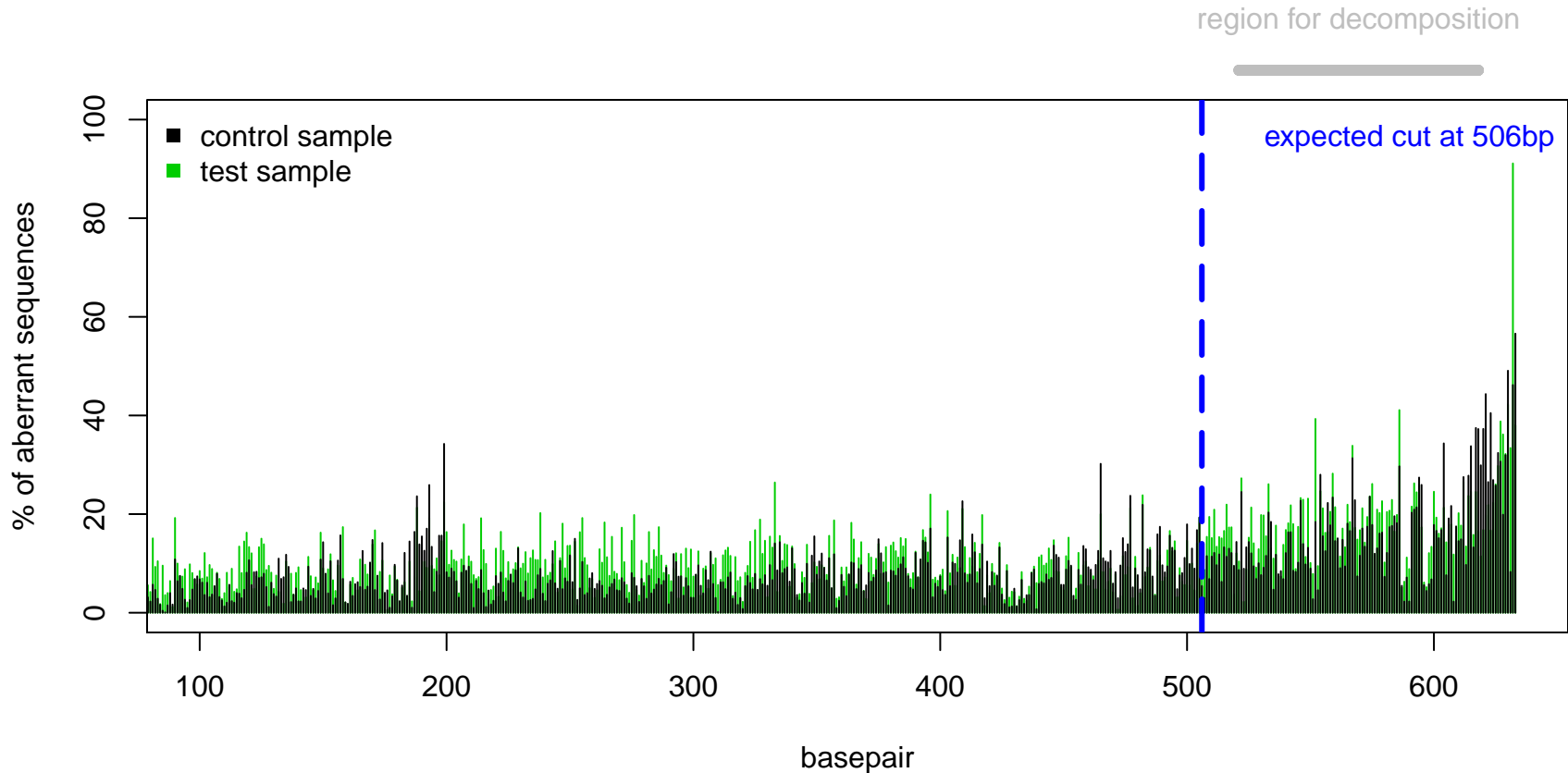
Warning: right boundary of decomposition window was adjusted to 618 . It must be at least 5bp plus the maximum indel size downstream of the expected break site

sample: WT/WT cell line, gRNA 2.4, forward
guide: TGGTAATGTCCCTCCTGGGG

total eff. = 8.2 %



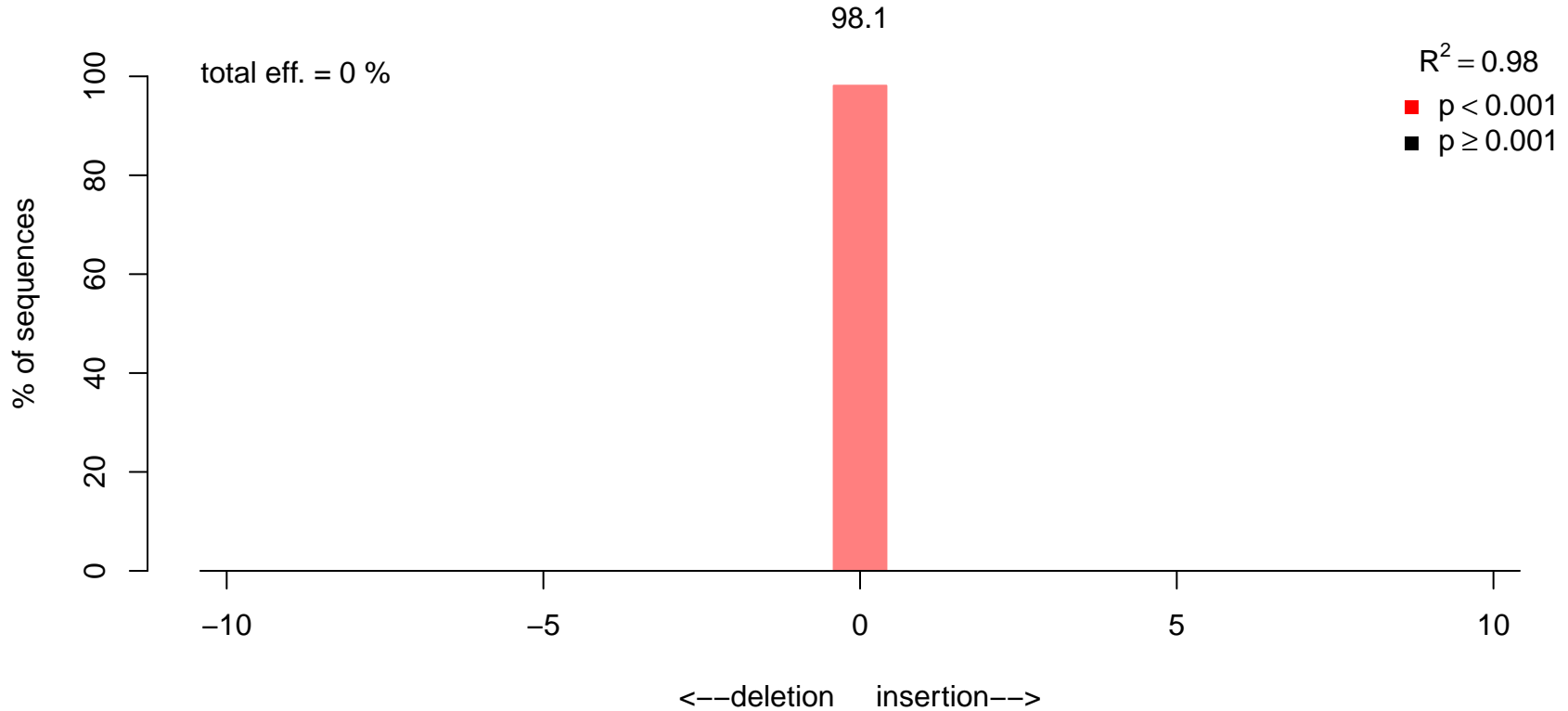
sample: WT/WT cell line, gRNA 2.4, forward
guide: TGGTAATGTCCCTCCTGGGG



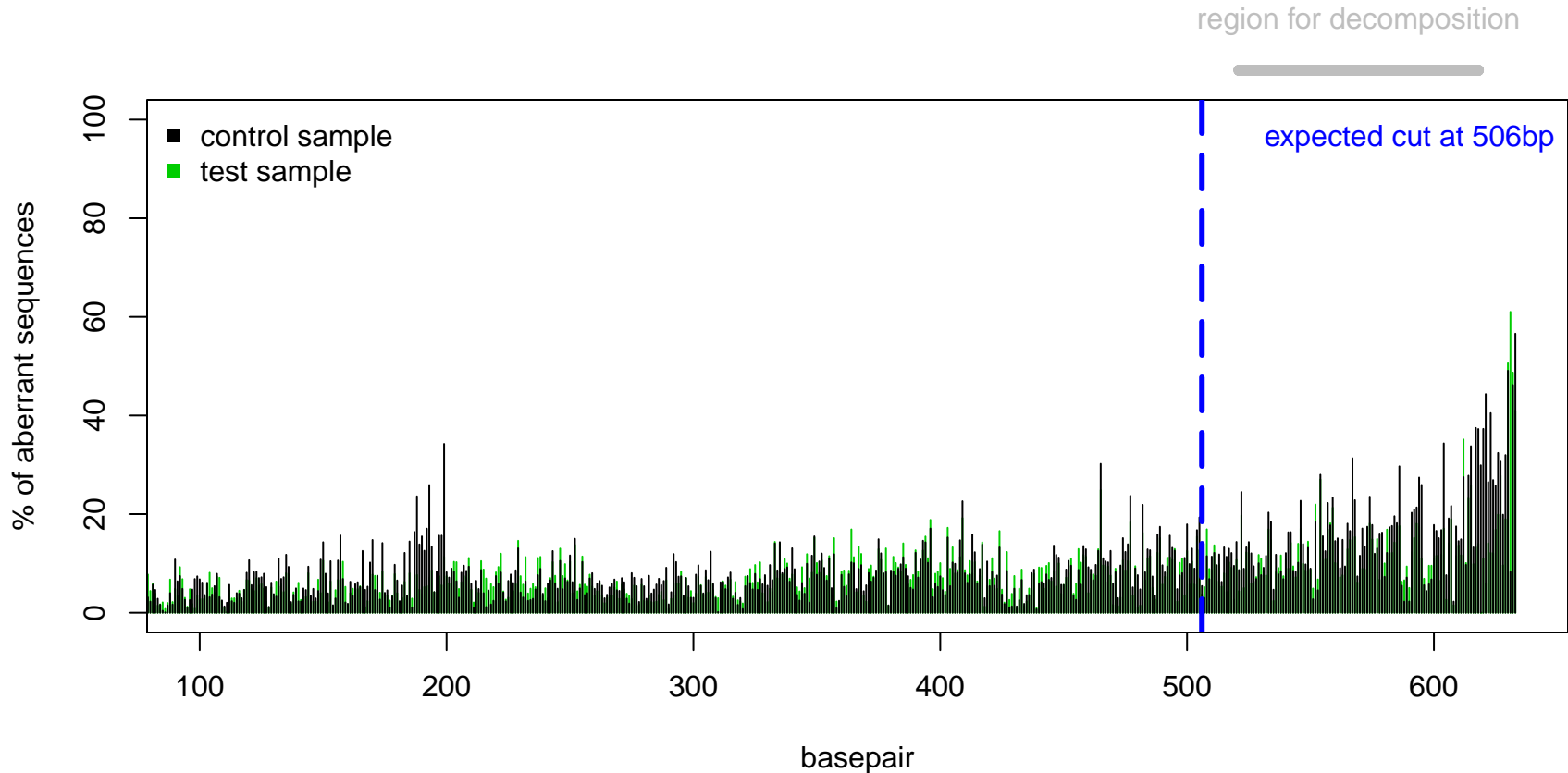
Warning: left boundary of decomposition window was adjusted 521 . It must be at least 5bp plus the maximum indel size downstream of the expected break site

Warning: right boundary of decomposition window was adjusted to 618 . It must be at least 5bp plus the maximum indel size downstream of the expected break site

sample: WT/WT cell line, gRNA 3.1, forward
guide: TGGTAATGTCCCTCCTGGGG



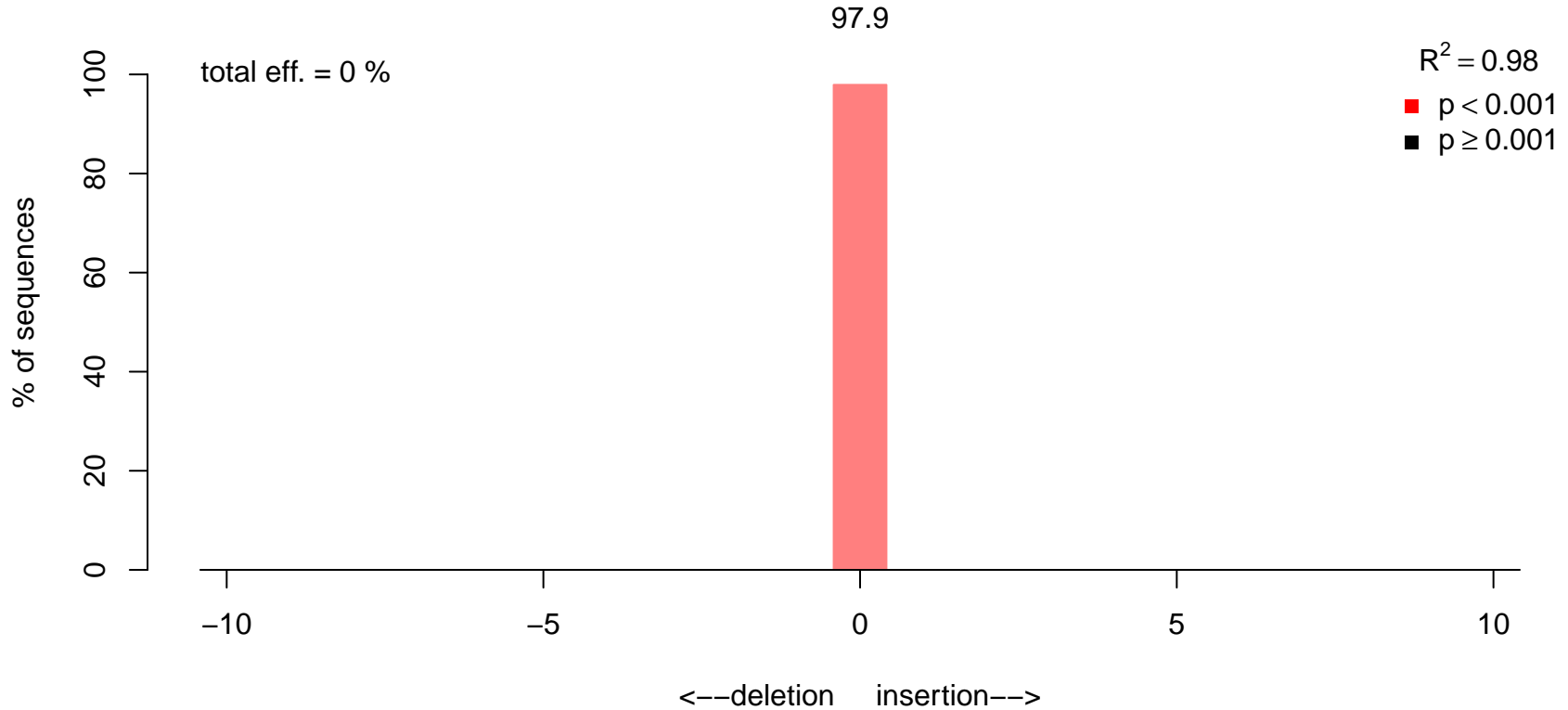
sample: WT/WT cell line, gRNA 3.1, forward
guide: TGGTAATGTCCCTCCTGGGG



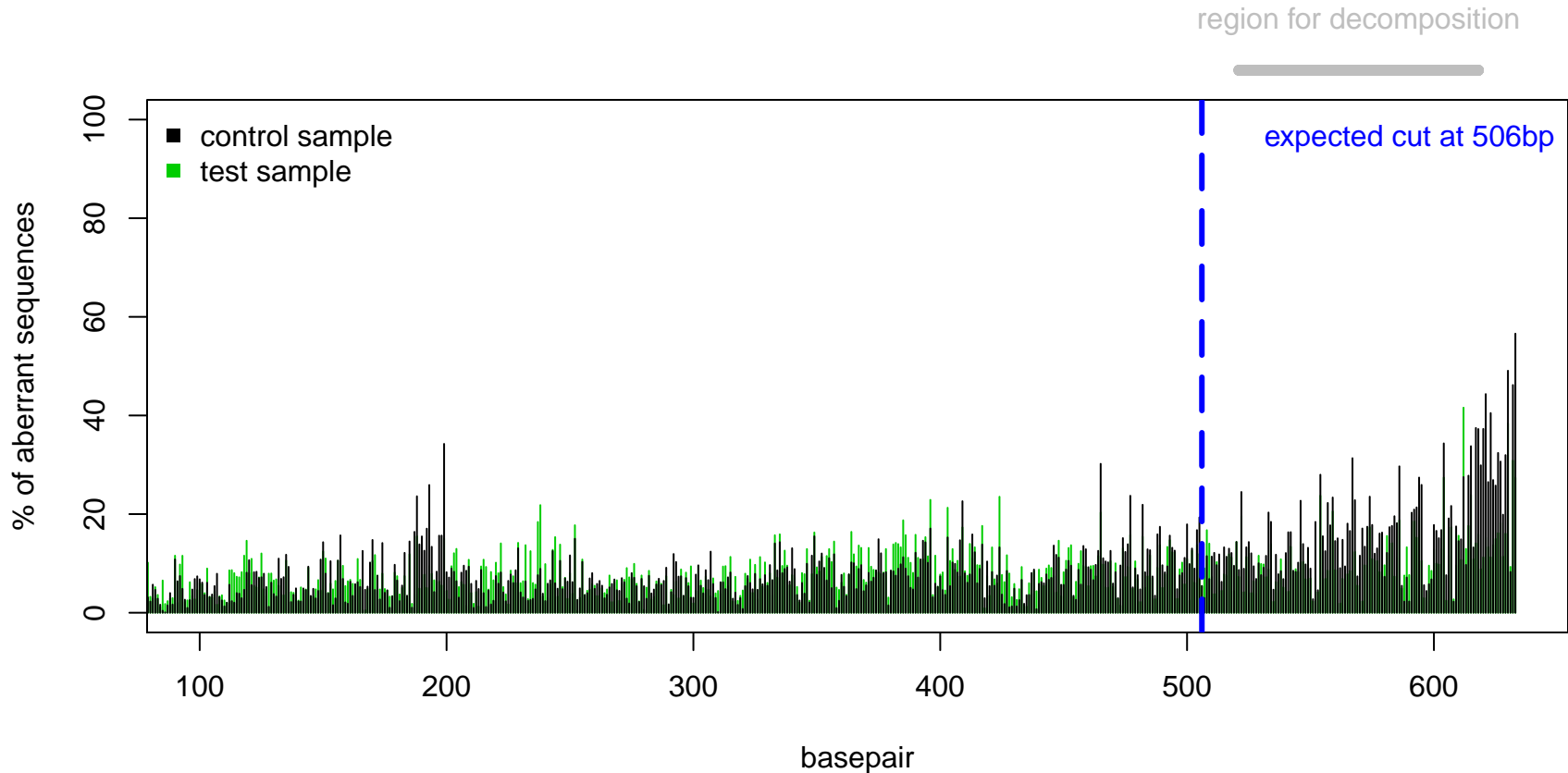
Warning: left boundary of decomposition window was adjusted 521 . It must be at least 5bp plus the maximum indel size downstream of the expected break site

Warning: right boundary of decomposition window was adjusted to 618 . It must be at least 5bp plus the maximum indel size downstream of the expected break site

sample: WT/WT cell line, gRNA 3.2, forward
guide: TGGTAATGTCCCTCCTGGGG



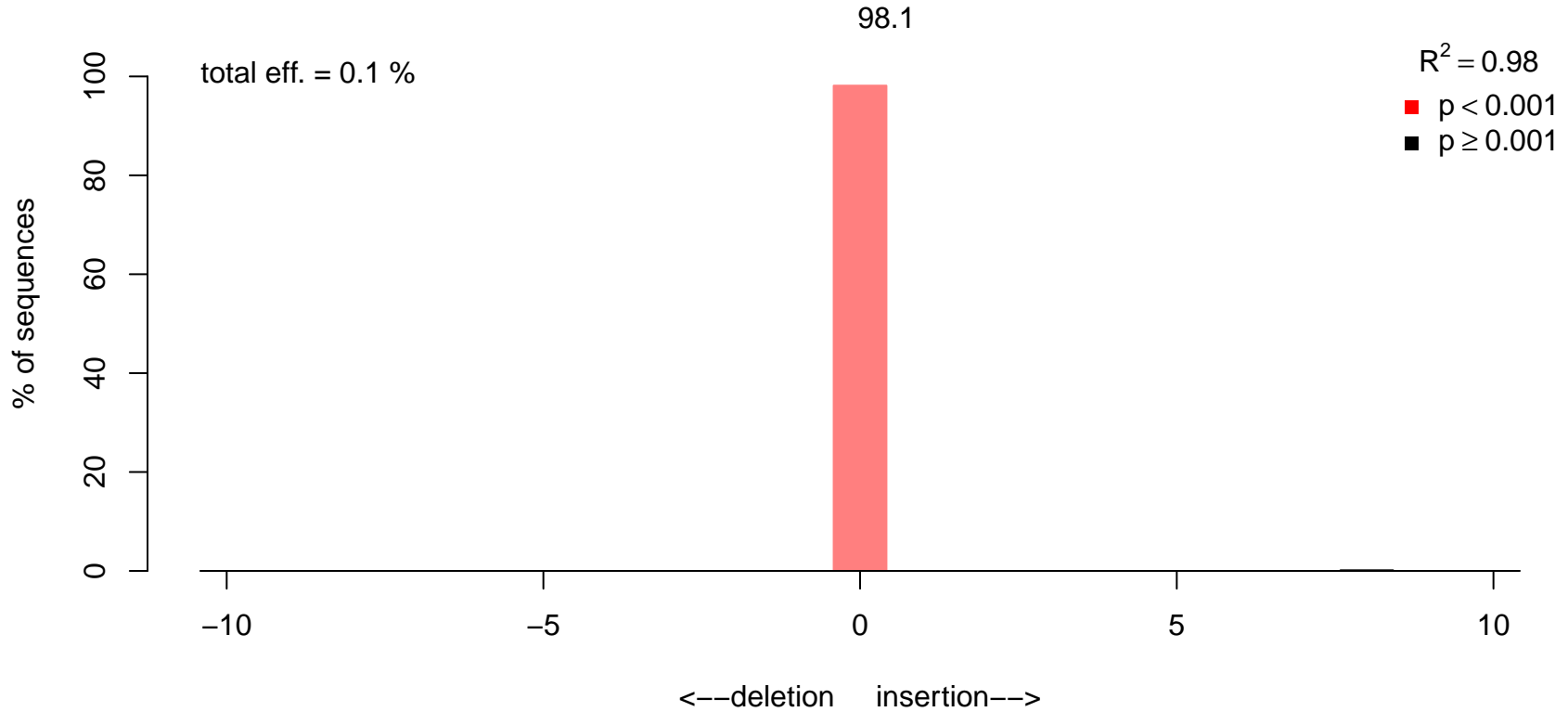
sample: WT/WT cell line, gRNA 3.2, forward
guide: TGGTAATGTCCCTCCTGGGG



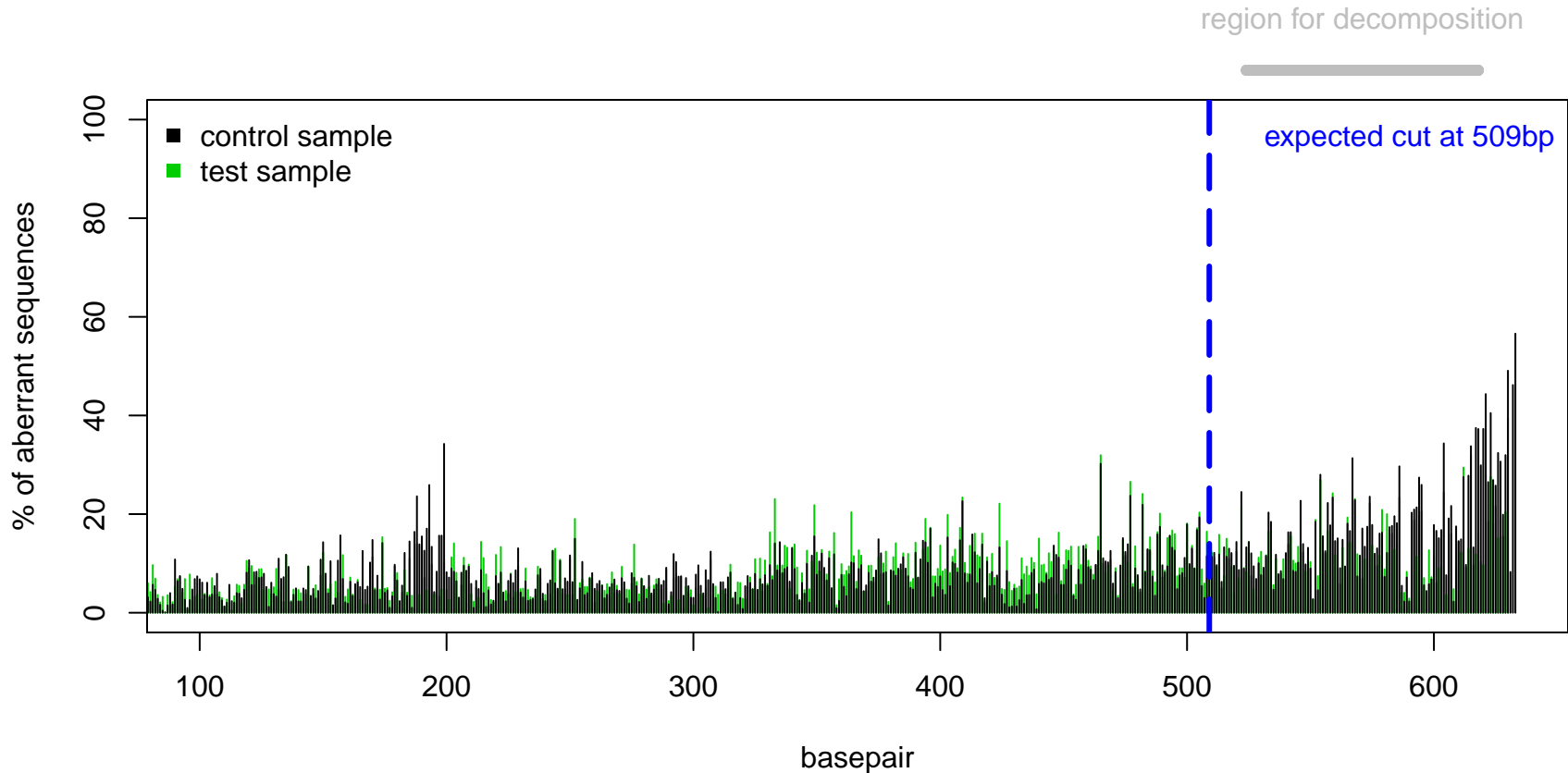
Warning: left boundary of decomposition window was adjusted 521 . It must be at least 5bp plus the maximum indel size downstream of the expected break site

Warning: right boundary of decomposition window was adjusted to 618 . It must be at least 5bp plus the maximum indel size downstream of the expected break site

sample: WT/WT cell line, gRNA 3,3, forward
guide: GGGTGGGACAGAACATCCCC



sample: WT/WT cell line, gRNA 3.3, forward
guide: GGGTGGGACAGAACATCCCC

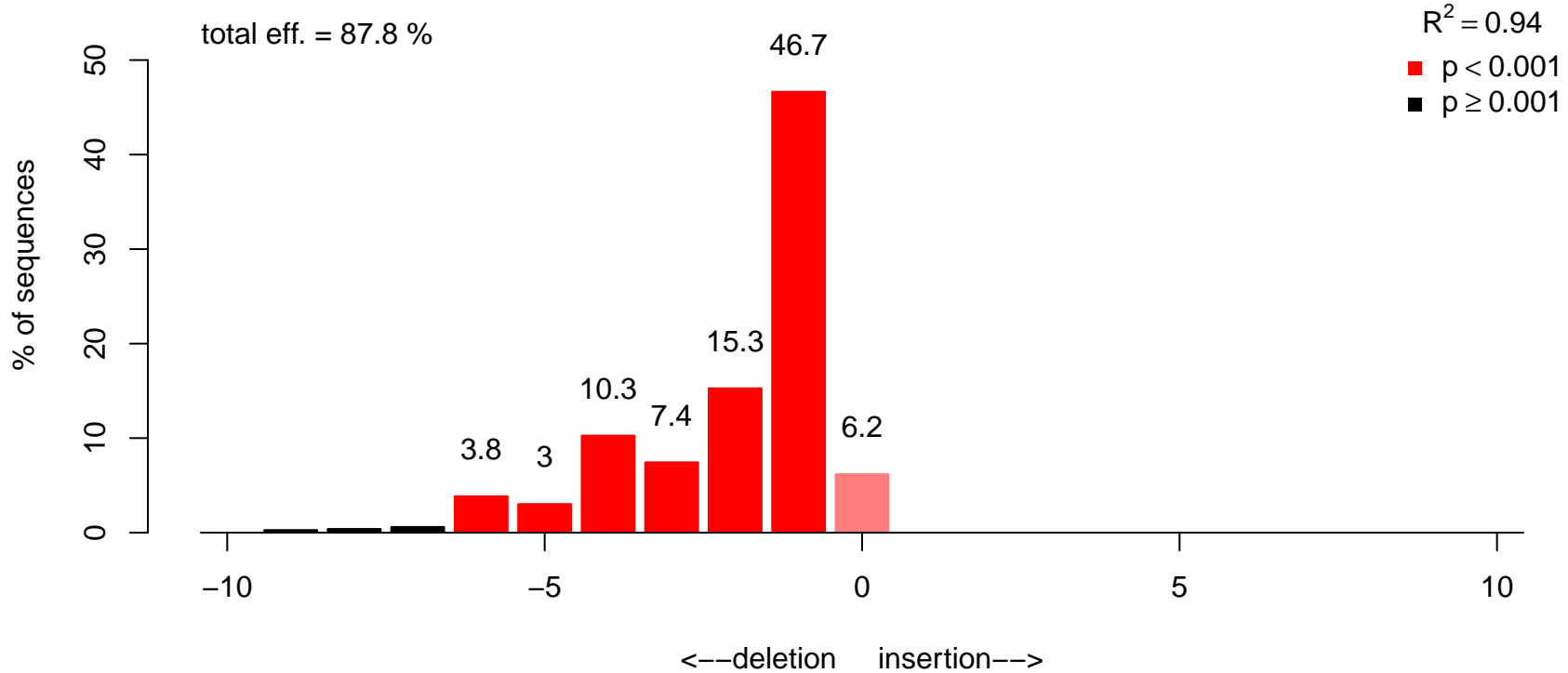


Warning: left boundary of decomposition window was adjusted 524 . It must be at least 5bp plus the maximum indel size downstream of the expected break site

Warning: right boundary of decomposition window was adjusted to 618 . It must be at least 5bp plus the maximum indel size downstream of the expected break site

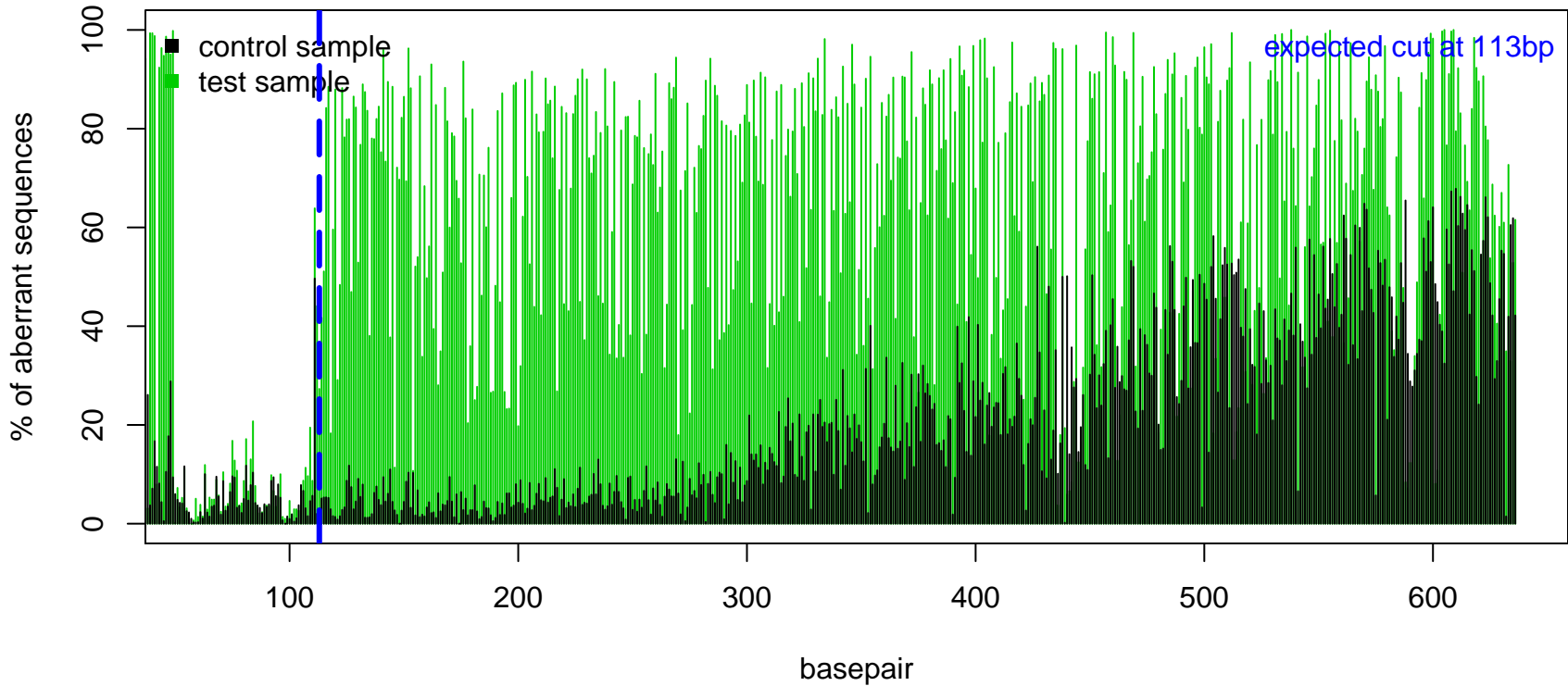
sample: Bth/WT cell line, gRNA WT, reverse
guide: GGGTGGGACAGAACTTCCCC

total eff. = 87.8 %



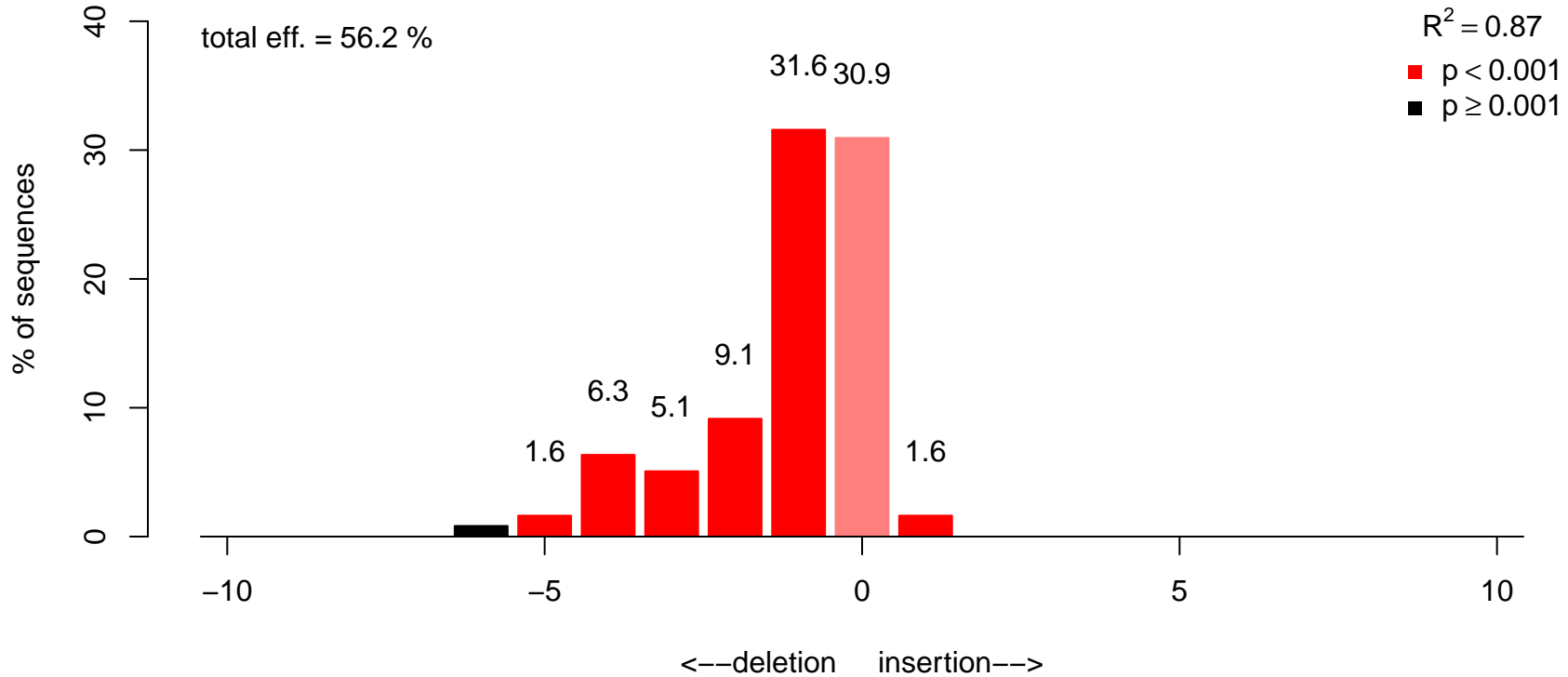
sample: Bth/WT cell line, gRNA WT, reverse
guide: GGGTGGGACAGAACTTCCCC

region for decomposition



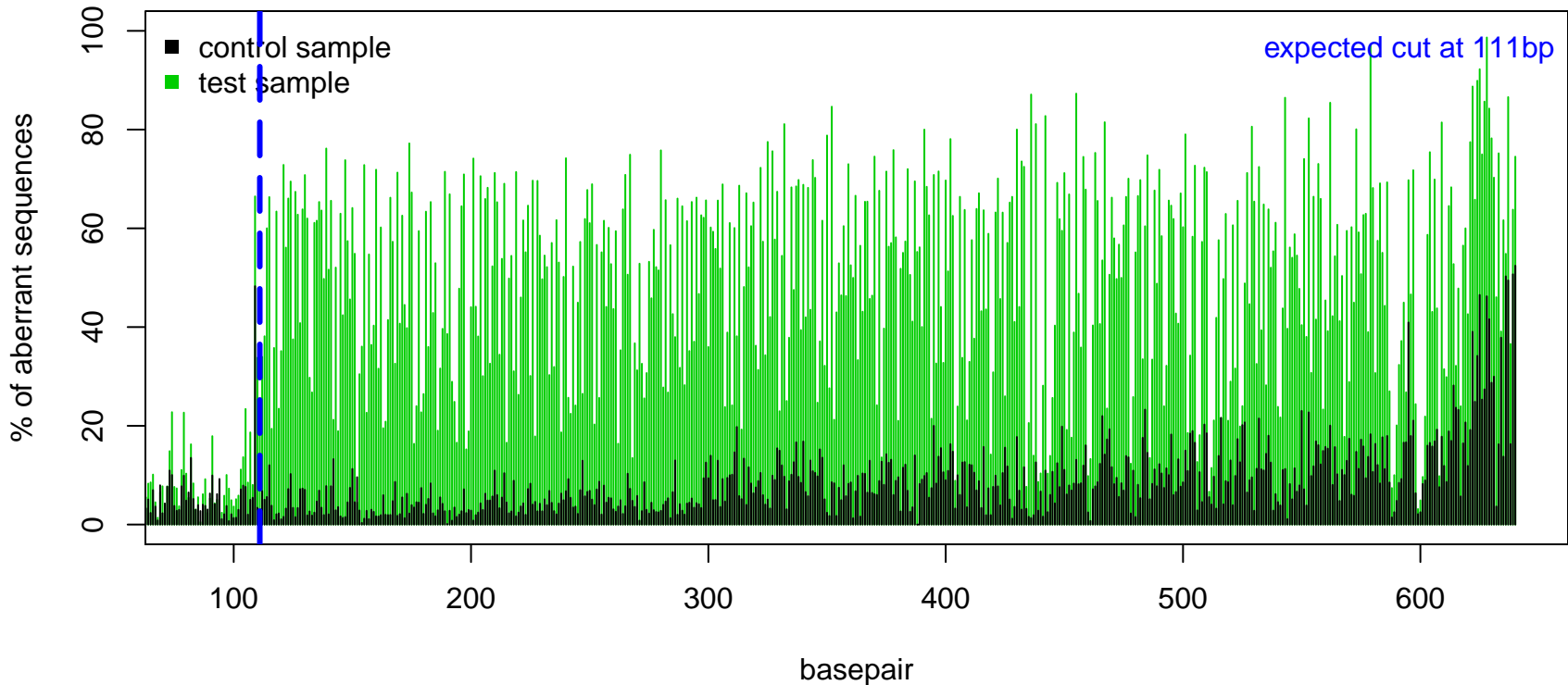
Warning: left boundary of decomposition window was adjusted 128 . It must be at least 5bp plus the maximum indel size downstream of the expected break site

sample: Bth/WT cell line, gRNA 1.1, reverse
guide: GGGTGGGACAGAACTTCCCC



sample: Bth/WT cell line, gRNA 1.1, reverse
guide: GGGTGGGACAGAACTTCCCC

region for decomposition

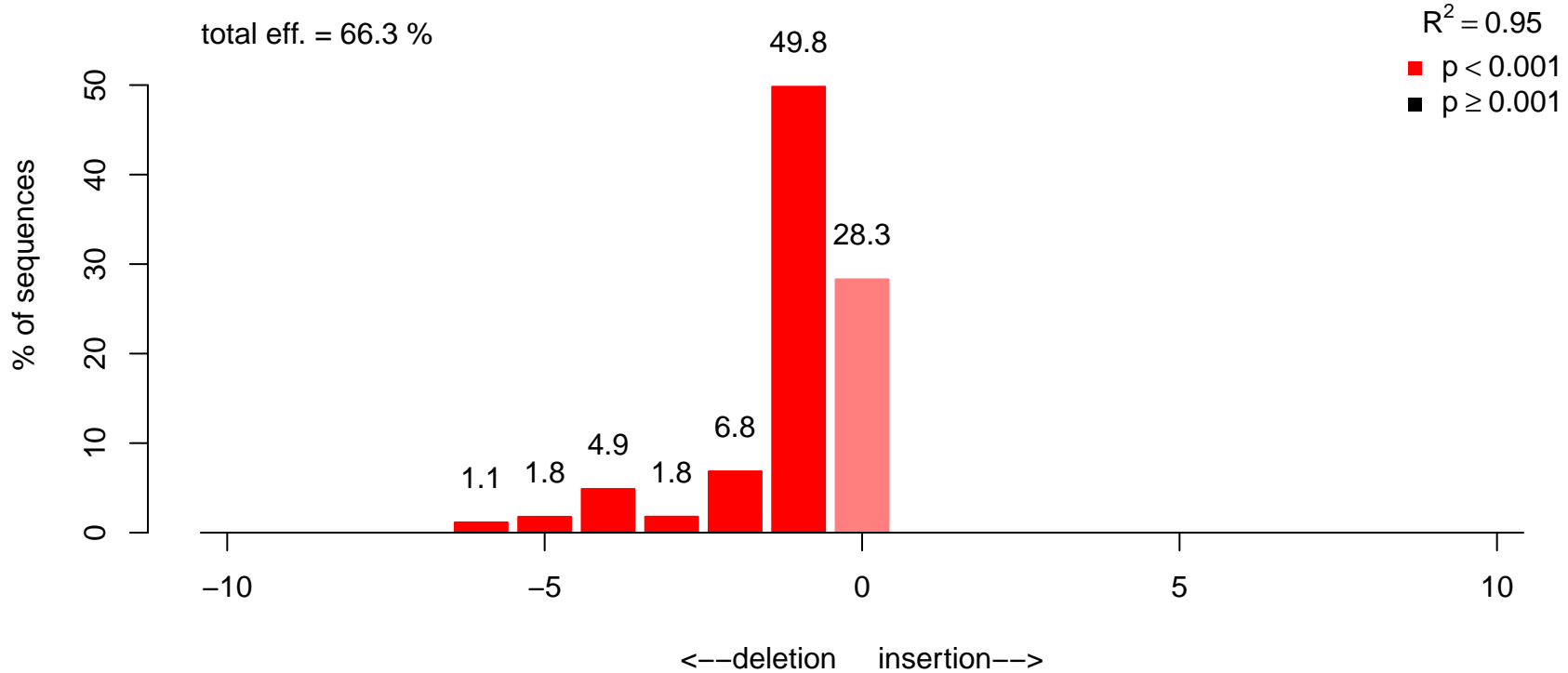


Warning: left boundary of decomposition window was adjusted 126 . It must be at least 5bp plus the maximum indel size downstream of the expected break site

Warning: right boundary of decomposition window was adjusted to 625 . It must be at least 5bp plus the maximum indel size downstream of the expected break site

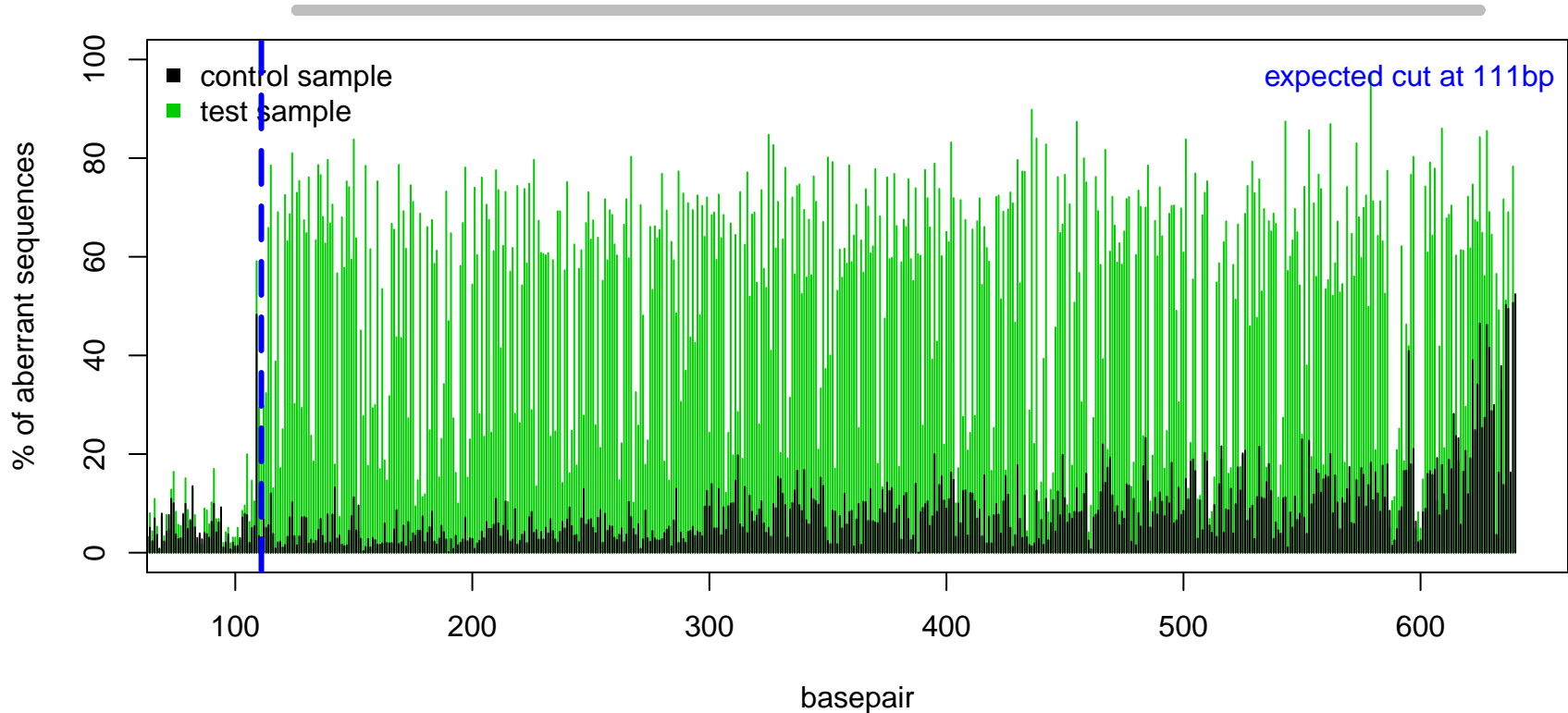
sample: Bth/WT cell line, gRNA 1.2, reverse
guide: GGGTGGGACAGAACTTCCCC

total eff. = 66.3 %



sample: Bth/WT cell line, gRNA 1.2, reverse
guide: GGGTGGGACAGAACTTCCCC

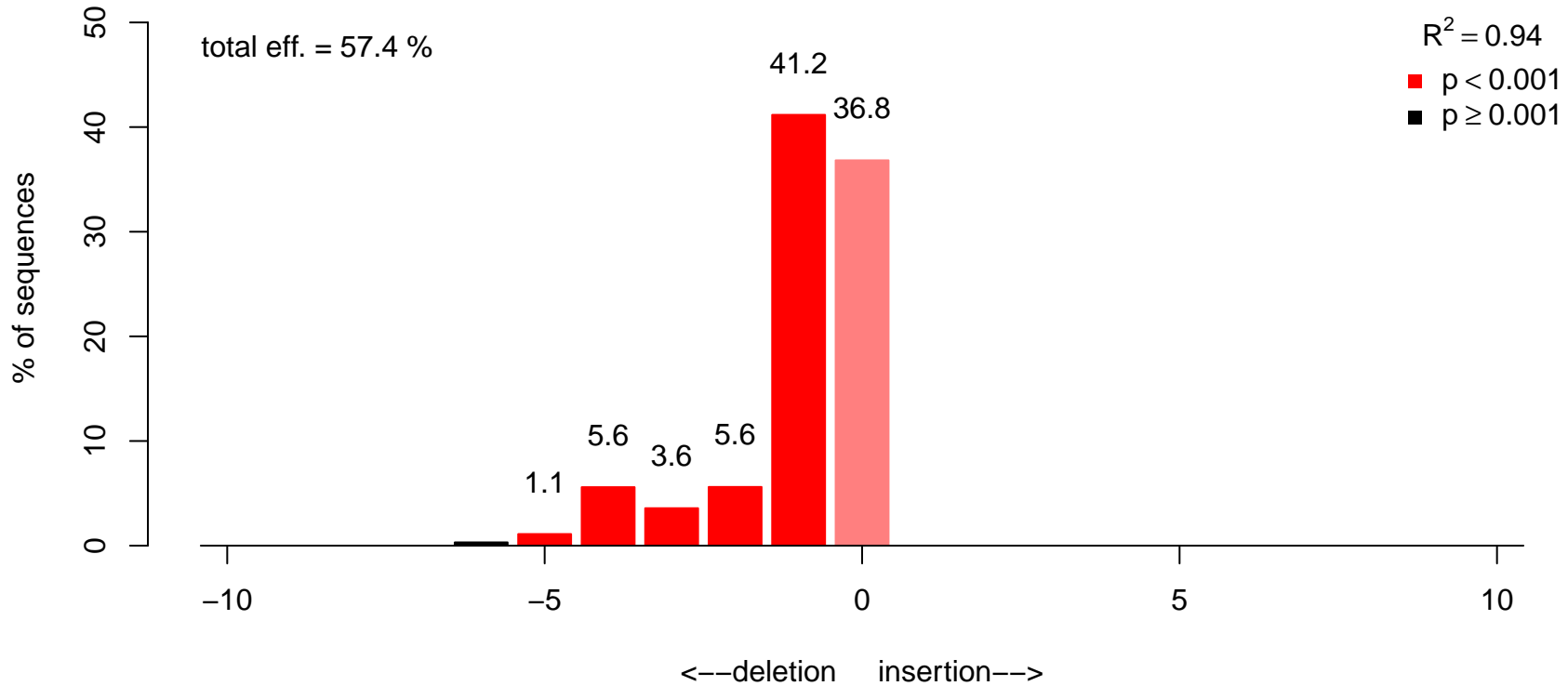
region for decomposition



Warning: left boundary of decomposition window was adjusted 126 . It must be at least 5bp plus the maximum indel size downstream of the expected break site

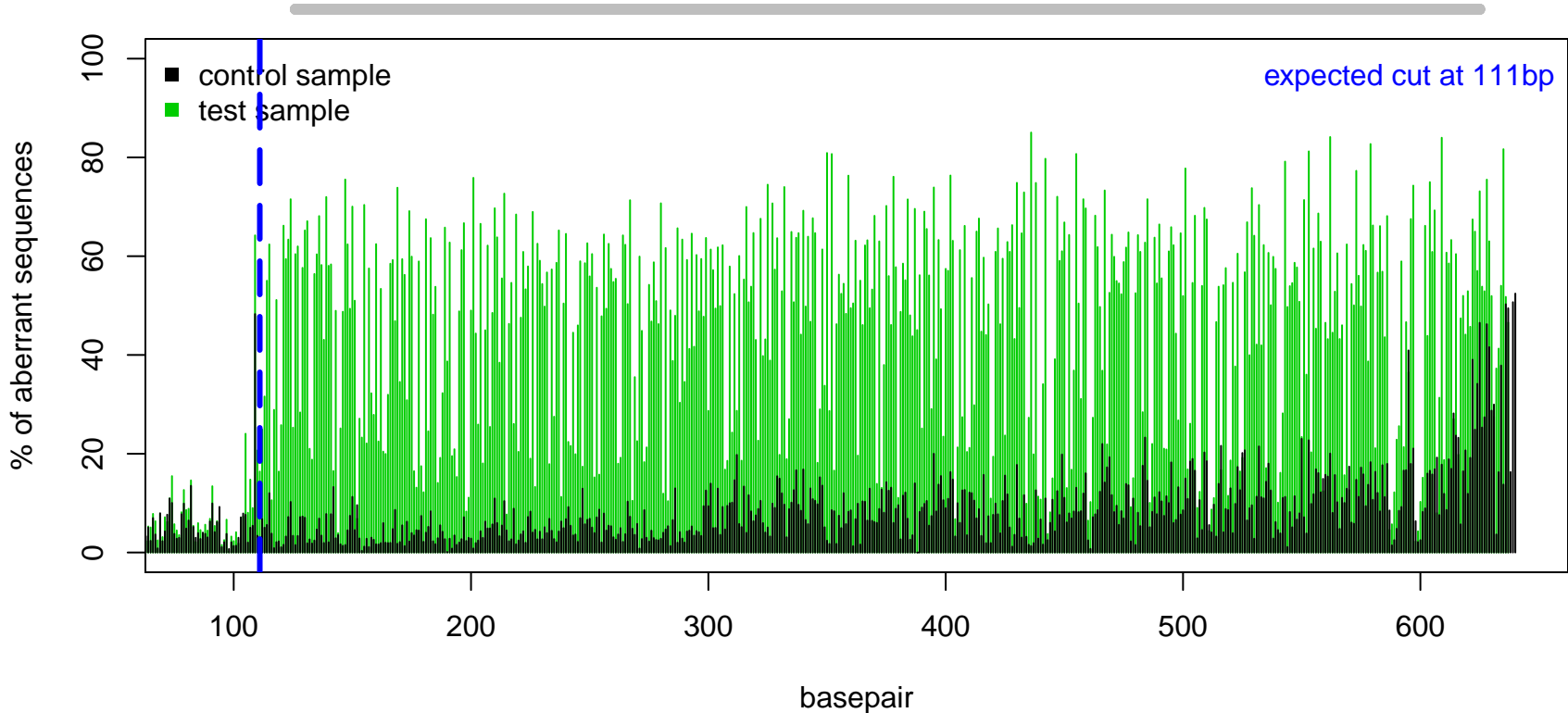
Warning: right boundary of decomposition window was adjusted to 625 . It must be at least 5bp plus the maximum indel size downstream of the expected break site

sample: Bth/WT cell line, gRNA 1.3, reverse
guide: GGGTGGGACAGAACTTCCCC



sample: Bth/WT cell line, gRNA 1.3, reverse
guide: GGGTGGGACAGAACTTCCCC

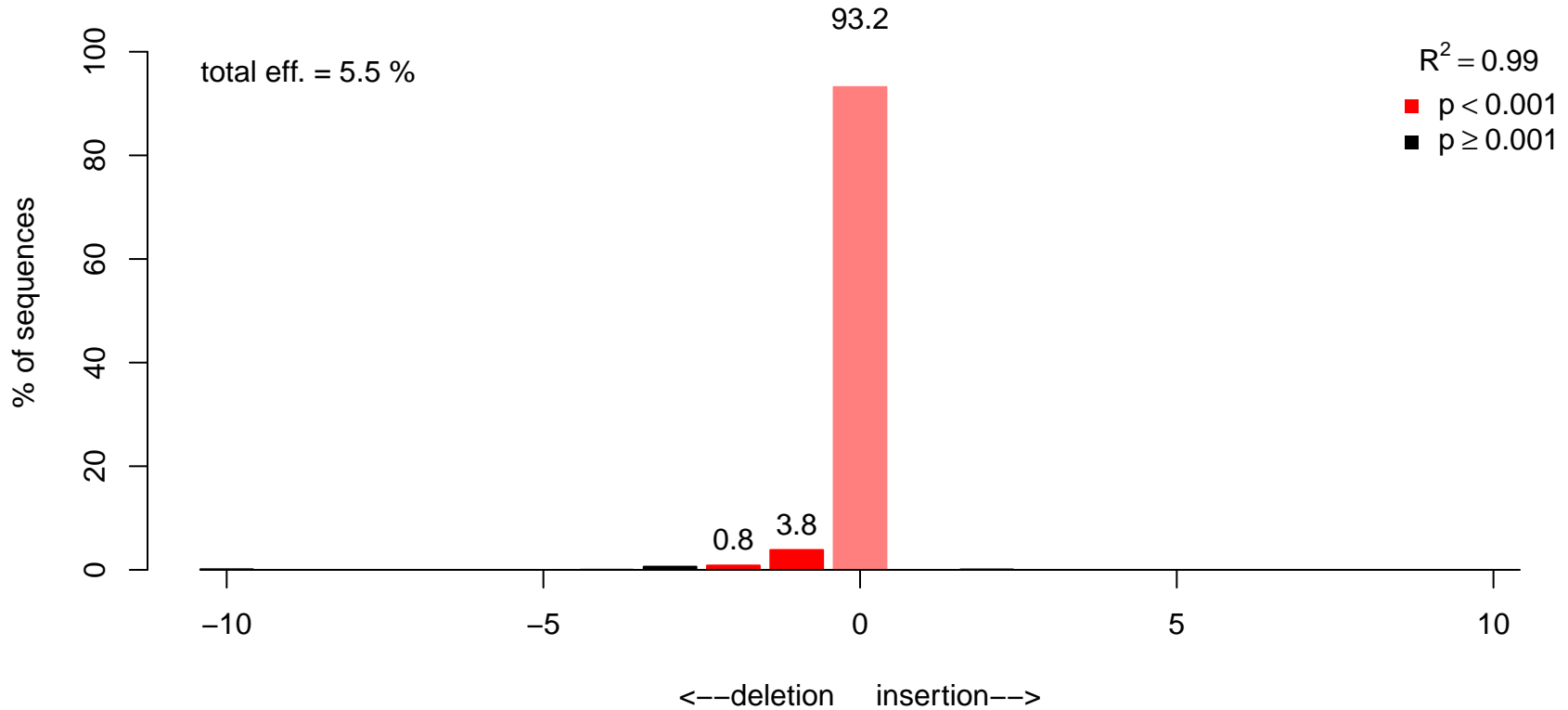
region for decomposition



Warning: left boundary of decomposition window was adjusted 126 . It must be at least 5bp plus the maximum indel size downstream of the expected break site

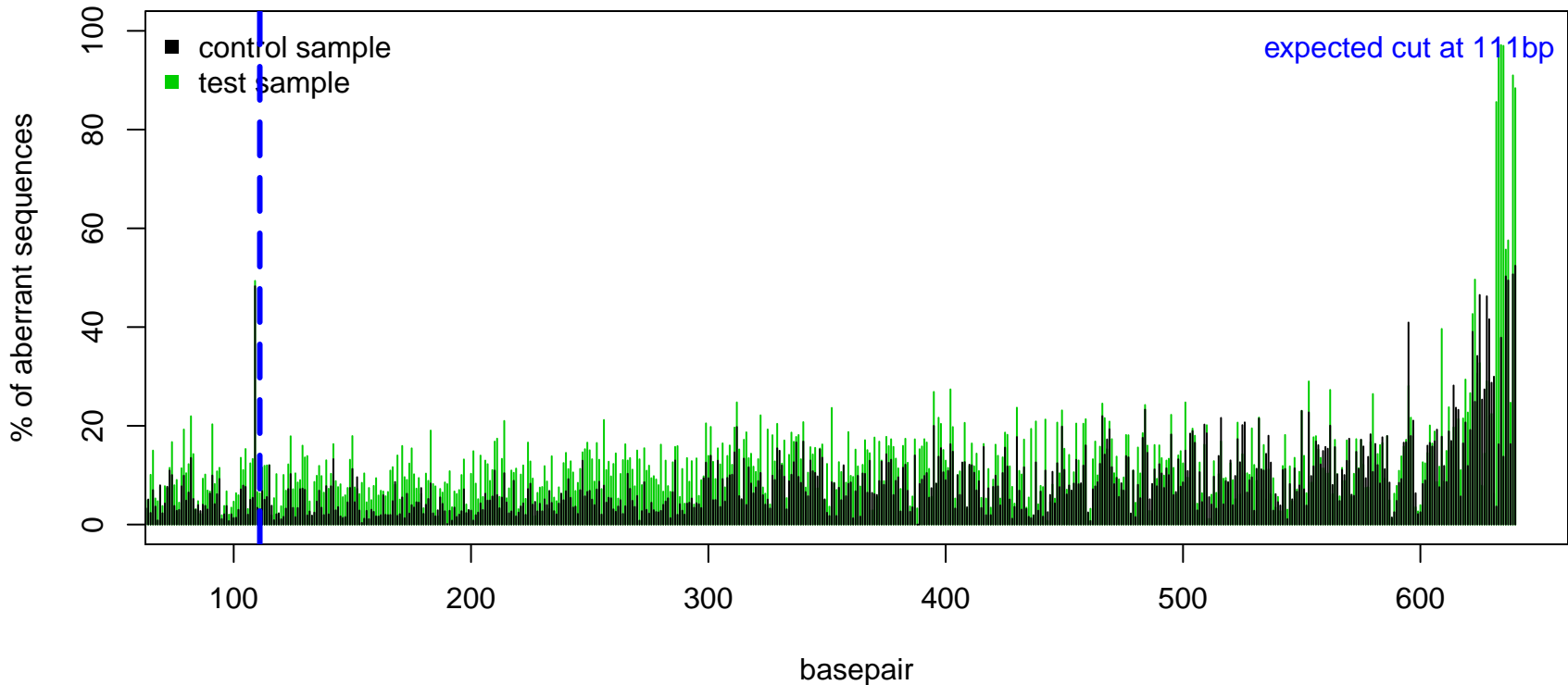
Warning: right boundary of decomposition window was adjusted to 625 . It must be at least 5bp plus the maximum indel size downstream of the expected break site

sample: Bth/WT cell line, gRNA 1.4, reverse
guide: GGGTGGGACAGAACTTCCCC



sample: Bth/WT cell line, gRNA 1.4, reverse
guide: GGGTGGGACAGAACTTCCCC

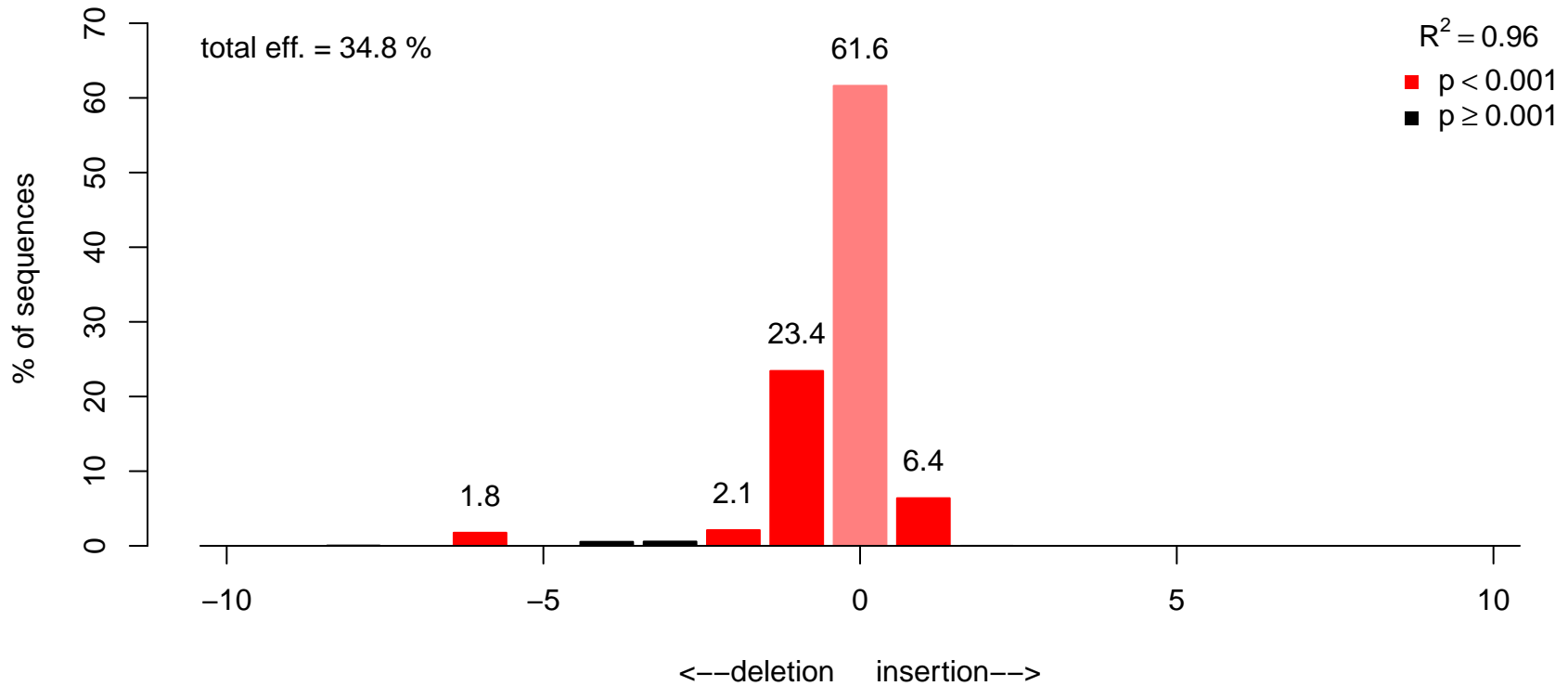
region for decomposition



Warning: left boundary of decomposition window was adjusted 126 . It must be at least 5bp plus the maximum indel size downstream of the expected break site

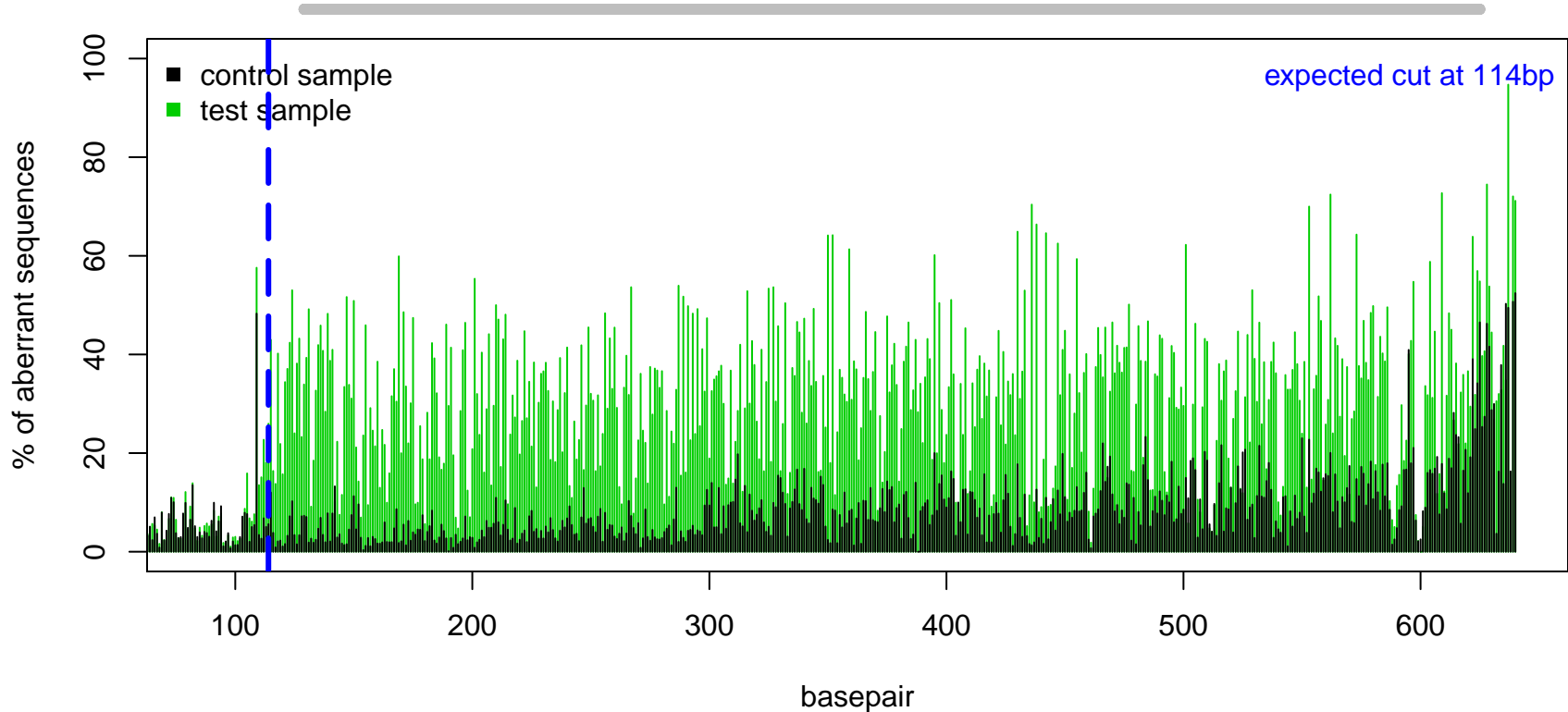
Warning: right boundary of decomposition window was adjusted to 625 . It must be at least 5bp plus the maximum indel size downstream of the expected break site

sample: Bth/WT cell line, gRNA 2.1, reverse
guide: TGGGACAGAACTTCCCCAGG



sample: Bth/WT cell line, gRNA 2.1, reverse
guide: TGGGACAGAACTTCCCCAGG

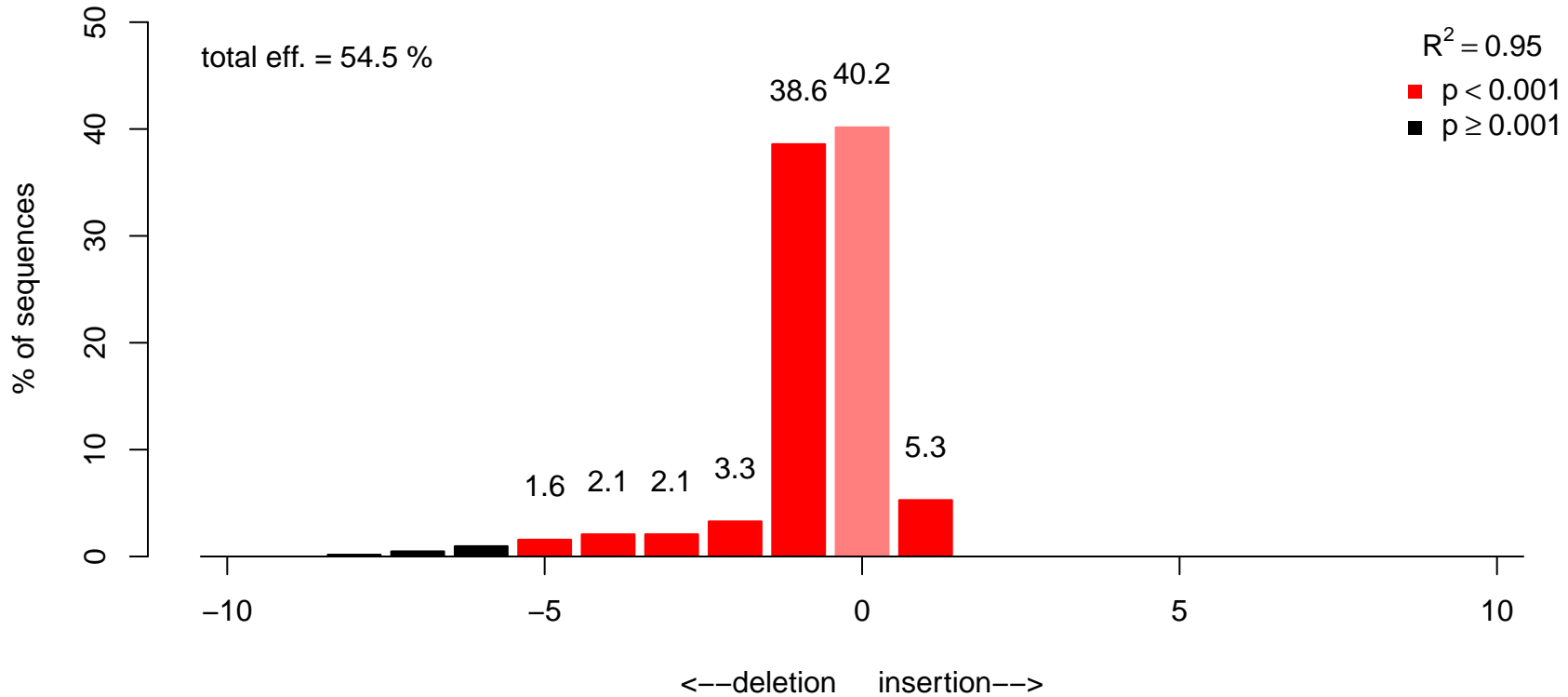
region for decomposition



Warning: left boundary of decomposition window was adjusted 129 . It must be at least 5bp plus the maximum indel size downstream of the expected break site

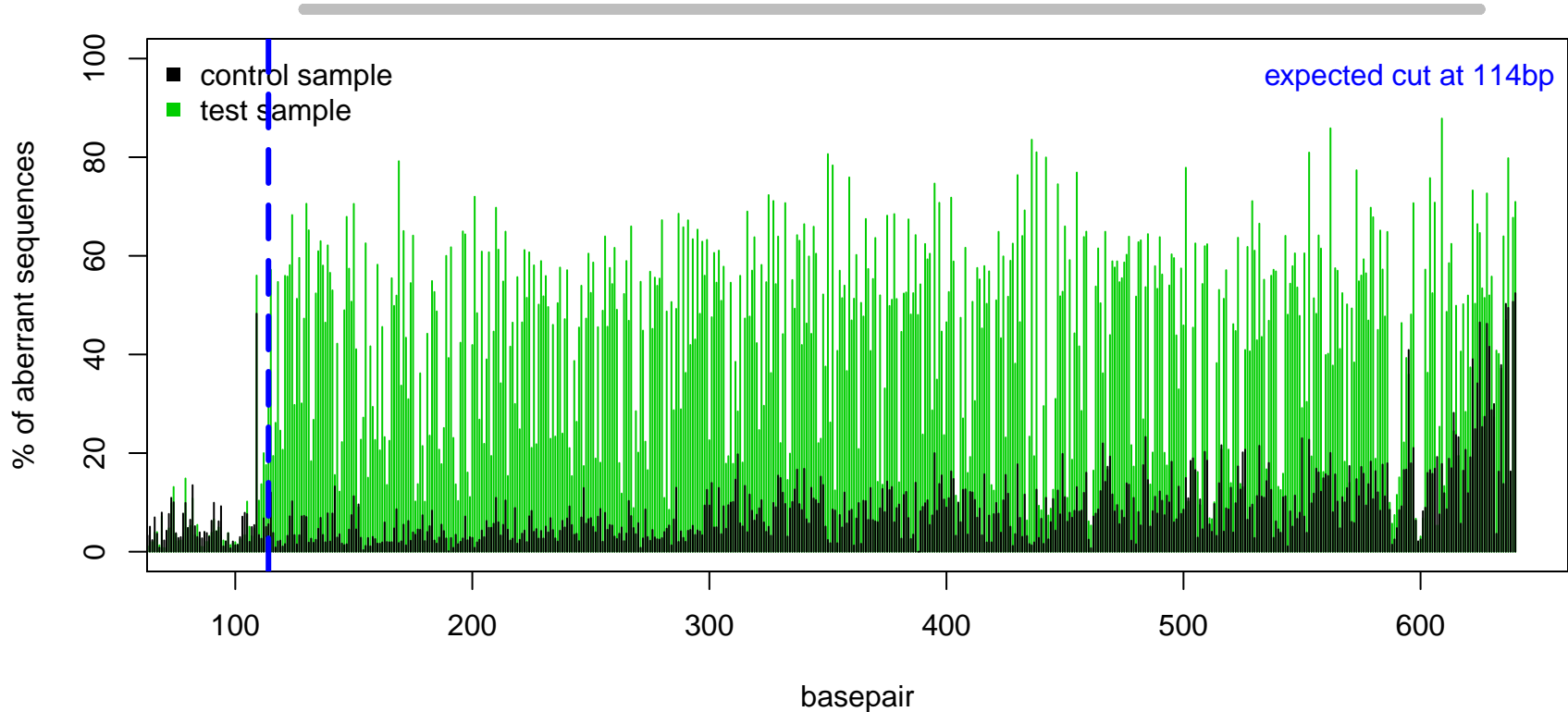
Warning: right boundary of decomposition window was adjusted to 625 . It must be at least 5bp plus the maximum indel size downstream of the expected break site

sample: Bth/WT cell line, gRNA 2.2, reverse
guide: TGGGACAGAACTTCCCCAGG



sample: Bth/WT cell line, gRNA 2.2, reverse
guide: TGGGACAGAACTTCCCCAGG

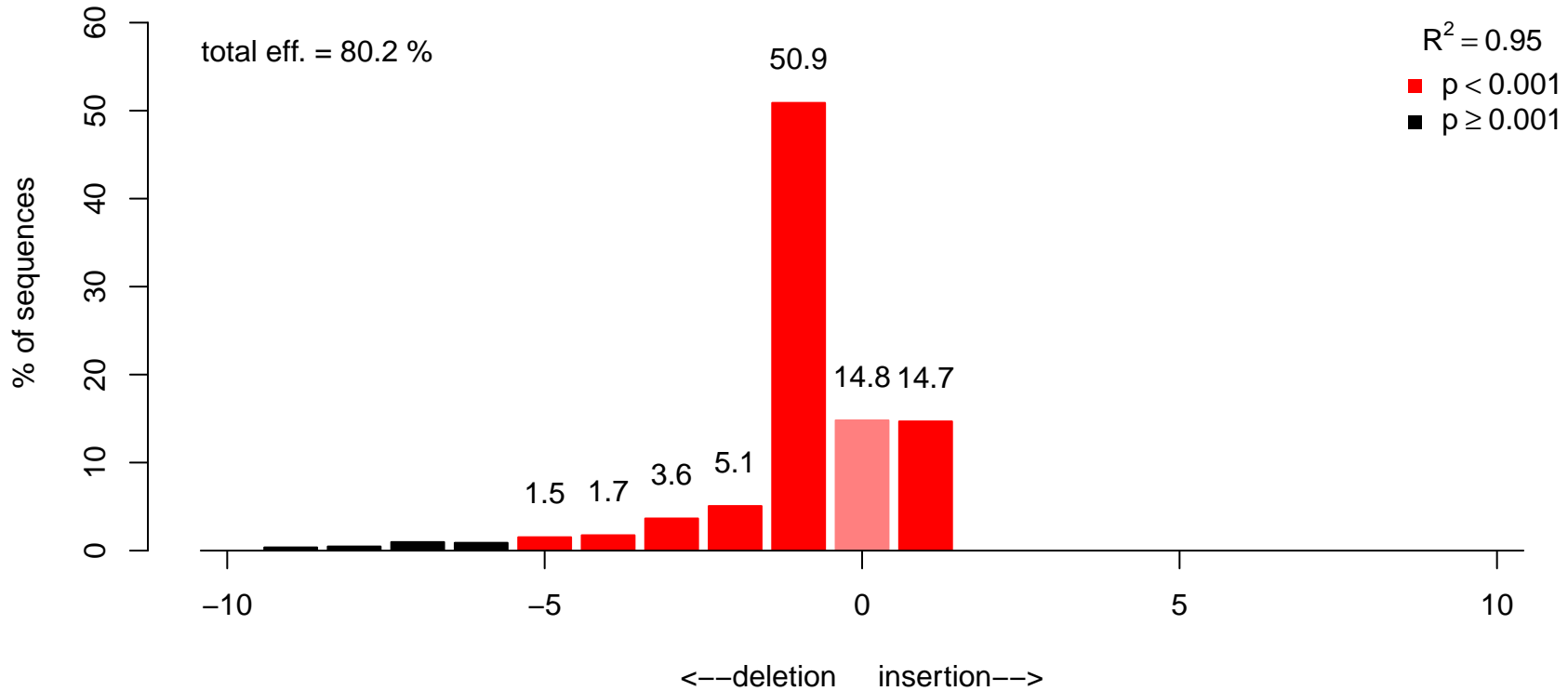
region for decomposition



Warning: left boundary of decomposition window was adjusted 129 . It must be at least 5bp plus the maximum indel size downstream of the expected break site

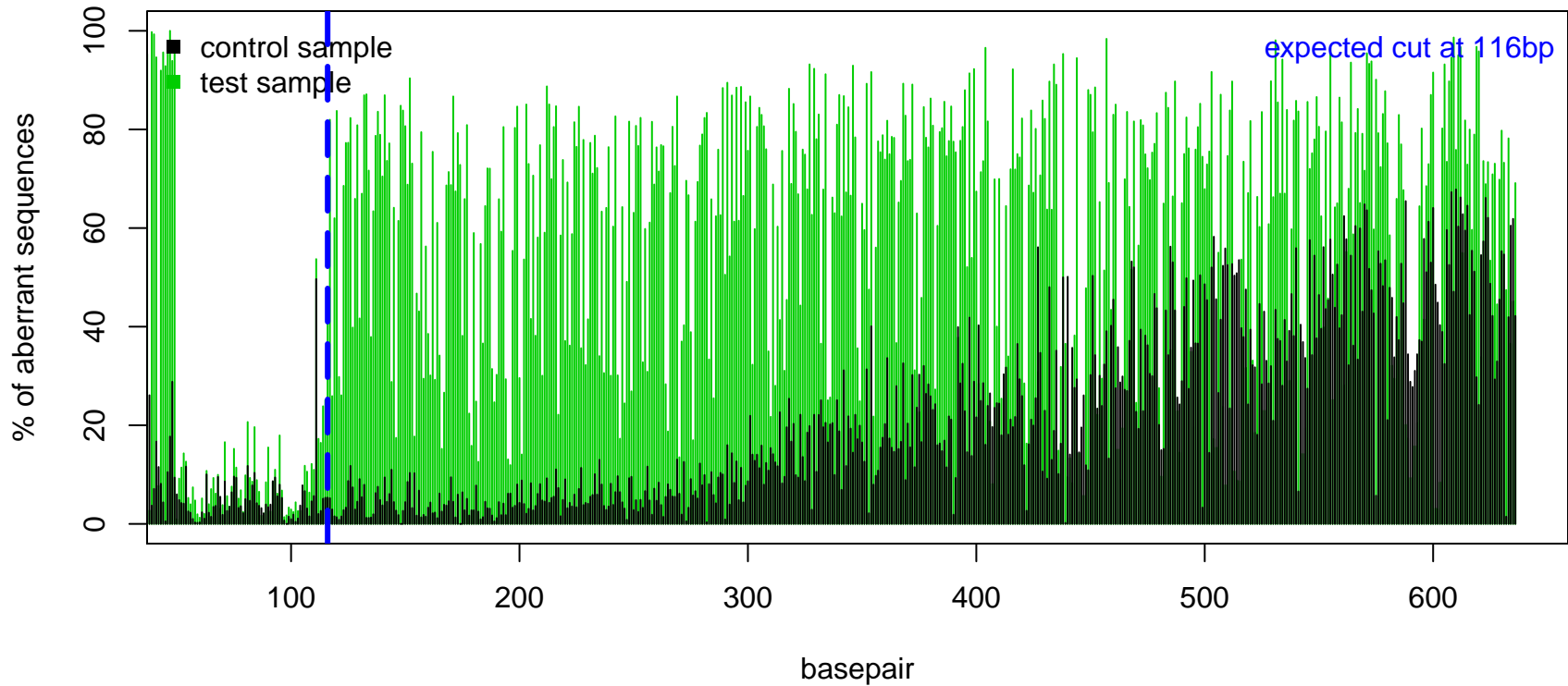
Warning: right boundary of decomposition window was adjusted to 625 . It must be at least 5bp plus the maximum indel size downstream of the expected break site

sample: Bth/WT cell line, gRNA 2.3, reverse
guide: TGGGACAGAACTTCCCCAGG



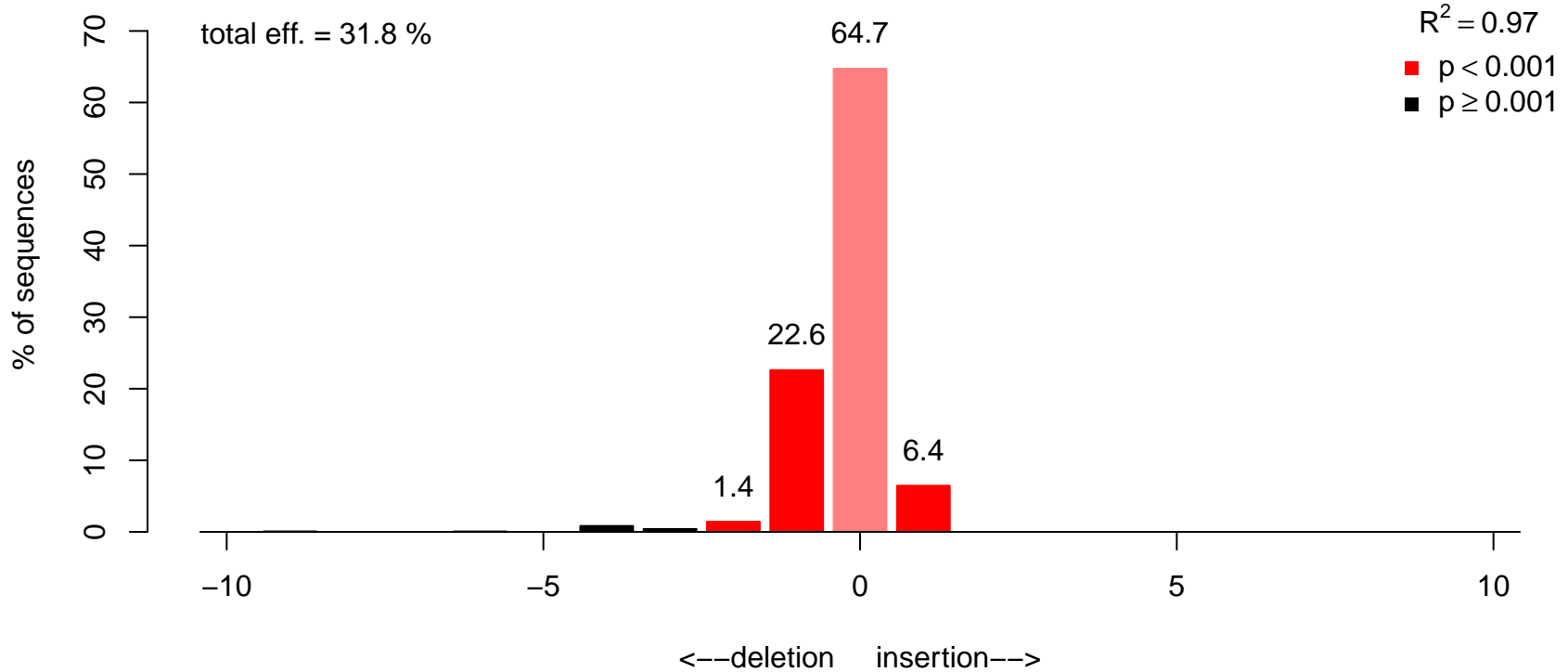
sample: Bth/WT cell line, gRNA 2.3, reverse
guide: TGGGACAGAACTTCCCCAGG

region for decomposition



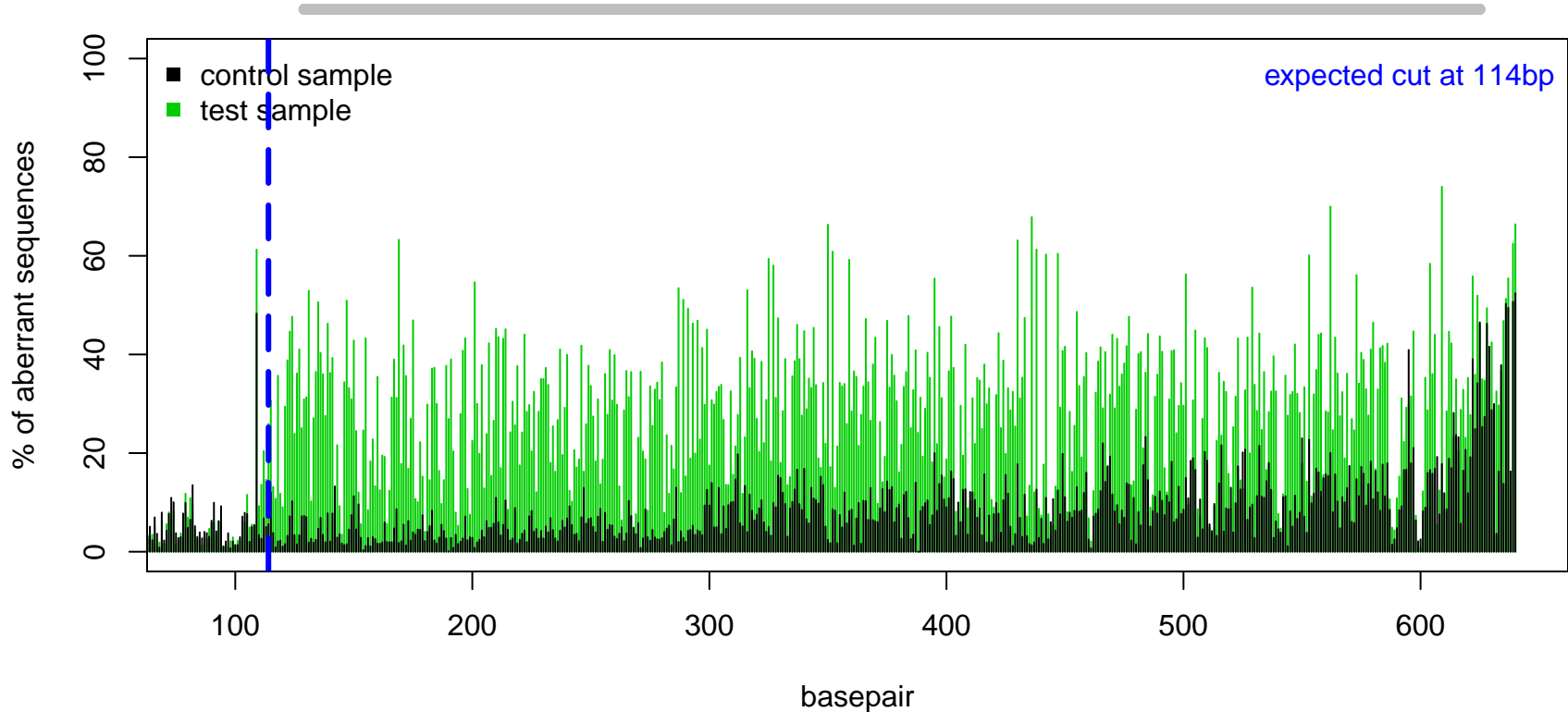
Warning: left boundary of decomposition window was adjusted 131 . It must be at least 5bp plus the maximum indel size downstream of the expected break site

sample: Bth/WT cell line, gRNA 2.4, reverse
guide: TGGGACAGAACTTCCCCAGG



sample: Bth/WT cell line, gRNA 2.4, reverse
guide: TGGGACAGAACTTCCCCAGG

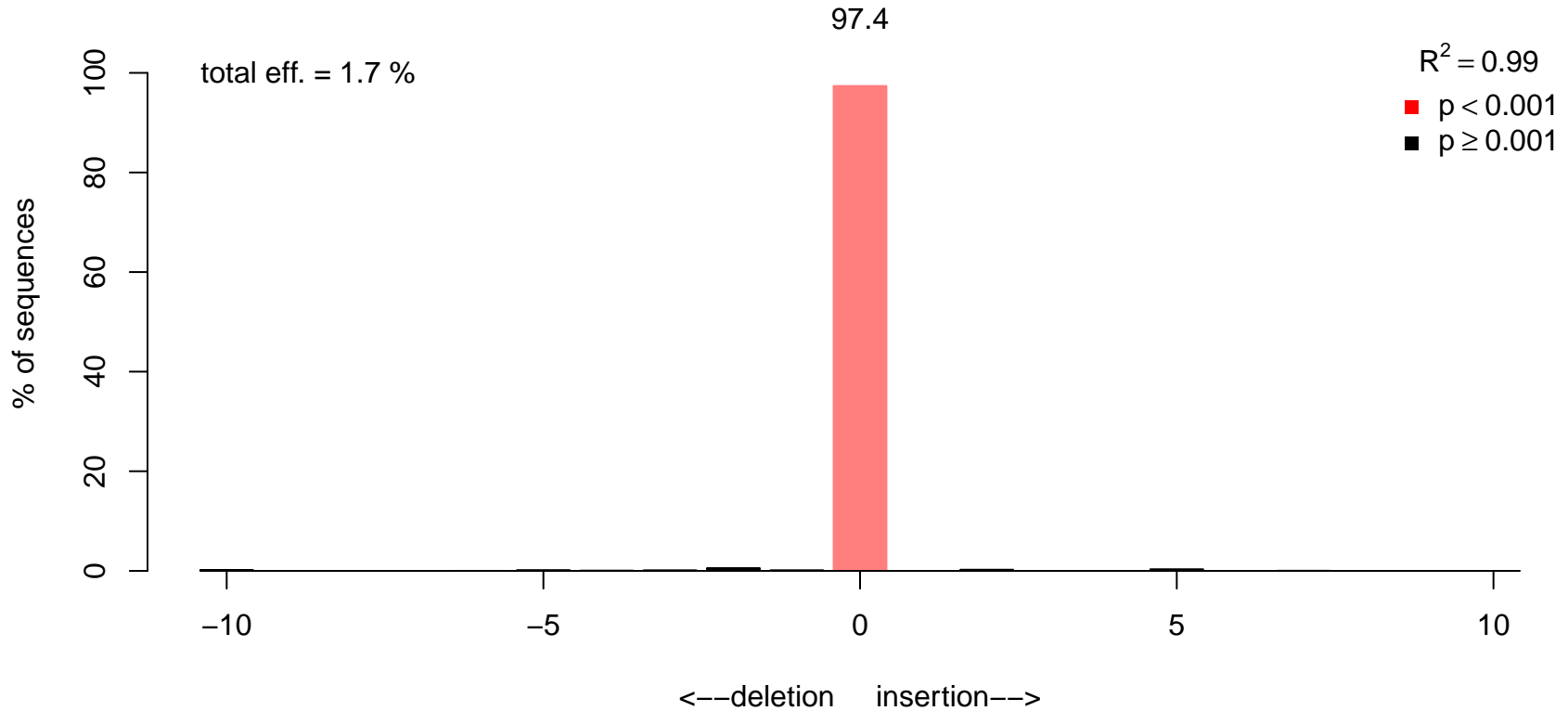
region for decomposition



Warning: left boundary of decomposition window was adjusted 129 . It must be at least 5bp plus the maximum indel size downstream of the expected break site

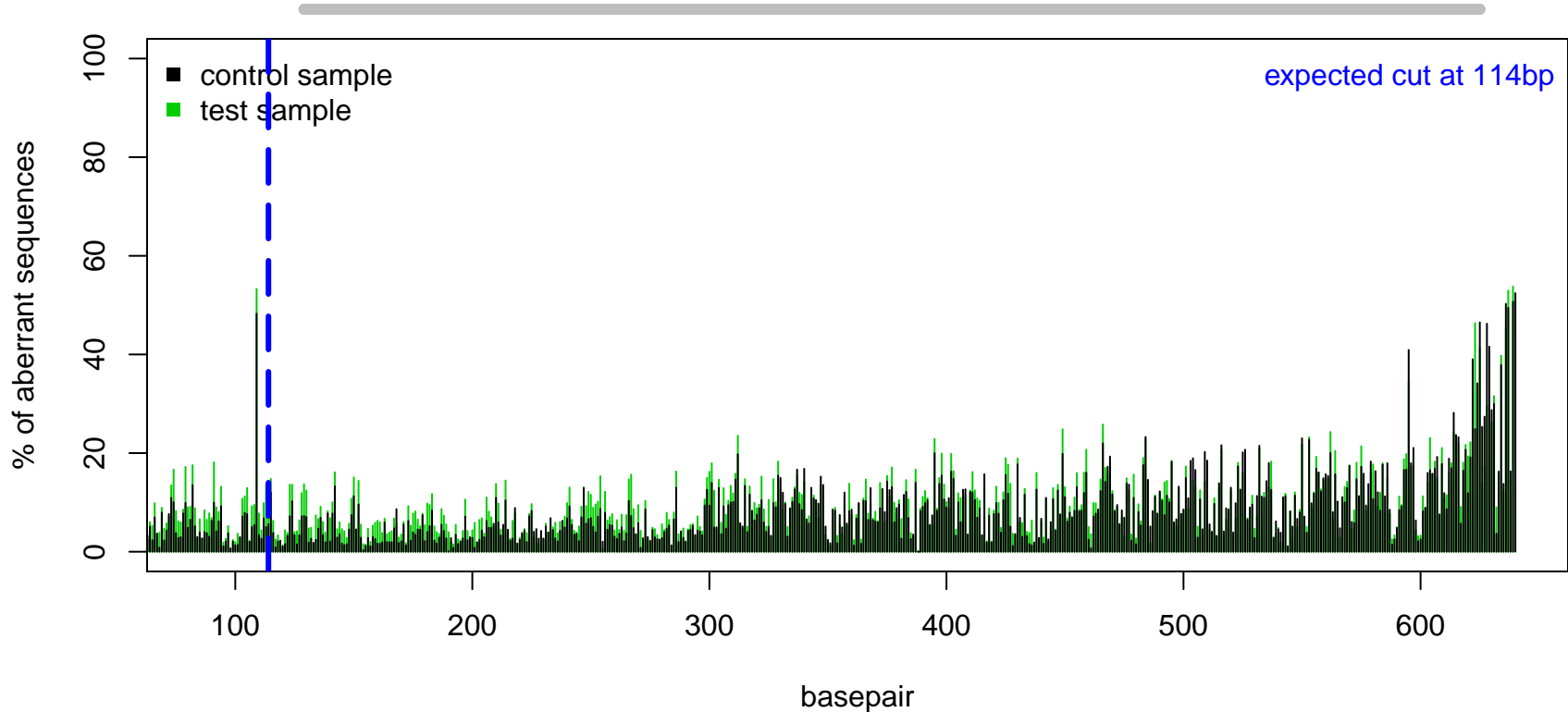
Warning: right boundary of decomposition window was adjusted to 625 . It must be at least 5bp plus the maximum indel size downstream of the expected break site

sample: Bth/WT cell line, gRNA 3.1, reverse
guide: TGGTAATGTCCCTCCTGGGG



sample: Bth/WT cell line, gRNA 3.1, reverse
guide: TGGTAATGTCCCTCCTGGGG

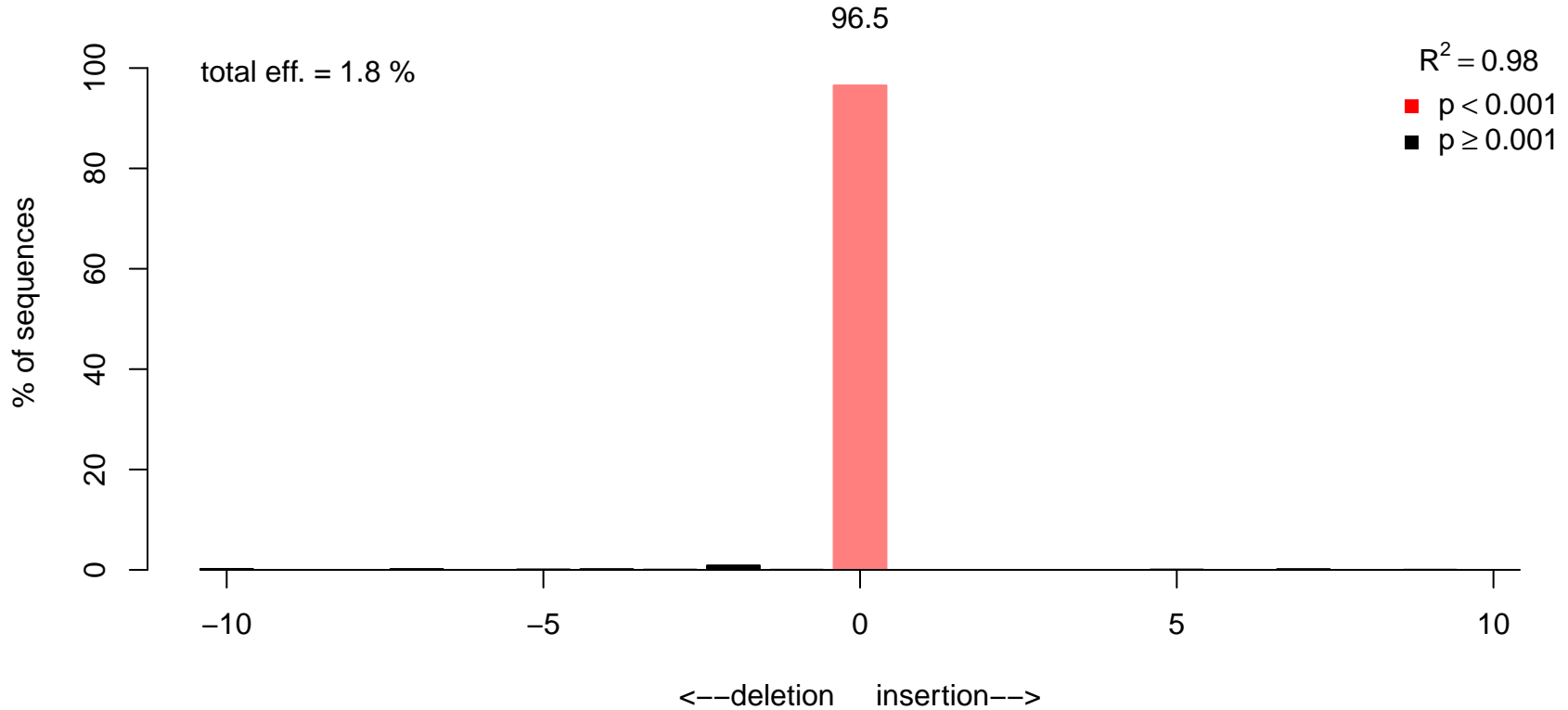
region for decomposition



Warning: left boundary of decomposition window was adjusted 129 . It must be at least 5bp plus the maximum indel size downstream of the expected break site

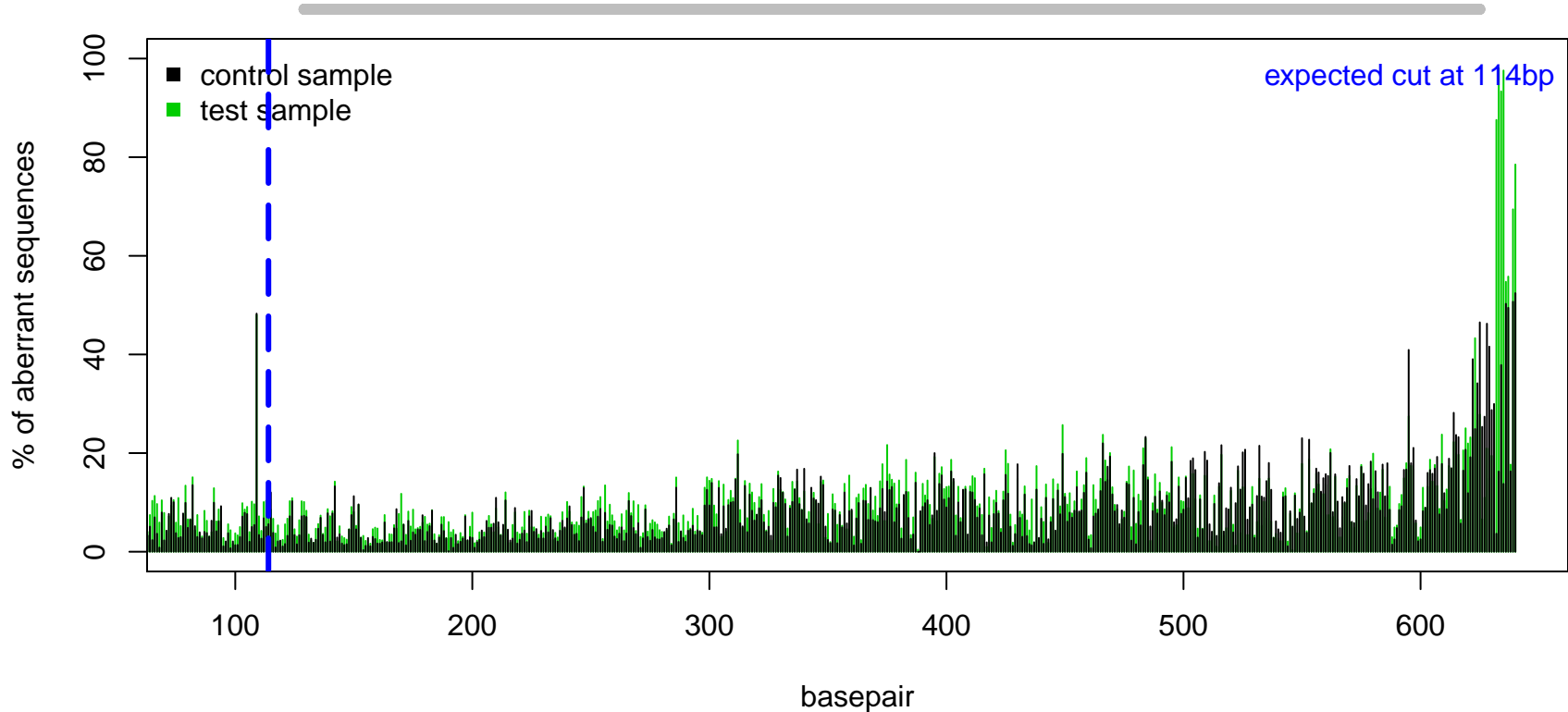
Warning: right boundary of decomposition window was adjusted to 625 . It must be at least 5bp plus the maximum indel size downstream of the expected break site

sample: Bth/WT cell line, gRNA 3.2, reverse
guide: TGGTAATGTCCCTCCTGGGG



sample: Bth/WT cell line, gRNA 3.2, reverse
guide: TGGTAATGTCCCTCCTGGGG

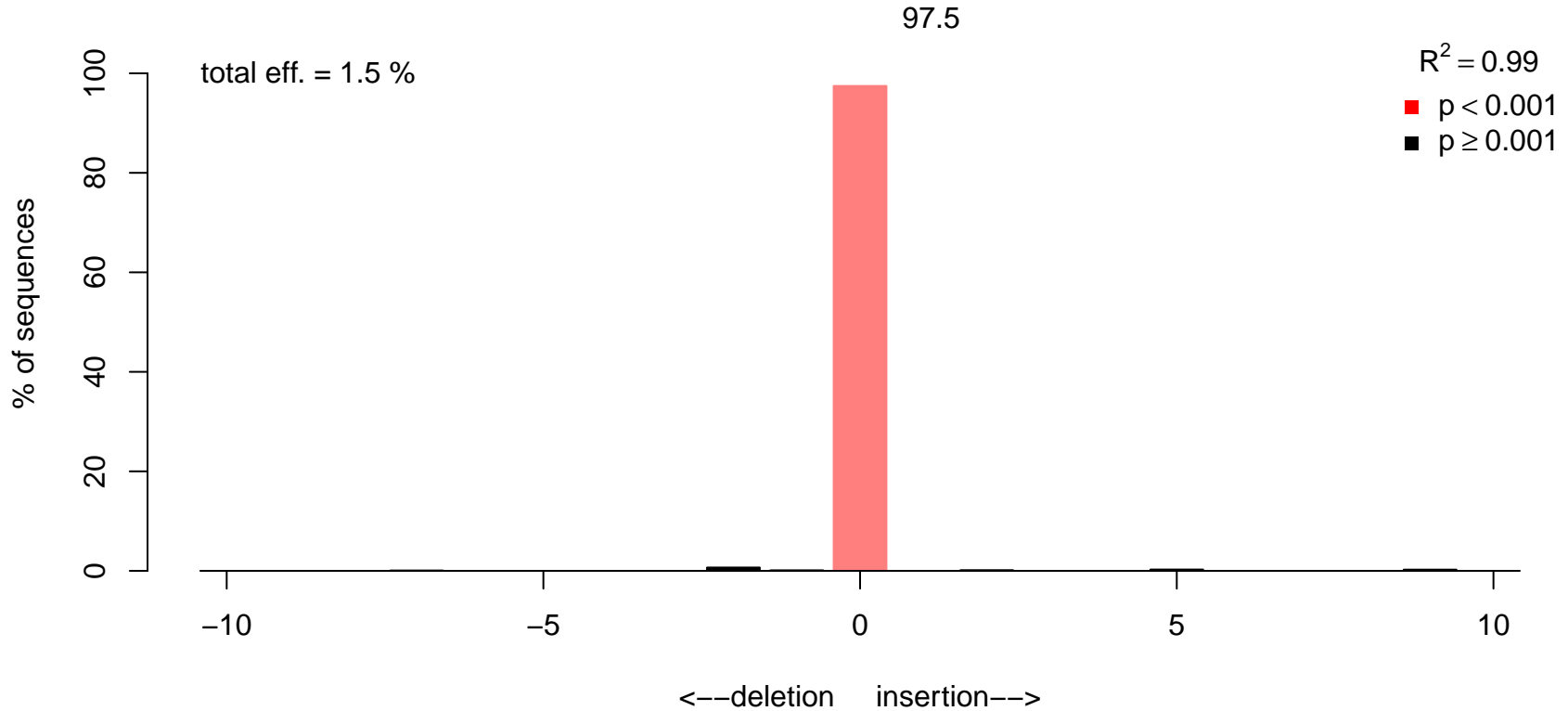
region for decomposition



Warning: left boundary of decomposition window was adjusted 129 . It must be at least 5bp plus the maximum indel size downstream of the expected break site

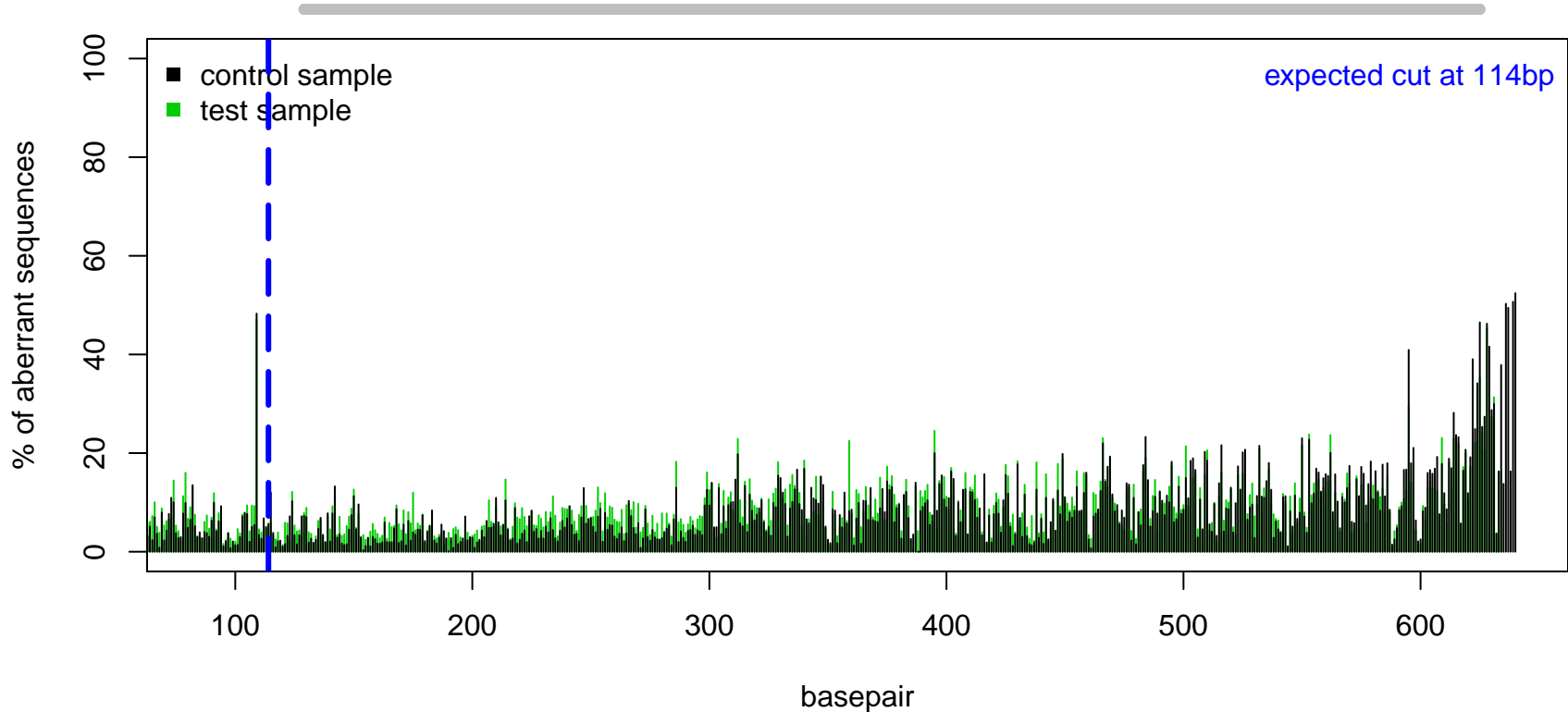
Warning: right boundary of decomposition window was adjusted to 625 . It must be at least 5bp plus the maximum indel size downstream of the expected break site

sample: Bth/WT cell line, gRNA 3.3, reverse
guide: TGGTAATGTCCCTCCTGGGG



sample: Bth/WT cell line, gRNA 3.3, reverse
guide: TGGTAATGTCCCTCCTGGGG

region for decomposition

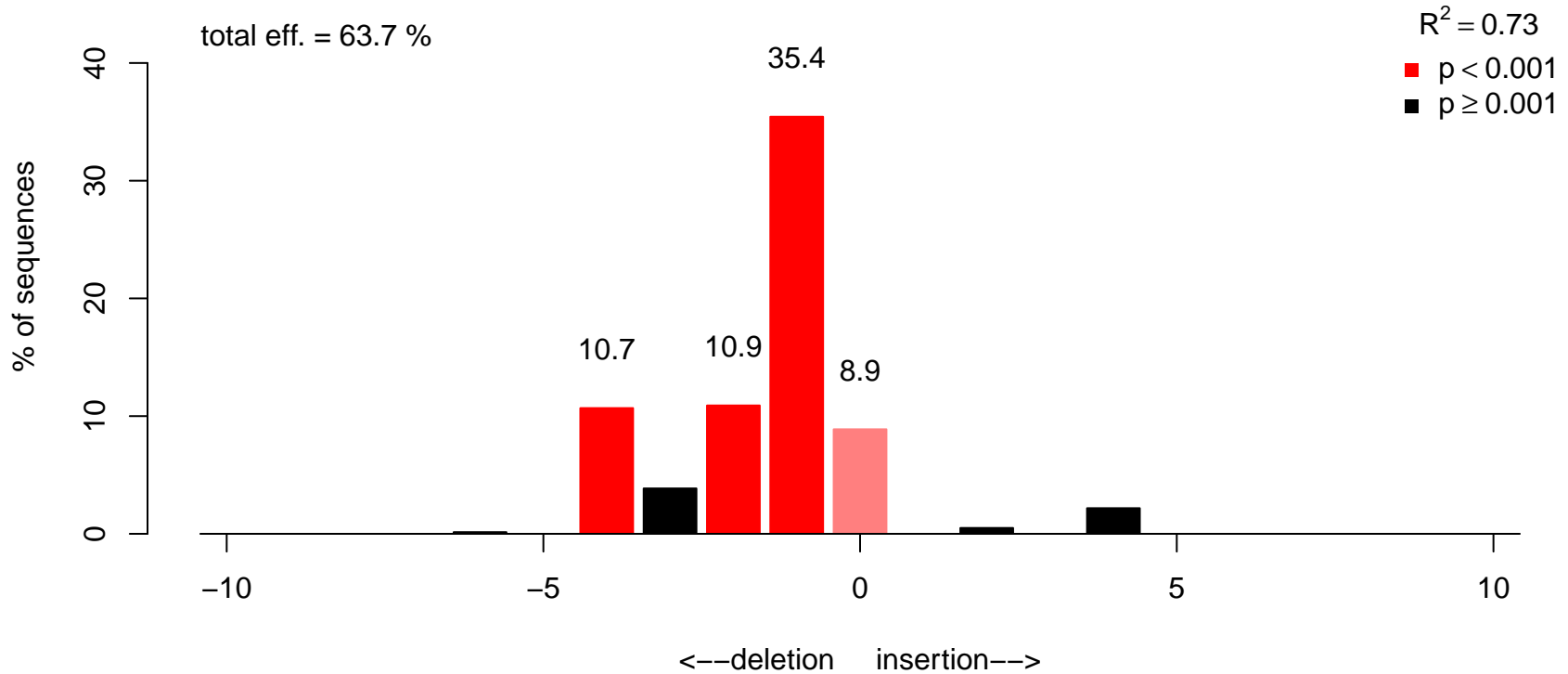


Warning: left boundary of decomposition window was adjusted 129 . It must be at least 5bp plus the maximum indel size downstream of the expected break site

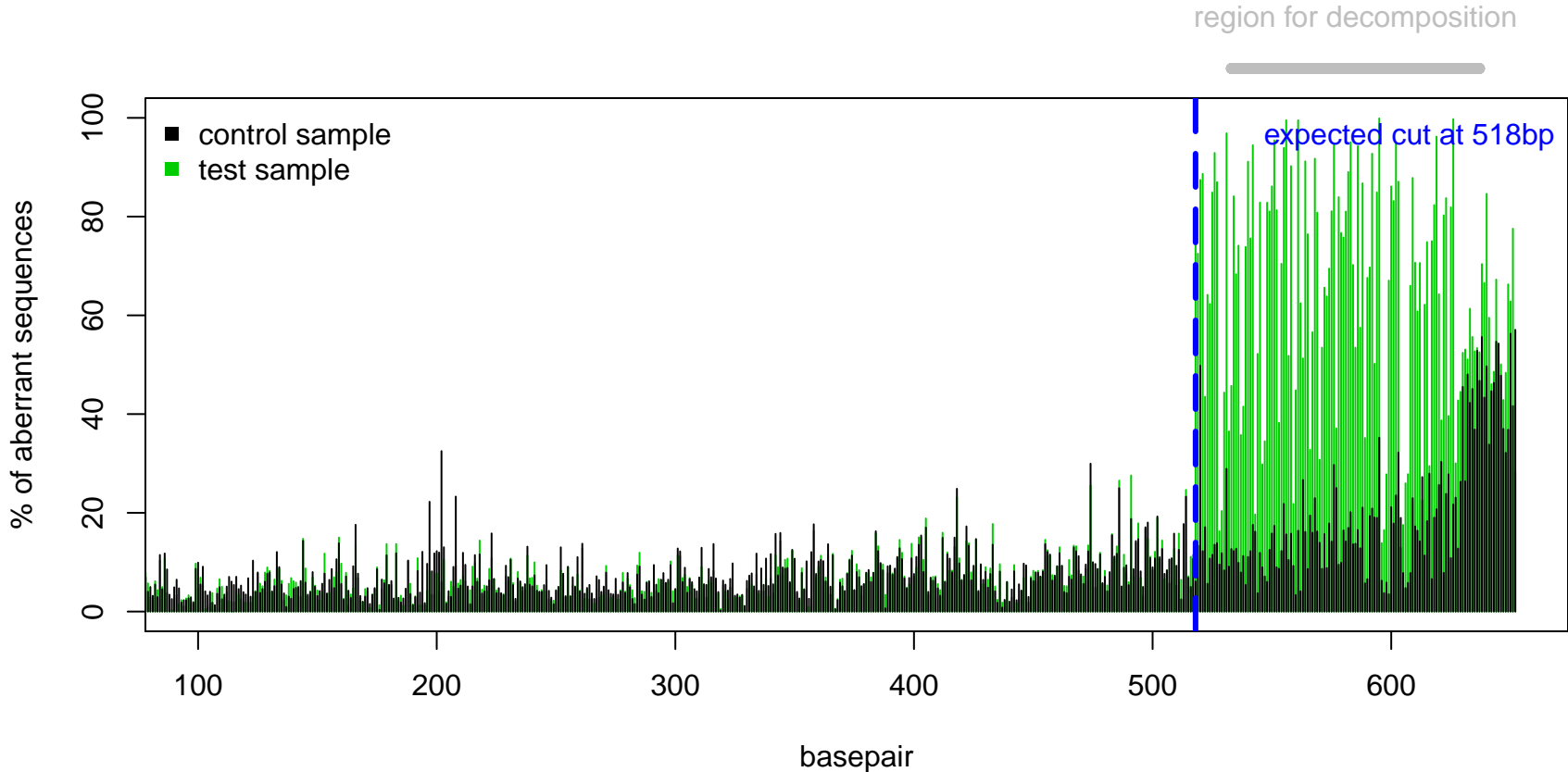
Warning: right boundary of decomposition window was adjusted to 625 . It must be at least 5bp plus the maximum indel size downstream of the expected break site

sample: Bth/WT cell line, gRNA WT, forward
guide: GGGTGGGACAGAACATCCCC

total eff. = 63.7 %



sample: Bth/WT cell line, gRNA WT, forward
guide: GGGTGGGACAGAACATCCCC



Warning: left boundary of decomposition window was adjusted 533 . It must be at least 5bp plus the maximum indel size downstream of the expected break site

Warning: right boundary of decomposition window was adjusted to 637 . It must be at least 5bp plus the maximum indel size downstream of the expected break site

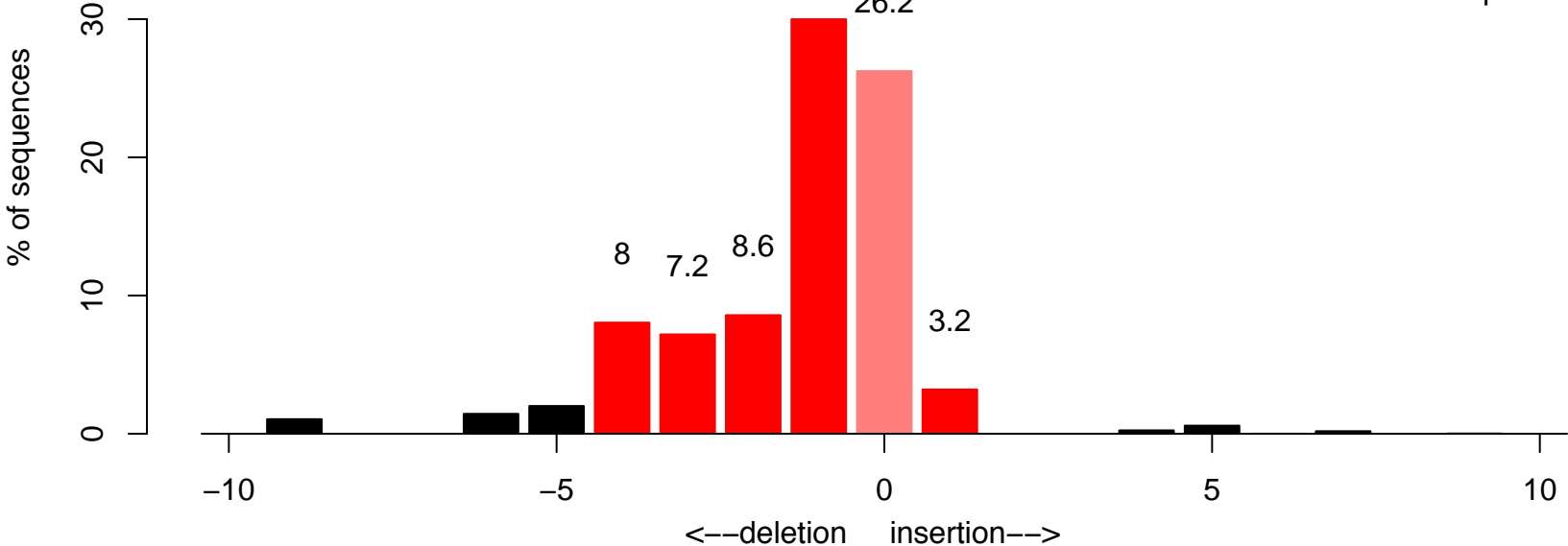
sample: Bth/WT cell line, gRNA 1.1, forward
guide: GGGTGGGACAGAACTTCCCC

total eff. = 62.5 %

$R^2 = 0.89$

■ $p < 0.001$

■ $p \geq 0.001$

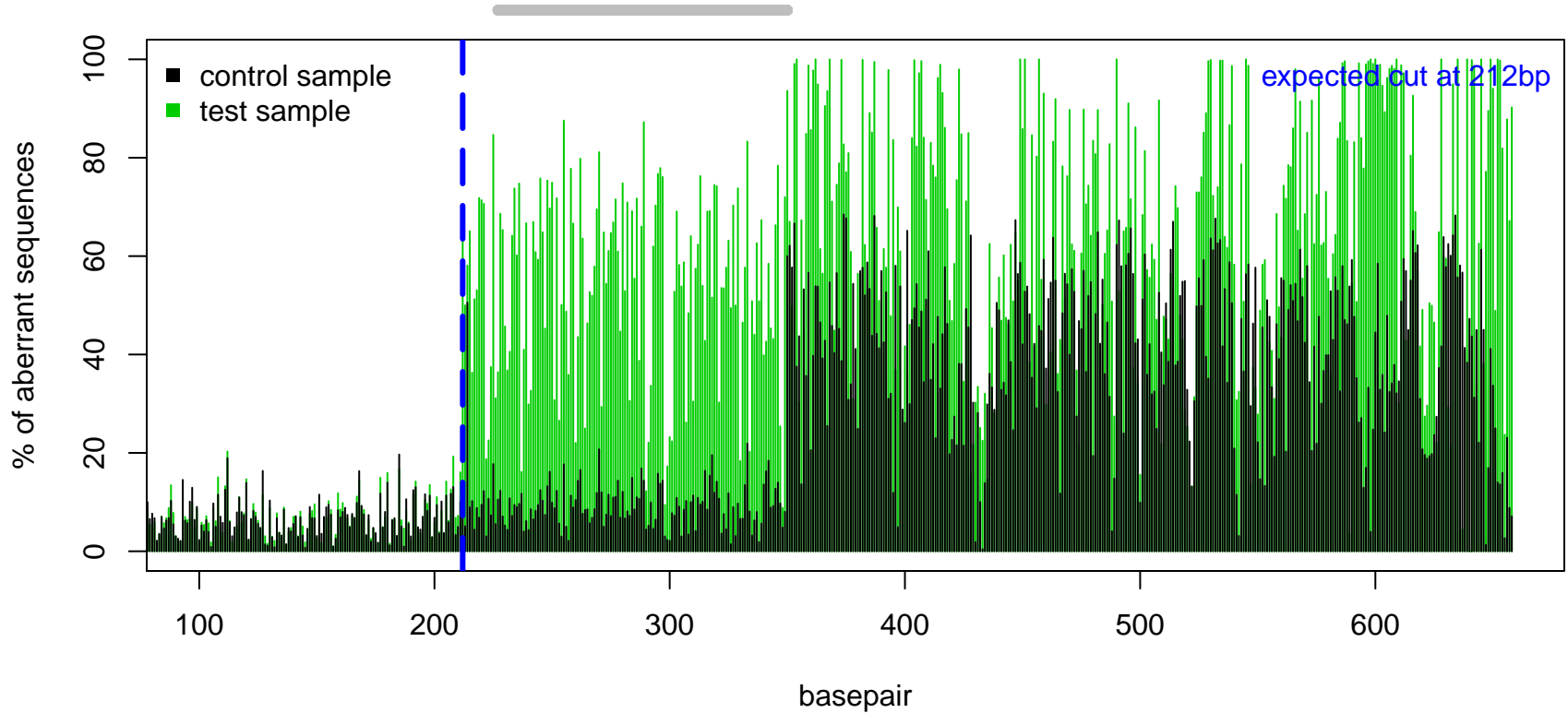


Warning: the spacing between the nucleotides in (one of) sanger sequence file(s) is not constant.

This might indicate for wrongly unannotated or wrongly additional annotated nucleotides.
Decomposition window lower and check the chromatogram for abnormalities.

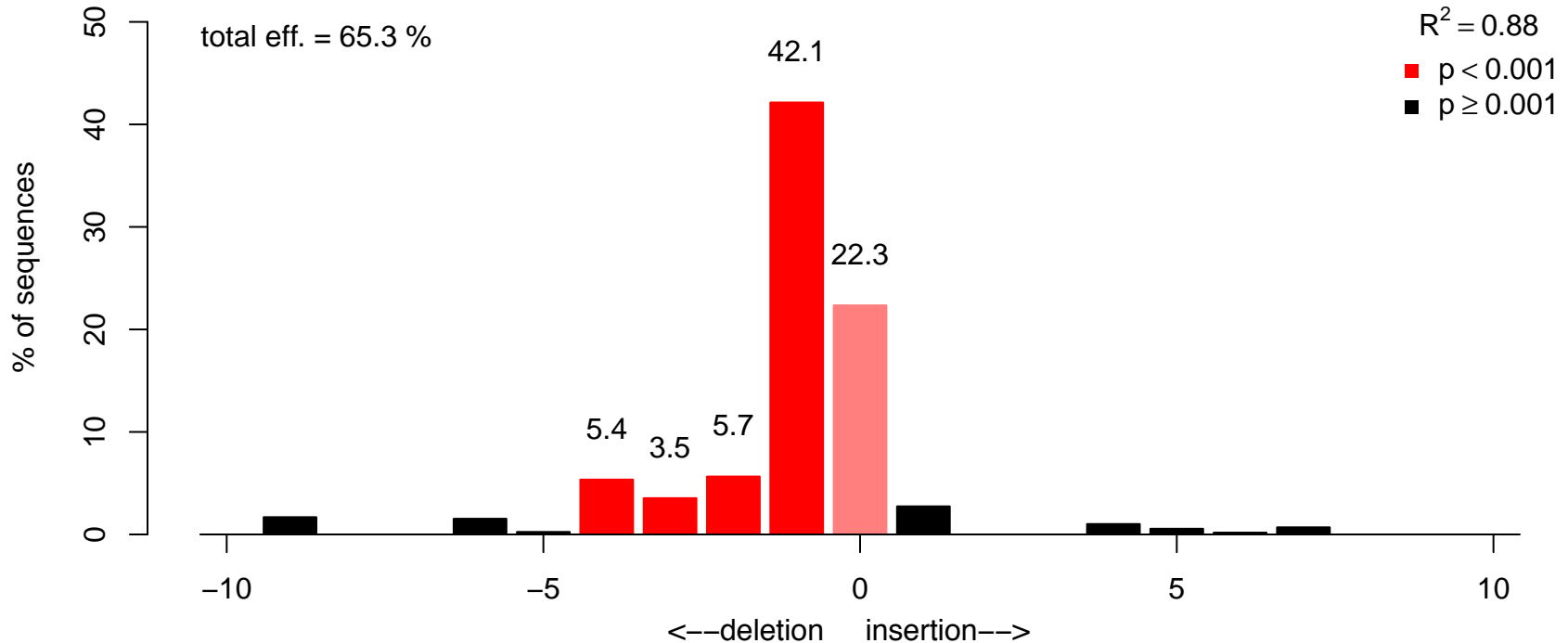
sample: Bth/WT cell line, gRNA 1.1, forward
guide: GGGTGGGACAGAACTTCCCC

region for decomposition



Warning: left boundary of decomposition window was adjusted 227 . It must be at least 5bp plus the maximum indel size downstream of the expected break site

sample: Bth/WT cell line, gRNA 1.2, forward
guide: GGGTGGGACAGAACTTCCCC

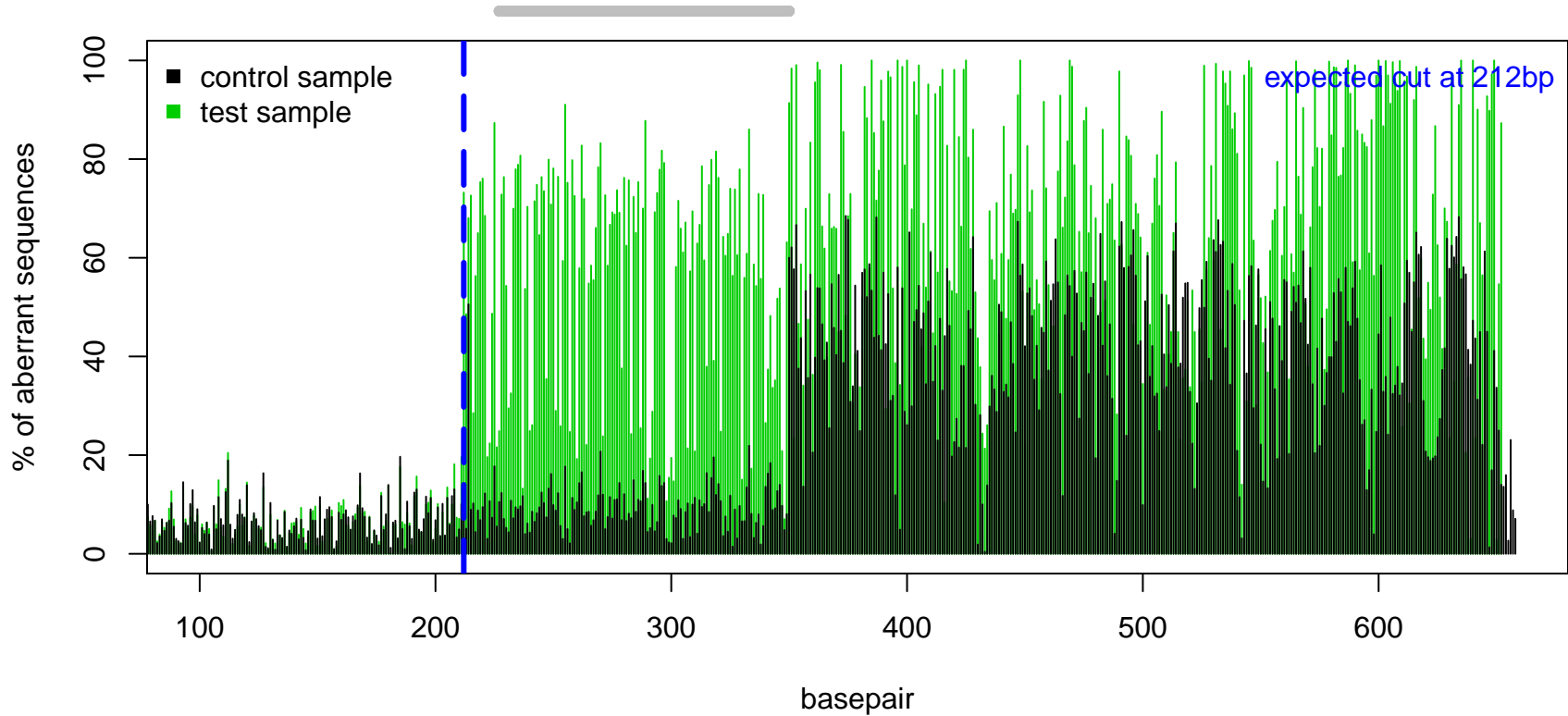


Warning: the spacing between the nucleotides in (one of) sanger sequence file(s) is not constant.

This might indicate for wrongly unannotated or wrongly additional annotated nucleotides.
Decomposition window lower and check the chromatogram for abnormalities.

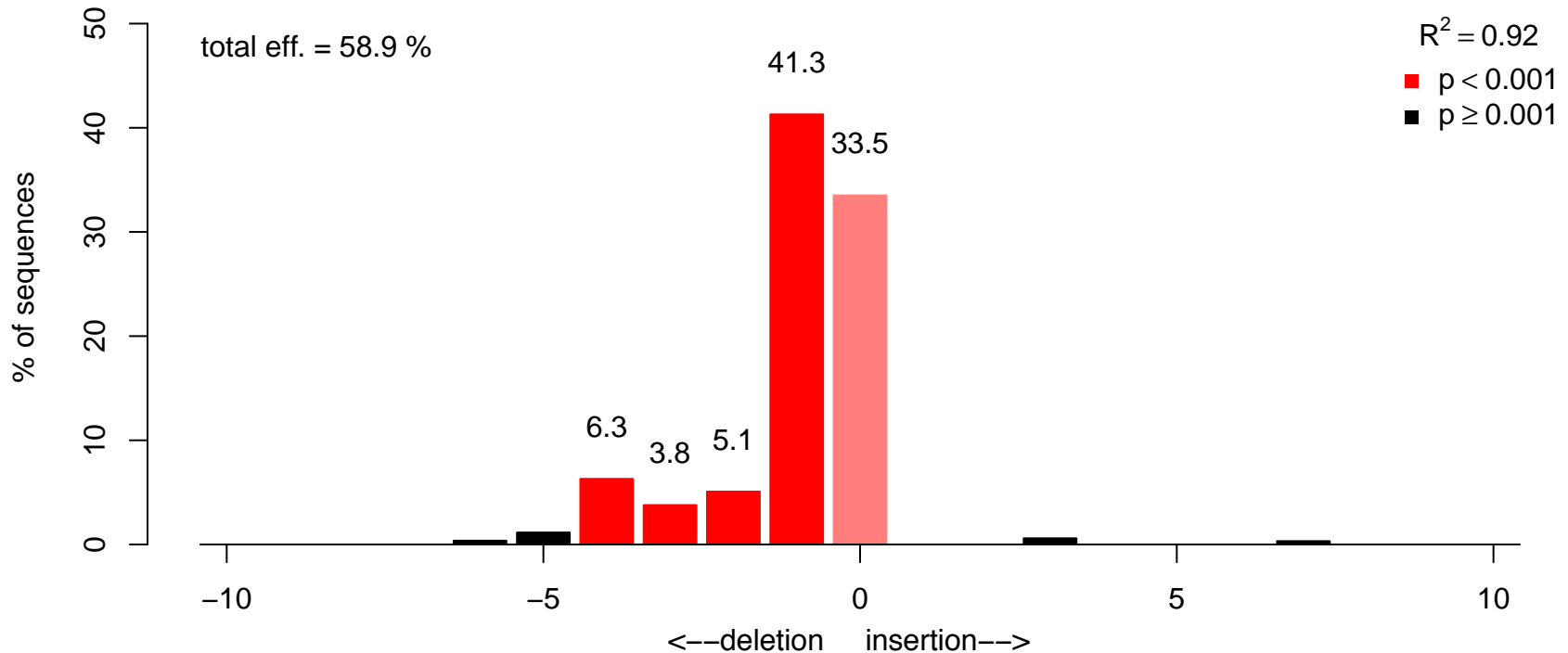
sample: Bth/WT cell line, gRNA 1.2, forward
guide: GGGTGGGACAGAACTTCCCC

region for decomposition



Warning: left boundary of decomposition window was adjusted 227 . It must be at least 5bp plus the maximum indel size downstream of the expected break site

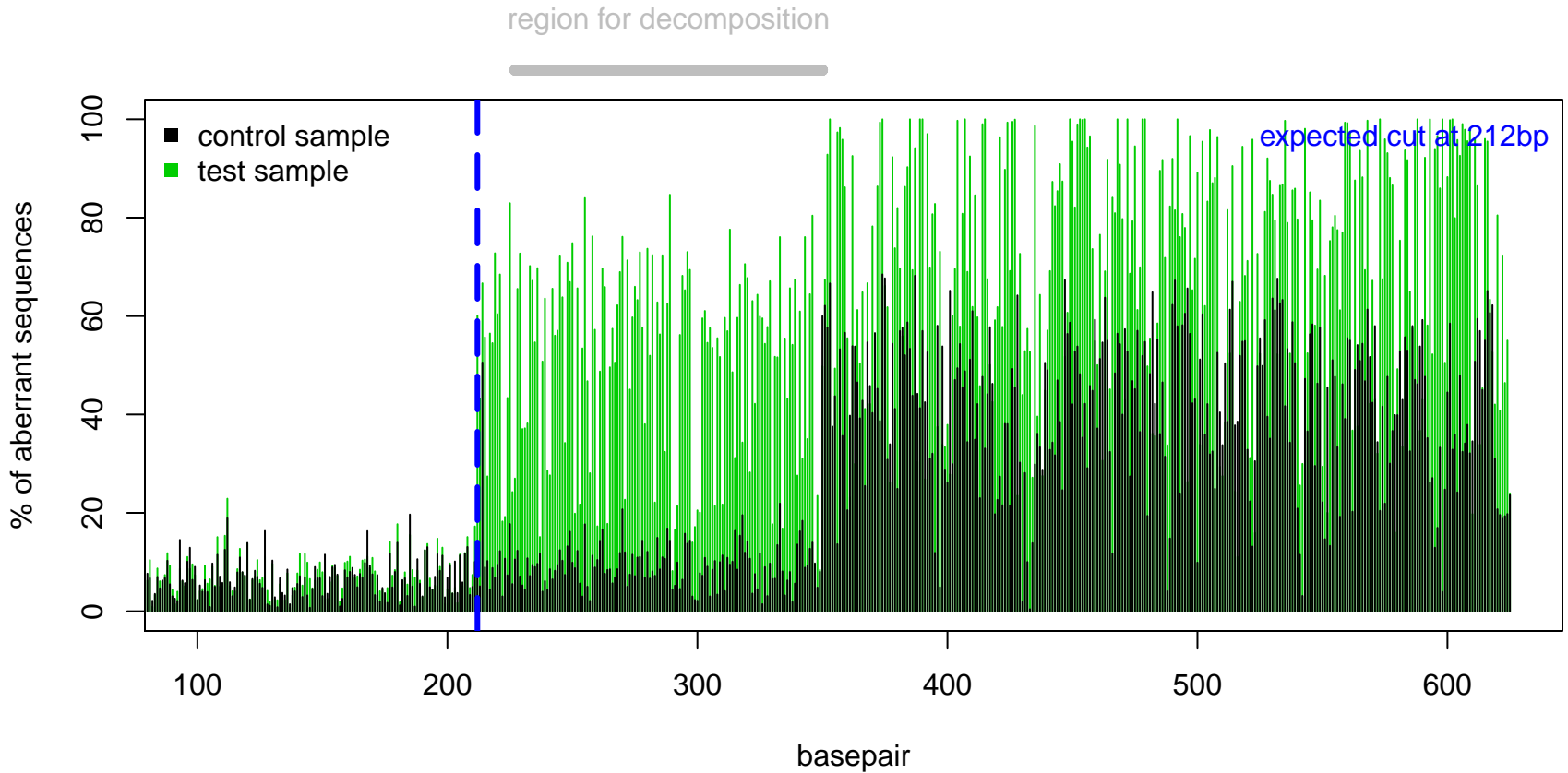
sample: Bth/WT cell line, gRNA 1.3, forward
guide: GGGTGGGACAGAACTTCCCC



Warning: the spacing between the nucleotides in (one of) sanger sequence file(s) is not constant.

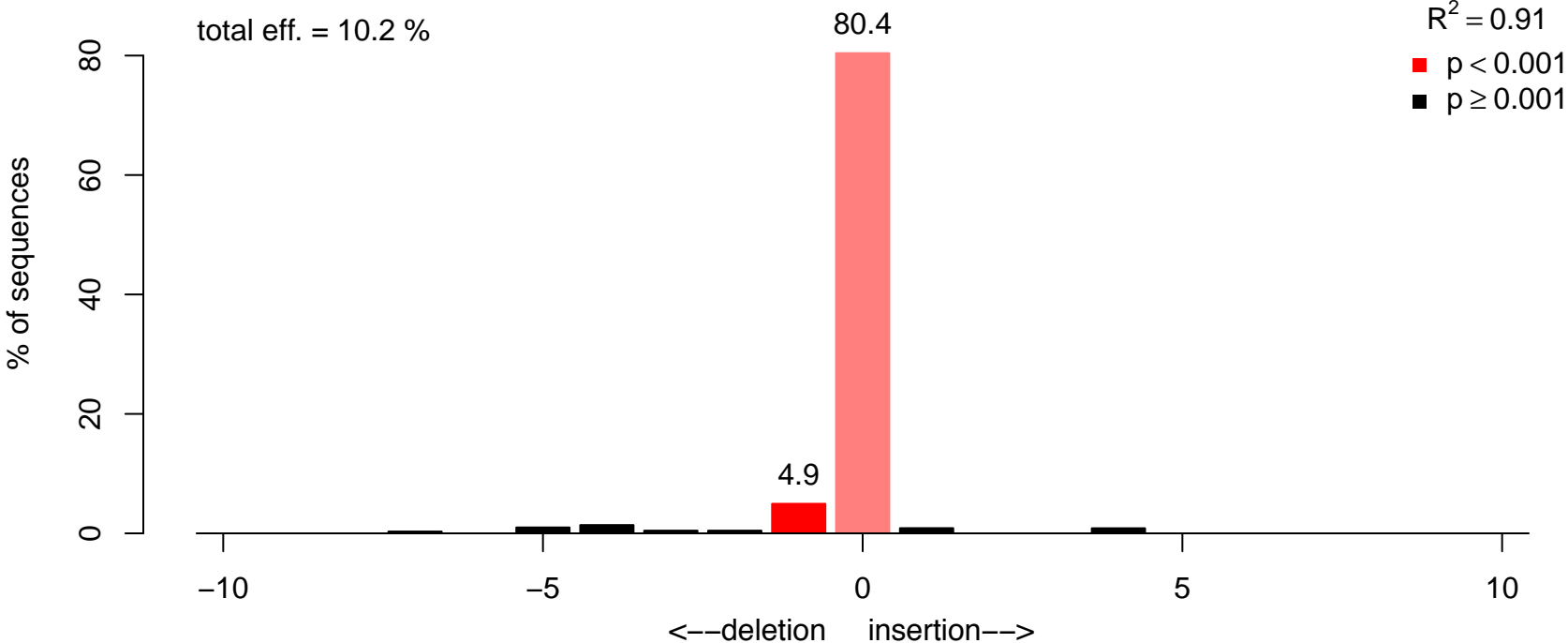
This might indicate for wrongly unannotated or wrongly additional annotated nucleotides.
Decomposition window lower and check the chromatogram for abnormalities.

sample: Bth/WT cell line, gRNA 1.3, forward
guide: GGGTGGGACAGAACTTCCCC



Warning: left boundary of decomposition window was adjusted 227 . It must be at least 5bp plus the maximum indel size downstream of the expected break site

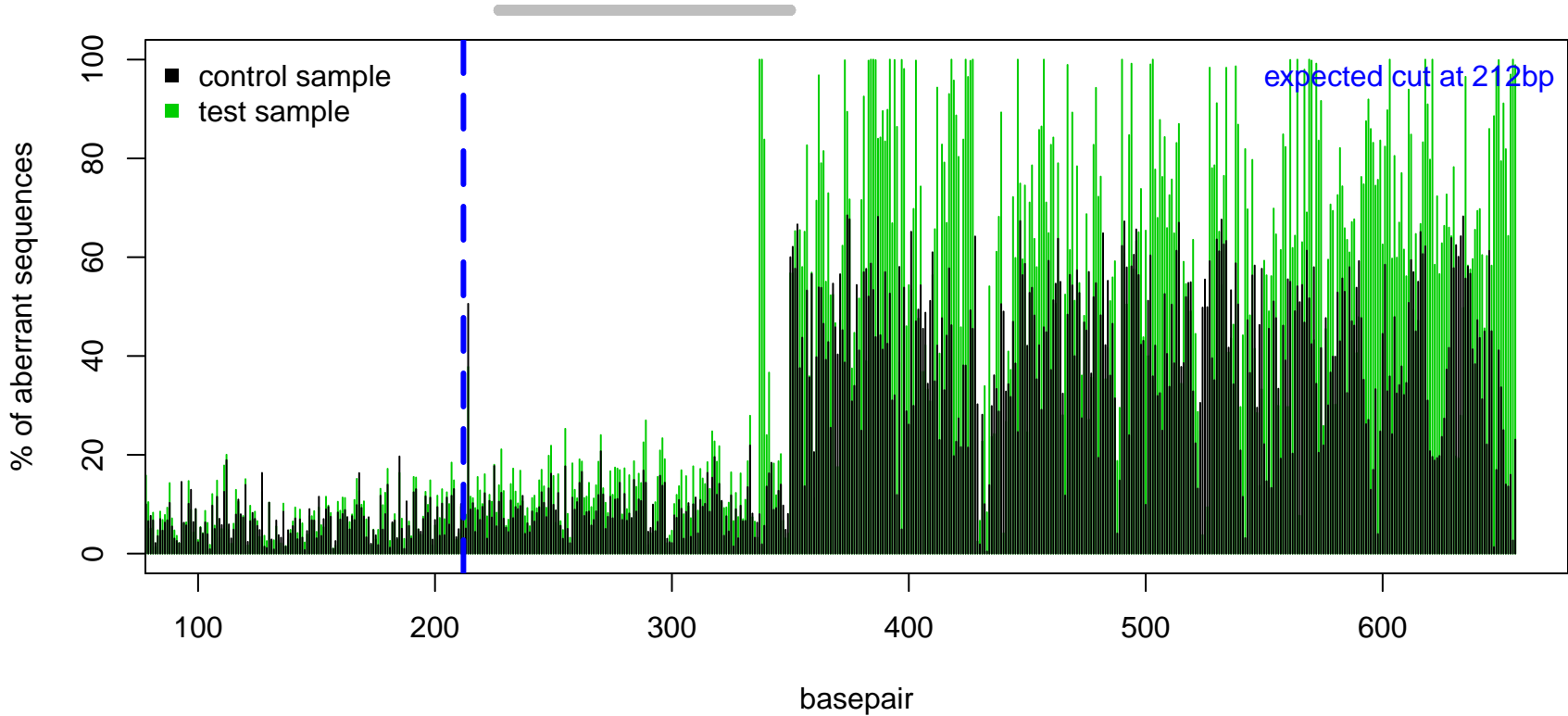
sample: Bth/WT cell line, gRNA 1.4, forward
guide: GGGTGGGACAGAACTTCCCC



Warning: the spacing between the nucleotides in (one of) sanger sequence file(s) is not constant.
This might indicate for wrongly unannotated or wrongly additional annotated nucleotides.
Decomposition window lower and check the chromatogram for abnormalities.

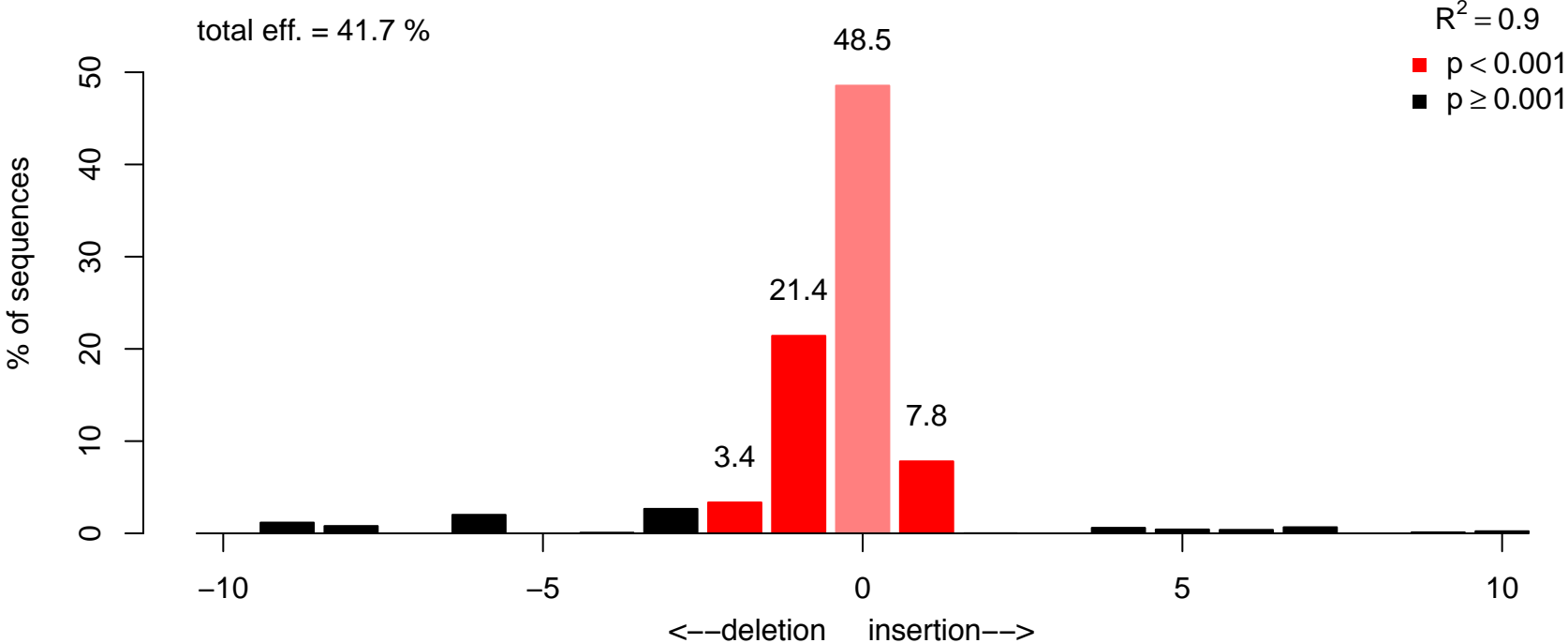
sample: Bth/WT cell line, gRNA 1.4, forward
guide: GGGTGGGACAGAACTTCCCC

region for decomposition



Warning: left boundary of decomposition window was adjusted 227 . It must be at least 5bp plus the maximum indel size downstream of the expected break site

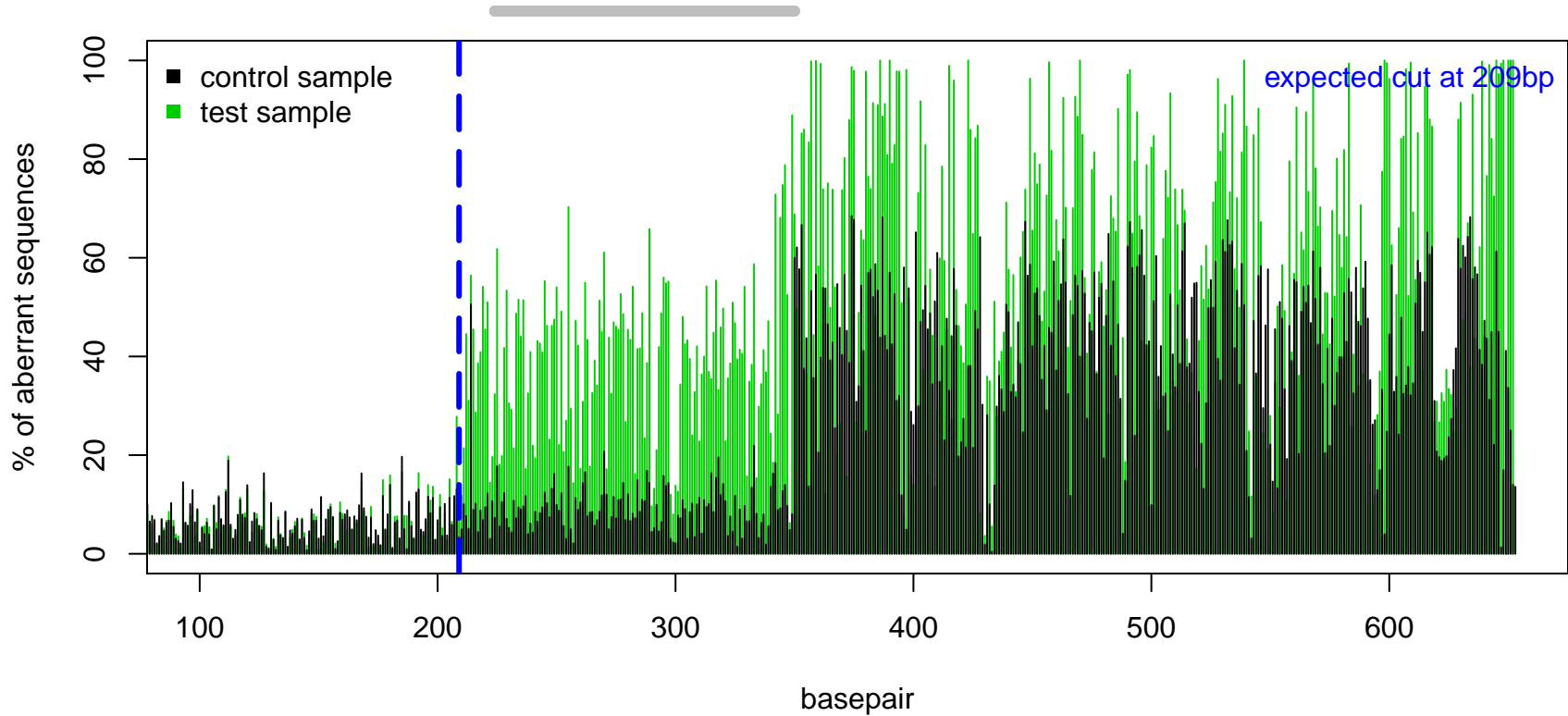
sample: Bth/WT cell line, gRNA 2.1, forward
guide: TGGGACAGAACTTCCCCAGG



Warning: the spacing between the nucleotides in (one of) sanger sequence file(s) is not constant.
This might indicate for wrongly unannotated or wrongly additional annotated nucleotides.
Decomposition window lower and check the chromatogram for abnormalities.

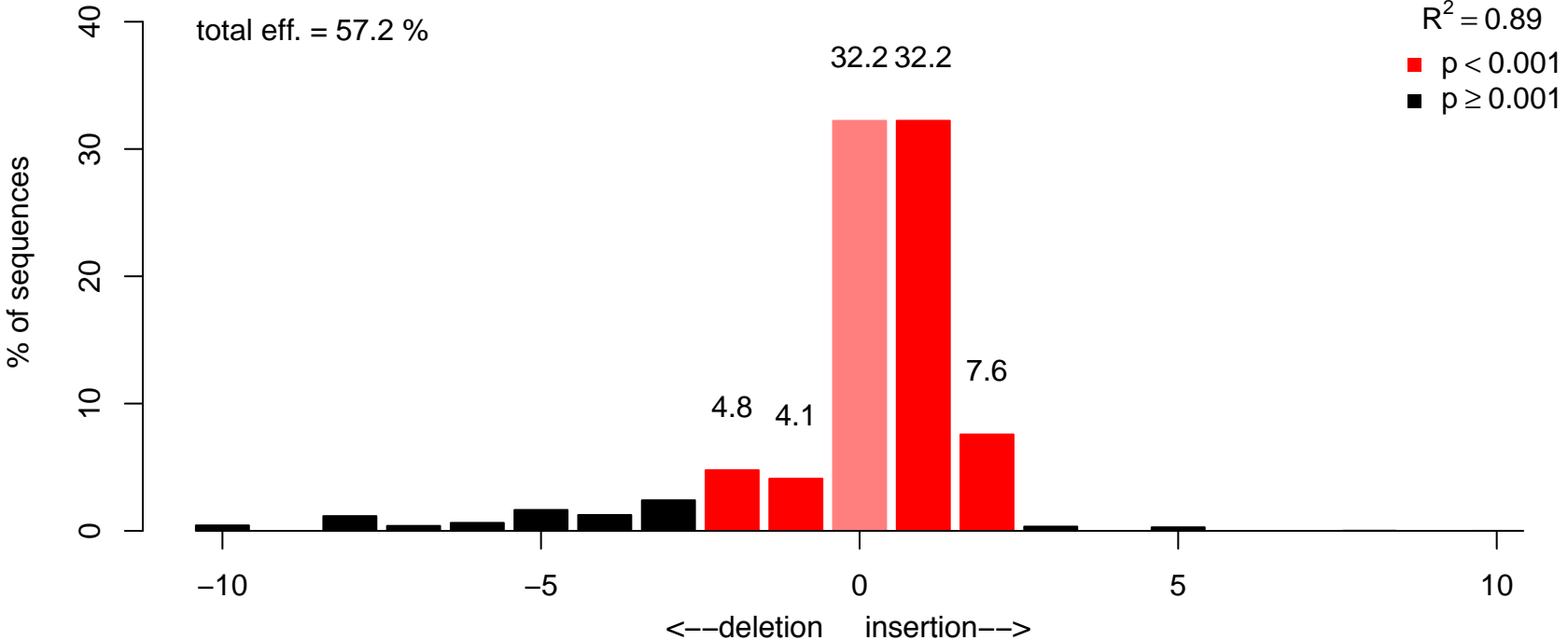
sample: Bth/WT cell line, gRNA 2.1, forward
guide: TGGGACAGAACTTCCCCAGG

region for decomposition



Warning: left boundary of decomposition window was adjusted 224 . It must be at least 5bp plus the maximum indel size downstream of the expected break site

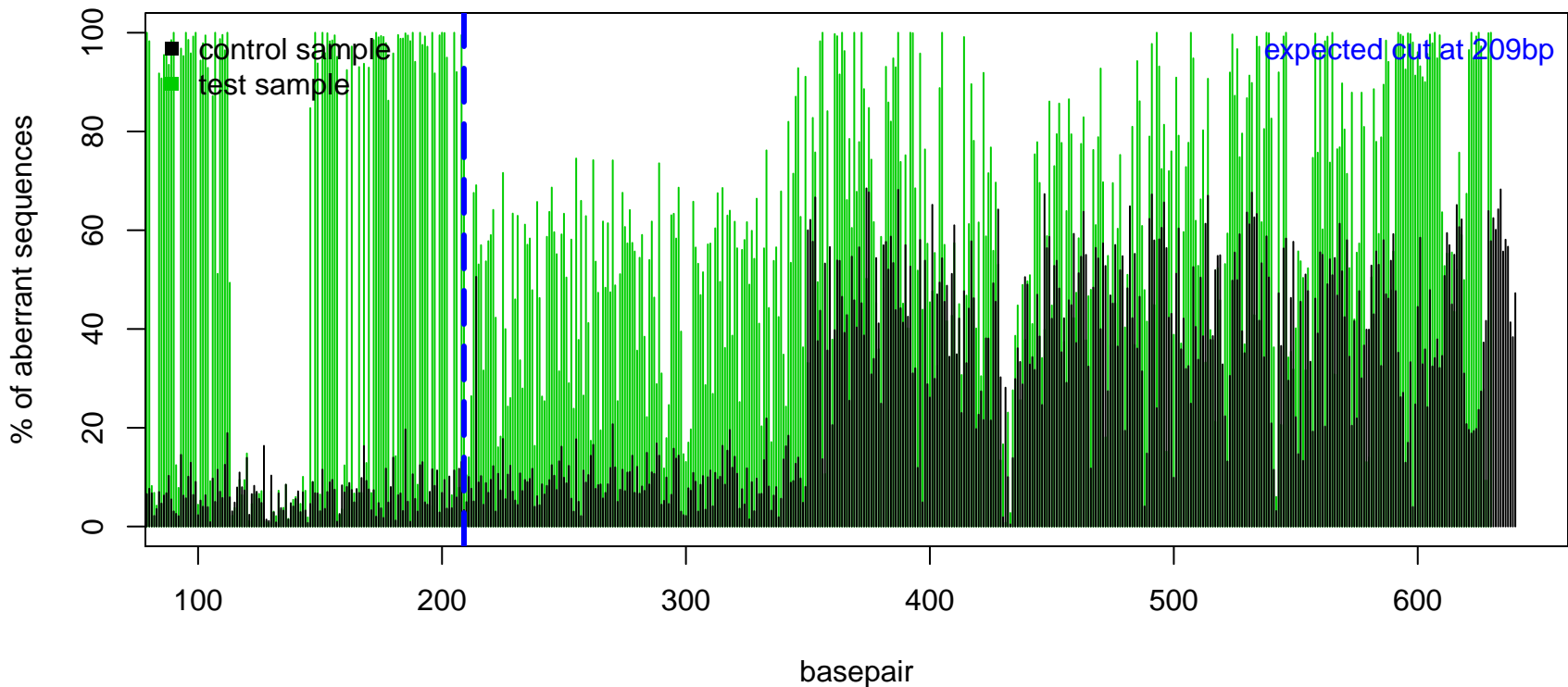
sample: Bth/WT cell line, gRNA 2.2, forward
6 guide: TGGGACAGAACTTCCCCAGG



Warning: the spacing between the nucleotides in (one of) sanger sequence file(s) is not constant.
This might indicate for wrongly unannotated or wrongly additional annotated nucleotides.
Decomposition window lower and check the chromatogram for abnormalities.

sample: Bth/WT cell line, gRNA 2.2, forward
guide: TGGGACAGAACTTCCCCAGG

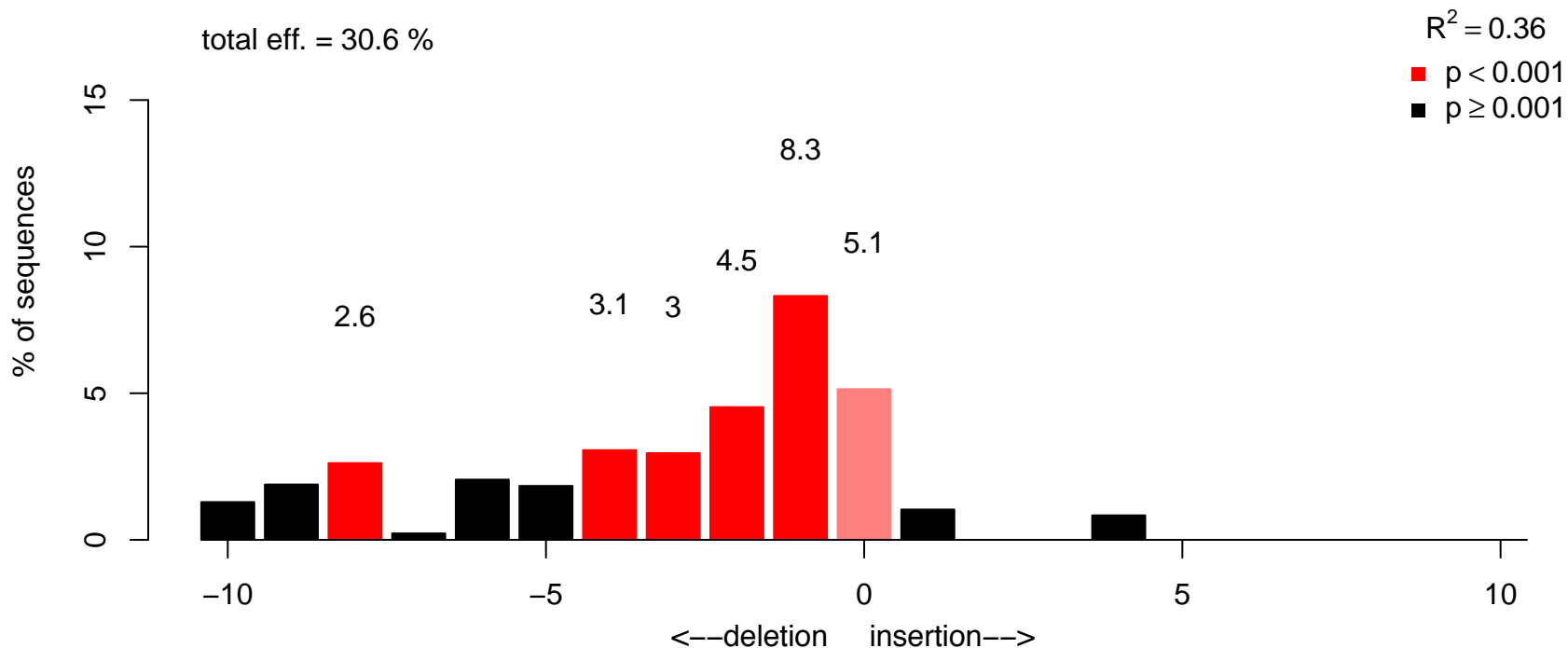
region for decomposition



Warning: left boundary of decomposition window was adjusted 224 . It must be at least 5bp plus the maximum indel size downstream of the expected break site

sample: Bth/WT cell line, gRNA 2.3, forward
guide: TGGGACAGAACTTCCCCAGG

total eff. = 30.6 %

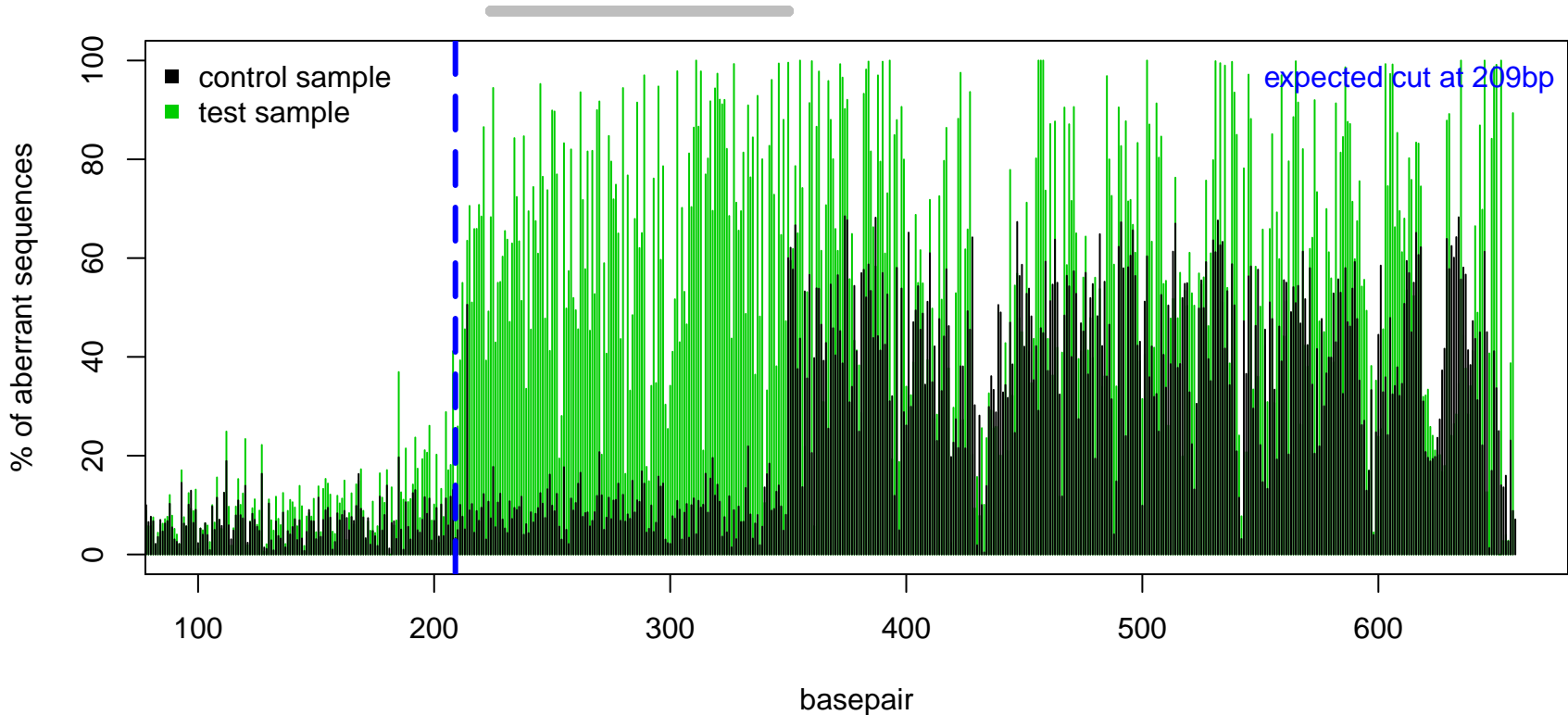


Warning: the spacing between the nucleotides in (one of) sanger sequence file(s) is not constant.

This might indicate for wrongly unannotated or wrongly additional annotated nucleotides.
Decomposition window lower and check the chromatogram for abnormalities.

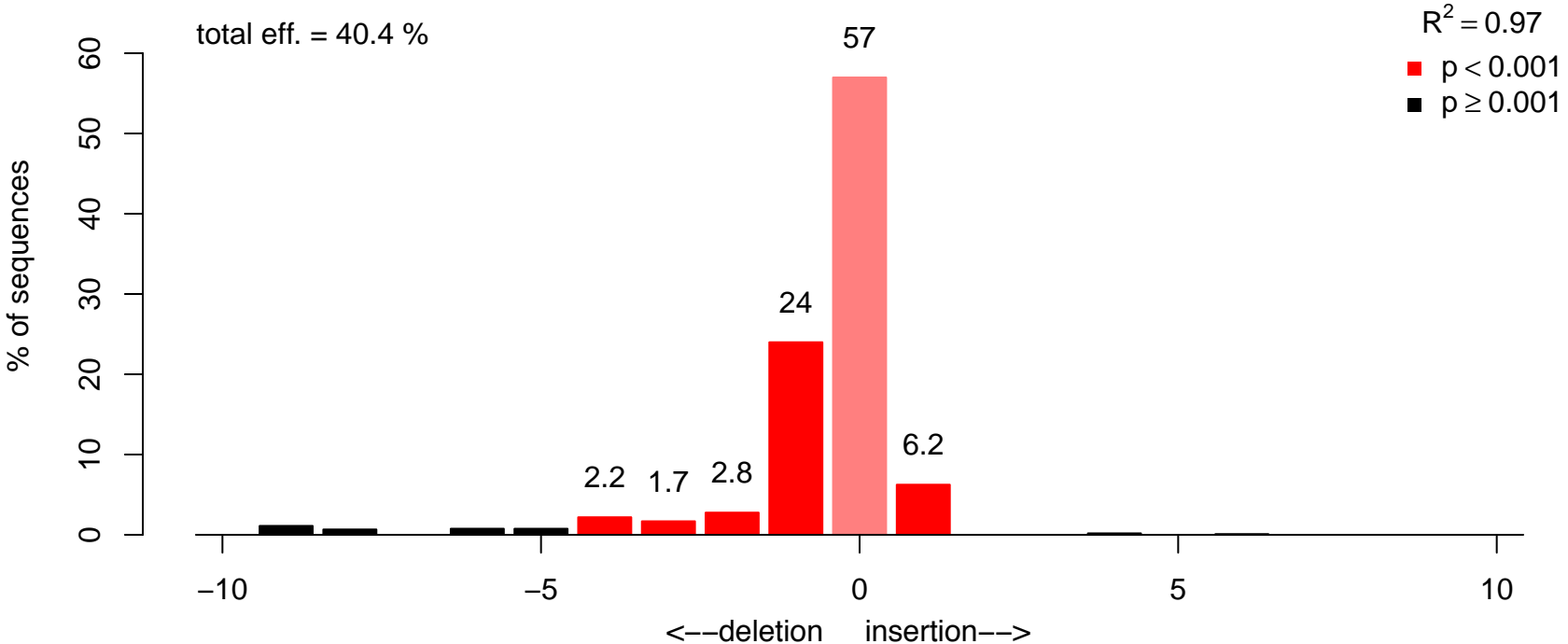
sample: Bth/WT cell line, gRNA 2.3, forward
guide: TGGGACAGAACTTCCCCAGG

region for decomposition



Warning: left boundary of decomposition window was adjusted 224 . It must be at least 5bp plus the maximum indel size downstream of the expected break site

sample: Bth/WT cell line, gRNA 2.4, forward
guide: TGGGACAGAACTTCCCCAGG

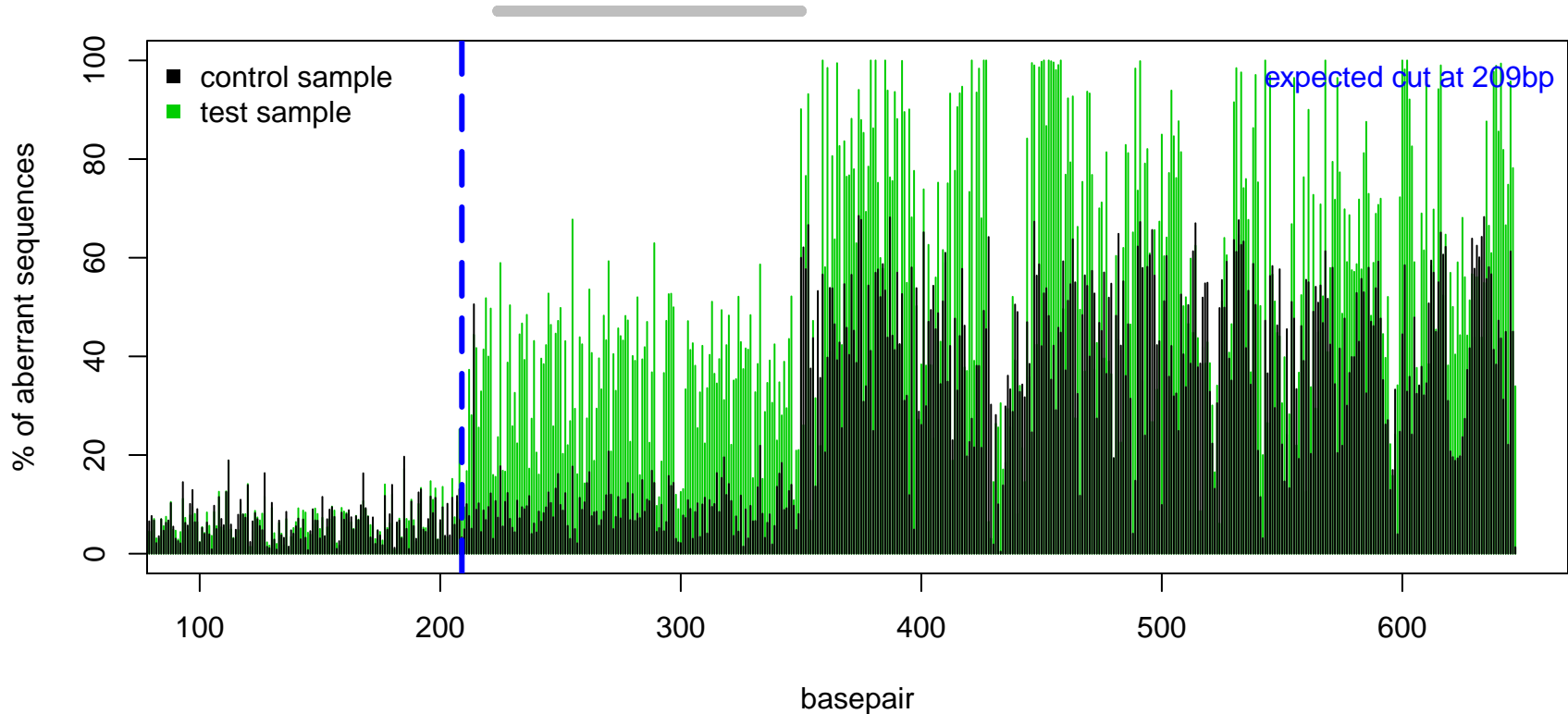


Warning: the spacing between the nucleotides in (one of) sanger sequence file(s) is not constant.

This might indicate for wrongly unannotated or wrongly additional annotated nucleotides.
Decomposition window lower and check the chromatogram for abnormalities.

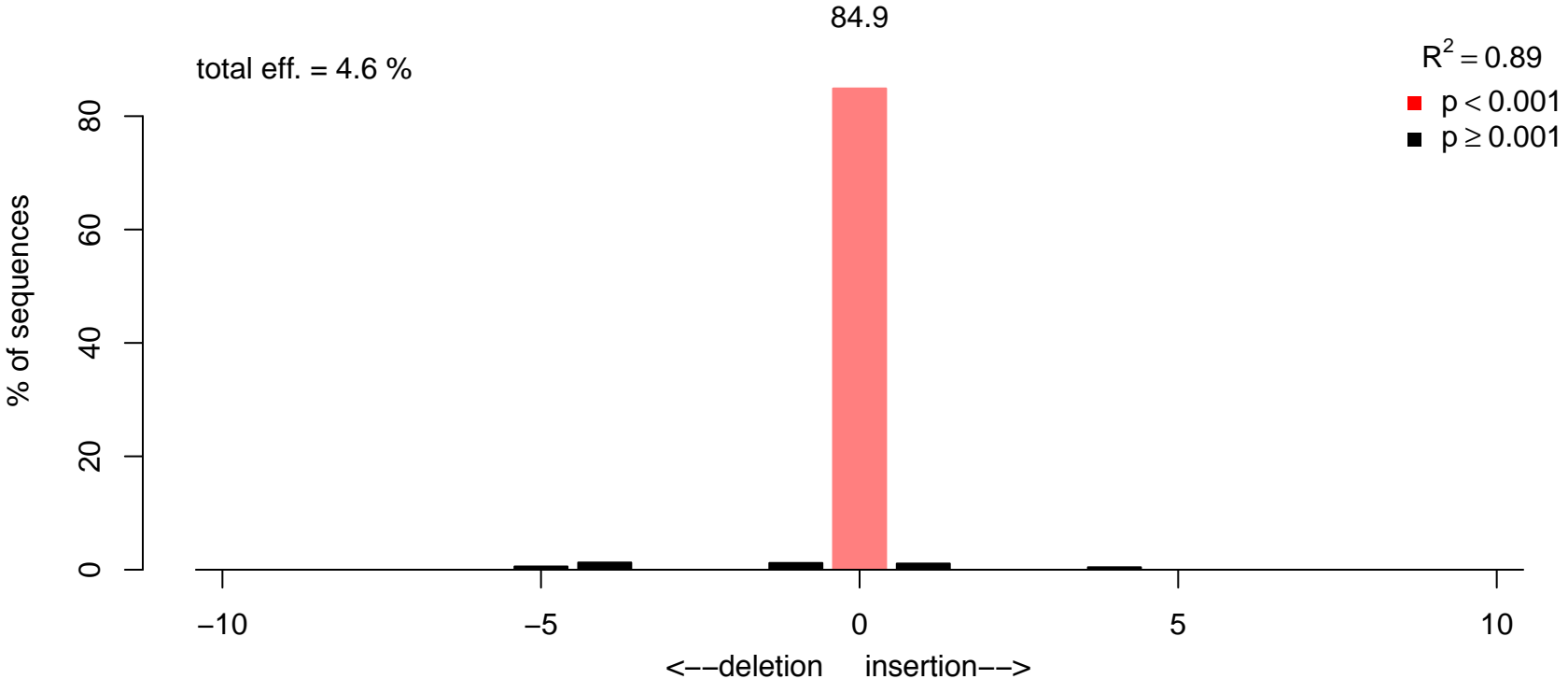
sample: Bth/WT cell line, gRNA 2.4, forward
guide: TGGGACAGAACTTCCCCAGG

region for decomposition



Warning: left boundary of decomposition window was adjusted 224 . It must be at least 5bp plus the maximum indel size downstream of the expected break site

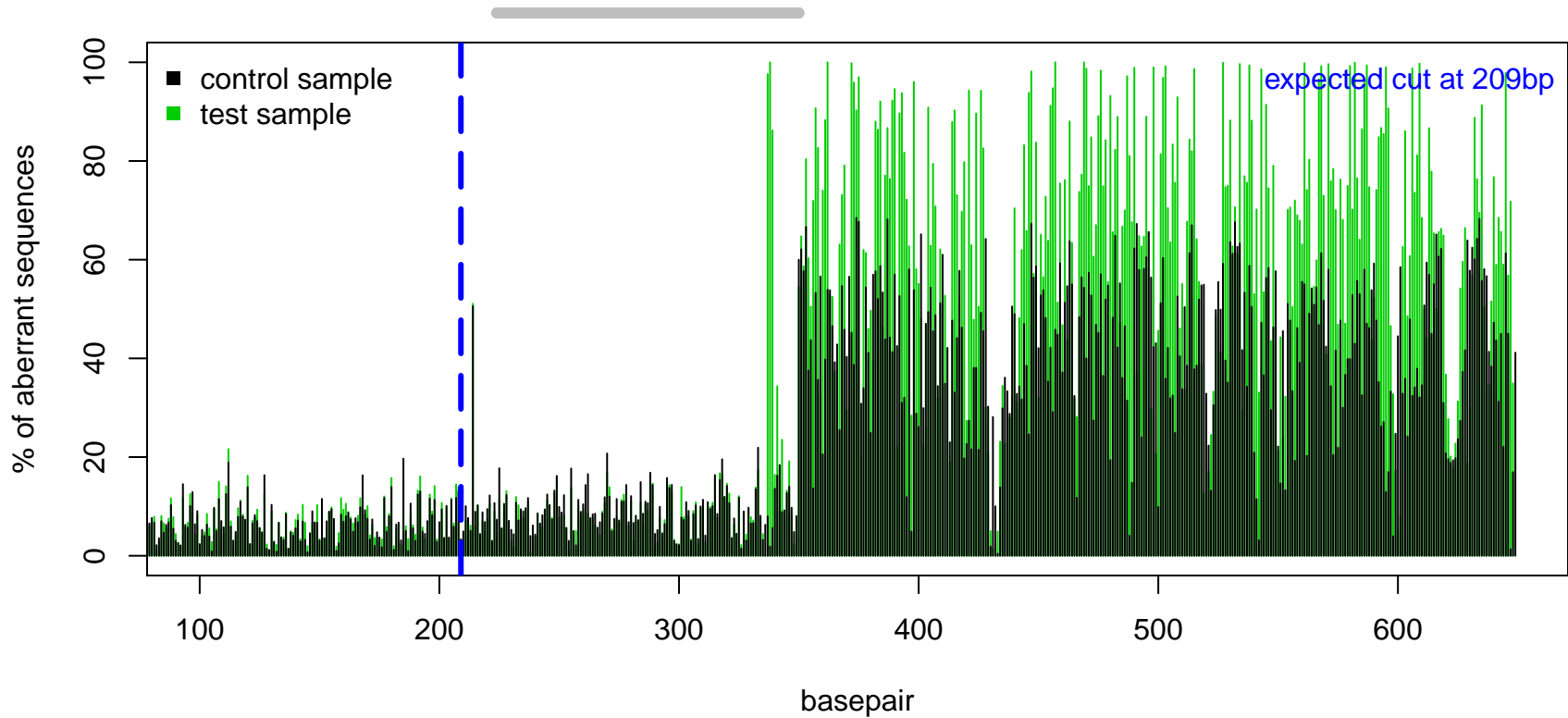
sample: Bth/WT cell line, gRNA 3.1, forward
guide: TGGTAATGTCCCTCCTGGGG



Warning: the spacing between the nucleotides in (one of) sanger sequence file(s) is not constant.
This might indicate for wrongly unannotated or wrongly additional annotated nucleotides.
Decomposition window lower and check the chromatogram for abnormalities.

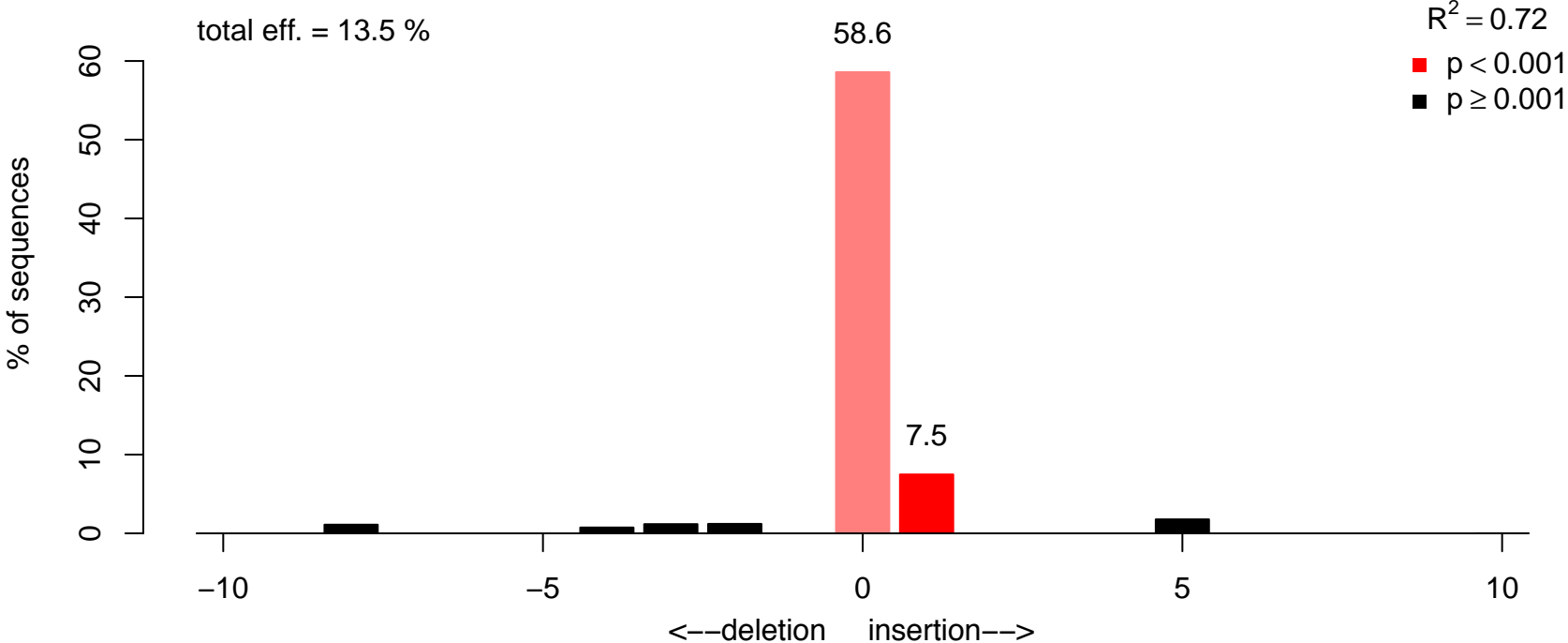
sample: Bth/WT cell line, gRNA 3.1, forward
guide: TGGTAATGTCCCTCCTGGGG

region for decomposition



Warning: left boundary of decomposition window was adjusted 224 . It must be at least 5bp plus the maximum indel size downstream of the expected break site

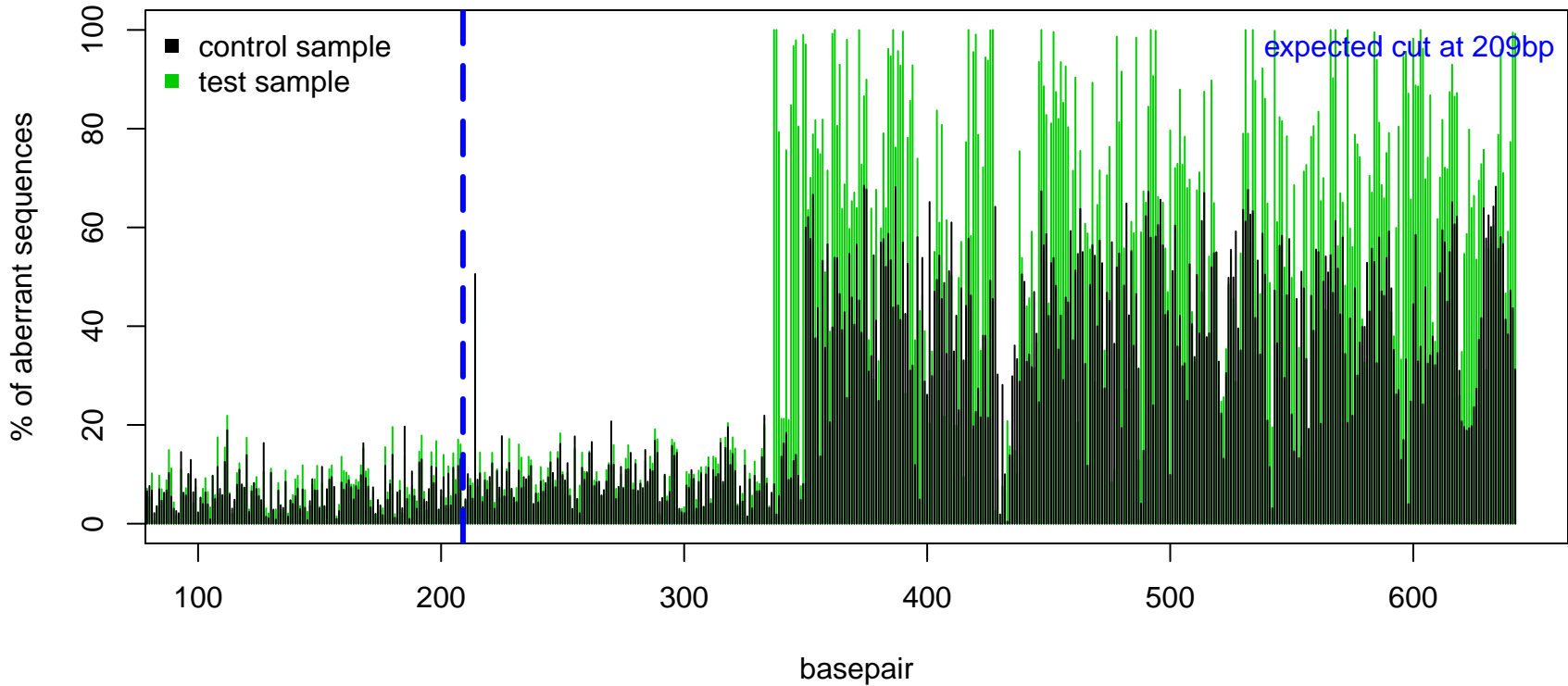
sample: Bth/WT cell line, gRNA 3.2, forward
guide: TGGTAATGTCCCTCCTGGGG



Warning: the spacing between the nucleotides in (one of) sanger sequence file(s) is not constant.
This might indicate for wrongly unannotated or wrongly additional annotated nucleotides.
Decomposition window lower and check the chromatogram for abnormalities.

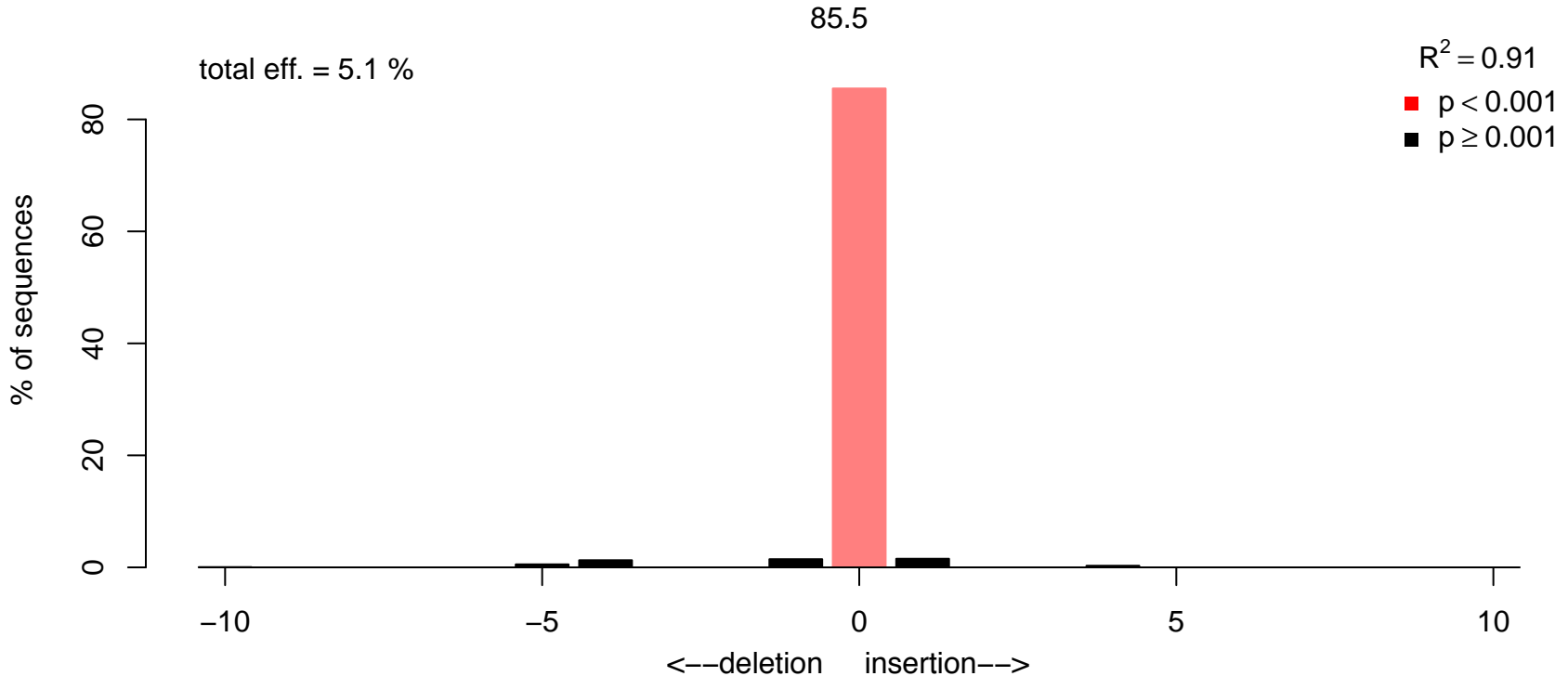
sample: Bth/WT cell line, gRNA 3.2, forward
guide: TGGTAATGTCCCTCCTGGGG

region for decomposition



Warning: left boundary of decomposition window was adjusted 224 . It must be at least 5bp plus the maximum indel size downstream of the expected break site

sample: Bth/WT cell line, gRNA 3.3, forward
guide: TGGTAATGTCCCTCCTGGGG

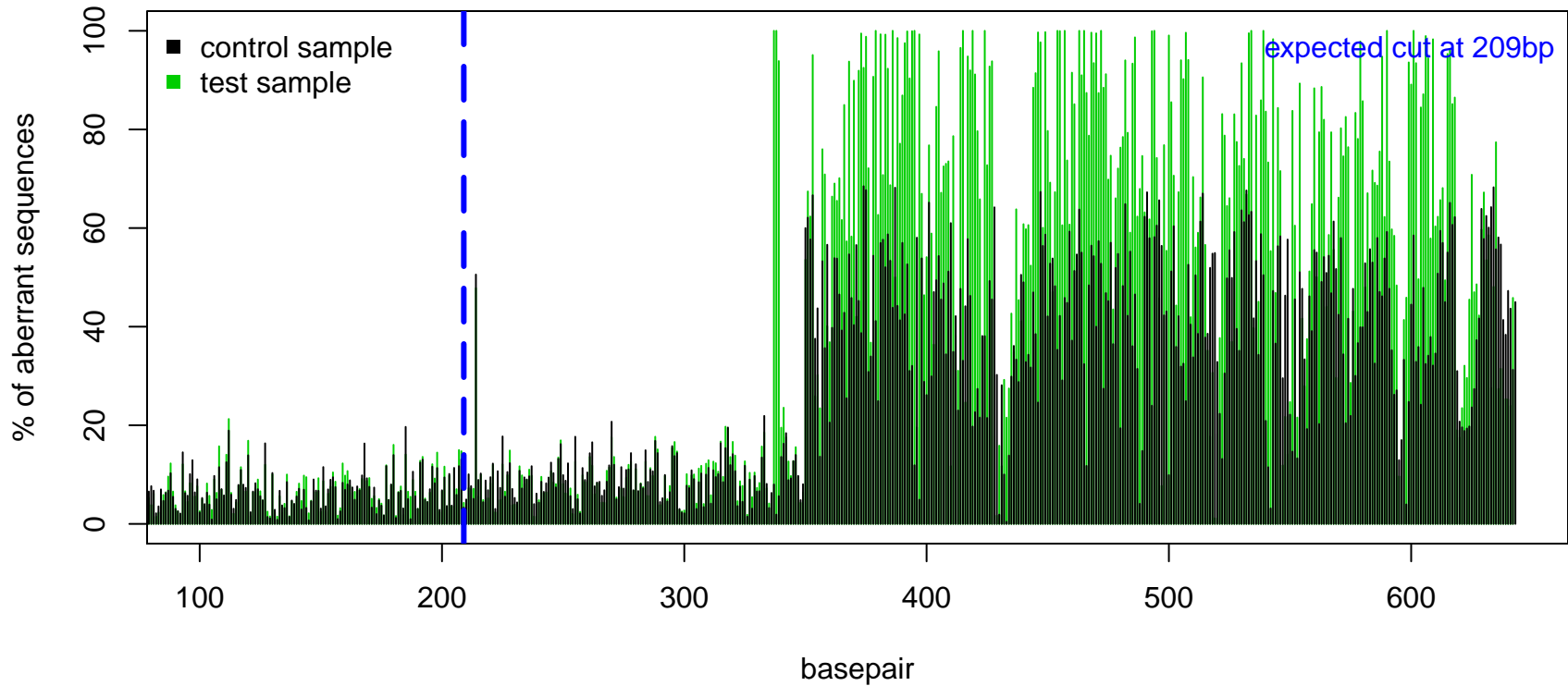


Warning: the spacing between the nucleotides in (one of) sanger sequence file(s) is not constant.

This might indicate for wrongly unannotated or wrongly additional annotated nucleotides.
Decomposition window lower and check the chromatogram for abnormalities.

sample: Bth/WT cell line, gRNA 3.3, forward
guide: TGGTAATGTCCCTCCTGGGG

region for decomposition



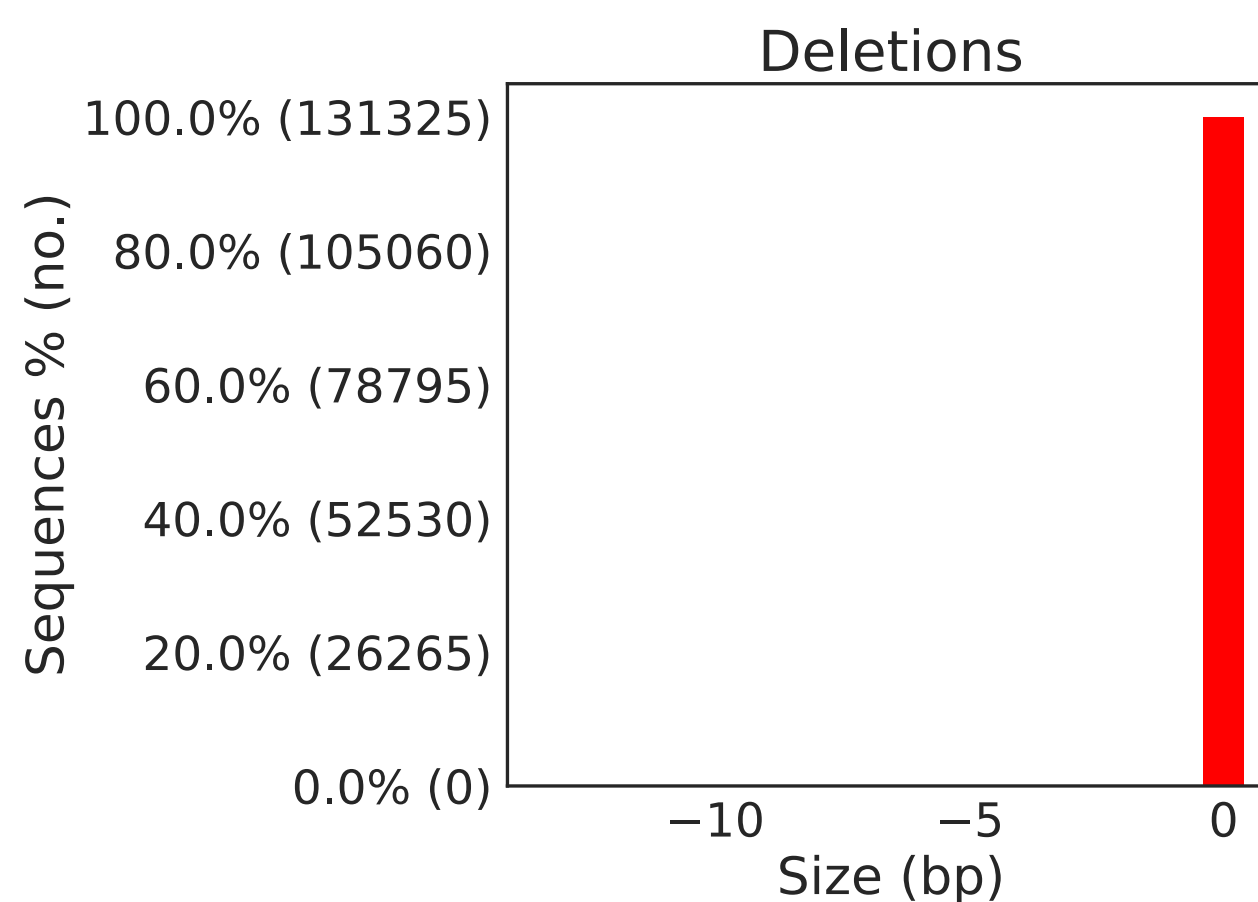
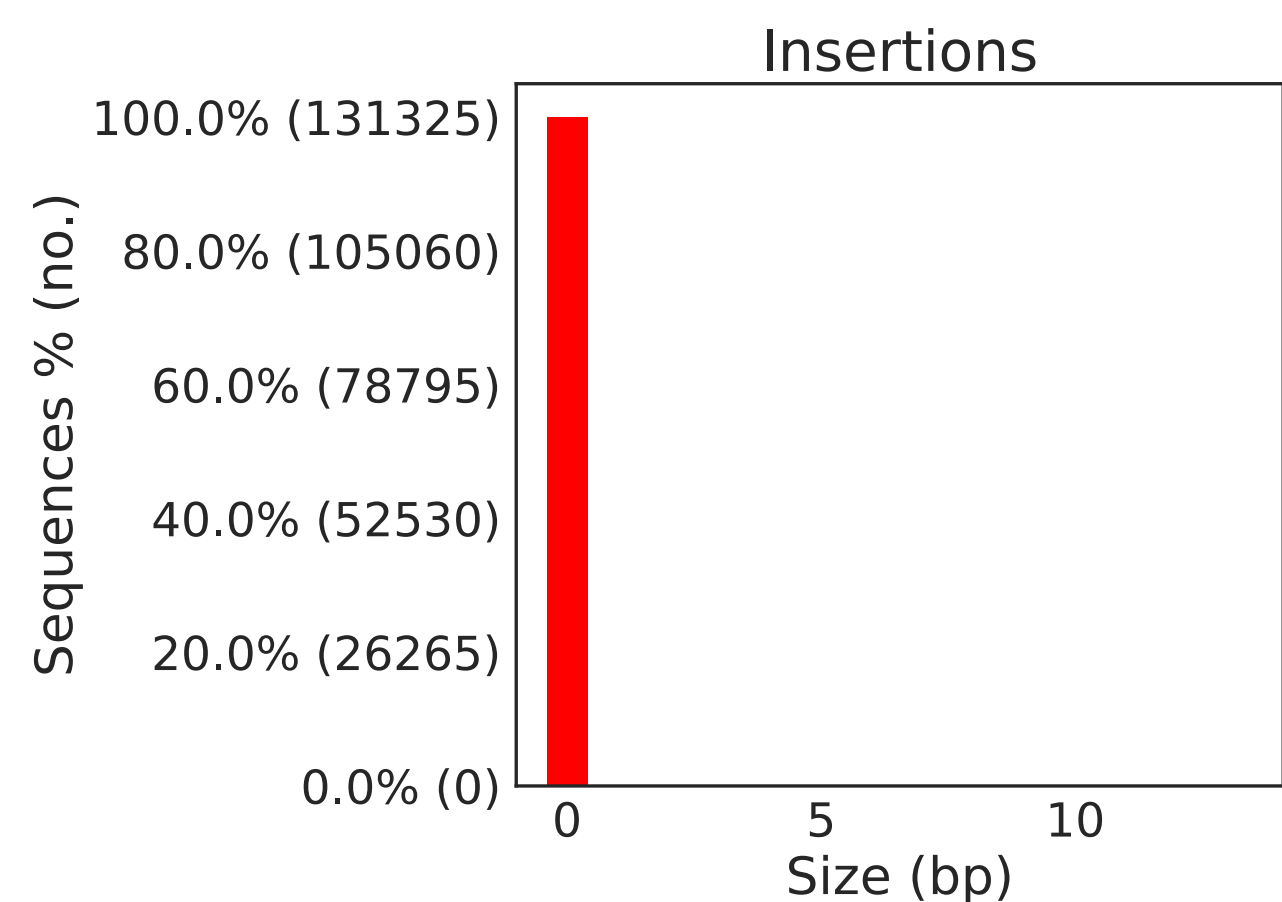
Warning: left boundary of decomposition window was adjusted 224 . It must be at least 5bp plus the maximum indel size downstream of the expected break site

Tmc1^{Bth/WT}, SpCas9 only, Bth allele only

- bold** Substitutions
- Insertions
- Deletions
- - -** Predicted cleavage position

A T G G T A A T G T C C C T C C T G G G G A A G T T C T G T C C C A C C C T G T Reference

A T G G T A A T G T C C C T C C T G G G G **G** A A G T T C T G T C C C A C C C T G T 98.27% (129057 reads)



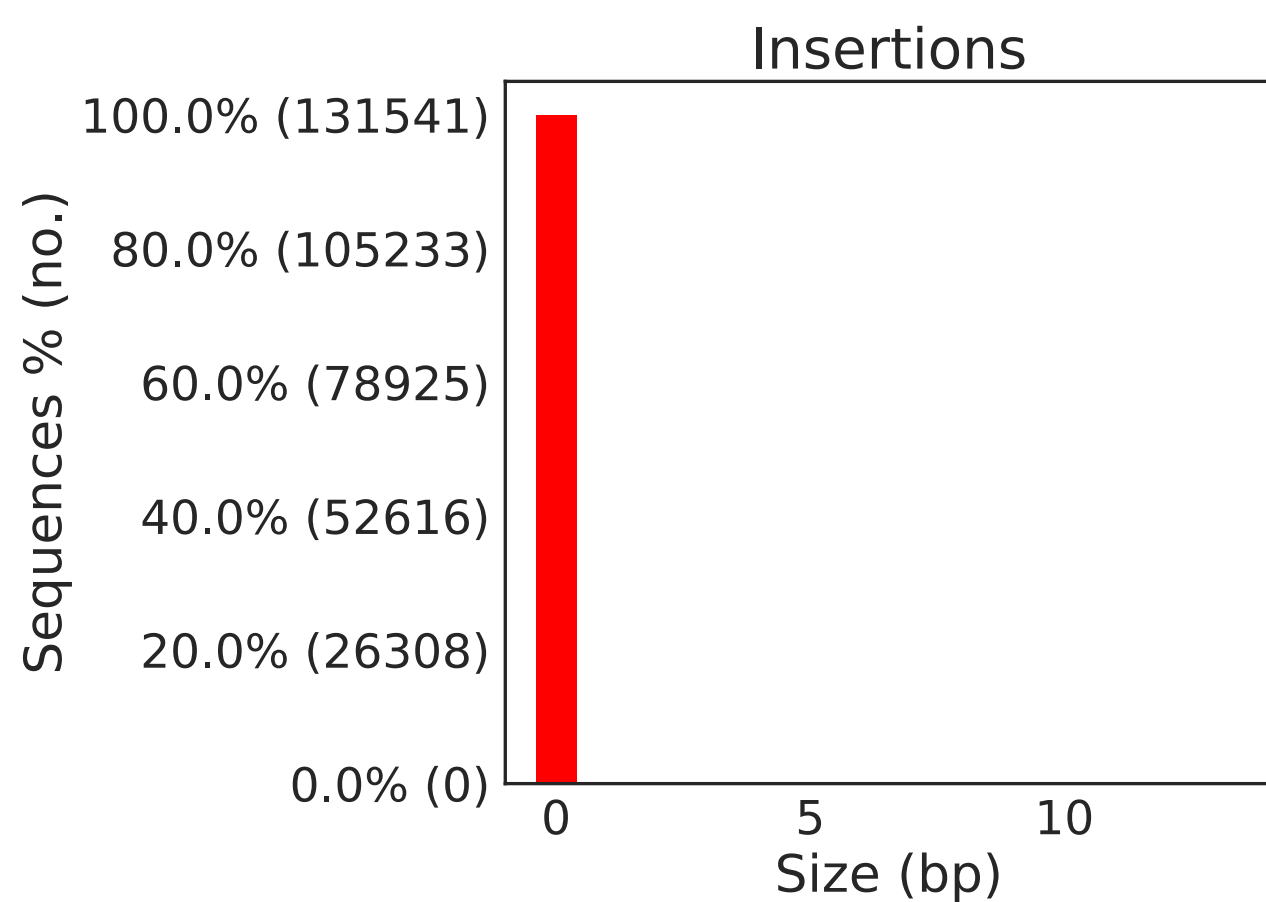
— Insertion
— Non-insertion

— Deletion
— Non-deletion

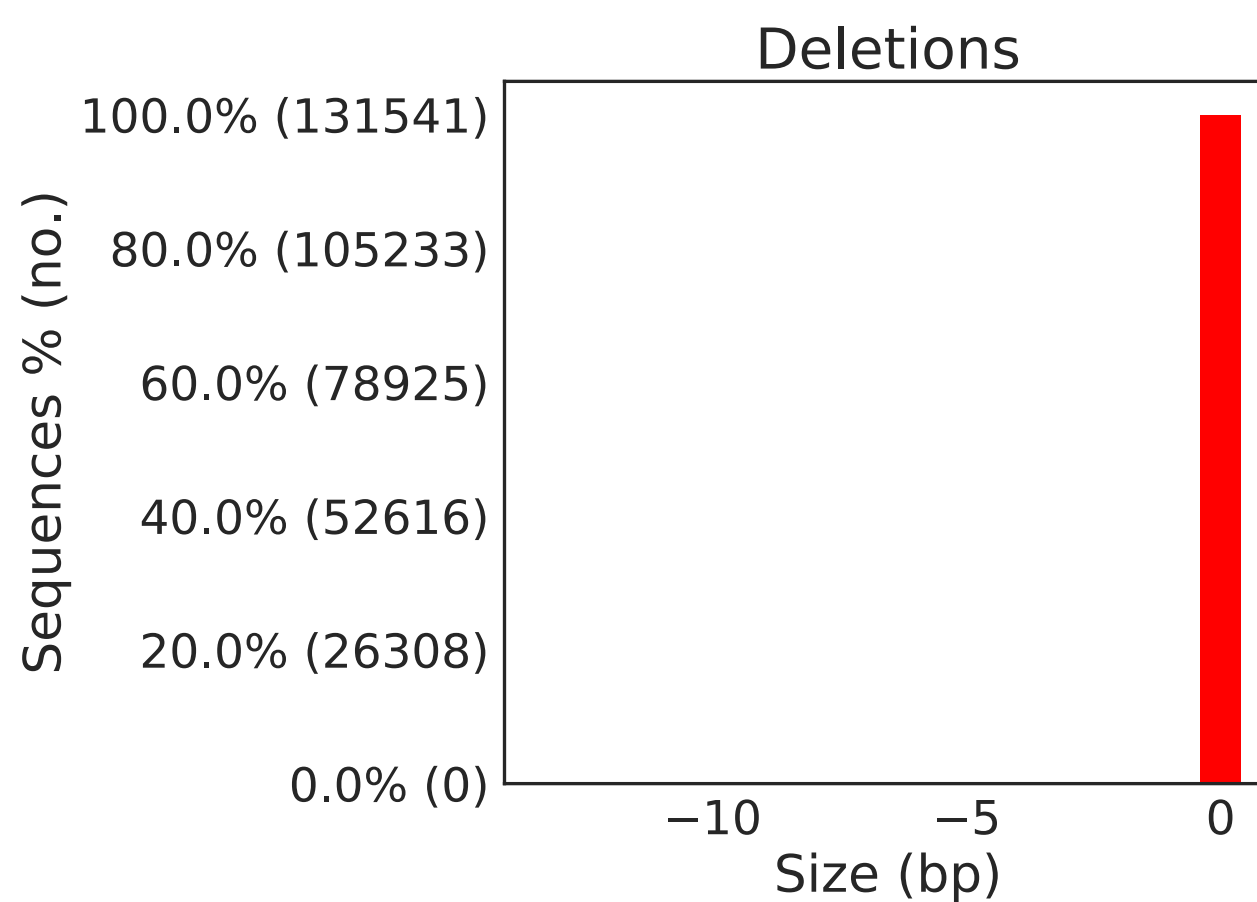
Tmc1^{Bth/WT}, SpCas9 only, WT allele only

bold Substitutions
 Insertions
 - Deletions
 - - - Predicted cleavage position

A T G G T A A T G T C C C T C C T G G G G A A G T T C T G T C C C A C C C T G T Reference
 A T G G T A A T G T C C C T C C T G G G **G** A T G T T C T G T C C C A C C C T G T 98.43% (129478 reads)



— Insertion
— Non-insertion

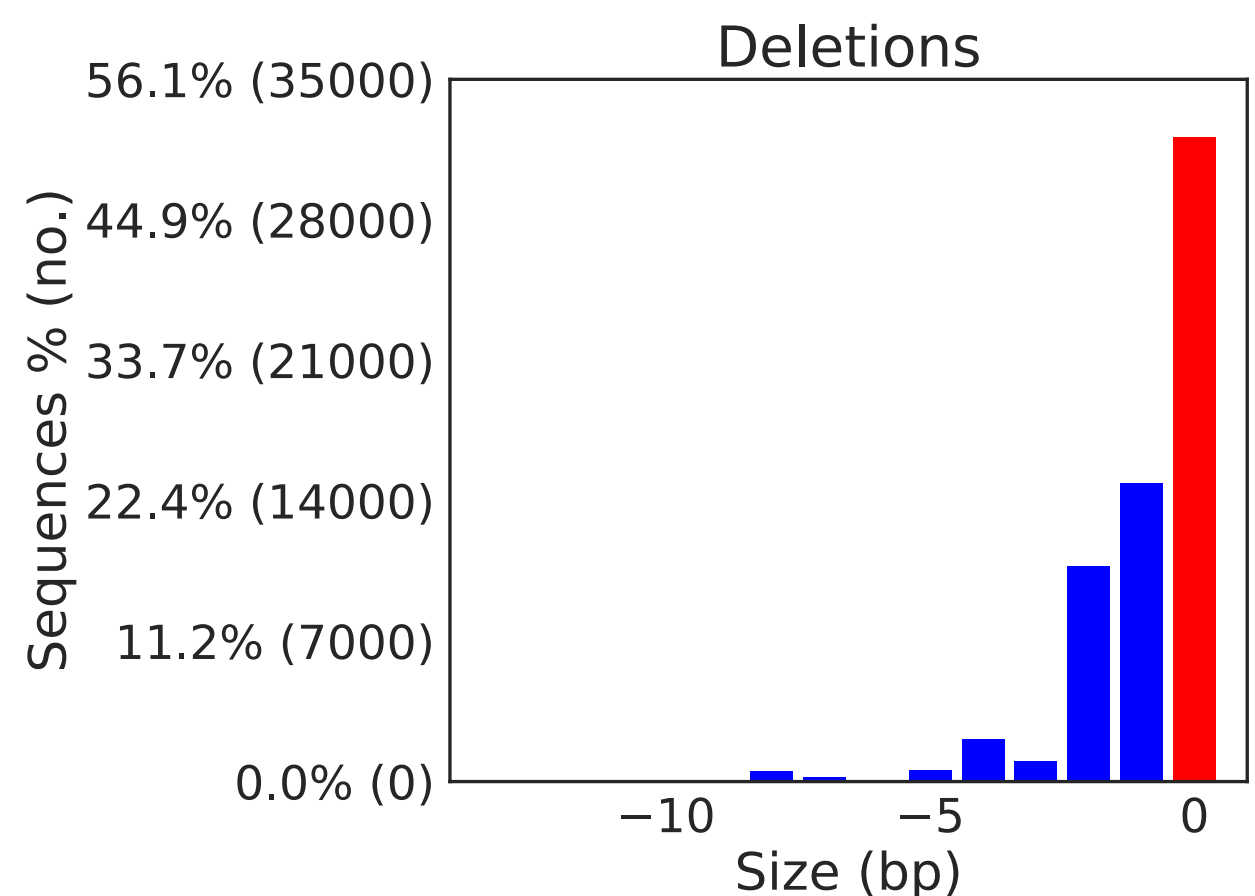
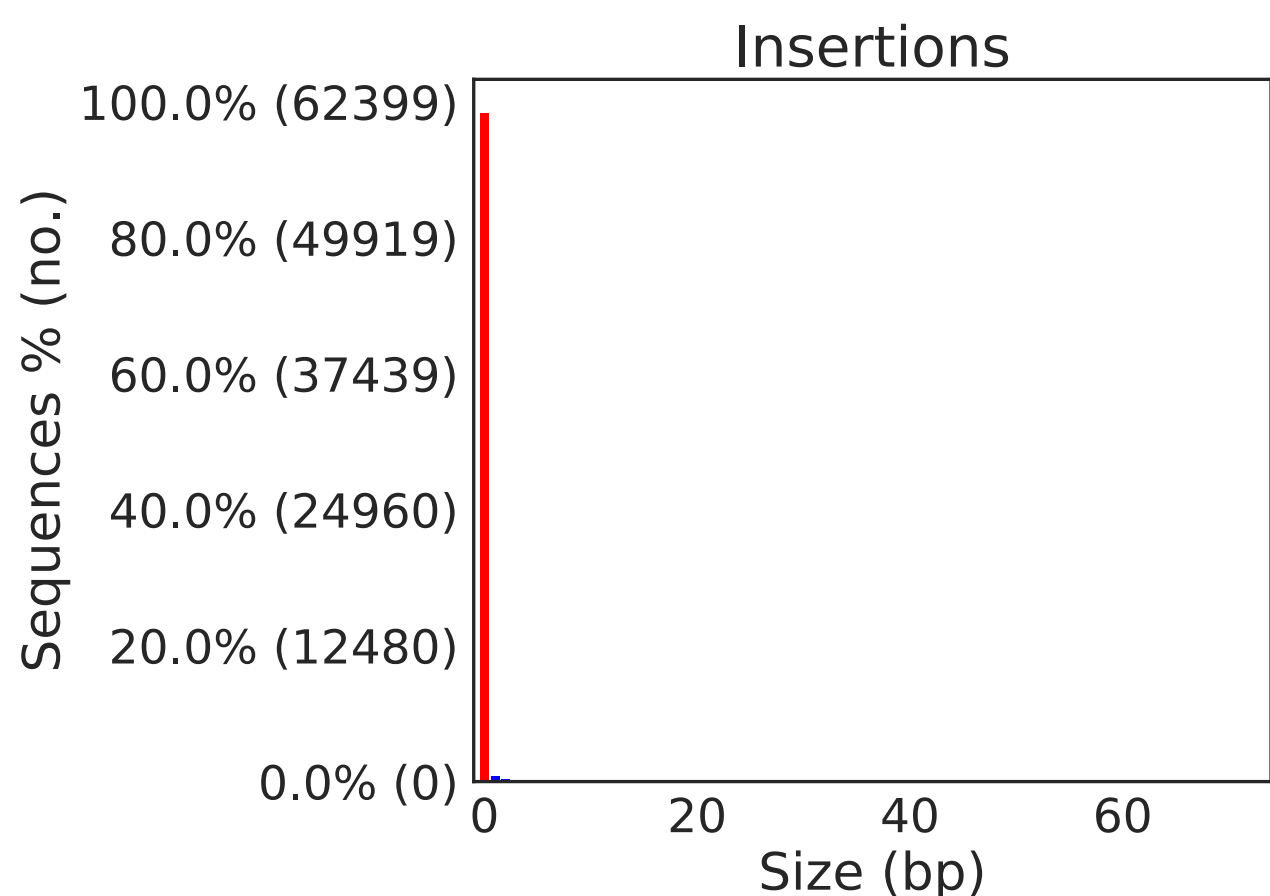


— Deletion
— Non-deletion

Tmc1^{Bth/WT}, SpCas9 + gRNA 1.1, Bth allele only

bold Substitutions
 Insertions
 - Deletions
 - - - Predicted cleavage position

Reference																																										
A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	G	G	G	G	A	A	G	T	T	C	T	G	T	C	C	C	A	C	C	C	T	G	T	23.21% (14481 reads)		
A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	G	G	G	I	-	A	A	G	T	T	C	T	G	T	C	C	C	A	C	C	C	T	G	T	23.08% (14400 reads)	
A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	G	G	G	G	A	A	G	T	T	C	T	G	T	C	C	C	A	C	C	C	T	G	T	22.84% (14253 reads)		
A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	G	G	G	-	-	A	A	G	T	T	C	T	G	T	C	C	C	A	C	C	C	T	G	T	14.59% (9101 reads)	
A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	-	-	-	-	G	A	A	G	T	T	C	T	G	T	C	C	C	A	C	C	C	T	G	T	2.65% (1656 reads)		
A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	G	G	-	-	A	A	G	T	T	C	T	G	T	C	C	C	A	C	C	C	T	G	T	1.26% (786 reads)		
A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	-	-	G	G	A	A	G	T	T	C	T	G	T	C	C	C	A	C	C	C	T	G	T	1.16% (723 reads)		
A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	G	G	G	A	G	A	A	G	T	T	C	T	G	T	C	C	C	A	C	C	C	T	G	T	0.78% (488 reads)	
A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	-	-	-	-	A	A	G	T	T	C	T	G	T	C	C	C	A	C	C	C	T	G	T	0.72% (448 reads)		
A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	-	-	-	-	-	G	A	A	G	T	T	C	T	G	T	C	C	C	A	C	C	C	T	G	T	0.65% (404 reads)		
A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	-	-	-	G	G	A	A	G	T	T	C	T	G	T	C	C	C	A	C	C	C	T	G	T	0.64% (399 reads)		
A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	-	G	G	G	G	A	A	G	T	T	C	T	G	T	C	C	C	A	C	C	C	T	G	T	0.60% (376 reads)		
A	T	G	G	T	A	A	T	G	T	C	C	C	T	-	-	-	-	-	-	-	A	A	G	T	T	C	T	G	T	C	C	C	A	C	C	C	T	G	T	0.47% (294 reads)		
A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	-	G	G	G	T	A	A	G	T	T	C	T	G	T	C	C	C	A	C	C	C	T	G	T	0.45% (283 reads)	
A	T	G	G	T	A	A	T	G	T	C	C	A	T	C	C	-	G	G	G	G	A	A	G	T	T	C	T	G	T	C	C	C	A	C	C	C	T	G	T	0.44% (274 reads)		
A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	G	G	G	A	A	G	A	A	G	T	T	C	T	G	T	C	C	C	A	C	C	C	T	G	T	0.41% (253 reads)
A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	G	G	G	T	A	-	G	T	T	C	T	G	T	C	C	C	A	C	C	C	T	G	T	0.39% (243 reads)		
A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	G	-	-	-	A	A	G	T	T	C	T	G	T	C	C	C	A	C	C	C	T	G	T	0.38% (235 reads)		
A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	-	-	-	G	A	A	G	T	T	C	T	G	T	C	C	C	A	C	C	C	T	G	T	0.36% (226 reads)		
A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	G	G	G	T	C	C	T	C	A	T	G	G	G	C	A	C	T	A	T	G	A	A	T	0.36% (222 reads)		
A	T	G	G	T	A	A	T	G	T	C	C	-	-	-	-	-	-	-	-	G	A	A	G	T	T	C	T	G	T	C	C	C	A	C	C	C	T	G	T	0.35% (216 reads)		
A	T	G	G	C	A	A	T	G	T	C	C	C	T	C	C	T	G	G	G	G	A	A	G	T	T	C	T	G	T	C	C	C	A	C	C	C	T	G	T	0.32% (200 reads)		
A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	-	-	-	-	-	A	A	G	T	T	C	T	G	T	C	C	C	A	C	C	C	T	G	T	0.27% (169 reads)		
A	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	G	A	A	G	T	T	C	T	G	T	C	C	C	A	C	C	C	T	G	T	0.27% (167 reads)	
A	T	A	G	T	A	A	T	G	T	C	C	C	T	C	C	T	G	G	G	G	A	A	G	T	T	C	T	G	T	C	C	C	A	C	C	C	T	G	T	0.21% (132 reads)		



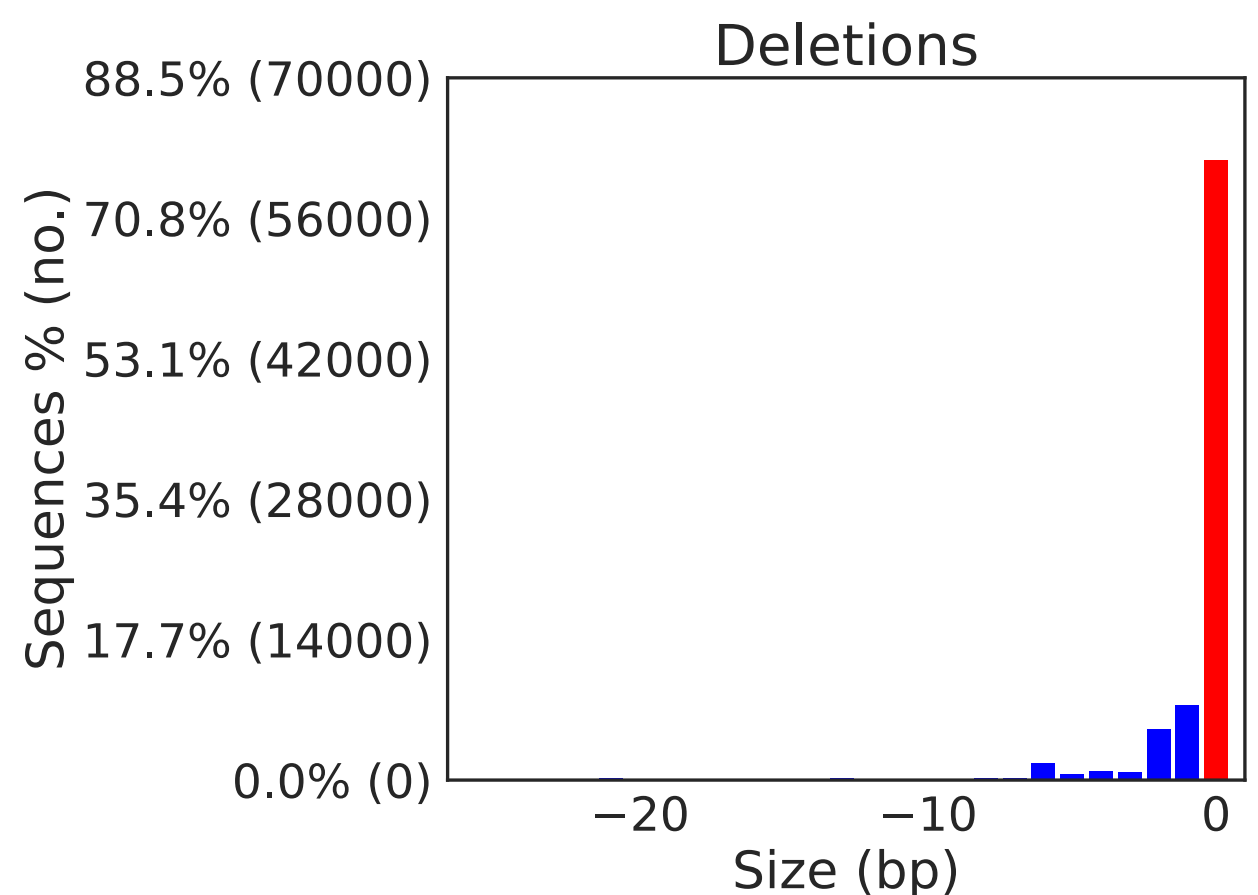
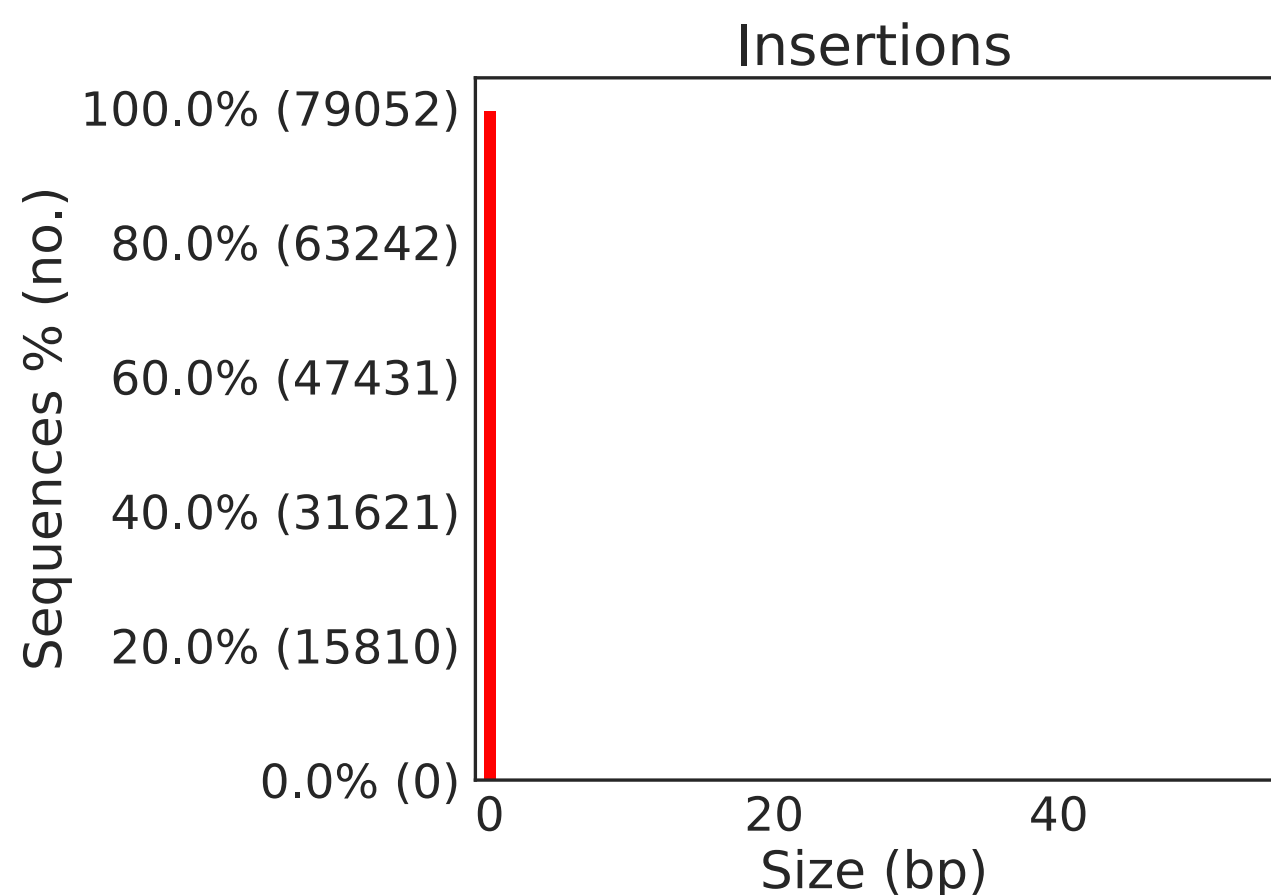
— Insertion
 — Non-insertion

— Deletion
 — Non-deletion

Tmc1^{Bth/WT}, SpCas9 + gRNA 1.1, WT allele only

bold Substitutions
 Insertions
 - Deletions
 - - - Predicted cleavage position

Reference																																								
A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	G	G	G	G	A	A	G	T	T	C	T	G	T	C	C	C	A	C	C	C	T	G	T	65.46% (51747 reads)
A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	-	G	G	G	A	T	G	T	T	C	T	G	T	C	C	C	A	C	C	C	T	G	T	9.71% (7675 reads)
A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	G	G	G	-	A	T	G	T	T	C	T	G	T	C	C	C	A	C	C	C	T	G	T	9.33% (7374 reads)
A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	G	G	G	-	-	T	G	T	T	C	T	G	T	C	C	C	A	C	C	C	T	G	T	2.39% (1887 reads)
A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	G	G	G	T	-	-	G	T	T	C	T	G	T	C	C	C	A	C	C	C	T	G	T	2.24% (1772 reads)
A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	-	-	-	-	-	-	G	T	T	C	T	G	T	C	C	C	A	C	C	C	T	G	T	1.08% (857 reads)
A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	G	-	-	-	-	-	-	T	T	C	T	G	T	C	C	C	A	C	C	C	T	G	T	0.99% (781 reads)
A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	-	-	-	-	G	A	T	G	T	T	C	T	G	T	C	C	C	A	C	C	C	T	G	T	0.84% (666 reads)
A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	G	G	-	-	A	T	G	T	T	C	T	G	T	C	C	C	A	C	C	C	T	G	T	0.68% (541 reads)
A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	-	-	G	G	A	T	G	T	T	C	T	G	T	C	C	C	A	C	C	C	T	G	T	0.67% (532 reads)
A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	-	G	G	G	G	A	T	G	T	T	C	T	G	T	C	C	C	A	C	C	C	T	G	T	0.55% (433 reads)
A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	G	G	G	T	G	G	T	G	G	T	A	G	T	T	G	T	T	G	A	T	C	T	C	0.48% (378 reads)
A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	G	-	-	-	A	T	G	T	T	C	T	G	T	C	C	C	A	C	C	C	T	G	T	0.38% (300 reads)
A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	-	-	-	G	A	T	G	T	T	C	T	G	T	C	C	C	A	C	C	C	T	G	T	0.34% (269 reads)
A	T	G	G	T	A	-	-	-	-	-	-	-	-	-	C	A	G	A	G	C	A	A	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0.30% (234 reads)
A	T	G	G	T	A	A	T	G	T	C	C	-	-	-	-	-	-	-	-	G	A	T	G	T	T	C	T	G	T	C	C	C	A	C	C	C	T	G	T	0.27% (211 reads)
A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	-	-	-	-	-	T	G	T	T	C	T	G	T	C	C	C	A	C	C	C	T	G	T	0.26% (202 reads)
A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	T	G	-	-	-	-	-	T	T	C	T	G	T	C	C	C	A	C	C	C	T	G	T	0.25% (201 reads)
A	T	G	G	T	A	A	T	G	T	C	C	C	-	-	-	-	-	-	-	G	A	T	G	T	T	C	T	G	T	C	C	C	A	C	C	C	T	G	T	0.24% (189 reads)
A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	-	-	-	-	-	G	A	T	G	T	T	C	T	G	T	C	C	C	A	C	C	C	T	G	T	0.22% (174 reads)
A	T	G	A	T	A	A	T	G	T	C	C	C	T	C	C	T	G	G	G	G	A	T	G	T	T	C	T	G	T	C	C	C	A	C	C	C	T	G	T	0.22% (171 reads)

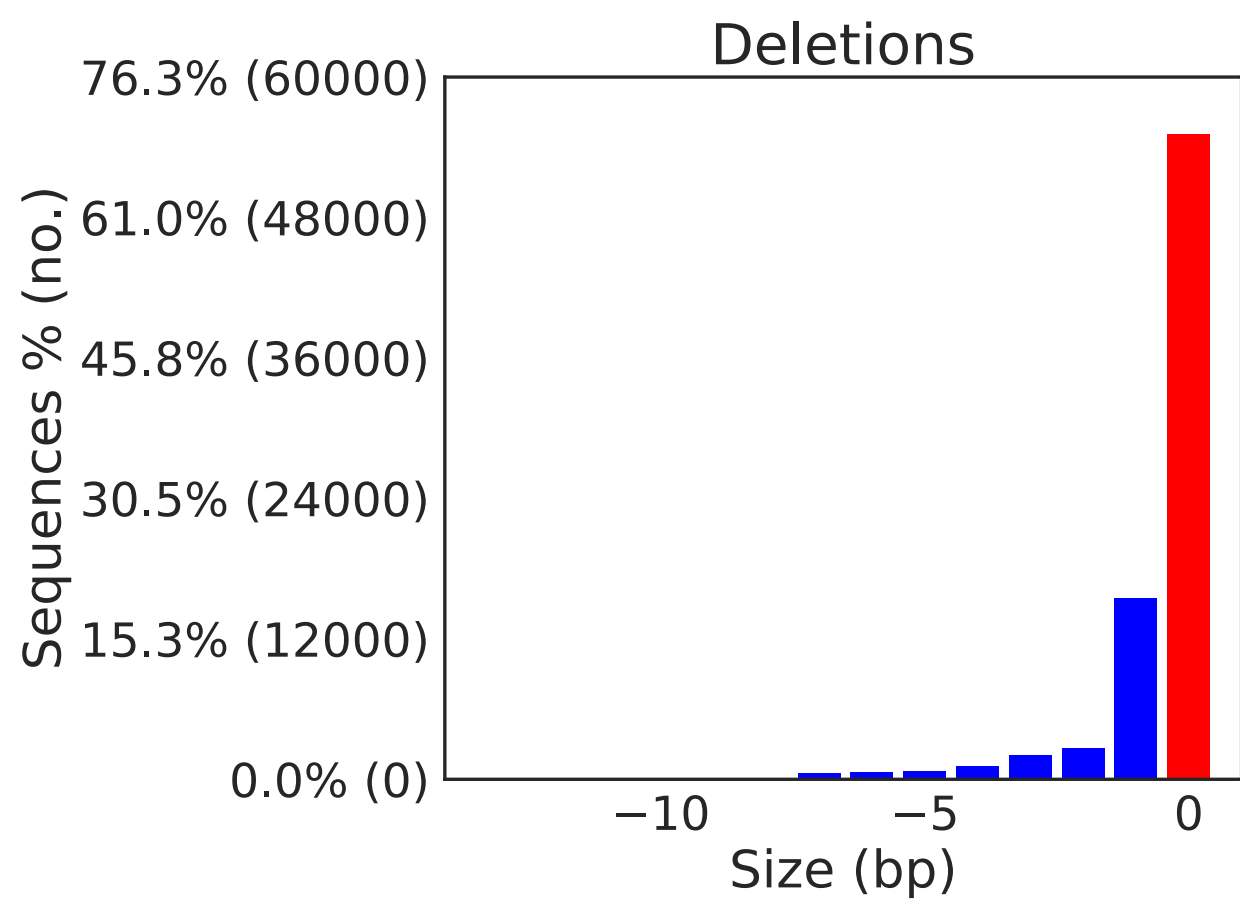
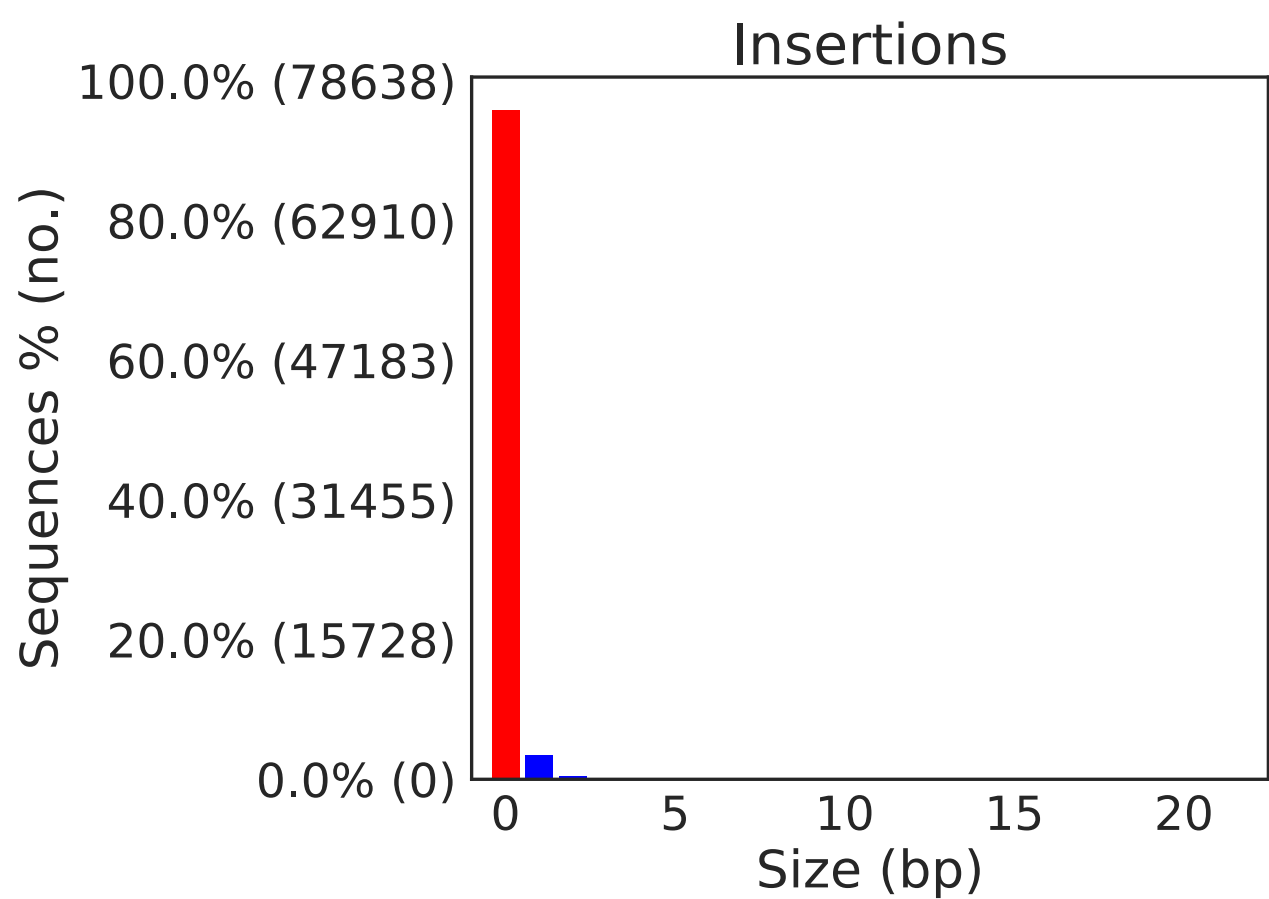
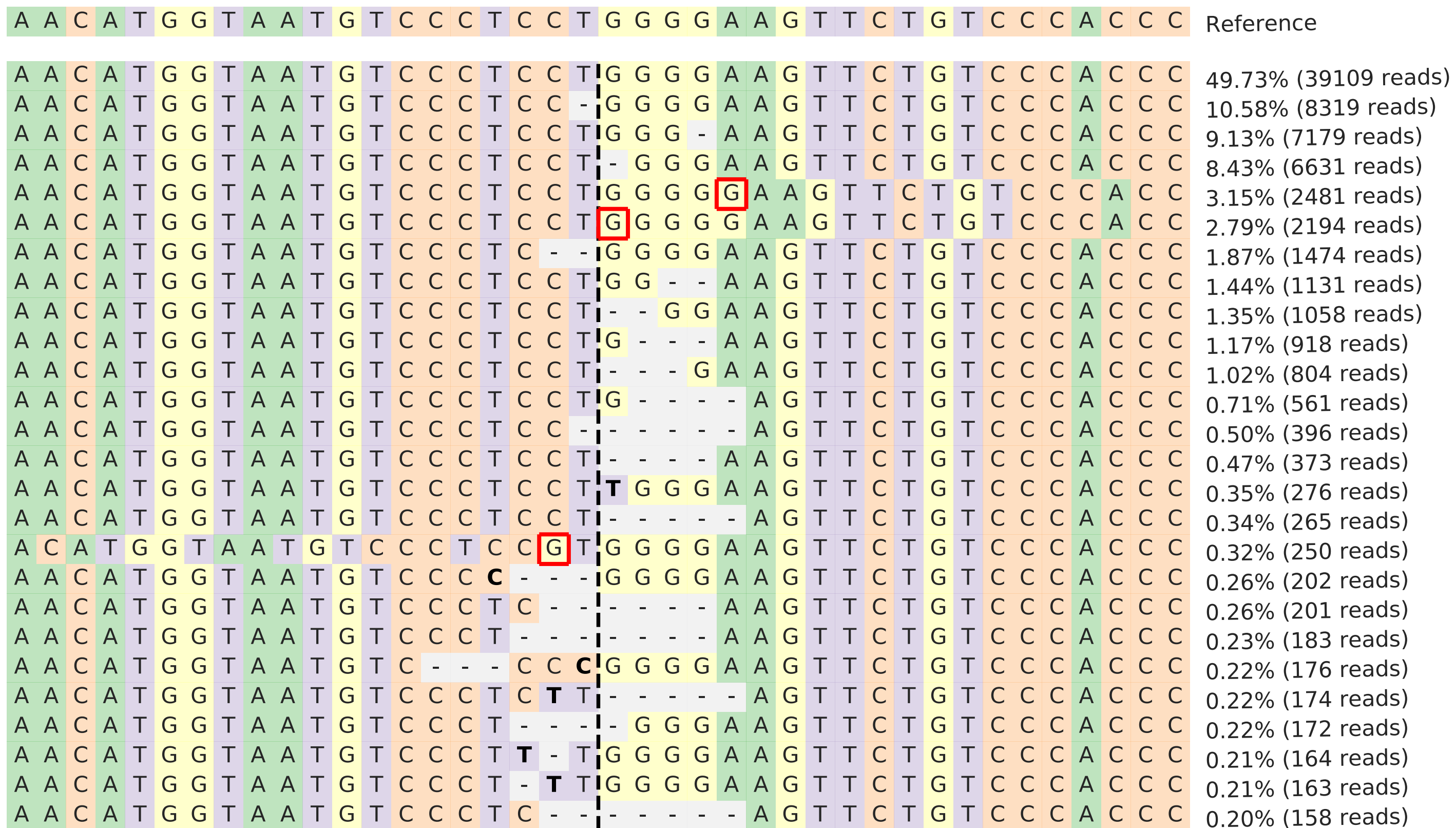


Insertion
 Non-insertion

Deletion
 Non-deletion

Tmc1^{Bth/WT}, SpCas9 + gRNA 2.1, Bth allele only

bold Substitutions
 Insertions
 - Deletions
 - - - Predicted cleavage position



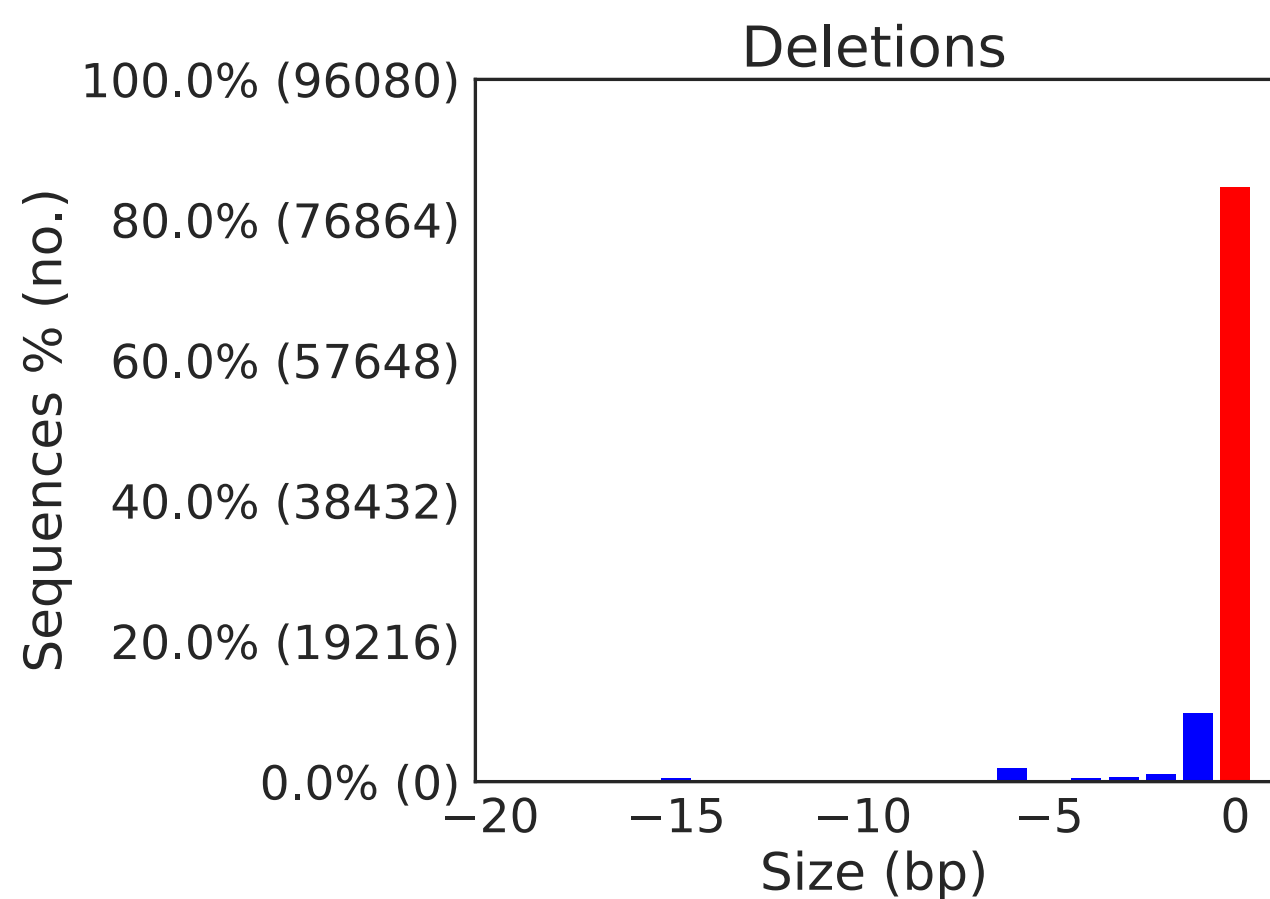
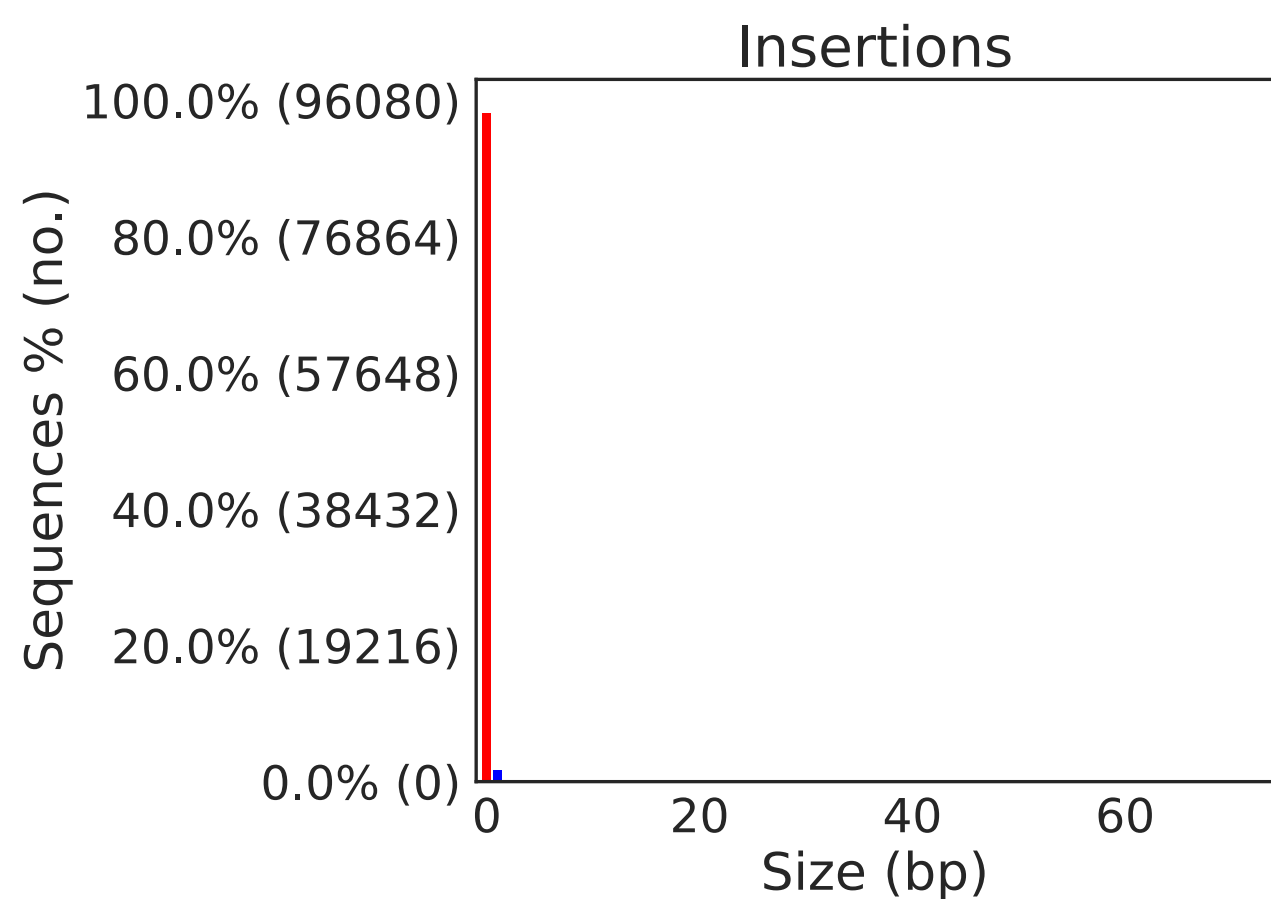
■ Insertion
 ■ Non-insertion

■ Deletion
 ■ Non-deletion

Tmc1^{Bth/WT}, SpCas9 + gRNA 2.1, WT allele only

bold Substitutions
 Insertions
 - Deletions
 - - - Predicted cleavage position

Reference																																									
A	A	C	A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	G	G	G	G	A	A	G	T	T	C	T	G	T	C	C	C	A	C	C	C	72.42% (69583 reads)	
A	A	C	A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	G	G	G	-	A	T	G	T	T	C	T	G	T	C	C	C	A	C	C	C	5.86% (5630 reads)	
A	A	C	A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	-	G	G	G	A	T	G	T	T	C	T	G	T	C	C	C	A	C	C	C	5.33% (5117 reads)	
A	A	C	A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	-	G	G	G	A	T	G	T	T	C	T	G	T	C	C	C	A	C	C	C	4.36% (4188 reads)		
A	A	C	A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	G	G	G	G	G	A	T	G	T	T	C	T	G	T	C	C	C	A	C	C	C	1.65% (1581 reads)
A	A	C	A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	G	G	G	G	A	T	G	T	T	C	T	G	T	C	C	C	A	C	C	C	1.42% (1365 reads)	
A	A	C	A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	G	-	-	-	-	-	-	T	T	C	T	G	T	C	C	C	A	C	C	C	0.99% (948 reads)	
A	A	C	A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	-	-	-	-	-	G	T	T	C	T	G	T	C	C	C	A	C	C	C	0.94% (905 reads)		
A	A	C	A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	G	G	-	-	A	T	G	T	T	C	T	G	T	C	C	C	A	C	C	C	0.90% (868 reads)	
A	A	C	A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	-	-	G	G	A	T	G	T	T	C	T	G	T	C	C	C	A	C	C	C	0.78% (752 reads)	
A	A	C	A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	-	-	G	G	G	A	T	G	T	T	C	T	G	T	C	C	C	A	C	C	C	0.31% (301 reads)	
A	A	C	A	T	G	G	T	A	A	T	-	-	-	-	-	-	-	-	-	-	-	-	-	-	G	T	T	C	T	G	T	C	C	C	A	C	C	C	0.28% (270 reads)		
A	A	C	A	T	G	G	T	A	A	T	G	T	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	T	C	T	G	T	C	C	C	A	C	C	C	0.25% (245 reads)	
A	A	C	A	T	G	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	T	T	C	T	G	T	C	C	C	A	C	C	C	0.23% (220 reads)	
A	A	C	A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	C	G	G	G	G	A	T	G	T	T	C	T	G	T	C	C	C	A	C	C	C	0.22% (211 reads)
A	A	C	A	T	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	G	T	T	C	T	G	T	C	C	C	A	C	C	C	0.22% (210 reads)		
A	A	C	A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	-	-	-	G	G	A	T	G	T	T	C	T	G	T	C	C	C	A	C	C	C	0.22% (208 reads)	
A	A	C	A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	G	T	G	-	-	-	-	T	T	C	T	G	T	C	C	C	A	C	C	C	0.21% (204 reads)	



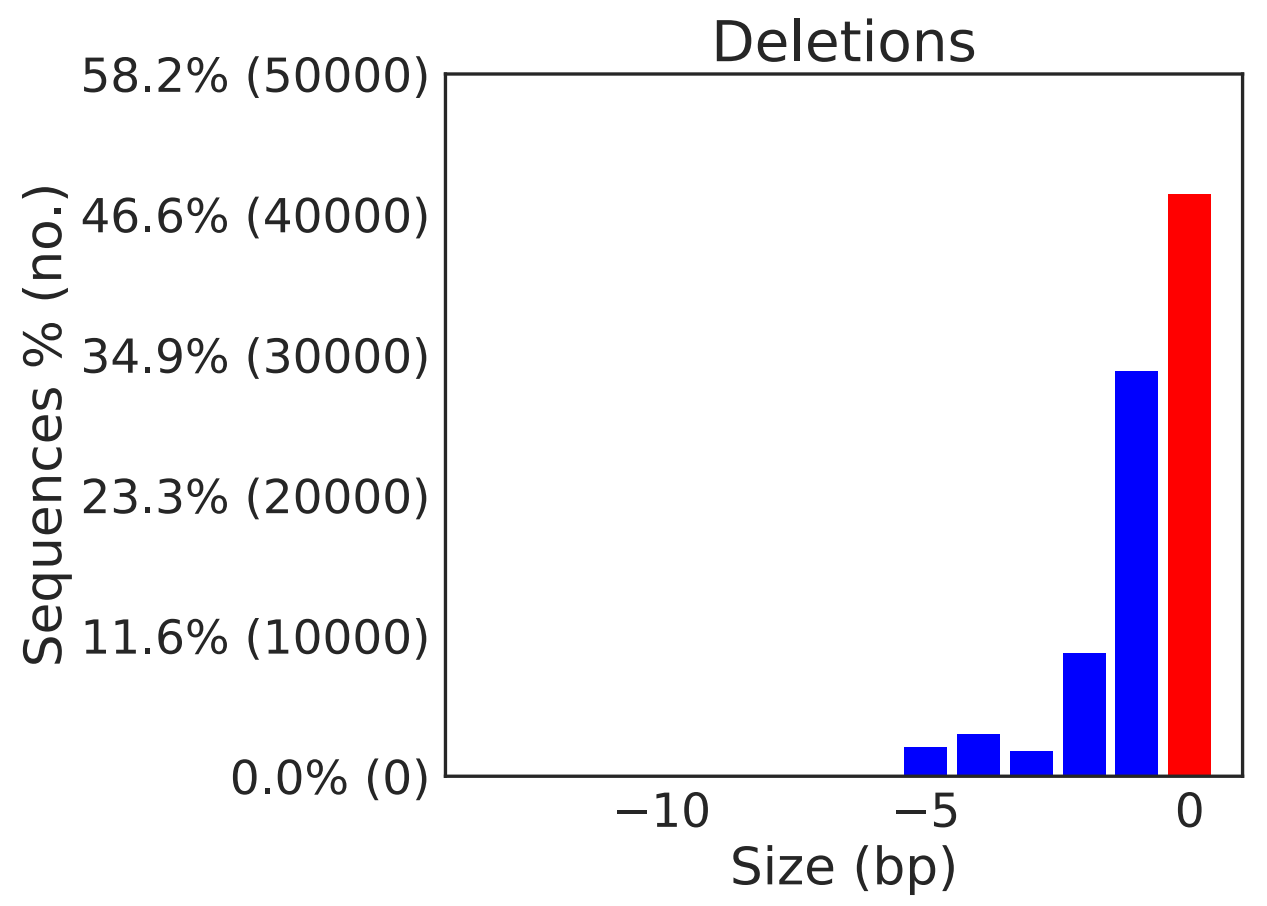
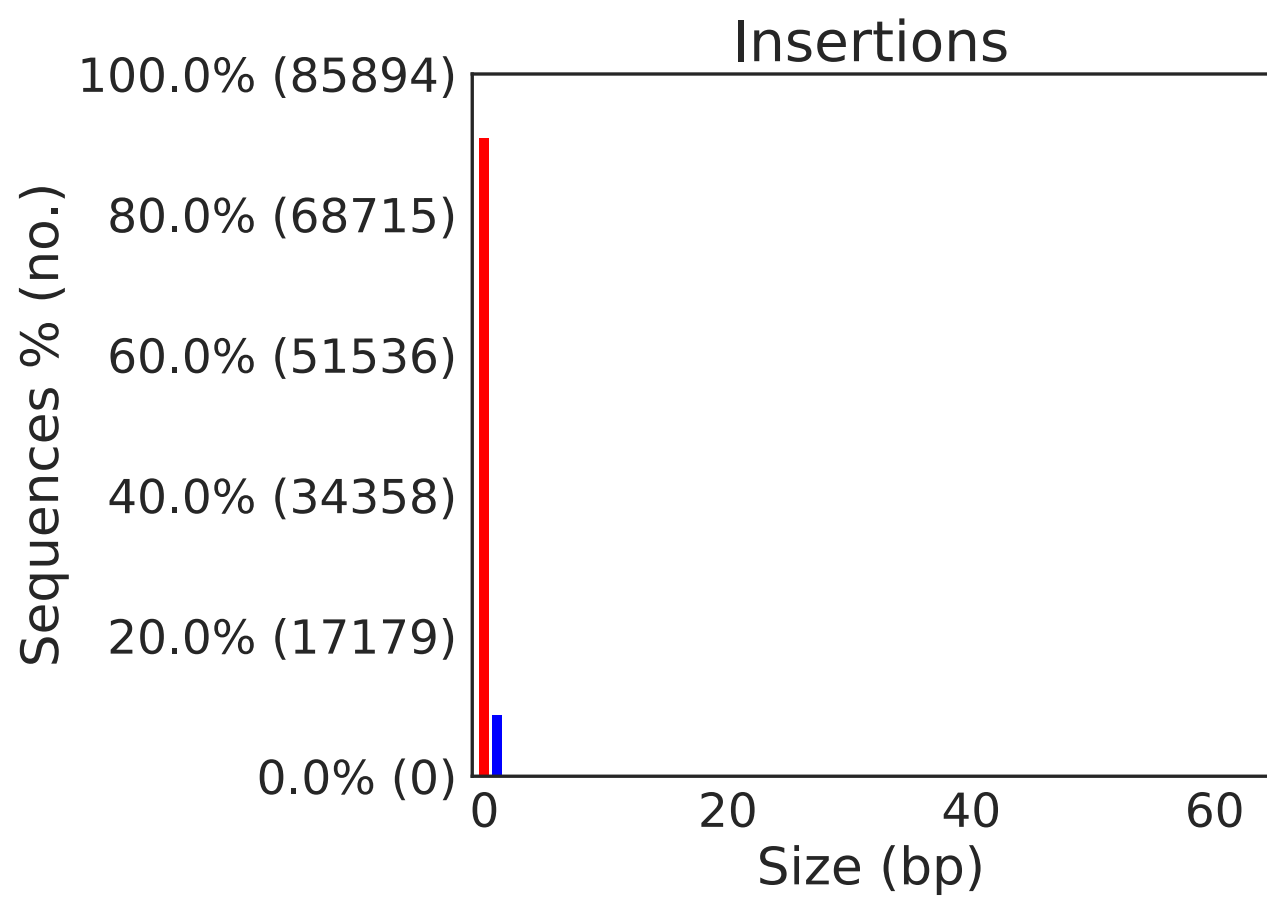
Insertion
 Non-insertion

Deletion
 Non-deletion

Tmc1^{Bth/WT}, SpCas9 + gRNA 2.4, Bth allele only

bold Substitutions
 Insertions
 - Deletions
 - - - Predicted cleavage position

Reference																																										
A	A	C	A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	G	G	G	G	A	A	G	T	T	C	T	G	T	C	C	C	A	C	C	C	18.73% (16088 reads)		
A	A	C	A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	C	C	T	G	G	G	A	A	G	T	T	C	T	G	T	C	C	C	A	C	C	C	15.01% (12896 reads)
A	A	C	A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	-	G	G	G	A	A	G	T	T	C	T	G	T	C	C	C	A	C	C	C	13.82% (11873 reads)		
A	A	C	A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	G	G	G	-	A	A	G	T	T	C	T	G	T	C	C	C	A	C	C	C	11.65% (10008 reads)		
A	A	C	A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	-	-	G	G	A	A	G	T	T	C	T	G	T	C	C	C	A	C	C	C	6.42% (5512 reads)		
A	A	C	A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	G	G	G	G	G	A	A	G	T	T	C	T	G	T	C	C	C	A	C	C	C	6.38% (5476 reads)	
A	A	C	A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	G	G	G	G	G	A	A	G	T	T	C	T	G	T	C	C	C	A	C	C	C	5.24% (4503 reads)	
A	A	C	A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	G	G	-	-	A	A	G	T	T	C	T	G	T	C	C	C	A	C	C	C	5.23% (4496 reads)		
A	A	C	A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	-	-	G	G	G	G	A	A	G	T	T	C	T	G	T	C	C	C	A	C	C	C	3.58% (3075 reads)		
A	A	C	A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	-	-	-	-	-	A	A	G	T	T	C	T	G	T	C	C	C	A	C	C	C	2.36% (2031 reads)	
A	A	C	A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	G	-	-	-	-	A	A	G	T	T	C	T	G	T	C	C	C	A	C	C	C	1.46% (1257 reads)	
A	C	A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	T	G	G	G	G	A	A	G	T	T	C	T	G	T	C	C	C	A	C	C	C	1.13% (969 reads)		
A	A	C	A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	-	-	-	-	A	A	G	T	T	C	T	G	T	C	C	C	A	C	C	C	1.07% (922 reads)		
A	A	C	A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	T	G	G	G	G	A	A	G	T	T	C	T	G	T	C	C	C	A	C	C	C	1.03% (883 reads)	
A	A	C	A	T	G	G	T	A	A	T	G	T	C	C	C	-	-	-	-	G	G	G	G	A	A	G	T	T	C	T	G	T	C	C	C	A	C	C	C	0.88% (752 reads)		
A	A	C	A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	-	-	-	G	A	A	G	T	T	C	T	G	T	C	C	C	A	C	C	C	0.76% (654 reads)		
A	A	C	A	T	G	G	T	A	A	T	G	T	C	-	-	-	C	C	T	G	G	G	G	A	A	G	T	T	C	T	G	T	C	C	C	A	C	C	C	0.73% (625 reads)		
A	A	C	A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	G	-	-	-	A	A	G	T	T	C	T	G	T	C	C	C	A	C	C	C	0.64% (552 reads)		
A	A	C	A	T	G	G	T	A	A	T	G	T	C	C	C	T	-	-	-	G	G	G	G	A	A	G	T	T	C	T	G	T	C	C	C	A	C	C	C	0.63% (540 reads)		
A	A	C	A	T	G	G	T	A	A	T	G	T	C	C	C	T	-	T	T	G	G	G	G	A	A	G	T	T	C	T	G	T	C	C	C	A	C	C	C	0.55% (470 reads)		
A	A	C	A	T	G	G	T	A	A	T	G	T	C	C	C	T	T	-	T	G	G	G	G	A	A	G	T	T	C	T	G	T	C	C	C	A	C	C	C	0.44% (380 reads)		



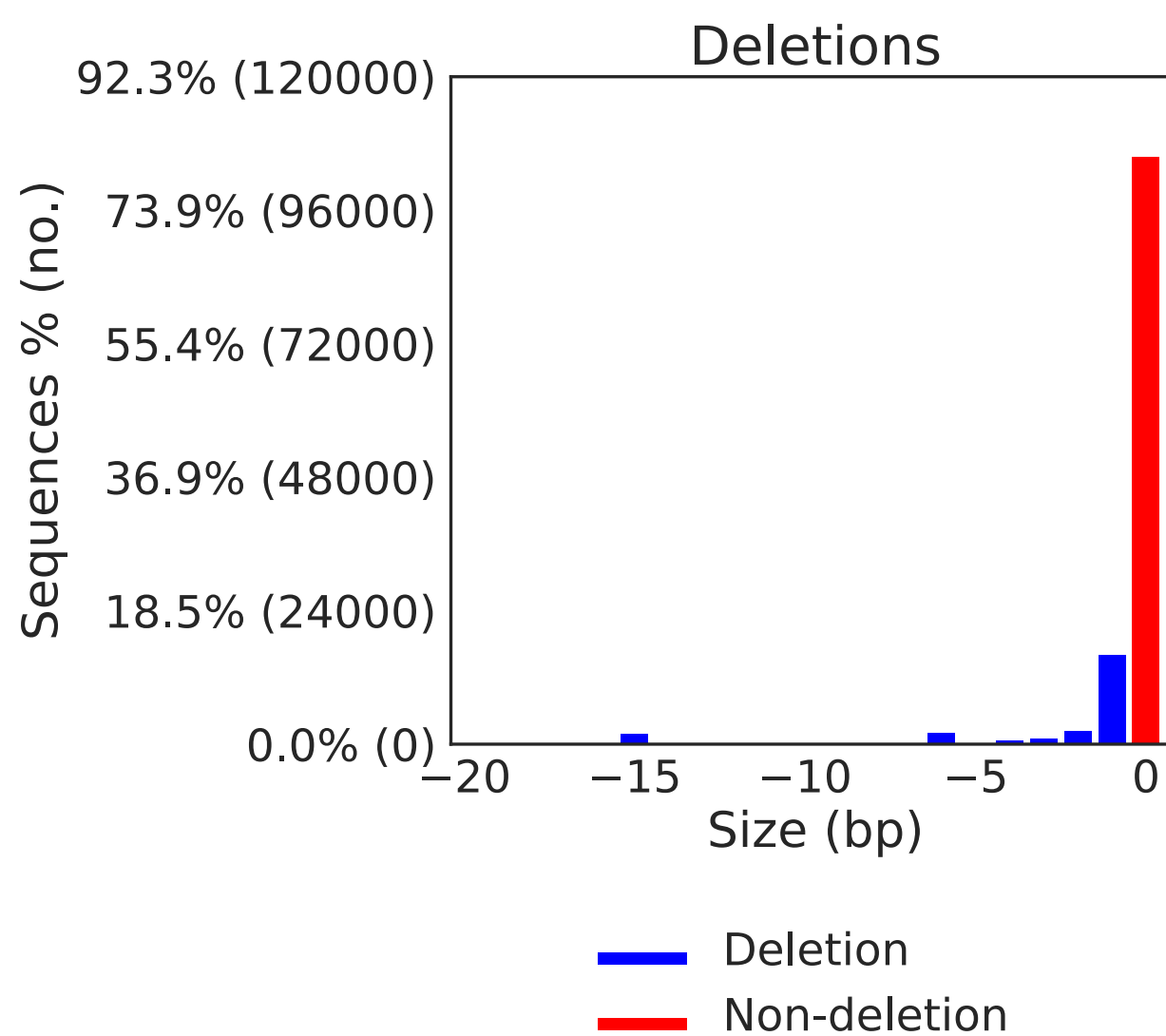
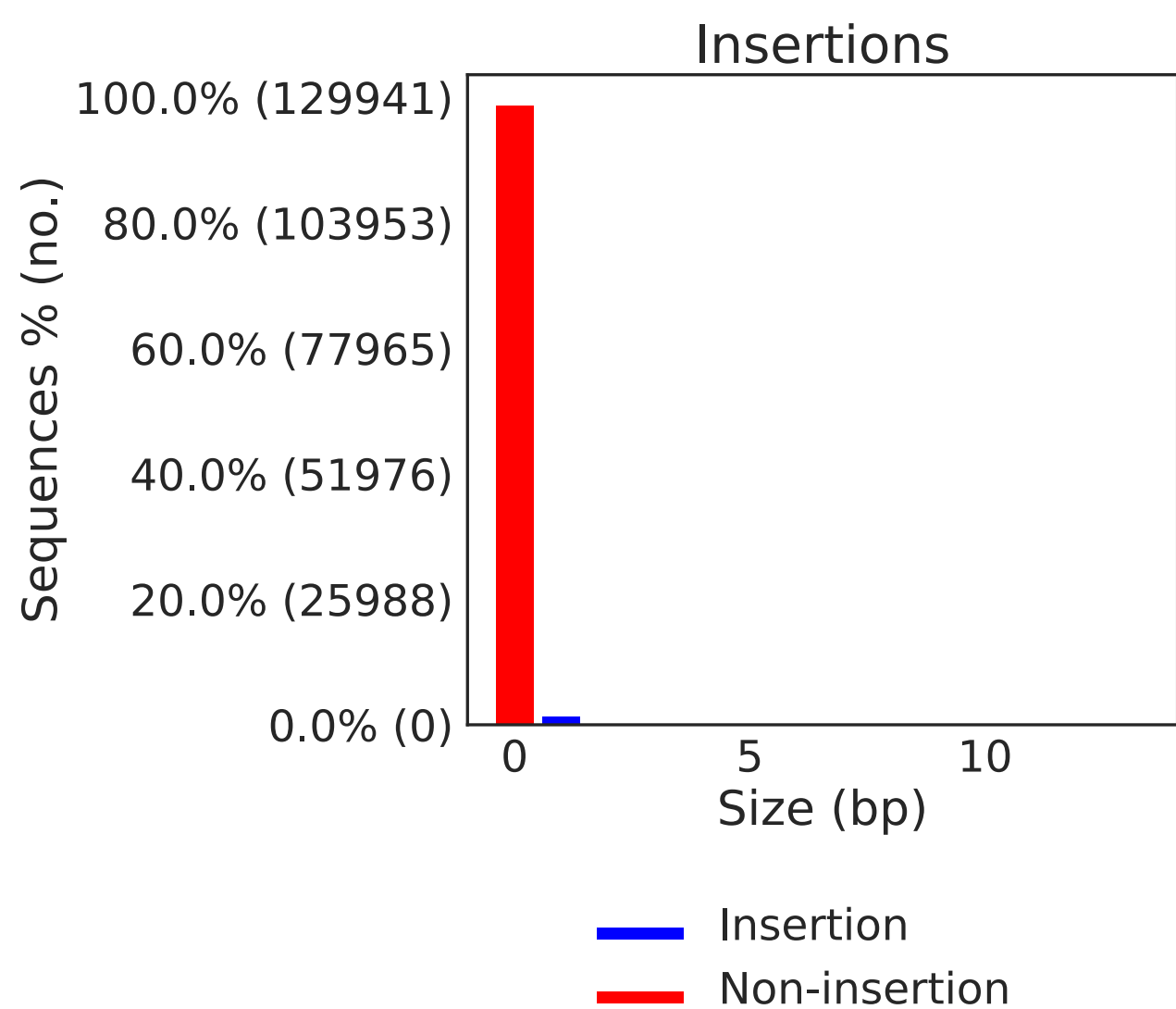
— Insertion
 — Non-insertion

— Deletion
 — Non-deletion

Tmc1^{Bth/WT}, SpCas9 + gRNA 2.4, WT allele only

bold Substitutions
 Insertions
 - Deletions
 - - - Predicted cleavage position

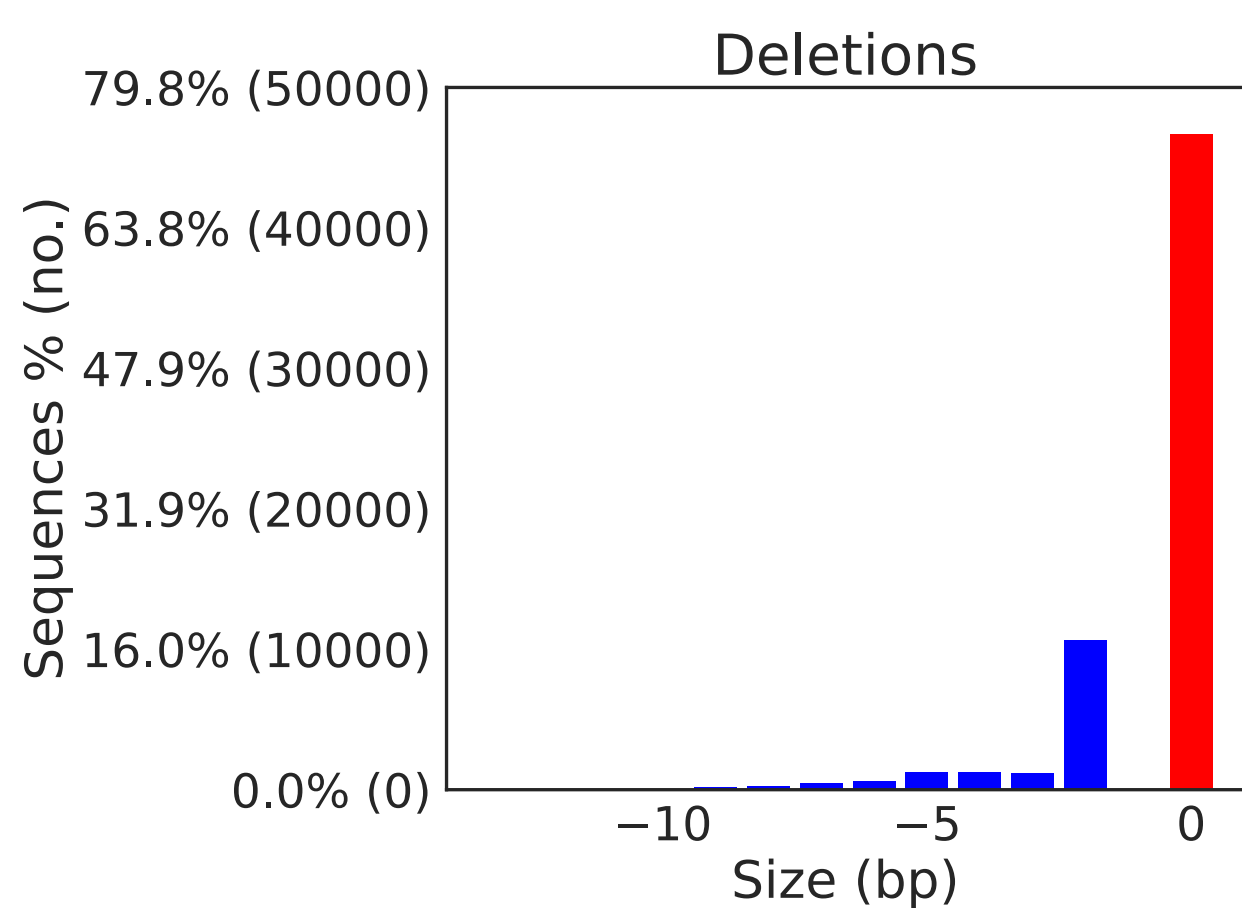
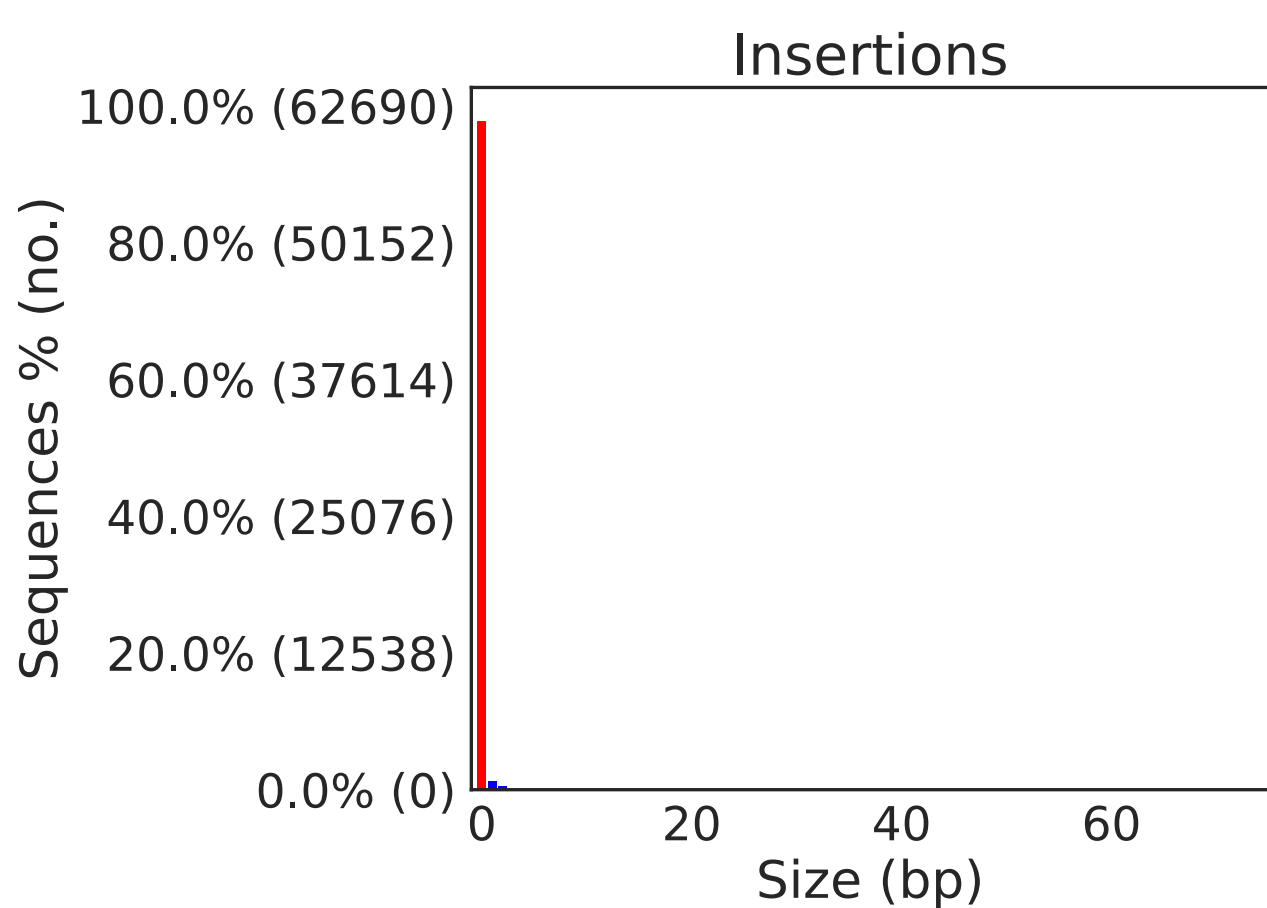
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A	A	C	A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	-	G	G	G	A	T	G	T	T	C	T	G	T	C	C	C	A	C	C	C	7.03% (9141 reads)	
A	A	C	A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	G	G	G	-	A	T	G	T	T	C	T	G	T	C	C	C	A	C	C	C	5.97% (7754 reads)	
A	A	C	A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	-	G	G	G	G	A	T	G	T	T	C	T	G	T	C	C	C	A	C	C	C	5.00% (6503 reads)	
A	A	C	A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	G	G	G	G	G	A	T	G	T	T	C	T	G	T	C	C	C	A	C	C	C	1.29% (1670 reads)
A	A	C	A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	G	G	G	G	G	A	T	G	T	T	C	T	G	T	C	C	C	A	C	C	C	1.05% (1368 reads)
A	A	C	A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	-	-	G	G	A	T	G	T	T	C	T	G	T	C	C	C	A	C	C	C	0.90% (1172 reads)	
A	A	C	A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	-	-	-	-	-	-	G	T	T	C	T	G	T	C	C	C	A	C	C	C	0.81% (1052 reads)	
A	A	C	A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	-	-	G	G	G	G	A	T	G	T	T	C	T	G	T	C	C	C	A	C	C	C	0.78% (1017 reads)	
A	A	C	A	T	G	G	T	A	A	T	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	G	T	T	C	T	G	T	C	C	C	A	C	C	C	0.78% (1008 reads)	
A	A	C	A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	G	G	-	-	A	T	G	T	T	C	T	G	T	C	C	C	A	C	C	C	0.69% (895 reads)	
A	A	C	A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	G	-	-	-	-	-	-	-	T	T	C	T	G	T	C	C	C	A	C	C	C	0.65% (846 reads)
A	A	C	A	T	G	G	T	A	A	T	G	T	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	T	C	T	G	T	C	C	C	A	C	C	C	0.60% (783 reads)	
A	A	C	A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	-	-	G	A	T	G	T	T	C	T	G	T	C	C	C	A	C	C	C	0.43% (564 reads)		
A	A	C	A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	-	-	-	-	T	T	G	T	T	C	T	G	T	C	C	C	A	C	C	C	0.42% (546 reads)	
A	A	C	A	T	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	G	T	T	C	T	G	T	C	C	C	A	C	C	C	0.36% (468 reads)	
A	A	C	A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	T	T	G	-	-	-	-	T	T	C	T	G	T	C	C	C	A	C	C	C	0.34% (443 reads)	
A	A	C	A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	G	-	-	-	A	T	G	T	T	C	T	G	T	C	C	C	A	C	C	C	0.33% (430 reads)	
A	A	C	A	T	G	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	T	T	C	T	G	T	C	C	C	A	C	C	C	0.31% (409 reads)	



Tmc1^{Bth/WT}, SpCas9 + gRNA WT, Bth allele only

bold Substitutions
 Insertions
 - Deletions
 - - - Predicted cleavage position

Reference																																										
A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	G	G	G	G	A	T	G	T	T	C	T	G	T	C	C	C	A	C	C	C	T	G	T	24.52% (15374 reads)		
A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	-	G	G	G	A	A	G	T	T	C	T	G	T	C	C	C	A	C	C	C	T	G	T	24.26% (15210 reads)		
A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	G	G	G	G	A	A	G	T	T	C	T	G	T	C	C	C	A	C	C	C	T	G	T	20.00% (12536 reads)		
A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	G	G	G	-	-	A	G	T	T	C	T	G	T	C	C	C	A	C	C	C	T	G	T	5.89% (3691 reads)		
A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	G	G	G	A	-	-	G	T	T	C	T	G	T	C	C	C	A	C	C	C	T	G	T	5.83% (3652 reads)		
A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	G	G	-	-	A	A	G	T	T	C	T	G	T	C	C	C	A	C	C	C	T	G	T	2.45% (1539 reads)		
A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	-	-	G	G	A	A	G	T	T	C	T	G	T	C	C	C	A	C	C	C	T	G	T	2.32% (1456 reads)		
A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	-	-	-	-	G	A	A	G	T	T	C	T	G	T	C	C	C	A	C	C	C	T	G	T	1.48% (927 reads)		
A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	-	-	-	-	-	G	A	A	G	T	T	C	T	G	T	C	C	C	A	C	C	C	T	G	T	1.14% (716 reads)		
A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	G	G	G	A	A	A	G	T	T	C	T	G	T	C	C	C	A	C	C	C	T	G	T	0.76% (476 reads)		
A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	-	-	-	G	A	A	G	T	T	C	T	G	T	C	C	C	A	C	C	C	T	G	T	0.64% (399 reads)		
A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	G	-	-	-	A	A	G	T	T	C	T	G	T	C	C	C	A	C	C	C	T	G	T	0.62% (390 reads)		
A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	G	G	G	A	G	A	A	G	T	T	C	T	G	T	C	C	C	A	C	C	C	T	G	T	0.53% (334 reads)	
A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	G	G	G	G	A	-	G	T	T	C	T	G	T	C	C	C	A	C	C	C	T	G	T	0.39% (243 reads)		
A	T	G	G	T	A	A	T	G	T	C	C	C	-	-	-	-	-	-	-	G	A	A	G	T	T	C	T	G	T	C	C	C	A	C	C	C	T	G	T	0.38% (238 reads)		
A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	G	G	G	T	G	A	A	G	T	T	C	T	G	T	C	C	C	A	C	C	C	T	G	T	0.37% (232 reads)	
A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	-	-	-	-	A	A	G	T	T	C	T	G	T	C	C	C	A	C	C	C	T	G	T	0.31% (195 reads)			
A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	G	G	G	T	A	-	G	T	T	C	T	G	T	C	C	C	A	C	C	C	T	G	T	0.28% (178 reads)		
A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	A	G	-	-	-	-	-	-	T	T	C	T	G	T	C	C	C	A	C	C	C	T	G	T	0.25% (156 reads)		
A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	G	G	G	A	A	G	A	A	G	T	T	C	T	G	T	C	C	C	A	C	C	C	T	G	T	0.25% (155 reads)
A	T	G	G	T	A	A	T	G	T	C	C	C	T	-	-	-	-	-	-	G	A	A	G	T	T	C	T	G	T	C	C	C	A	C	C	C	T	G	T	0.24% (148 reads)		
A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	-	-	-	-	-	A	G	T	T	C	T	G	T	C	C	C	A	C	C	C	T	G	T	0.23% (147 reads)			
A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	G	G	A	G	-	-	-	T	T	C	T	G	T	C	C	C	A	C	C	C	T	G	T	0.22% (140 reads)		
A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	A	G	-	-	-	-	-	T	T	C	T	G	T	C	C	C	A	C	C	C	T	G	T	0.21% (131 reads)		
A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	G	G	-	-	-	A	G	T	T	C	T	G	T	C	C	C	A	C	C	C	T	G	T	0.21% (129 reads)		



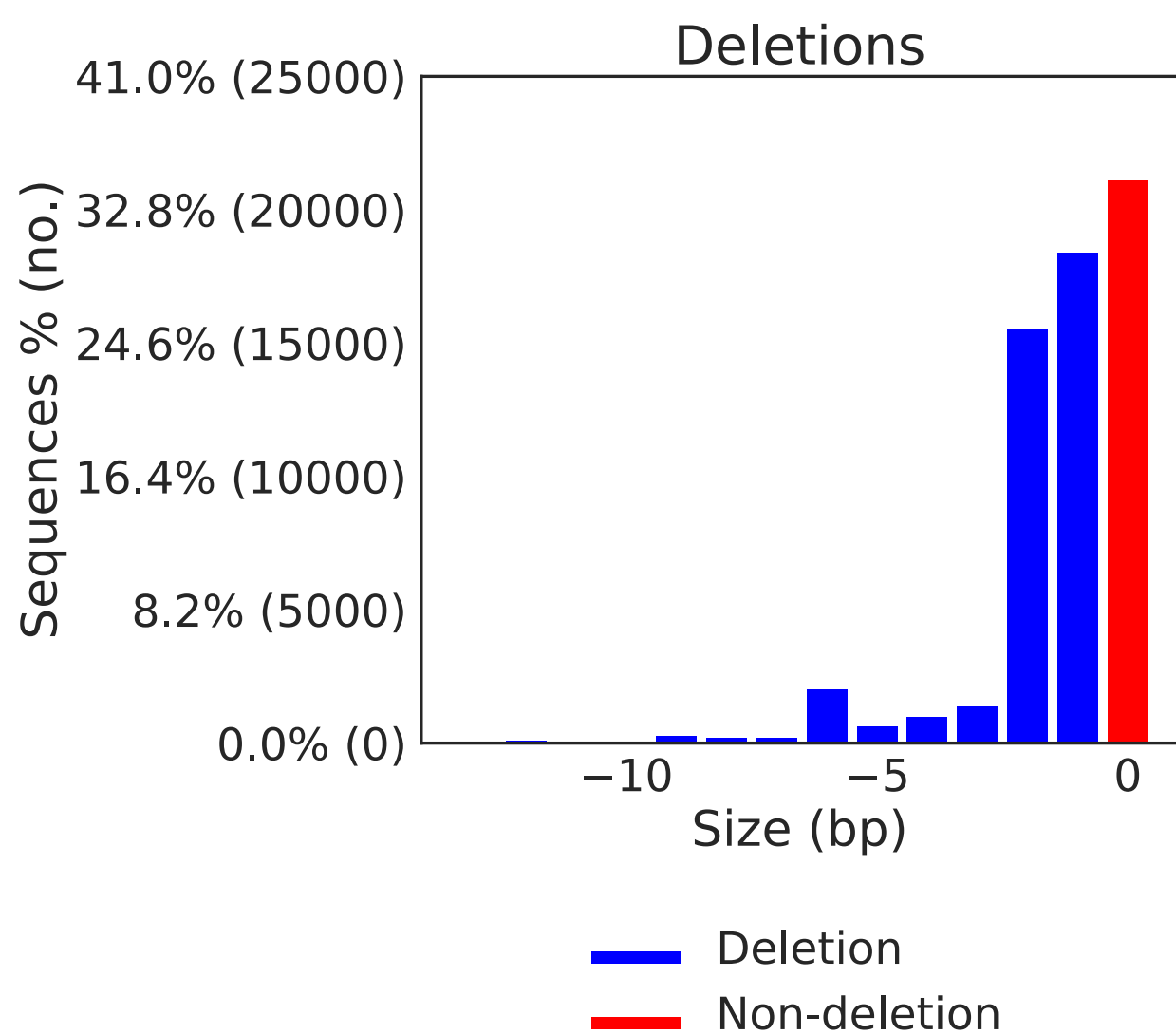
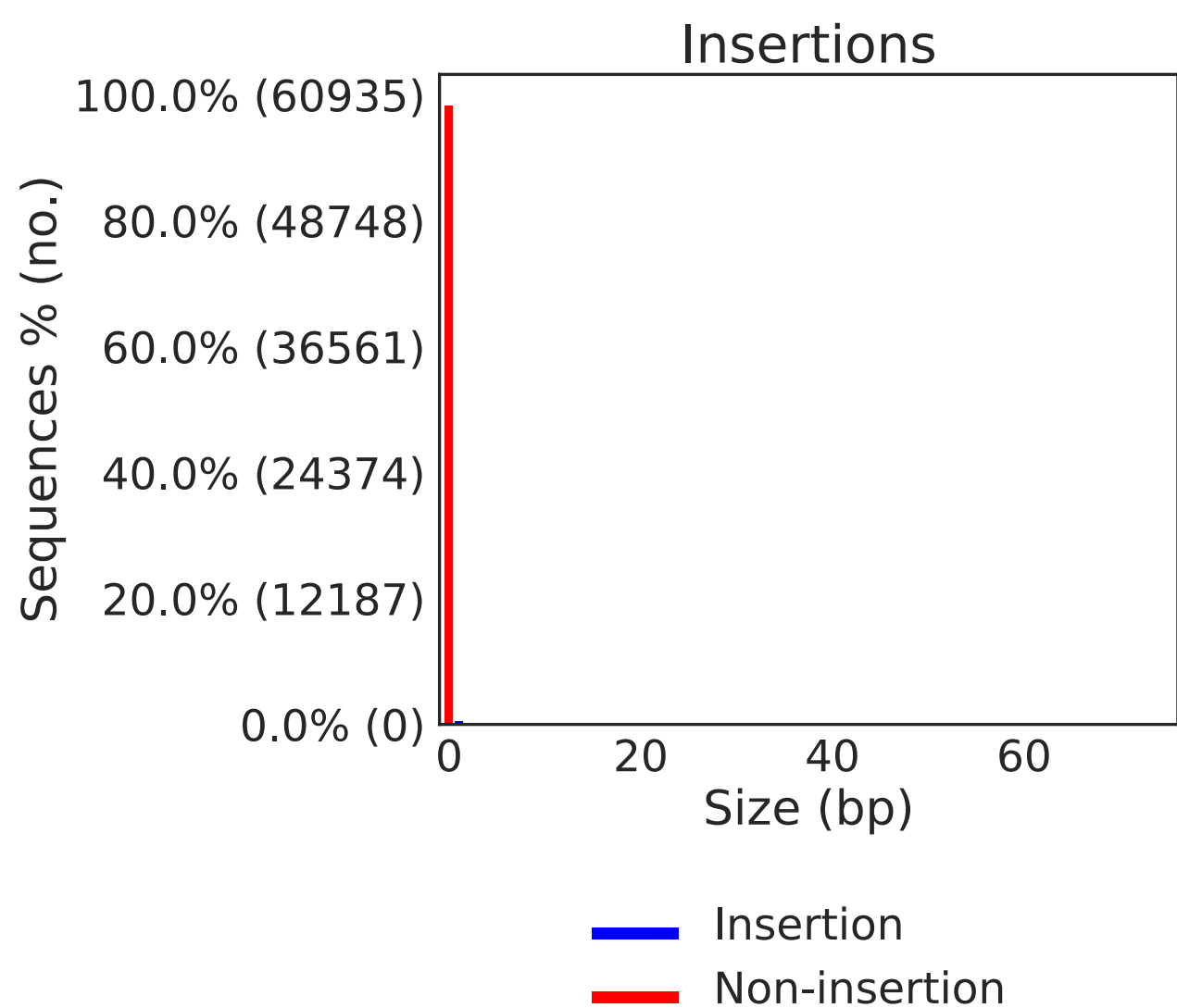
█ Insertion
█ Non-insertion

█ Deletion
█ Non-deletion

Tmc1^{Bth/WT}, SpCas9 + gRNA WT, WT allele only

bold Substitutions
 Insertions
 - Deletions
 - - - Predicted cleavage position

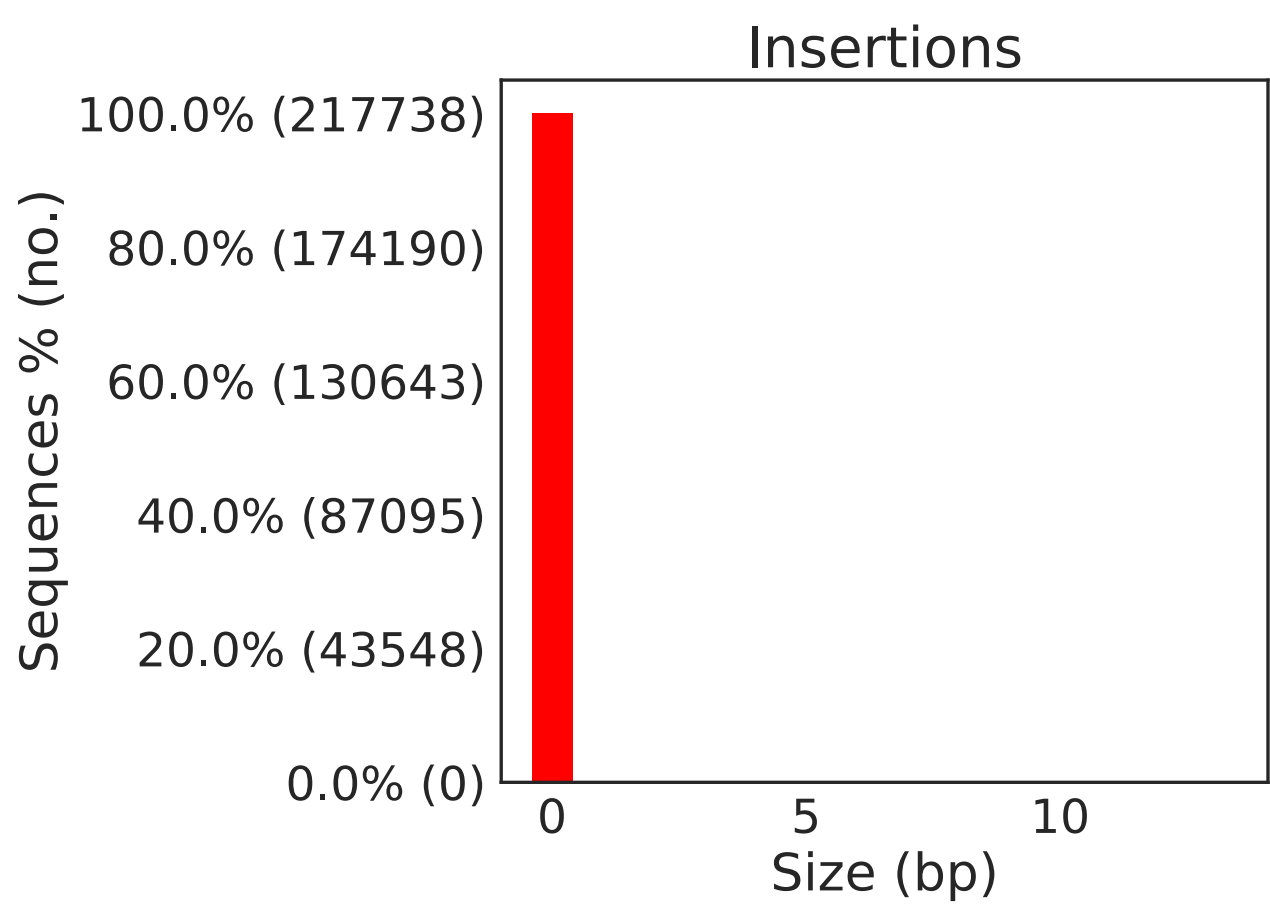
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A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	-	G	G	G	A	T	G	T	T	C	T	G	T	C	C	C	A	C	C	C	T	G	T	28.68% (17475 reads)	
A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	G	G	G	-	-	T	G	T	T	C	T	G	T	C	C	C	A	C	C	C	T	G	T	19.41% (11827 reads)	
A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	G	G	G	G	A	T	G	T	T	C	T	G	T	C	C	C	A	C	C	C	T	G	T	3.36% (2045 reads)	
A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	G	G	-	-	A	T	G	T	T	C	T	G	T	C	C	C	A	C	C	C	T	G	T	2.88% (1757 reads)	
A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	-	-	G	G	A	T	G	T	T	C	T	G	T	C	C	C	A	C	C	C	T	G	T	2.63% (1602 reads)	
A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	G	-	-	-	-	-	-	T	T	C	T	G	T	C	C	C	A	C	C	C	T	G	T	1.36% (830 reads)	
A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	-	-	-	-	-	-	T	G	T	T	C	T	G	T	C	C	C	A	C	C	C	T	G	T	1.33% (810 reads)	
A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	-	-	-	-	G	A	T	G	T	T	C	T	G	T	C	C	C	A	C	C	C	T	G	T	1.18% (718 reads)	
A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	-	-	-	G	A	T	G	T	T	C	T	G	T	C	C	C	A	C	C	C	T	G	T	0.75% (460 reads)	
A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	-	-	-	-	G	A	T	G	T	T	C	T	G	T	C	C	C	A	C	C	C	T	G	T	0.75% (459 reads)	
A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	G	-	-	-	A	T	G	T	T	C	T	G	T	C	C	C	A	C	C	C	T	G	T	0.73% (447 reads)	
A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	G	G	G	A	G	A	T	G	T	T	C	T	G	T	C	C	C	A	C	C	C	T	G	T	0.41% (252 reads)
A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	G	G	-	-	-	T	G	T	T	C	T	G	T	C	C	C	A	C	C	C	T	G	T	0.35% (213 reads)	
A	T	G	G	T	A	A	T	G	T	C	C	C	T	-	-	-	-	-	-	G	A	T	G	T	T	C	T	G	T	C	C	C	A	C	C	C	T	G	T	0.33% (200 reads)	
A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	G	G	G	-	T	G	T	T	C	T	G	T	C	C	C	A	C	C	C	T	G	T	0.25% (154 reads)		
A	T	G	G	T	A	A	T	G	T	C	C	C	T	-	-	-	-	-	-	-	-	G	T	T	C	T	G	T	C	C	C	A	C	C	C	T	G	T	0.22% (134 reads)		
A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	G	-	-	-	-	T	G	T	T	C	T	G	T	C	C	C	A	C	C	C	T	G	T	0.21% (127 reads)	



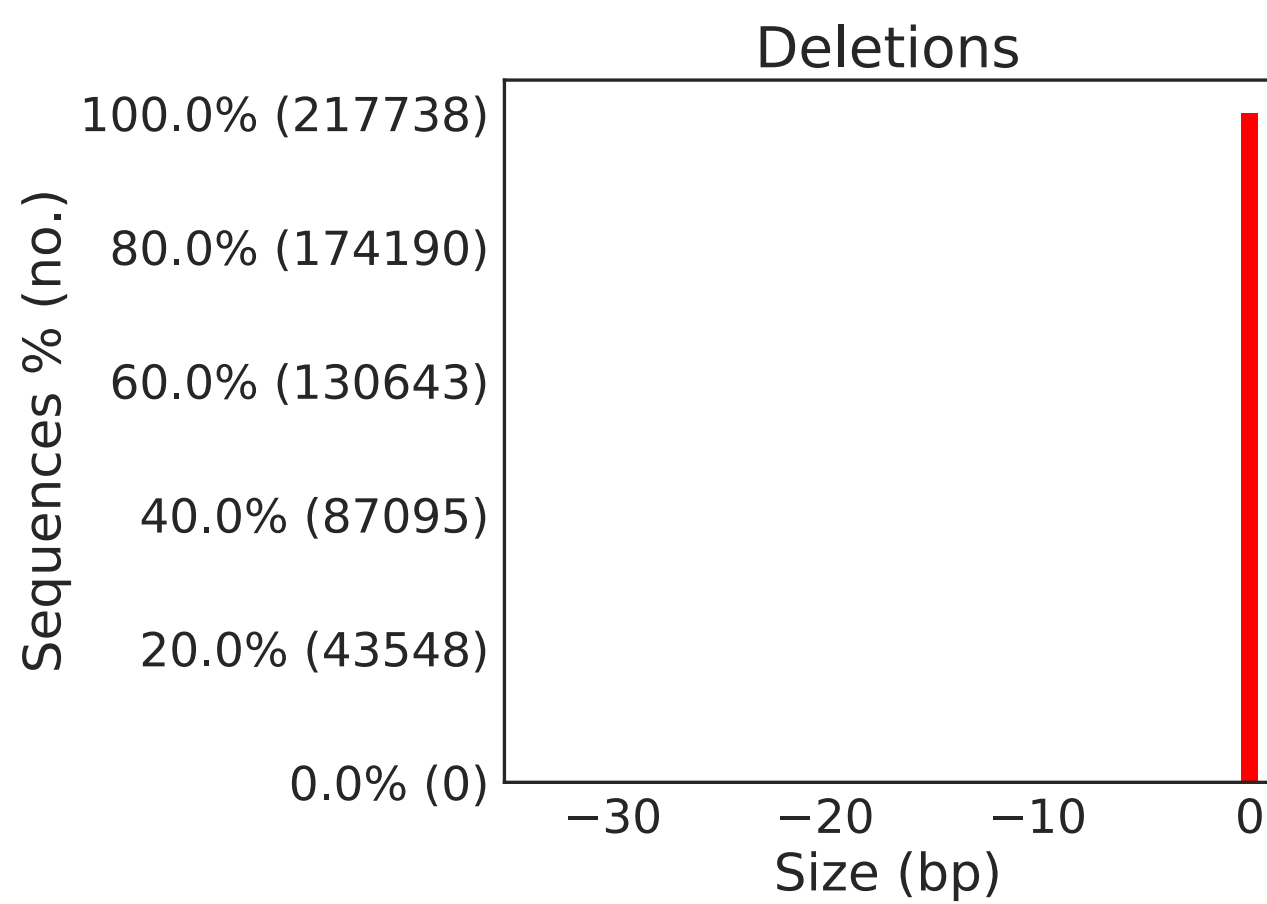
Tmc1^{WT/WT}, SpCas9 only

bold Substitutions
 Insertions
 - Deletions
 - - - Predicted cleavage position

A T G G T A A T G T C C C T C C T G G G G A A G T T C T G T C C C A C C C T G T Reference
 A T G G T A A T G T C C C T C C T G G G **G** A **T** G T T C T G T C C C A C C C T G T 97.75% (212831 reads)



— Insertion
— Non-insertion

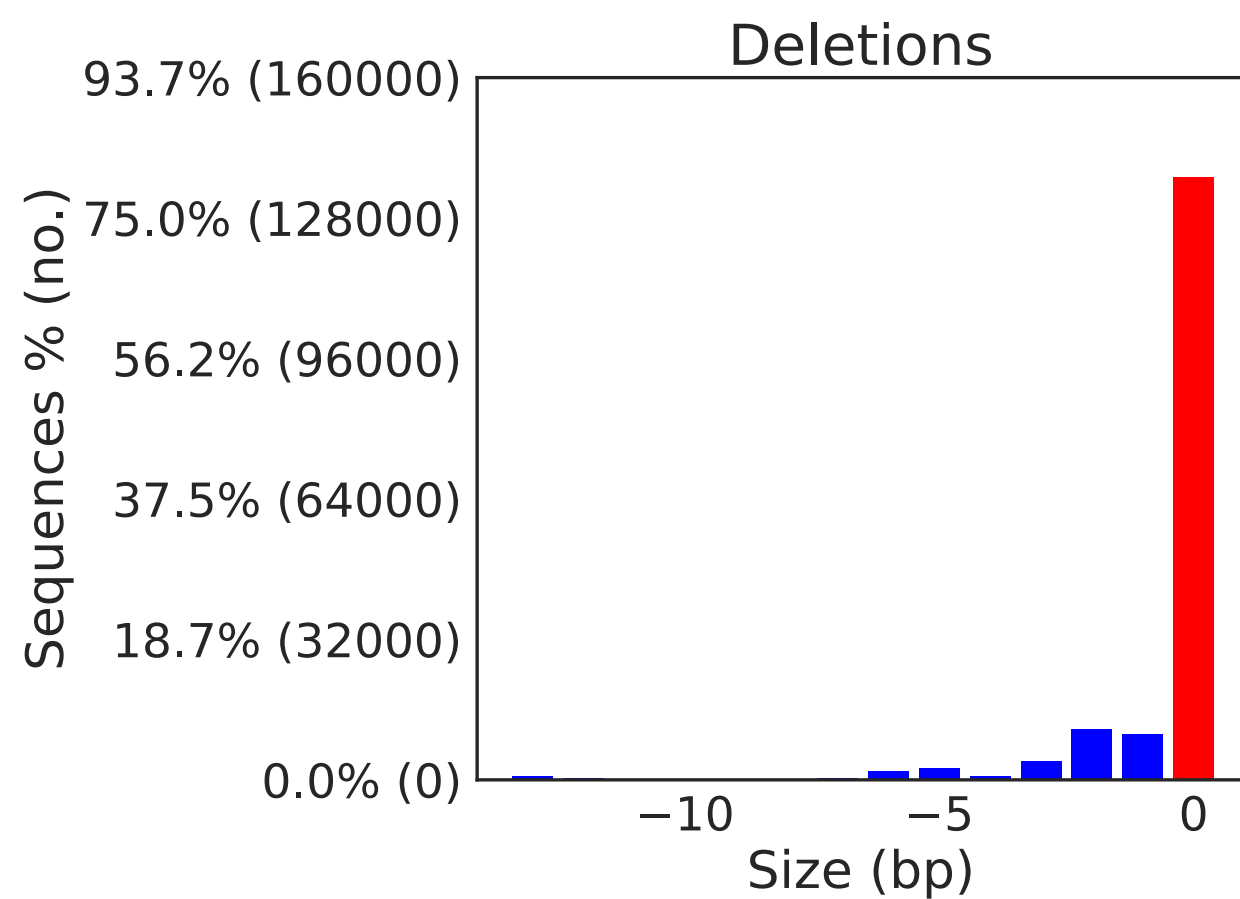
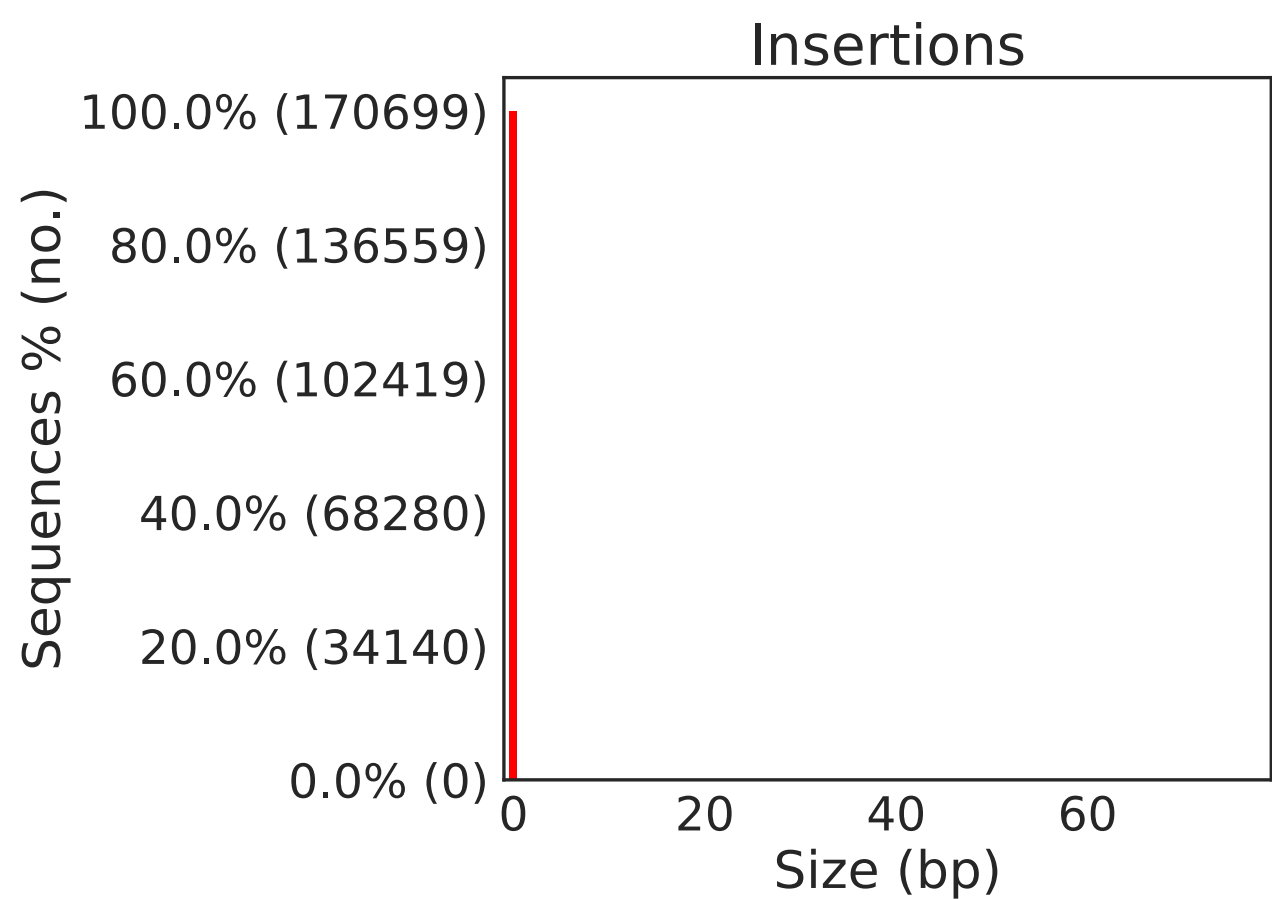


— Deletion
— Non-deletion

Tmc1^{WT/WT}, SpCas9 + gRNA 1.1

bold Substitutions
 Insertions
 - Deletions
 - - - Predicted cleavage position

Reference																																								
A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	G	G	G	G	A	A	G	T	T	C	T	G	T	C	C	C	A	C	C	C	T	G	T	71.19% (121524 reads)
A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	G	G	G	-	A	T	G	T	T	C	T	G	T	C	C	C	A	C	C	C	T	G	T	5.71% (9740 reads)
A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	-	G	G	G	A	T	G	T	T	C	T	G	T	C	C	C	A	C	C	C	T	G	T	5.03% (8593 reads)
A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	G	G	G	T	-	-	G	T	T	C	T	G	T	C	C	C	A	C	C	C	T	G	T	2.89% (4927 reads)
A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	G	G	G	-	-	T	G	T	T	C	T	G	T	C	C	C	A	C	C	C	T	G	T	2.50% (4273 reads)
A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	G	G	G	-	-	-	-	-	T	C	T	G	T	C	C	C	A	C	C	C	T	G	T	1.53% (2612 reads)
A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	G	G	G	G	A	A	G	T	T	C	T	G	T	C	C	C	A	C	C	C	T	G	T	1.04% (1778 reads)
A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	G	G	G	-	-	-	-	-	C	T	G	T	C	C	C	A	C	C	C	T	G	T	1.03% (1752 reads)	
A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	G	G	G	G	-	-	-	T	T	C	T	G	T	C	C	C	A	C	C	C	T	G	T	0.95% (1626 reads)
A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	G	G	G	-	-	-	G	T	T	C	T	G	T	C	C	C	A	C	C	C	T	G	T	0.87% (1491 reads)
A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	G	G	-	-	A	T	G	T	T	C	T	G	T	C	C	C	A	C	C	C	T	G	T	0.67% (1140 reads)
A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	-	-	G	G	A	T	G	T	T	C	T	G	T	C	C	C	A	C	C	C	T	G	T	0.56% (955 reads)
A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	G	G	T	G	-	-	-	T	T	C	T	G	T	C	C	C	A	C	C	C	T	G	T	0.31% (528 reads)
A	T	G	G	C	A	A	T	G	T	C	C	C	T	C	C	T	G	G	G	G	A	T	G	T	T	C	T	G	T	C	C	C	A	C	C	C	T	G	T	0.28% (484 reads)
A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	G	G	-	-	-	T	G	T	T	C	T	G	T	C	C	C	A	C	C	C	T	G	T	0.26% (452 reads)
A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	G	G	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0.22% (372 reads)
A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	G	G	G	-	-	-	-	-	-	-	T	G	T	C	C	C	A	C	C	C	T	G	T	0.21% (357 reads)



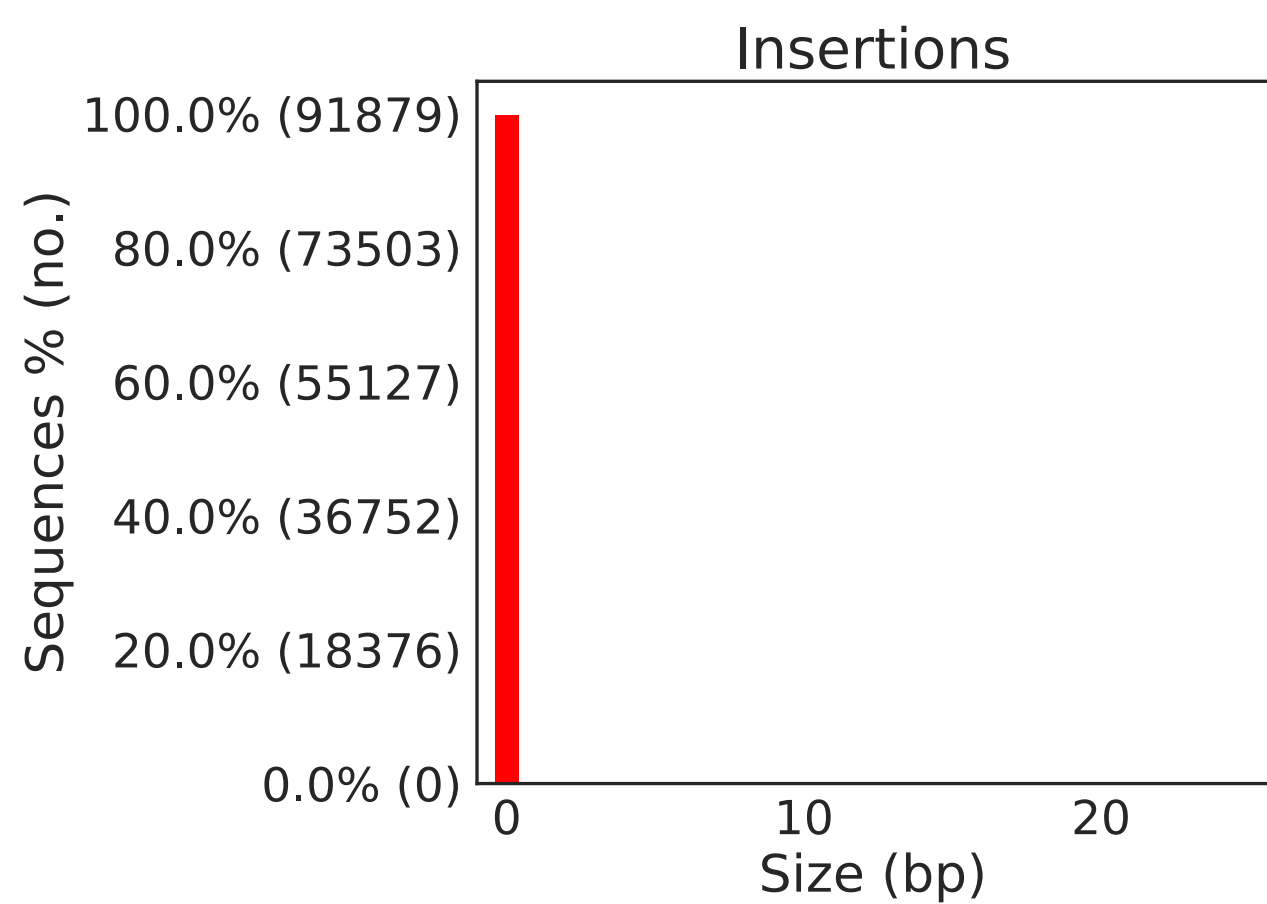
■ Insertion
 ■ Non-insertion

■ Deletion
 ■ Non-deletion

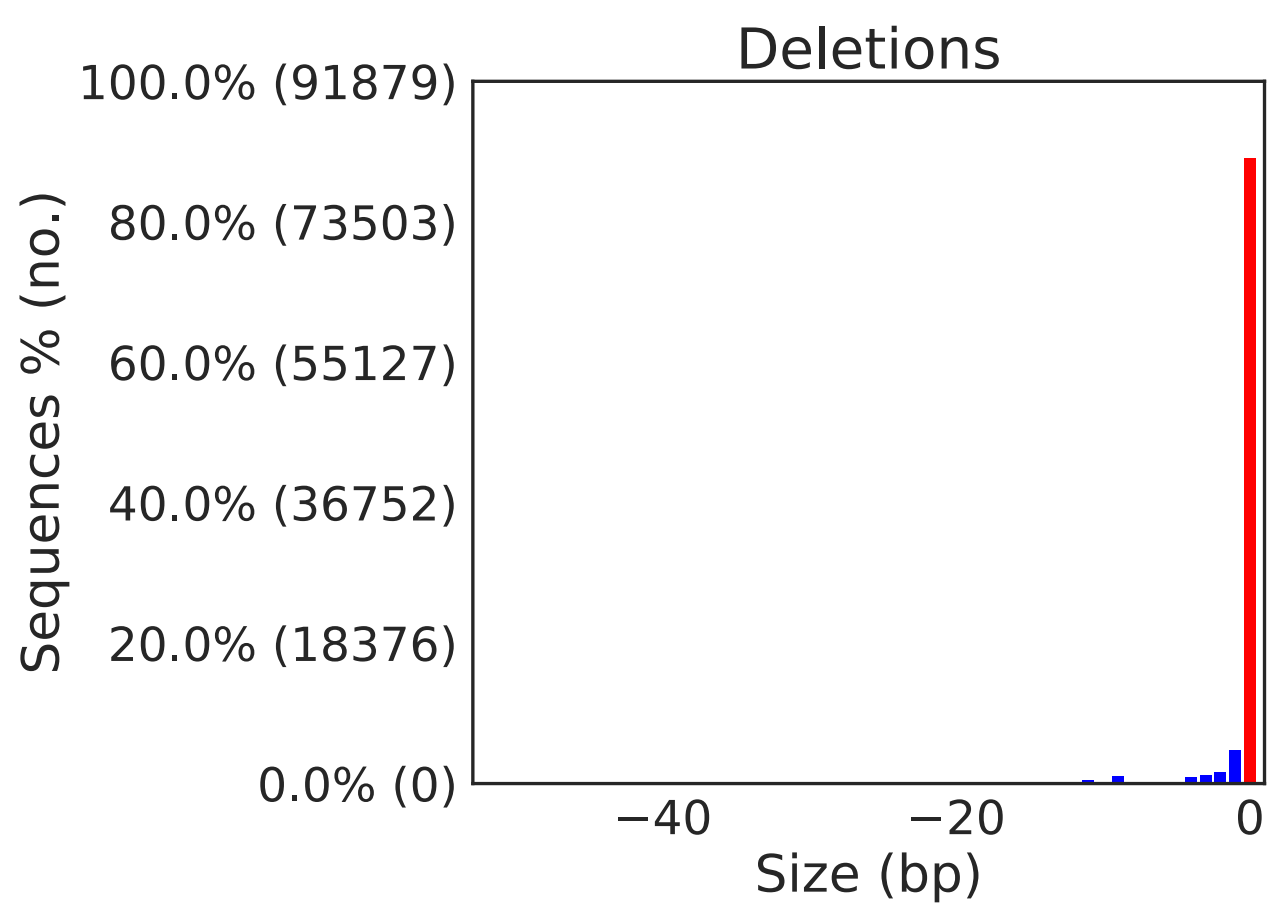
Tmc1^{WT/WT}, SpCas9 + gRNA 2.1

bold Substitutions
 Insertions
 - Deletions
 - - - Predicted cleavage position

Reference																																										
A	A	C	A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	G	G	G	G	A	A	G	T	T	C	T	G	T	C	C	C	A	C	C	C	81.91% (75262 reads)		
A	A	C	A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	-	G	G	G	G	A	T	G	T	T	C	T	G	T	C	C	C	A	C	C	C	3.37% (3095 reads)		
A	A	C	A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	G	G	G	G	A	A	G	T	T	C	T	G	T	C	C	C	A	C	C	C	2.45% (2249 reads)		
A	A	C	A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	G	G	G	-	A	T	G	T	T	C	T	G	T	C	C	C	A	C	C	C	1.31% (1206 reads)		
A	A	C	A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	-	-	G	G	G	G	A	T	G	T	T	C	T	G	T	C	C	C	A	C	C	C	1.25% (1147 reads)		
A	A	C	A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	-	G	G	G	A	T	G	T	T	C	T	G	T	C	C	C	A	C	C	C	1.23% (1133 reads)		
A	A	C	A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	G	-	-	-	A	T	G	T	T	C	T	G	T	C	C	C	A	C	C	C	0.60% (549 reads)		
A	A	C	A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	-	-	-	-	A	T	G	T	T	C	T	G	T	C	C	C	A	C	C	C	0.58% (529 reads)		
A	A	C	A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	-	-	-	G	A	T	G	T	T	C	T	G	T	C	C	C	A	C	C	C	0.56% (517 reads)		
A	A	C	A	T	G	G	T	A	A	T	G	T	C	C	C	T	-	-	-	-	-	-	-	-	G	T	T	C	T	G	T	C	C	C	A	C	C	C	0.55% (503 reads)			
A	A	C	A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	G	G	G	-	-	A	G	T	T	C	T	G	T	C	C	C	A	C	C	C	0.32% (290 reads)		
A	A	C	A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0.30% (274 reads)	
A	A	C	A	T	G	G	T	A	A	T	G	T	C	C	C	-	-	-	-	G	G	G	G	A	T	G	T	T	C	T	G	T	C	C	C	A	C	C	C	0.29% (270 reads)		
A	A	C	A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0.28% (257 reads)	
A	A	C	A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	G	T	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0.27% (249 reads)
A	A	C	A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	G	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0.25% (233 reads)
A	A	C	A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	G	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0.25% (230 reads)
A	A	C	A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0.22% (198 reads)



■ Insertion
 ■ Non-insertion

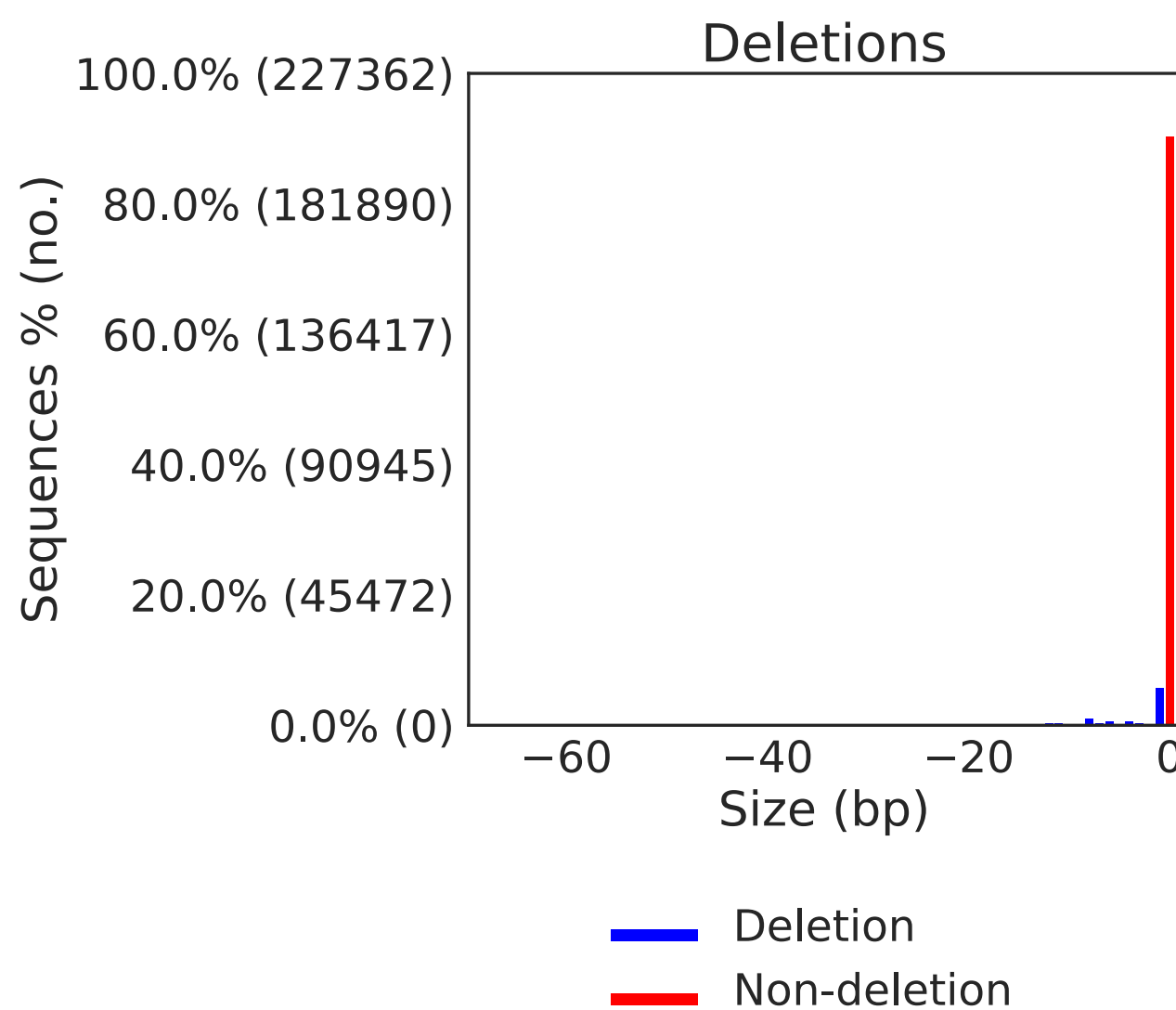
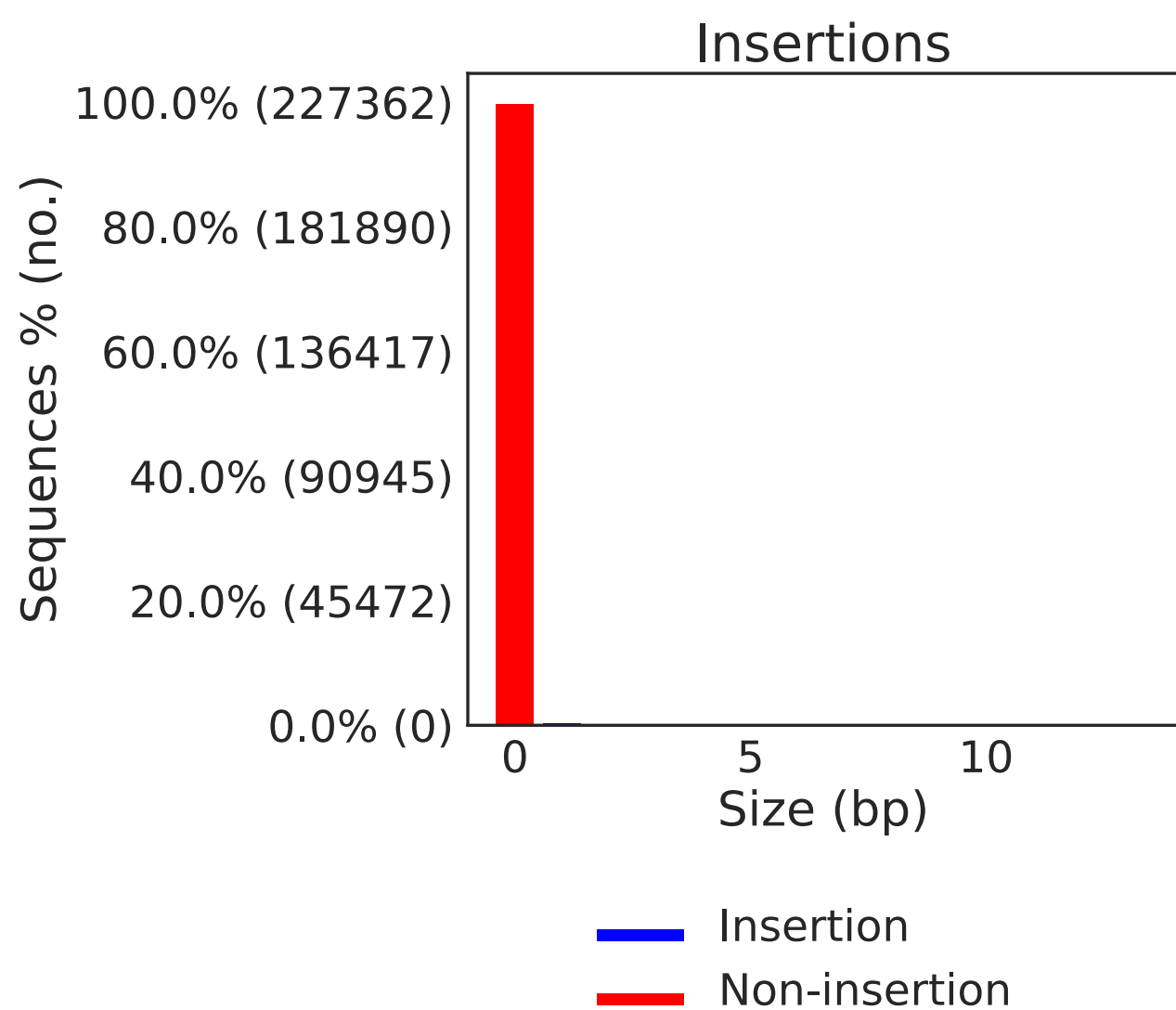


■ Deletion
 ■ Non-deletion

Tmc1^{WT/WT}, SpCas9 + gRNA 2.4

bold Substitutions
 Insertions
 - Deletions
 - - - Predicted cleavage position

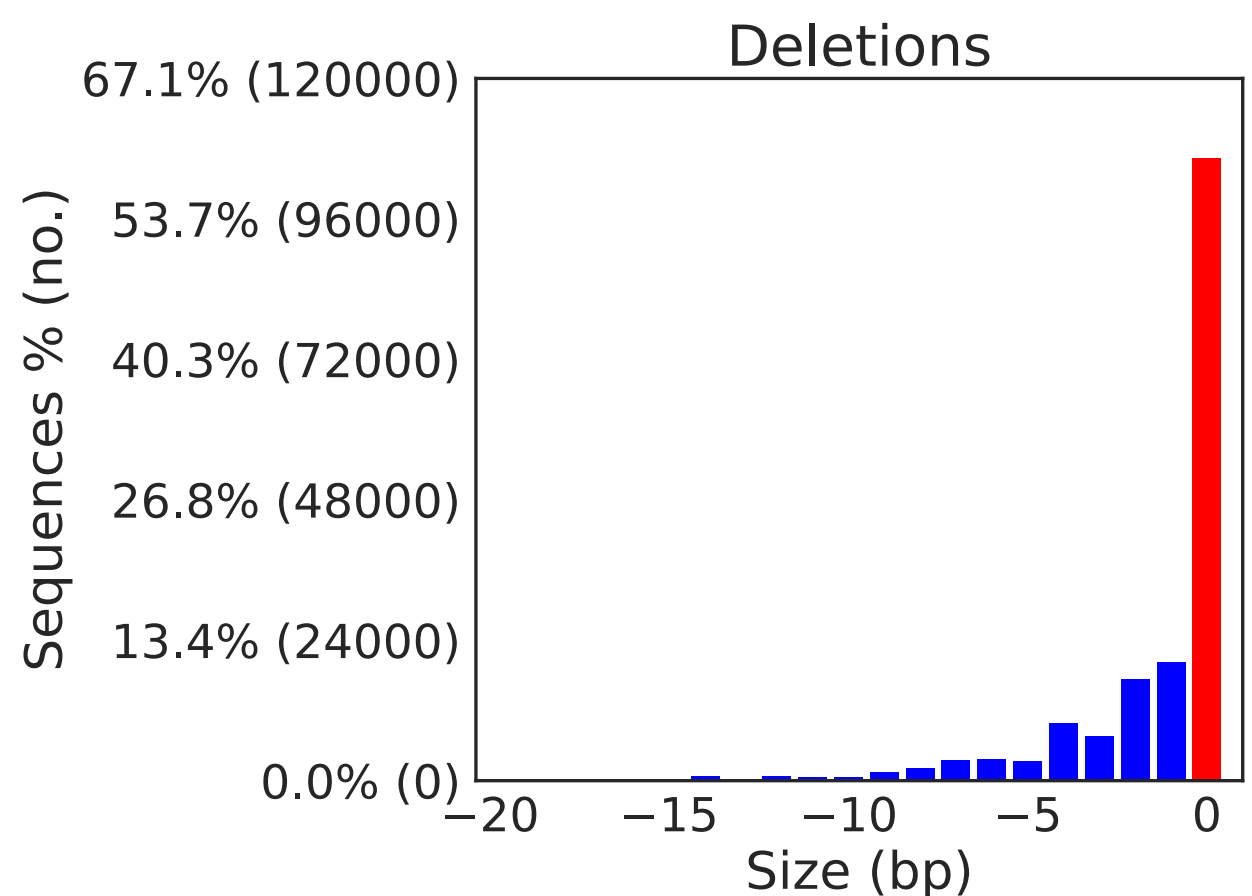
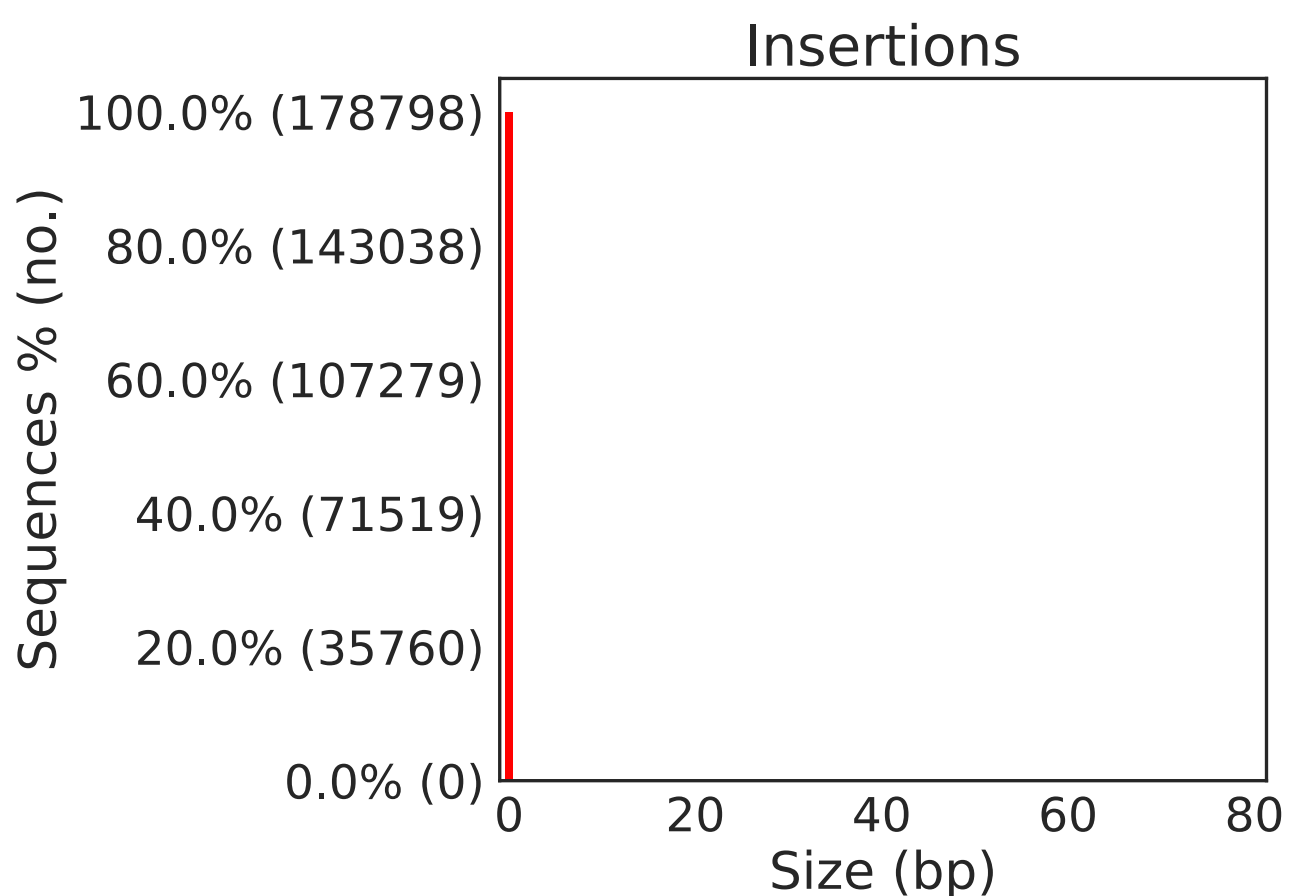
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A	A	C	A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	G	G	G	G	A	T	G	T	T	C	T	G	T	C	C	C	A	C	C	C	82.51% (187593 reads)		
A	A	C	A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	G	G	G	-	A	T	G	T	T	C	T	G	T	C	C	C	A	C	C	C	3.61% (8203 reads)		
A	A	C	A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	-	G	G	G	A	T	G	T	T	C	T	G	T	C	C	C	A	C	C	C	3.51% (7987 reads)		
A	A	C	A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	-	G	G	G	G	A	T	G	T	T	C	T	G	T	C	C	C	A	C	C	C	2.11% (4789 reads)		
A	A	C	A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	G	G	G	G	A	A	G	T	T	C	T	G	T	C	C	C	A	C	C	C	0.92% (2098 reads)		
A	A	C	A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	G	-	-	-	-	-	-	-	-	-	-	C	T	G	T	C	C	C	A	C	C	C	0.78% (1763 reads)
A	A	C	A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	-	-	-	-	A	T	G	T	T	C	T	G	T	C	C	C	A	C	C	C	0.43% (982 reads)		
A	A	C	A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	G	G	G	G	G	A	T	G	T	T	C	T	G	T	C	C	C	A	C	C	C	0.34% (772 reads)	
A	A	C	A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	G	G	G	G	A	T	G	T	T	C	T	G	T	C	C	C	A	C	C	C	0.34% (766 reads)		
A	A	C	A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	-	-	-	G	G	A	T	G	T	T	C	T	G	T	C	C	C	A	C	C	C	0.29% (649 reads)		
A	A	C	A	T	G	G	T	A	A	T	G	T	C	C	C	-	-	-	-	-	-	-	-	A	T	G	T	T	C	T	G	T	C	C	C	A	C	C	C	0.28% (636 reads)		
A	A	C	A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	G	-	-	-	-	-	-	-	-	-	T	C	T	G	T	C	C	C	A	C	C	C	0.28% (628 reads)
A	A	C	A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	-	-	-	-	-	-	G	T	T	C	T	G	T	C	C	C	A	C	C	C	0.27% (611 reads)		
A	A	C	A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	G	-	-	-	-	-	-	-	T	T	C	T	G	T	C	C	C	A	C	C	C	0.25% (566 reads)	
-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0.24% (546 reads)



Tmc1^{WT/WT}, SpCas9 + gRNA WT

bold Substitutions
 Insertions
 - Deletions
 - - - Predicted cleavage position

A T G G T A A T G T C C C T C C T G G G G A T G T T C T G T C C C A C C C T G T																									Reference																	
A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	G	G	G	G	A	T	G	T	T	C	T	G	T	C	C	C	A	C	C	C	T	G	T	35.76% (63934 reads)		
A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	-	G	G	G	A	T	G	T	T	C	T	G	T	C	C	C	A	C	C	C	T	G	T	12.72% (22743 reads)		
A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	G	G	G	-	A	T	G	T	T	C	T	G	T	C	C	C	A	C	C	C	T	G	T	11.05% (19766 reads)		
A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	G	G	G	A	A	G	T	T	C	T	G	T	C	C	C	A	C	C	C	T	G	T	9.37% (16761 reads)			
A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	G	G	G	-	-	T	G	T	T	C	T	G	T	C	C	C	A	C	C	C	T	G	T	6.51% (11631 reads)		
A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	G	G	-	-	-	G	T	T	C	T	G	T	C	C	C	A	C	C	C	T	G	T	2.18% (3904 reads)			
A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	G	G	G	-	-	-	T	T	C	T	G	T	C	C	C	A	C	C	C	T	G	T	1.95% (3480 reads)			
A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	G	G	G	-	-	-	G	T	T	C	T	G	T	C	C	C	A	C	C	C	T	G	T	1.77% (3164 reads)		
A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	-	-	G	G	A	T	G	T	T	C	T	G	T	C	C	C	A	C	C	C	T	G	T	1.56% (2792 reads)		
A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	G	G	G	G	-	-	-	T	T	C	T	G	T	C	C	C	A	C	C	C	T	G	T	1.55% (2766 reads)		
A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	G	G	G	-	-	-	-	-	-	-	-	-	T	G	T	C	C	C	A	C	C	C	T	G	T	1.55% (2763 reads)
A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	G	G	-	-	A	T	G	T	T	C	T	G	T	C	C	C	A	C	C	C	T	G	T	1.38% (2459 reads)		
A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	G	G	G	-	-	-	-	-	-	-	-	C	T	G	T	C	C	C	A	C	C	C	T	G	T	1.21% (2160 reads)
A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	G	G	G	-	-	-	-	-	-	-	T	C	T	G	T	C	C	C	A	C	C	C	T	G	T	0.91% (1635 reads)
A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	G	G	G	G	-	-	-	-	-	-	T	C	T	G	T	C	C	C	A	C	C	C	T	G	T	0.48% (861 reads)
A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	G	-	-	-	-	-	G	T	T	C	T	G	T	C	C	C	A	C	C	C	T	G	T	0.47% (832 reads)		
A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	-	-	-	-	-	-	A	T	G	T	T	C	T	G	T	C	C	C	A	C	C	C	T	G	T	0.43% (761 reads)		
A	T	G	G	T	A	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	G	A	T	G	T	T	C	T	G	T	C	C	C	A	C	C	C	T	G	T	0.42% (748 reads)	
A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	G	G	-	-	-	-	-	-	-	T	T	C	T	G	T	C	C	C	A	C	C	C	T	G	T	0.41% (741 reads)
A	T	G	G	T	A	A	T	G	T	C	C	C	C	C	-	-	-	-	-	-	-	-	-	-	-	T	T	C	T	G	T	C	C	C	A	C	C	C	T	G	T	0.41% (741 reads)
A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	-	-	-	-	-	-	-	-	G	T	T	C	T	G	T	C	C	C	A	C	C	C	T	G	T	0.41% (738 reads)		
A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	G	G	G	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0.41% (725 reads)	
A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	G	-	-	-	-	-	-	-	-	-	T	C	T	G	T	C	C	C	A	C	C	C	T	G	T	0.39% (703 reads)
A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	G	-	-	-	-	-	-	-	-	-	-	C	T	G	T	C	C	C	A	C	C	C	T	G	T	0.37% (662 reads)
A	T	G	G	T	A	A	T	G	T	C	C	C	T	-	-	-	-	-	-	-	-	-	-	-	-	T	T	C	T	G	T	C	C	C	A	C	C	C	T	G	T	0.34% (614 reads)
A	T	G	G	T	A	A	T	G	T	C	C	A	T	C	C	T	G	G	G	G	A	A	G	T	T	C	T	G	T	C	C	C	A	C	C	C	T	G	T	0.24% (435 reads)		
A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	-	-	-	G	A	T	G	T	T	C	T	G	T	C	C	C	A	C	C	C	T	G	T	0.24% (432 reads)		
A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	G	-	-	-	A	T	G	T	T	C	T	G	T	C	C	C	A	C	C	C	T	G	T	0.23% (419 reads)		
A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	-	-	-	-	-	-	-	T	G	T	T	C	T	G	T	C	C	C	A	C	C	C	T	G	T	0.22% (389 reads)	
A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	-	-	-	-	G	G	T	G	T	T	C	T	G	T	C	C	C	A	C	C	C	T	G	T	0.21% (382 reads)		
A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	G	G	-	-	-	-	-	-	-	-	-	G	T	C	C	C	A	C	C	C	T	G	T	0.21% (373 reads)		
A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	-	-	-	C	G	A	T	G	T	T	C	T	G	T	C	C	C	A	C	C	C	T	G	T	0.21% (373 reads)		



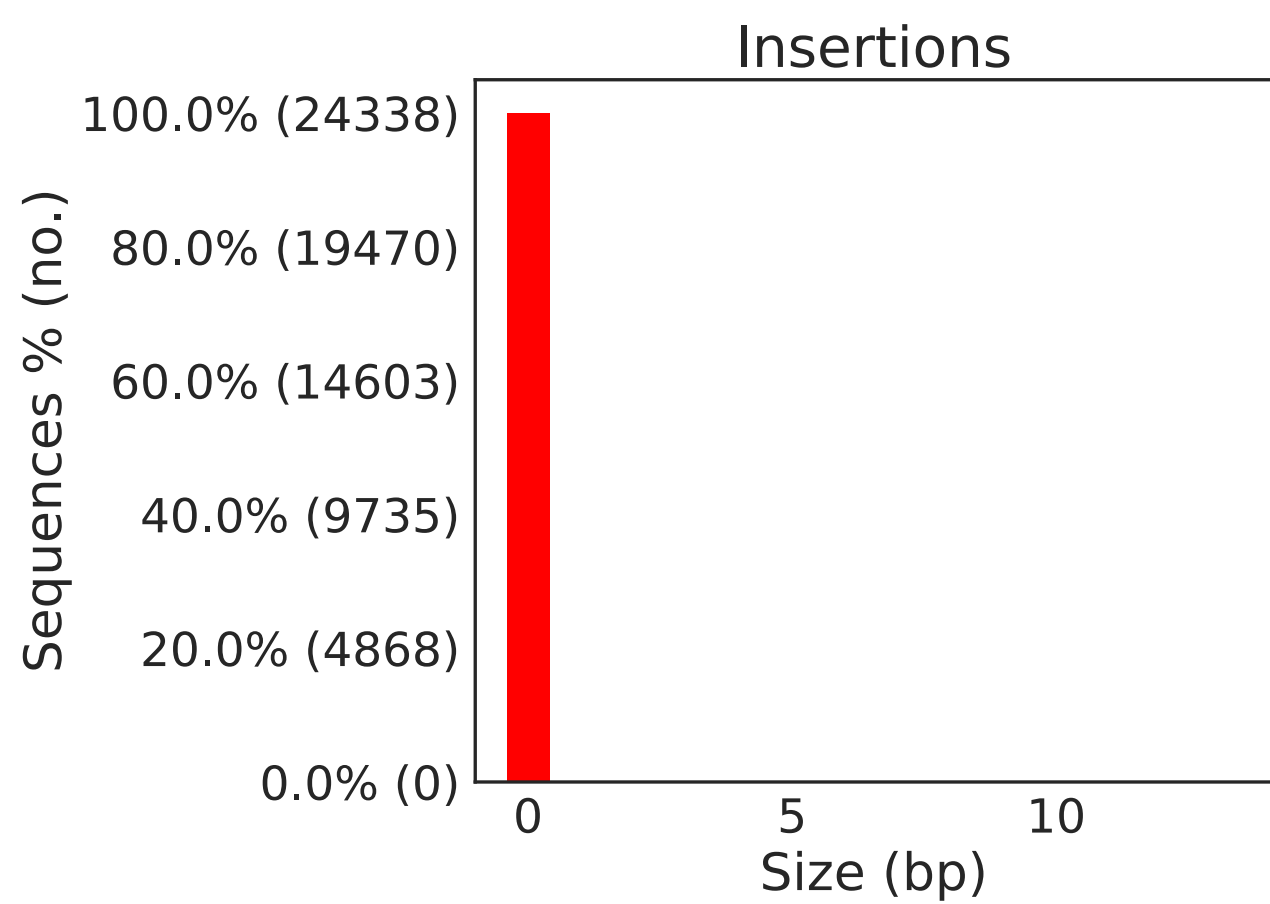
Insertion
 Non-insertion

Deletion
 Non-deletion

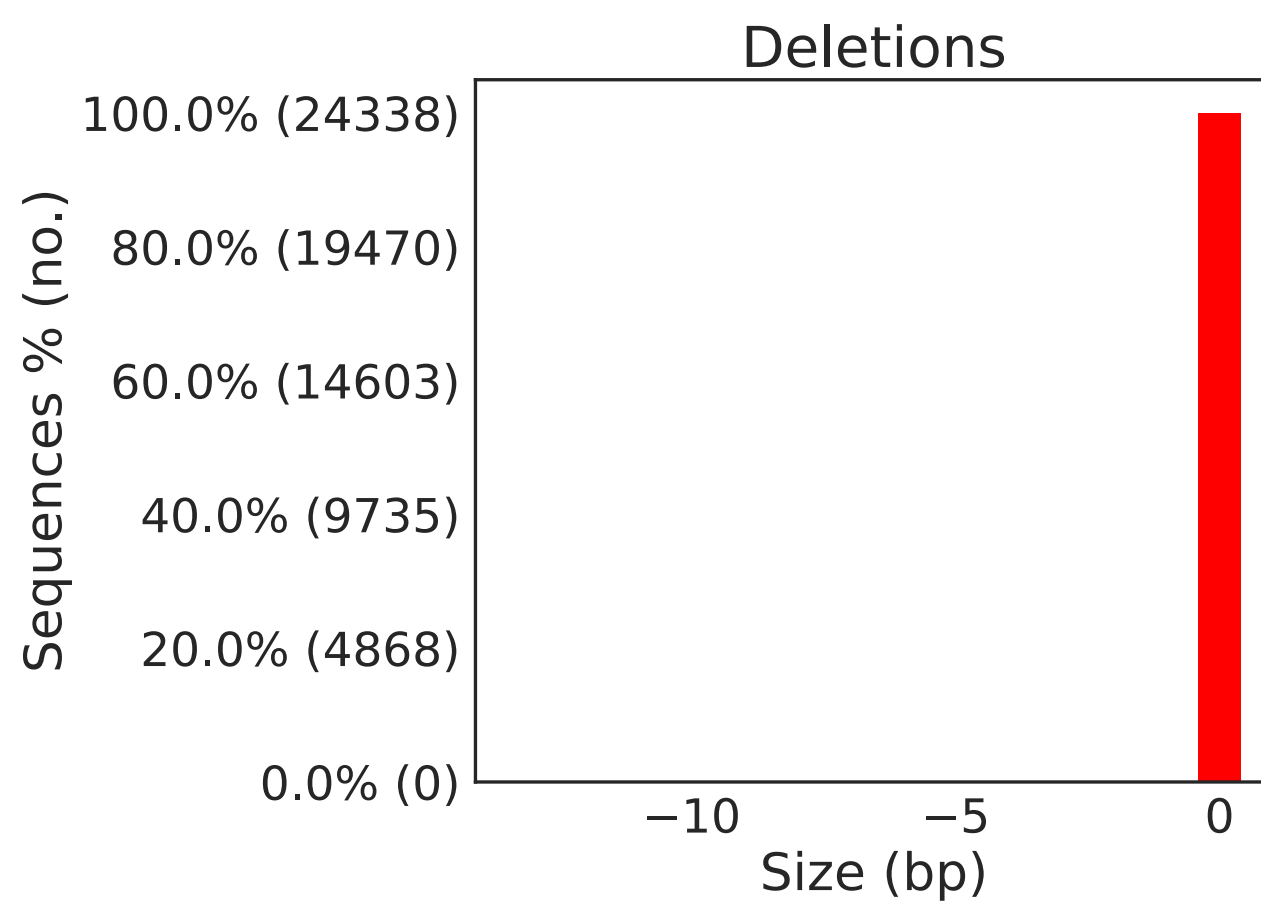
Tmc^{Bth/WT}, SpCas9 only, Bth allele

bold Substitutions
 Insertions
 - Deletions
 - - - Predicted cleavage position

A T G G T A A T G T C C C T C C T G G G G A A G T T C T G T C C C A C C C T G T Reference
 A T G G T A A T G T C C C T C C T G G G **G** A A G T T C T G T C C C A C C C T G T 98.27% (23918 reads)



— Insertion
— Non-insertion

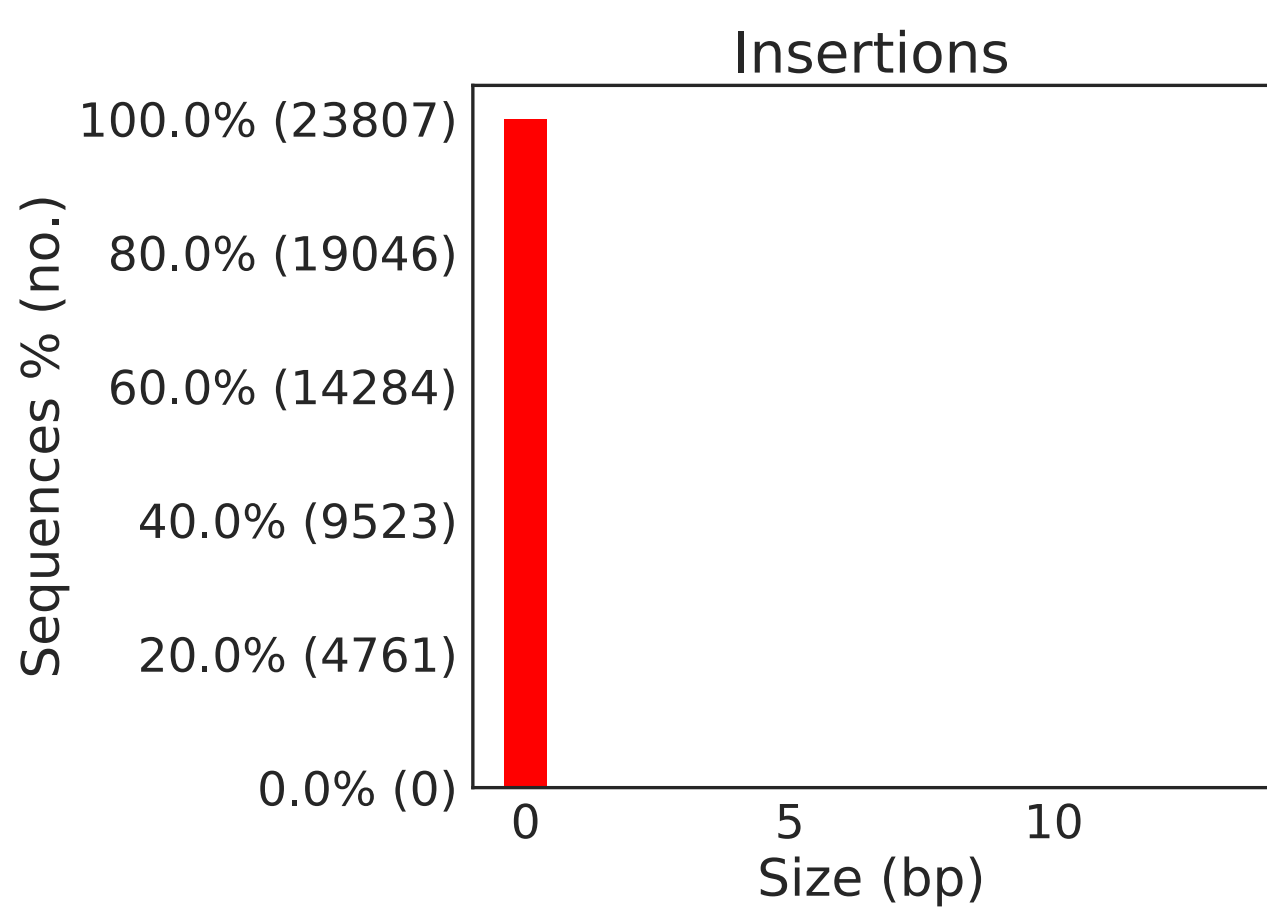


— Deletion
— Non-deletion

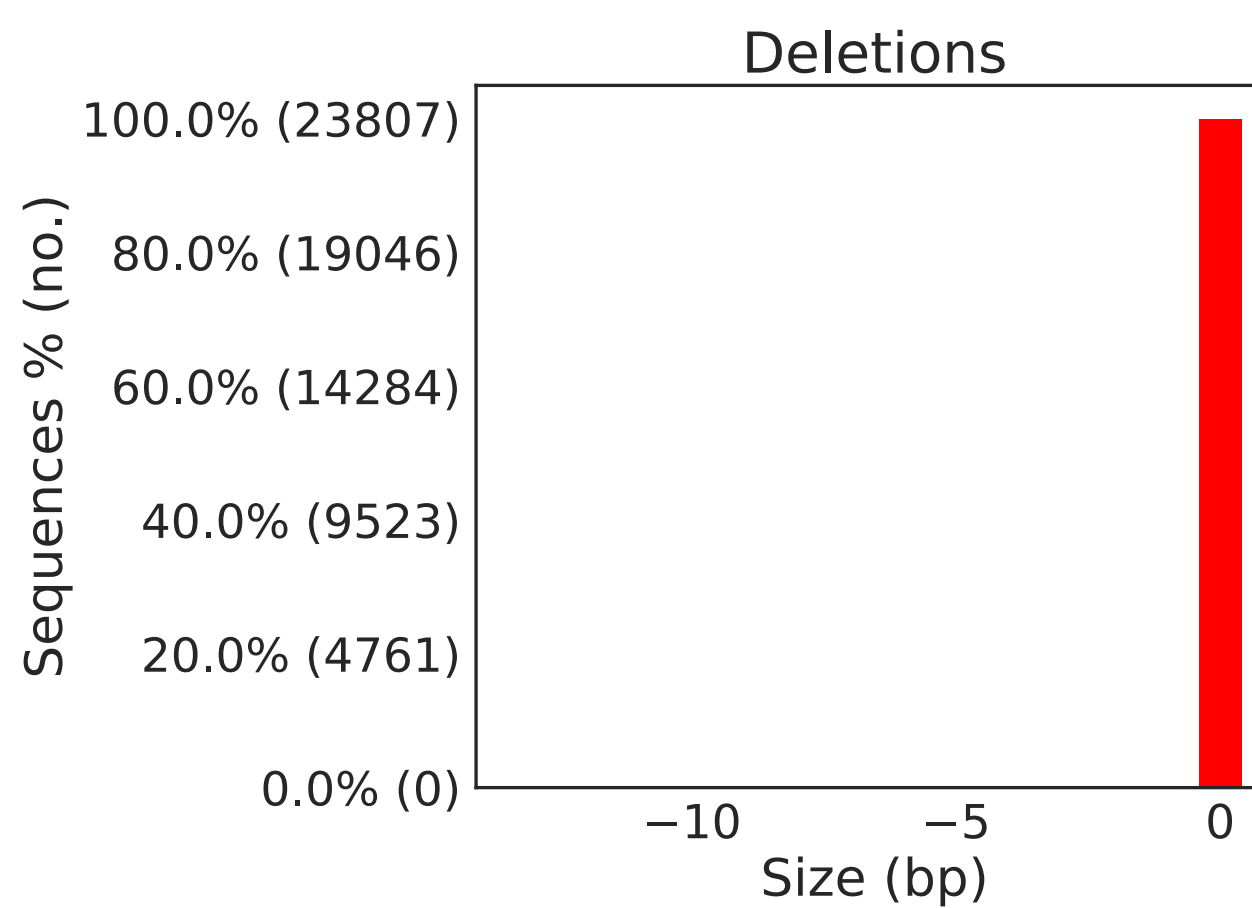
Tmc^{Bth/WT}, SpCas9 only, WT allele

bold Substitutions
 Insertions
 - Deletions
 - - - Predicted cleavage position

A T G G T A A T G T C C C T C C T G G G G A A G T T C T G T C C C A C C C T G T Reference
 A T G G T A A T G T C C C T C C T G G G **G** A **T** G T T C T G T C C C A C C C T G T 98.25% (23391 reads)



— Insertion
— Non-insertion

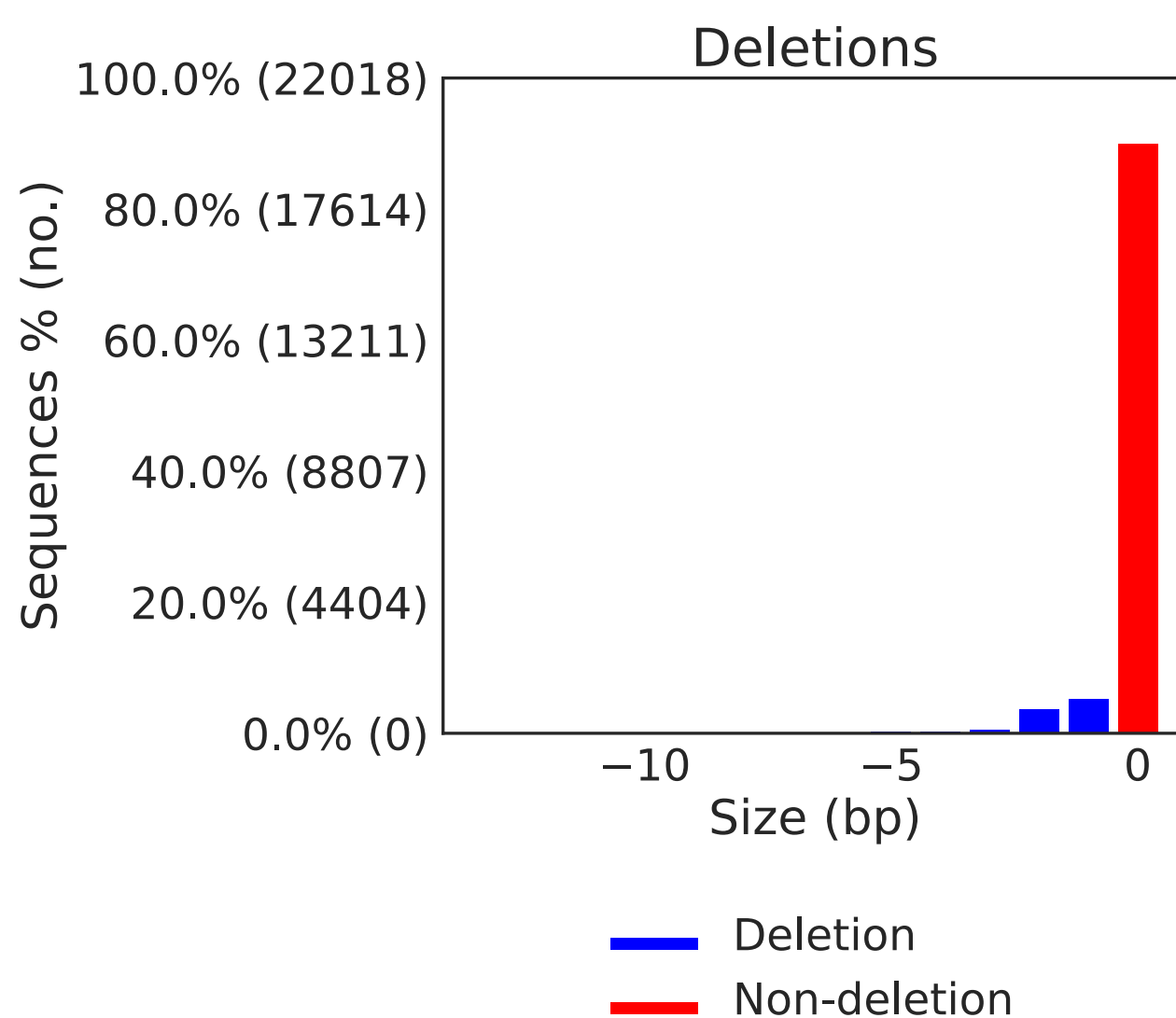
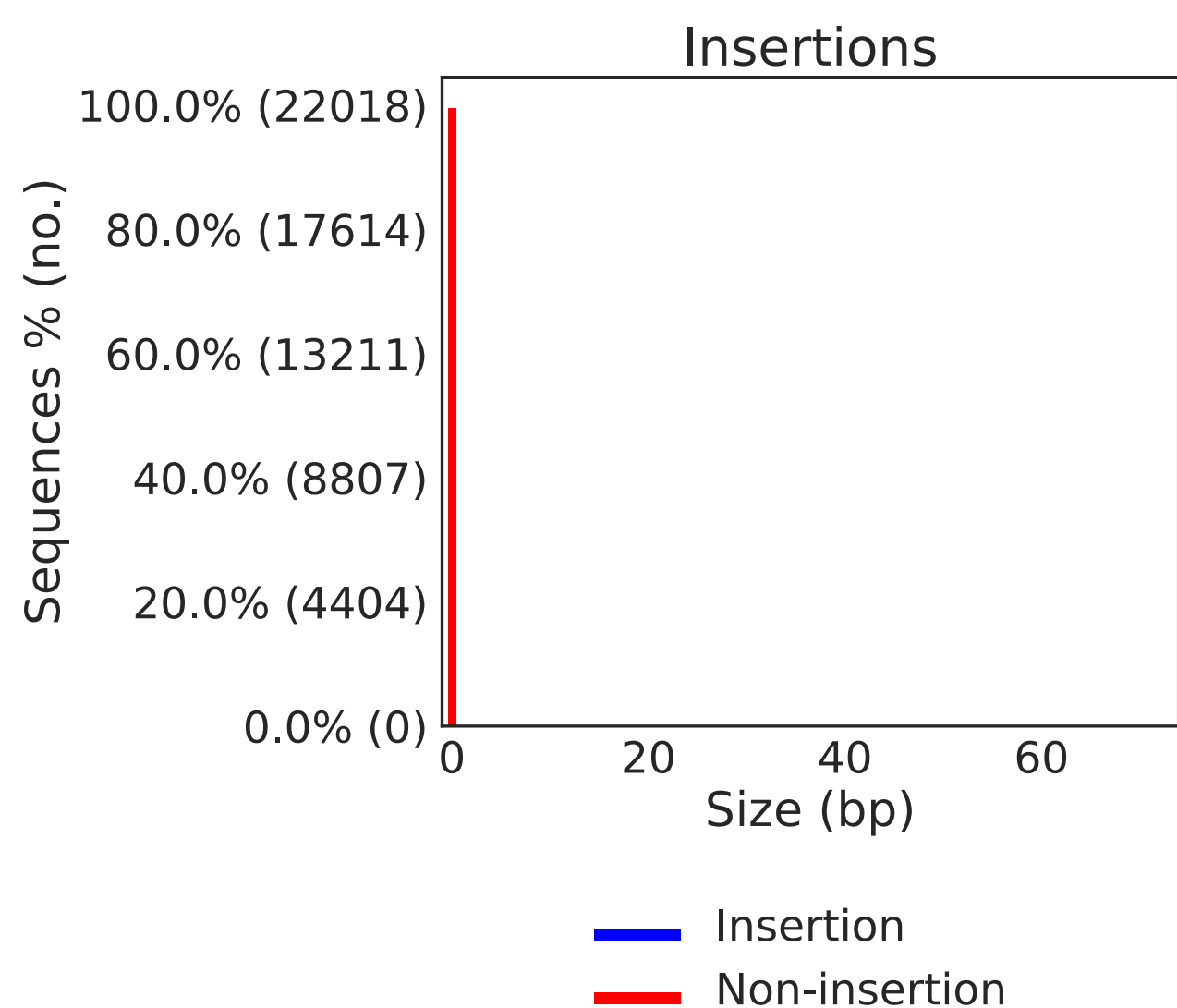


— Deletion
— Non-deletion

Tmc^{Bth/WT}, SpCas9 + gRNA 1.1, Bth allele

bold Substitutions
 Insertions
 - Deletions
 - - - Predicted cleavage position

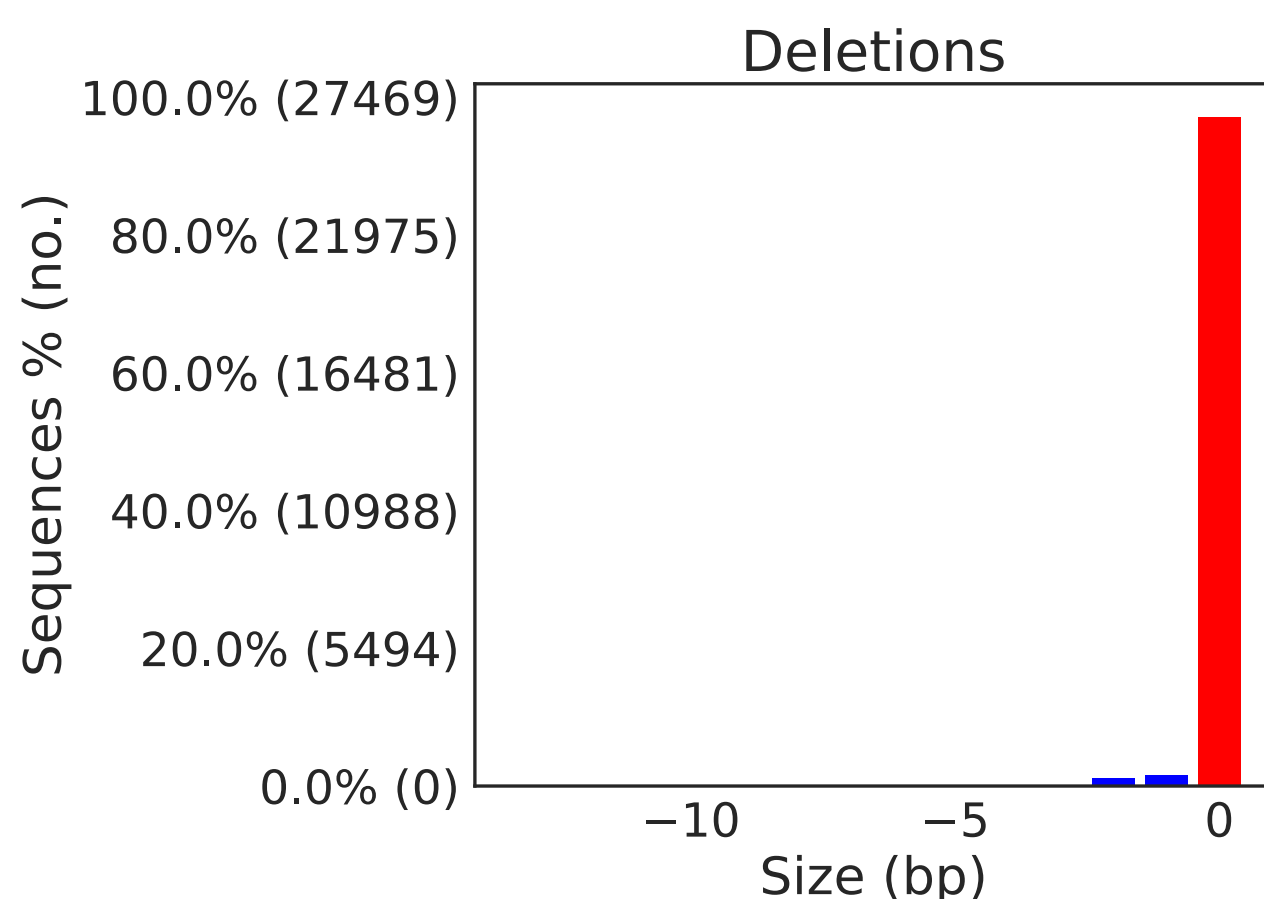
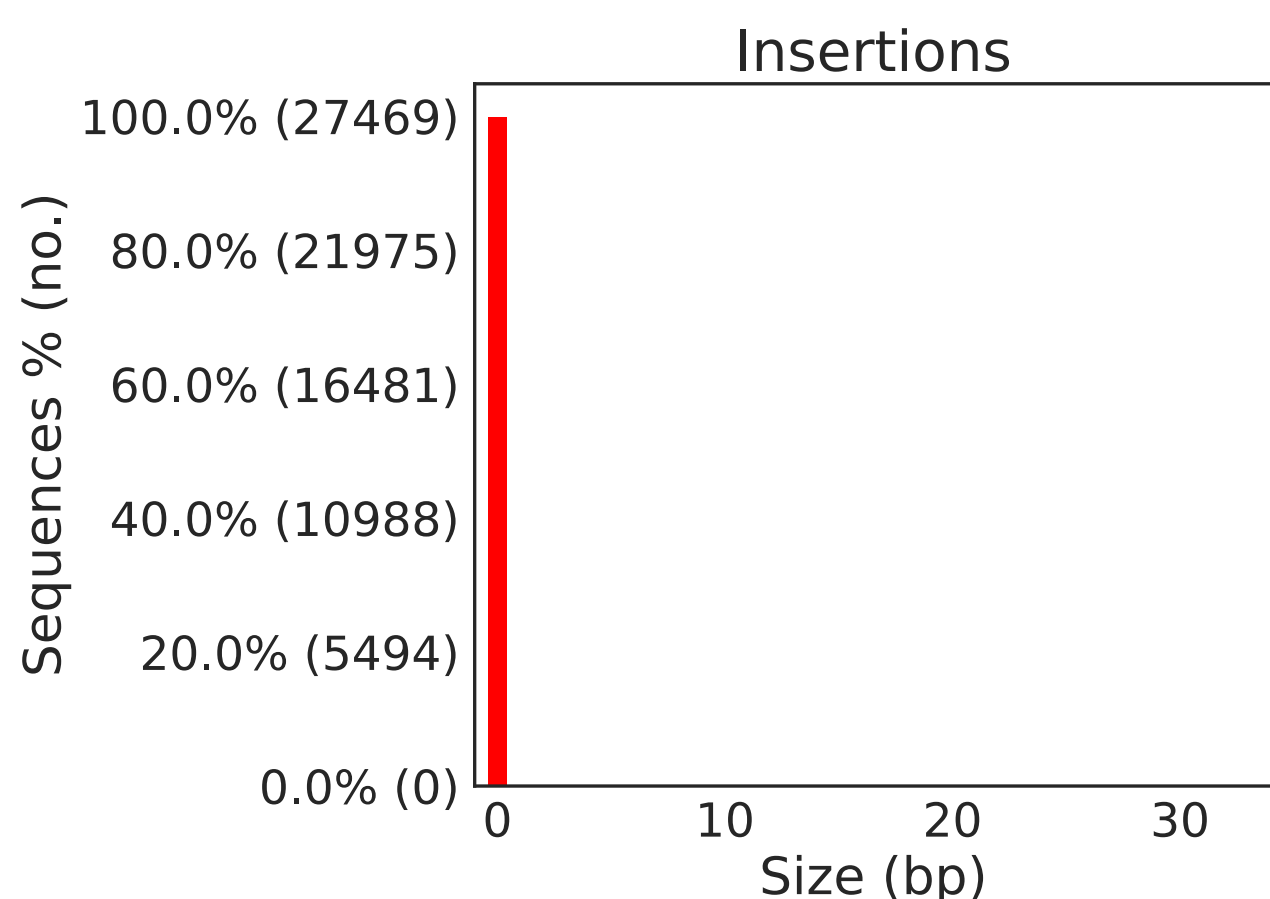
A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	G	G	G	G	A	A	G	T	T	C	T	G	T	C	C	C	A	C	C	C	T	G	T	Reference	
A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	G	G	G	G	A	A	G	T	T	C	T	G	T	C	C	C	A	C	C	C	T	G	T	81.34% (17909 reads)	
A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	G	G	G	-	A	A	G	T	T	C	T	G	T	C	C	C	A	C	C	C	T	G	T	5.10% (1122 reads)	
A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	-	G	G	G	A	A	G	T	T	C	T	G	T	C	C	C	A	C	C	C	T	G	T	4.91% (1082 reads)	
A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	G	G	G	-	-	A	A	G	T	T	C	T	G	T	C	C	C	A	C	C	C	T	G	T	2.77% (610 reads)
A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	G	G	-	-	A	A	G	T	T	C	T	G	T	C	C	C	A	C	C	C	T	G	T	0.41% (91 reads)	
A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	-	-	G	G	A	A	G	T	T	C	T	G	T	C	C	C	A	C	C	C	T	G	T	0.41% (90 reads)	
A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	-	-	-	-	-	G	A	A	G	T	T	C	T	G	T	C	C	C	A	C	C	C	T	G	T	0.20% (45 reads)	



Tmc^{Bth/WT}, SpCas9 + gRNA 1.1, WT allele

bold Substitutions
 Insertions
 - Deletions
 - - - Predicted cleavage position

A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	G	G	G	G	A	A	G	T	T	C	T	G	T	C	C	C	A	C	C	C	T	G	T	Reference
A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	G	G	G	G	A	T	G	T	T	C	T	G	T	C	C	C	A	C	C	C	T	G	T	92.48% (25403 reads)
A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	-	G	G	G	A	T	G	T	T	C	T	G	T	C	C	C	A	C	C	C	T	G	T	1.56% (429 reads)
A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	G	G	G	-	A	T	G	T	T	C	T	G	T	C	C	C	A	C	C	C	T	G	T	1.46% (402 reads)
A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	G	G	G	T	-	-	G	T	T	C	T	G	T	C	C	C	A	C	C	C	T	G	T	0.40% (111 reads)
A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	G	G	G	-	-	T	G	T	T	C	T	G	T	C	C	C	A	C	C	C	T	G	T	0.39% (108 reads)



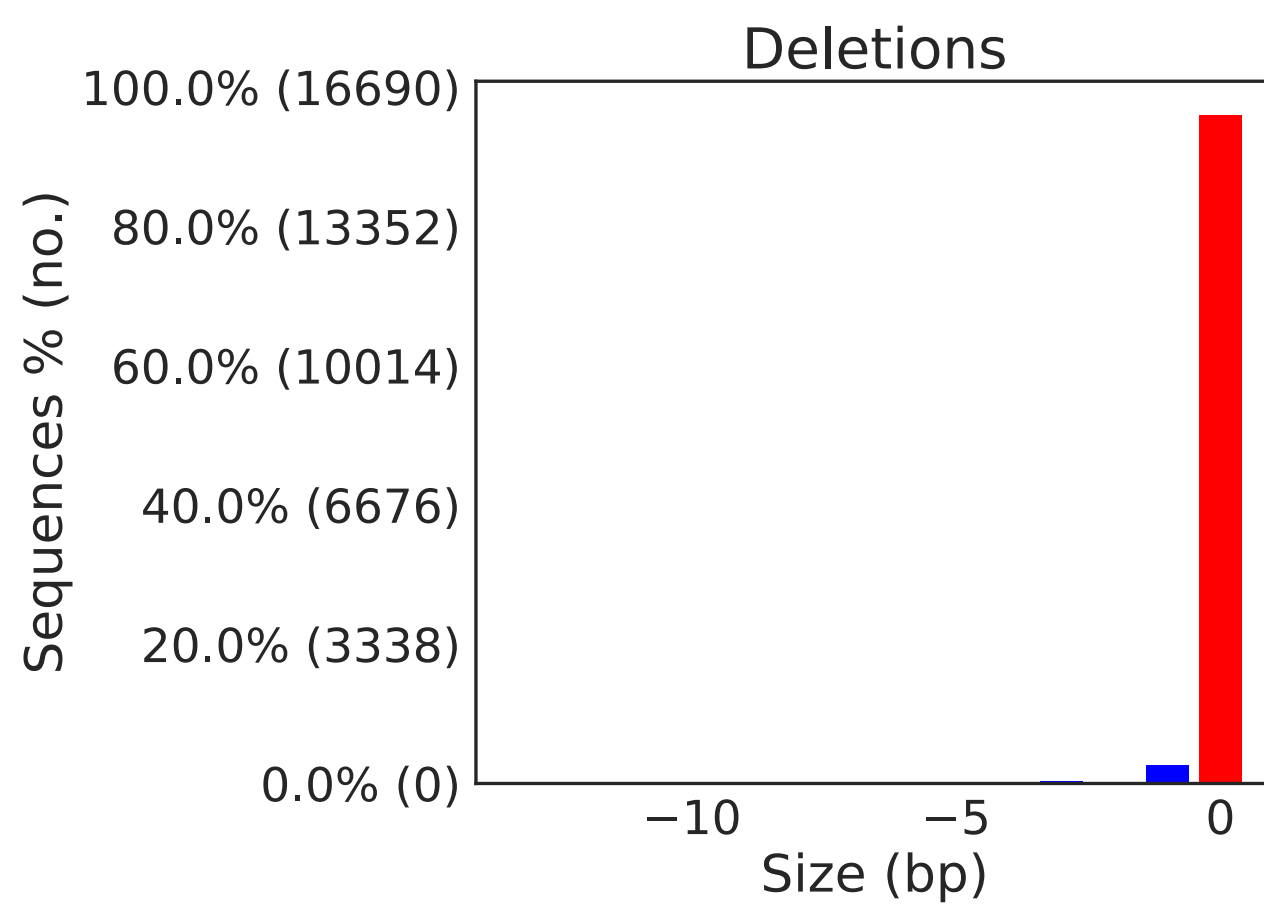
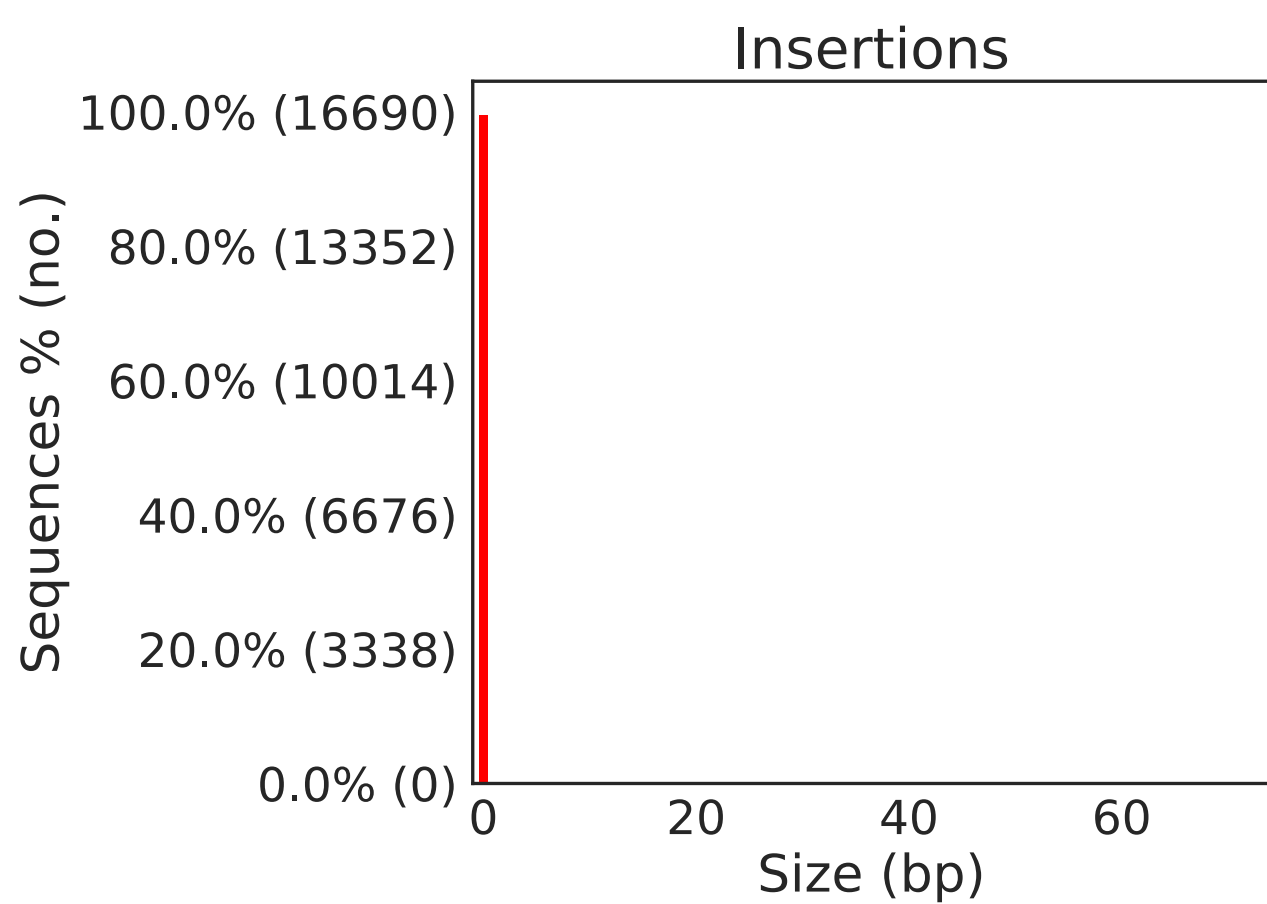
█ Insertion
█ Non-insertion

█ Deletion
█ Non-deletion

Tmc^{Bth/WT}, SpCas9 + gRNA 2.1, Bth allele

bold Substitutions
 Insertions
 - Deletions
 - - - Predicted cleavage position

A	A	C	A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	G	G	G	G	A	A	G	T	T	C	T	G	T	C	C	C	A	C	C	C	Reference
A	A	C	A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	G	G	G	G	A	A	G	T	T	C	T	G	T	C	C	C	A	C	C	C	90.87% (15166 reads)
A	A	C	A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	G	G	G	G	A	A	G	T	T	C	T	G	T	C	C	C	A	C	C	C	1.52% (254 reads)
A	A	C	A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	G	G	G	G	A	A	G	T	T	C	T	G	T	C	C	C	A	C	C	C	1.04% (173 reads)
A	A	C	A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	G	G	G	G	A	A	G	T	T	C	T	G	T	C	C	C	A	C	C	C	1.01% (168 reads)



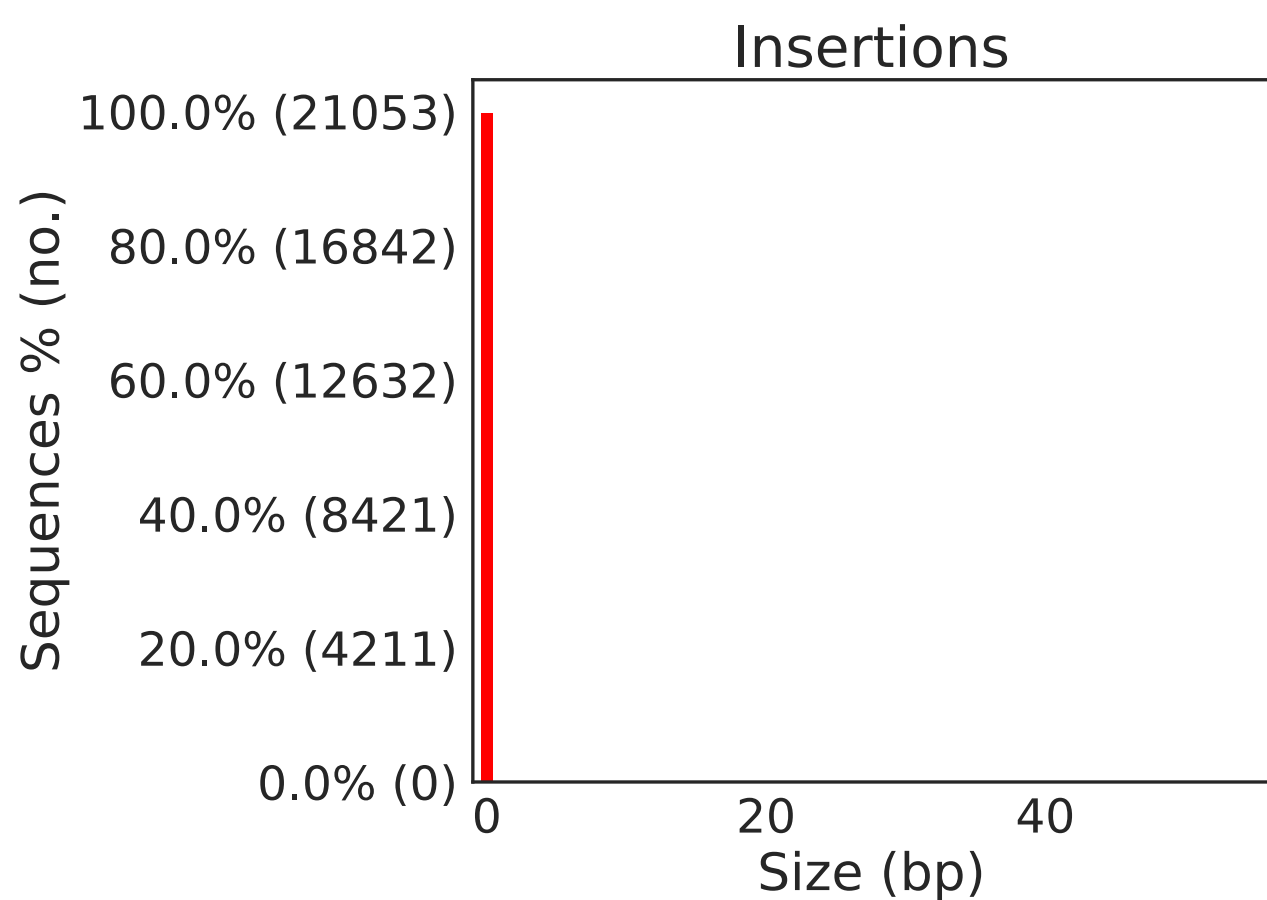
— Insertion
— Non-insertion

— Deletion
— Non-deletion

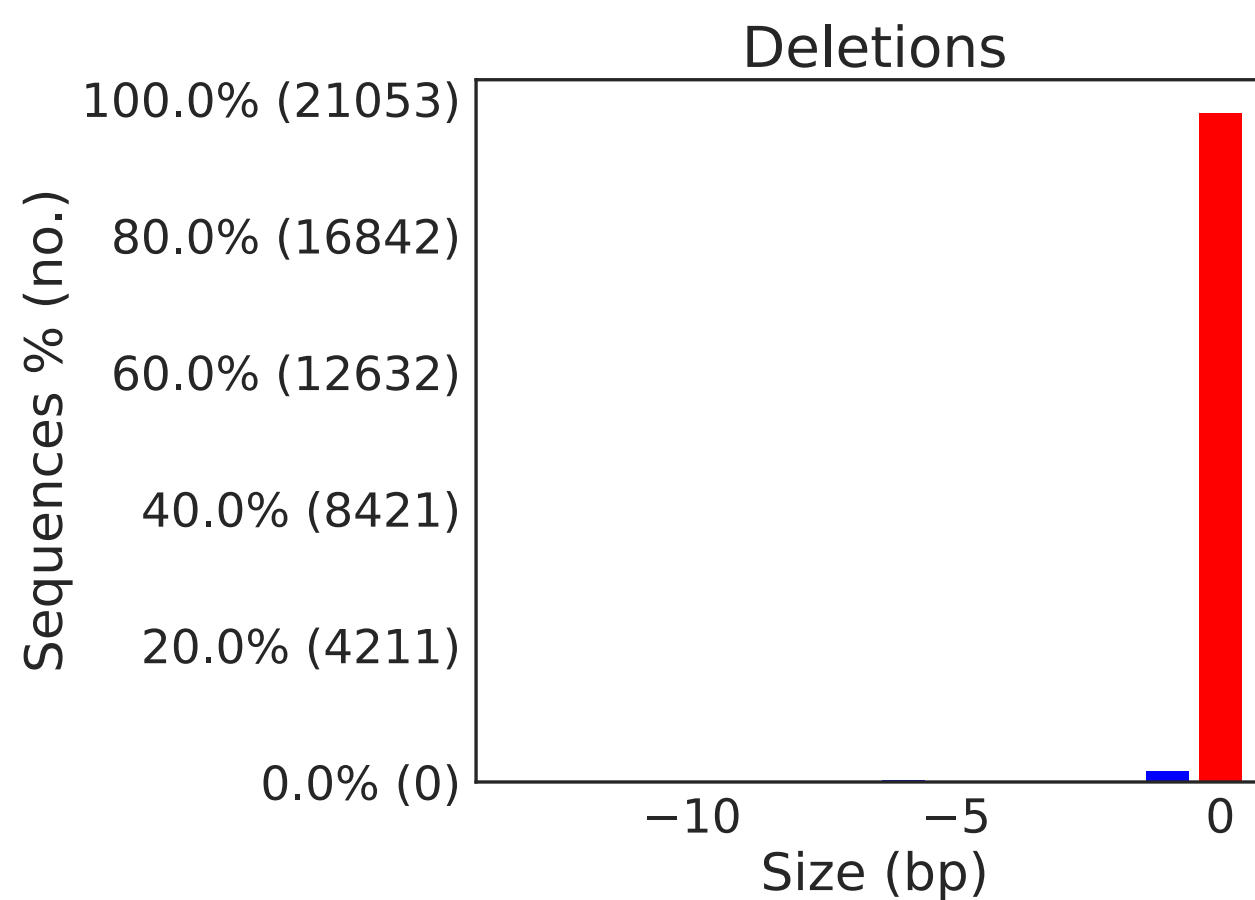
Tmc^{Bth/WT}, SpCas9 + gRNA 2.1, WT allele

bold Substitutions
 Insertions
 - Deletions
 - - - Predicted cleavage position

A	A	C	A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	G	G	G	G	A	A	G	T	T	C	T	G	T	C	C	C	A	C	C	C	Reference
A	A	C	A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	G	G	G	G	A	T	G	T	T	C	T	G	T	C	C	C	A	C	C	C	93.33% (19648 reads)
A	A	C	A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	G	G	G	G	A	T	G	T	T	C	T	G	T	C	C	C	A	C	C	C	0.75% (157 reads)
A	A	C	A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	G	G	G	G	A	T	G	T	T	C	T	G	T	C	C	C	A	C	C	C	0.69% (145 reads)
A	A	C	A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	G	G	G	G	A	T	G	T	T	C	T	G	T	C	C	C	A	C	C	C	0.64% (134 reads)



— Insertion
 — Non-insertion

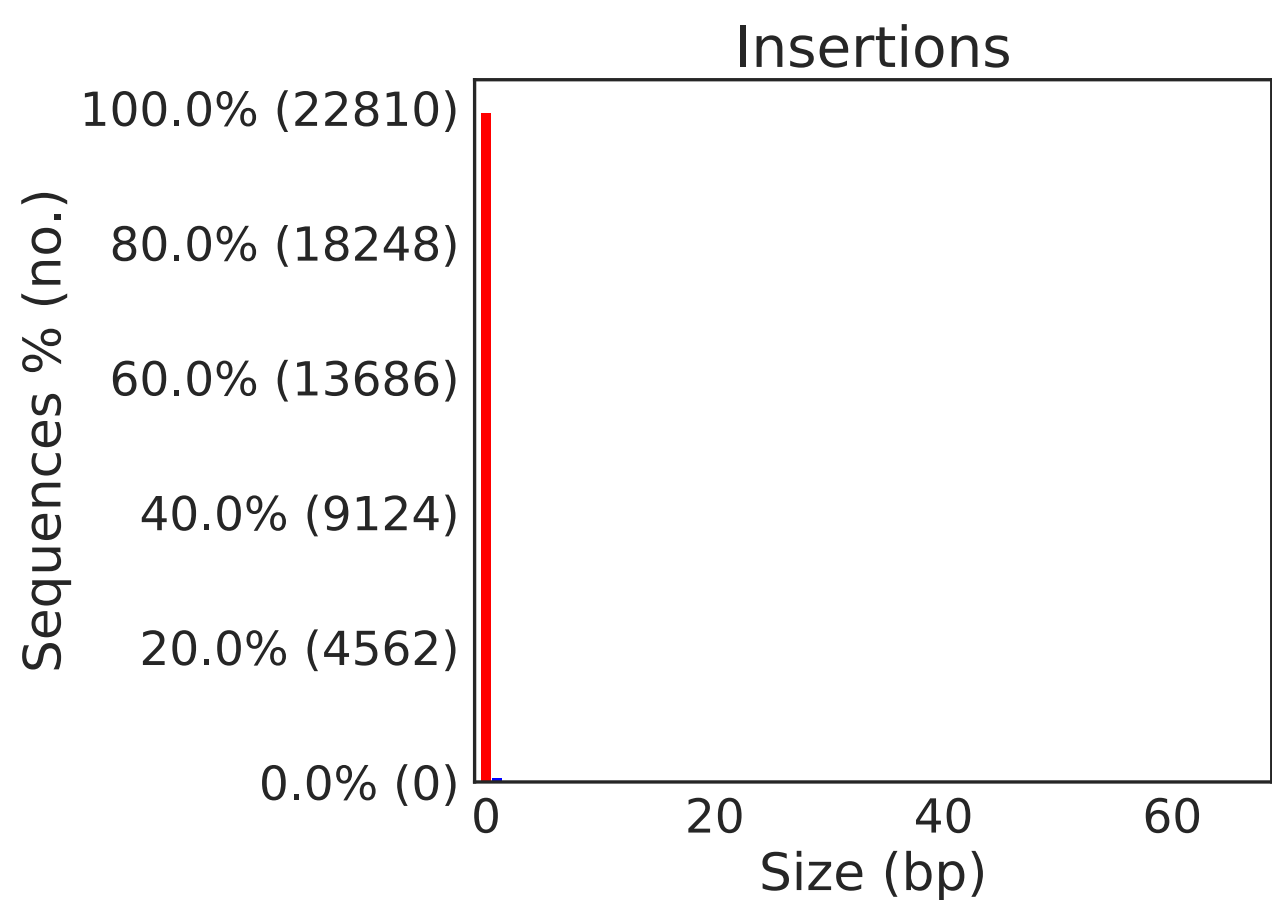


— Deletion
 — Non-deletion

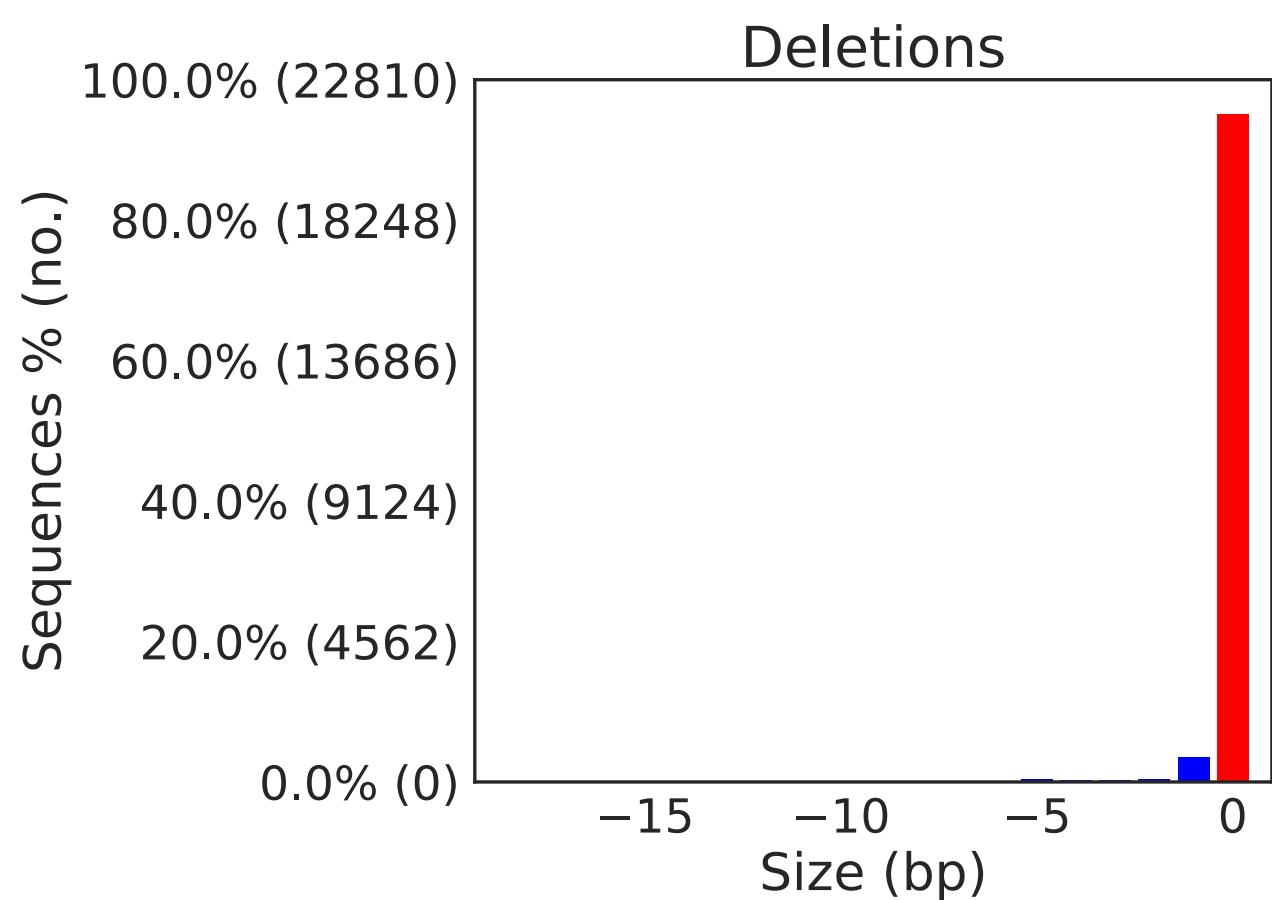
Tmc^{Bth/WT}, SpCas9 + gRNA 2.4, Bth allele

bold Substitutions
 Insertions
 - Deletions
 - - - Predicted cleavage position

A	A	C	A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	G	G	G	G	A	A	G	T	T	C	T	G	T	C	C	C	A	C	C	C	Reference	
A	A	C	A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	G	G	G	G	A	A	G	T	T	C	T	G	T	C	C	C	A	C	C	C	88.91% (20281 reads)	
A	A	C	A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	-	G	G	G	G	A	A	G	T	T	C	T	G	T	C	C	C	A	C	C	C	1.81% (413 reads)	
A	A	C	A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	G	G	G	-	A	A	G	T	T	C	T	G	T	C	C	C	A	C	C	C	1.65% (376 reads)	
A	A	C	A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	-	G	G	G	A	A	G	T	T	C	T	G	T	C	C	C	A	C	C	C	1.62% (369 reads)	
A	A	C	A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	G	G	G	G	A	A	G	T	T	C	T	G	T	C	C	C	A	C	C	C	0.37% (85 reads)	
A	A	C	A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	G	G	G	G	G	A	A	G	T	T	C	T	G	T	C	C	C	A	C	C	C	0.35% (79 reads)
A	A	C	A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	-	-	G	G	G	G	A	A	G	T	T	C	T	G	T	C	C	C	A	C	C	C	0.21% (47 reads)	



— Insertion
— Non-insertion

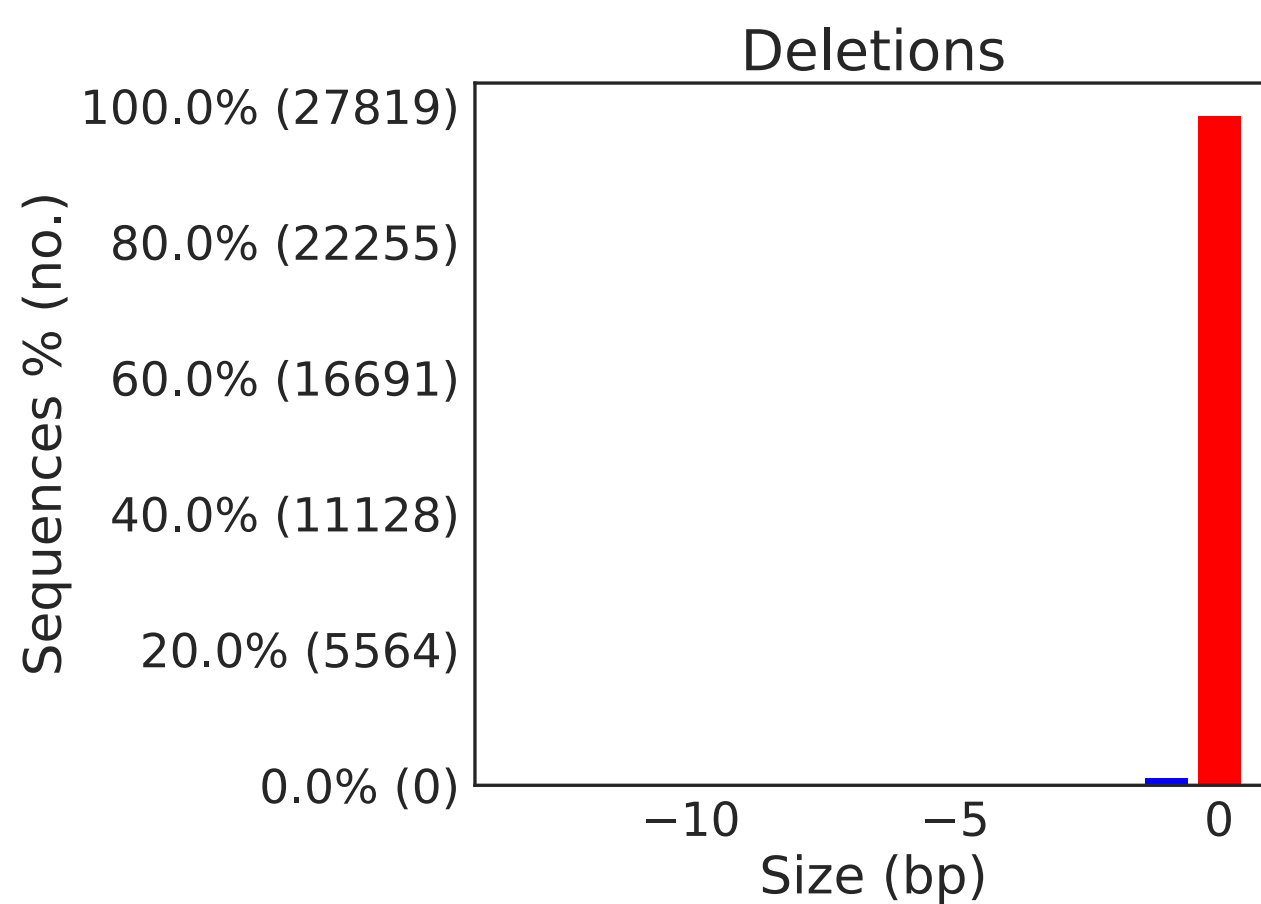
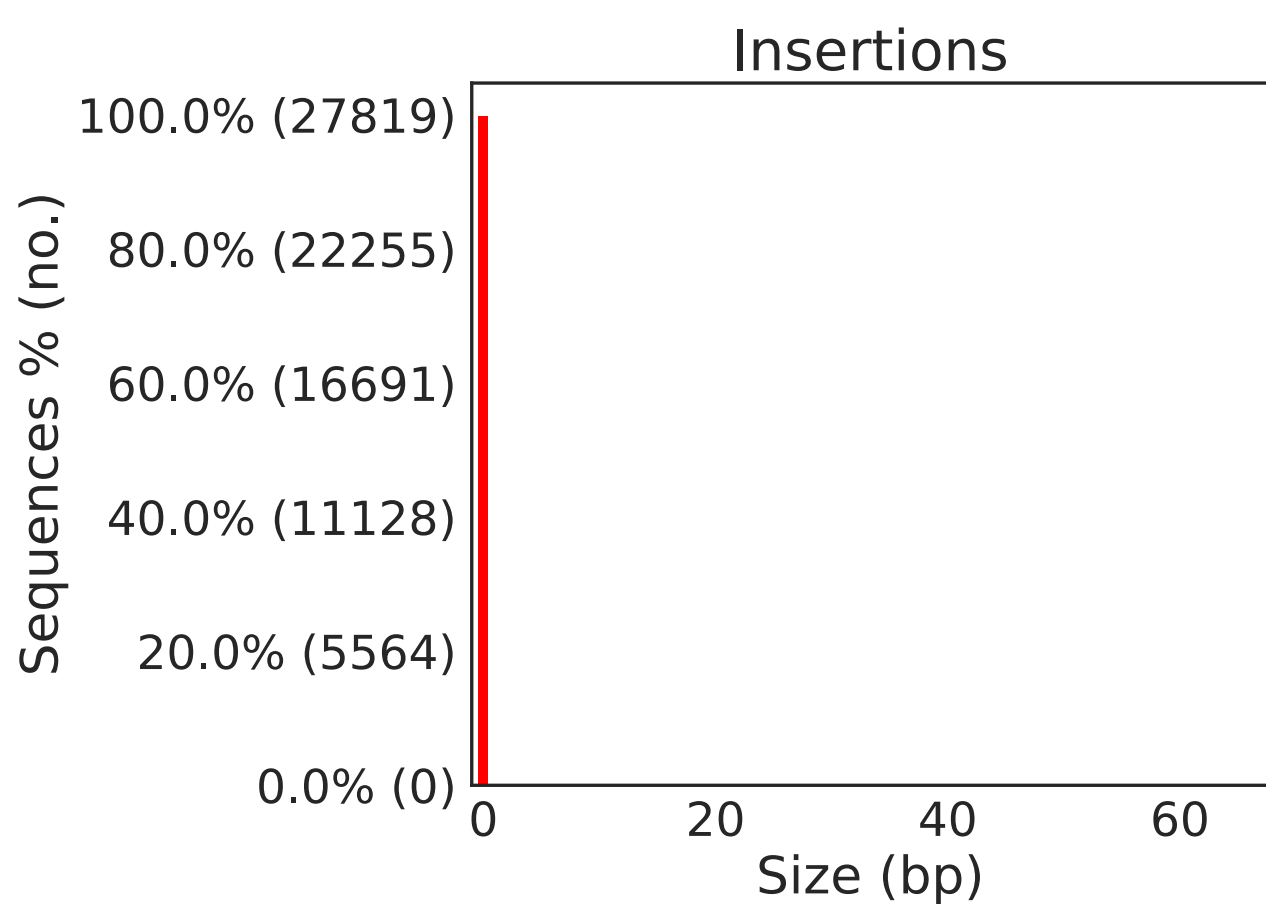


— Deletion
— Non-deletion

Tmc^{Bth/WT}, SpCas9 + gRNA 2.4, WT allele

bold Substitutions
 Insertions
 - Deletions
 - - - Predicted cleavage position

A	A	C	A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	G	G	G	G	A	A	G	T	T	C	T	G	T	C	C	C	A	C	C	C	Reference
A	A	C	A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	G	G	G	G	A	T	G	T	T	C	T	G	T	C	C	C	A	C	C	C	94.40% (26262 reads)
A	A	C	A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	-	G	G	G	A	T	G	T	T	C	T	G	T	C	C	C	A	C	C	C	0.59% (163 reads)
A	A	C	A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	-	G	G	G	A	T	G	T	T	C	T	G	T	C	C	C	A	C	C	C	0.47% (132 reads)	
A	A	C	A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	G	G	G	-	A	T	G	T	T	C	T	G	T	C	C	C	A	C	C	C	0.43% (121 reads)
A	A	C	A	T	G	A	T	A	A	T	G	T	C	C	C	T	C	C	T	G	G	G	G	A	T	G	T	T	C	T	G	T	C	C	C	A	C	C	C	0.20% (57 reads)



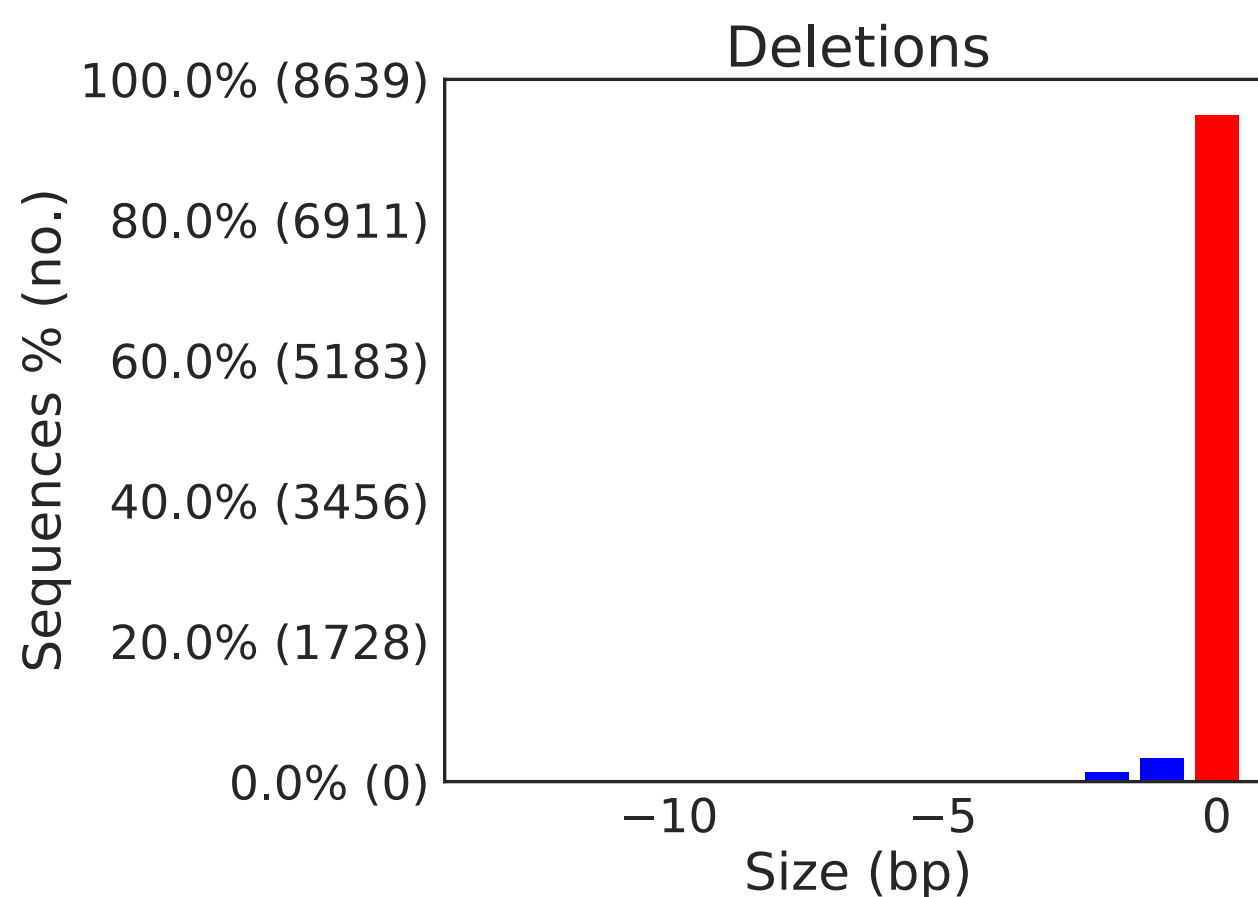
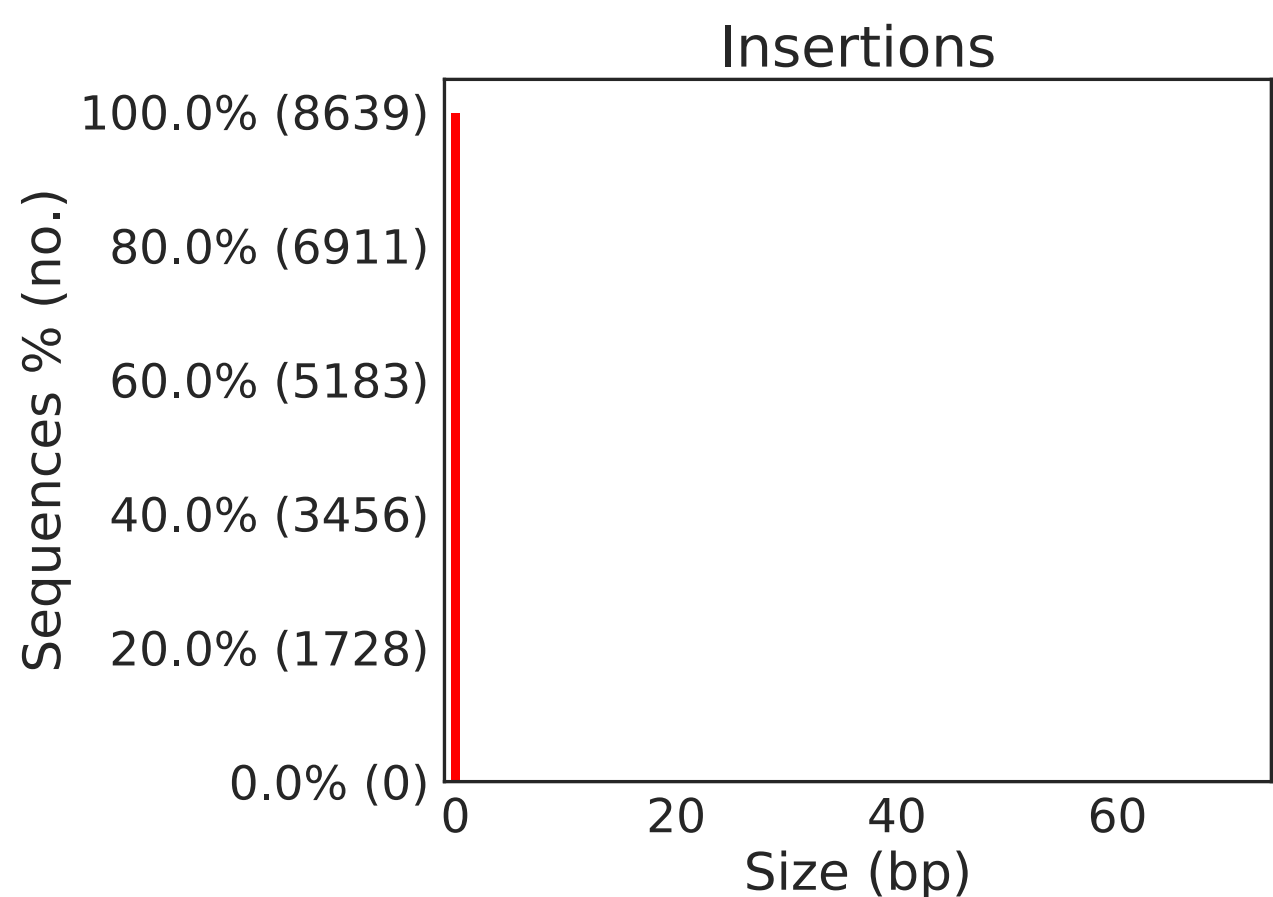
— Insertion
— Non-insertion

— Deletion
— Non-deletion

Tmc^{Bth/WT}, eSpCas9 + gRNA 1.1, Bth allele

bold Substitutions
 Insertions
 - Deletions
 - - - Predicted cleavage position

A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	G	G	G	G	A	A	G	T	T	C	T	G	T	C	C	C	A	C	C	C	T	G	T	Reference	
A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	G	G	G	G	A	A	G	T	T	C	T	G	T	C	C	C	A	C	C	C	T	G	T	88.47% (7643 reads)	
A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	G	G	G	-	A	A	G	T	T	C	T	G	T	C	C	C	A	C	C	C	T	G	T	3.16% (273 reads)	
A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	-	G	G	G	A	A	G	T	T	C	T	G	T	C	C	C	A	C	C	C	T	G	T	2.57% (222 reads)	
A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	G	G	G	-	-	A	A	G	T	T	C	T	G	T	C	C	C	A	C	C	C	T	G	T	0.87% (75 reads)
A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	G	G	-	-	A	A	G	T	T	C	T	G	T	C	C	C	A	C	C	C	T	G	T	0.24% (21 reads)	
A	T	G	A	T	A	A	T	G	T	C	C	C	T	C	C	T	G	G	G	G	A	A	G	T	T	C	T	G	T	C	C	C	A	C	C	C	T	G	T	0.22% (19 reads)	



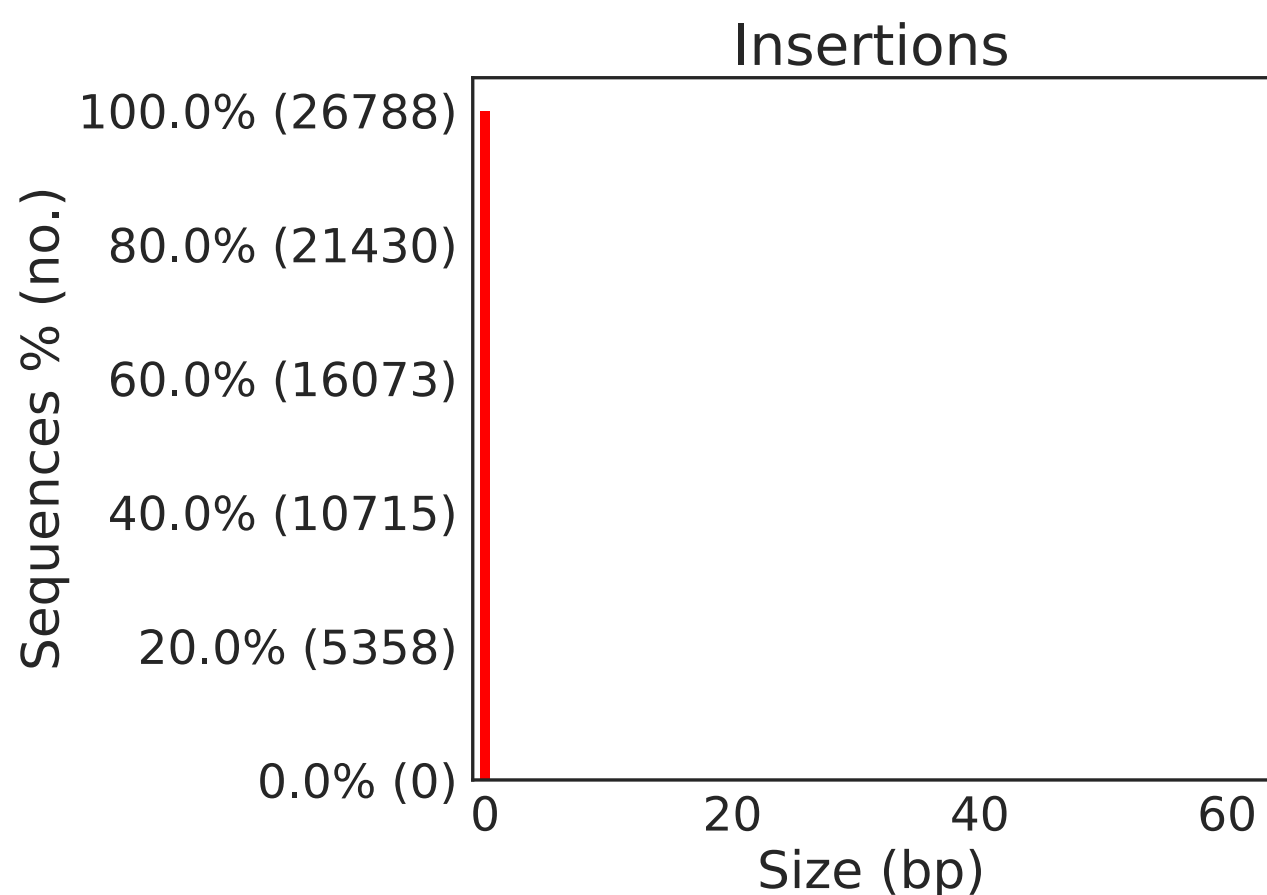
Insertion
 Non-insertion

Deletion
 Non-deletion

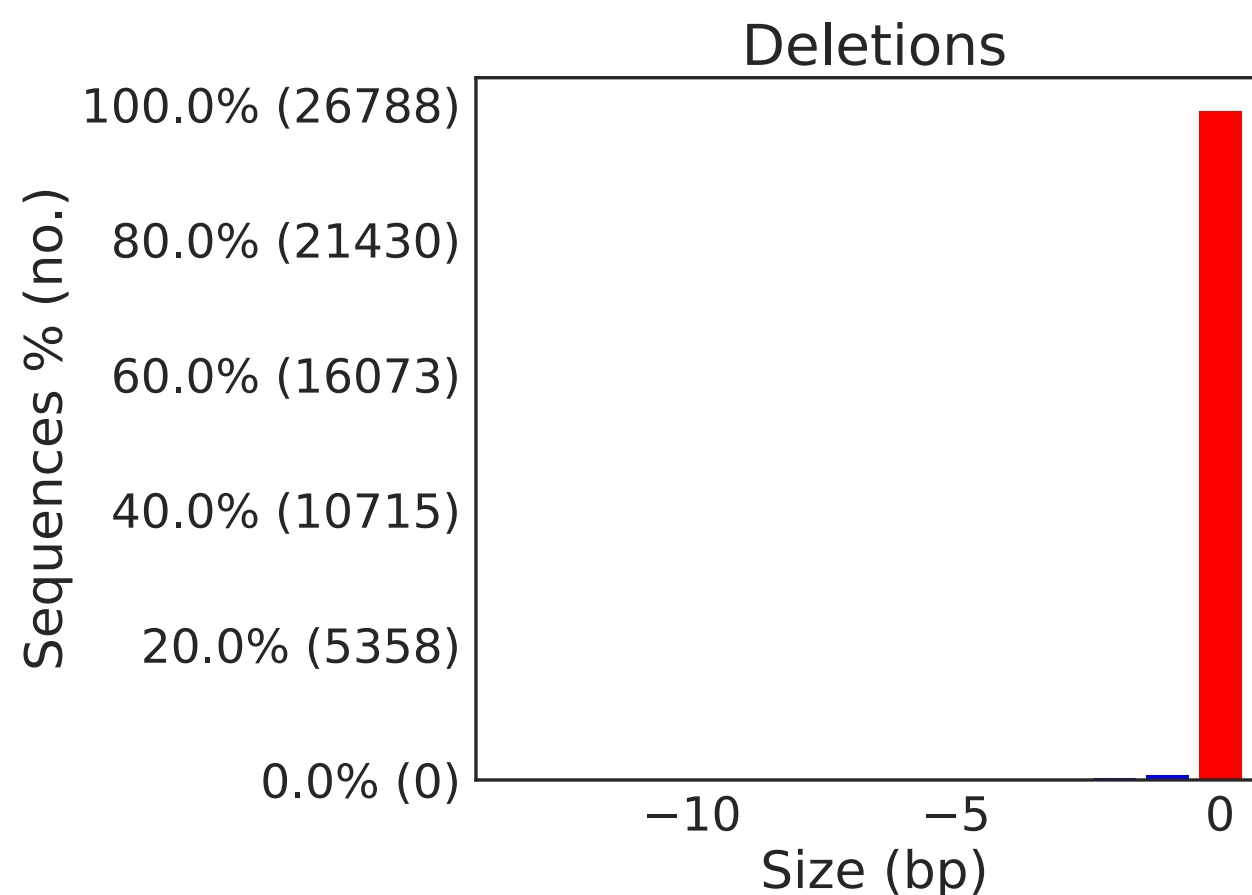
Tmc^{Bth/WT}, eSpCas9 + gRNA 1.1, WT allele

bold Substitutions
 Insertions
 - Deletions
 - - - Predicted cleavage position

A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	G	G	G	G	A	A	G	T	T	C	T	G	T	C	C	C	A	C	C	C	T	G	T	Reference	
A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	G	G	G	G	G	A	T	G	T	T	C	T	G	T	C	C	C	A	C	C	C	T	G	T	94.83% (25404 reads)
A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	G	G	G	G	-	A	T	G	T	T	C	T	G	T	C	C	C	A	C	C	C	T	G	T	0.59% (159 reads)
A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	-	G	G	G	-	A	T	G	T	T	C	T	G	T	C	C	C	A	C	C	C	T	G	T	0.57% (153 reads)



— Insertion
 — Non-insertion

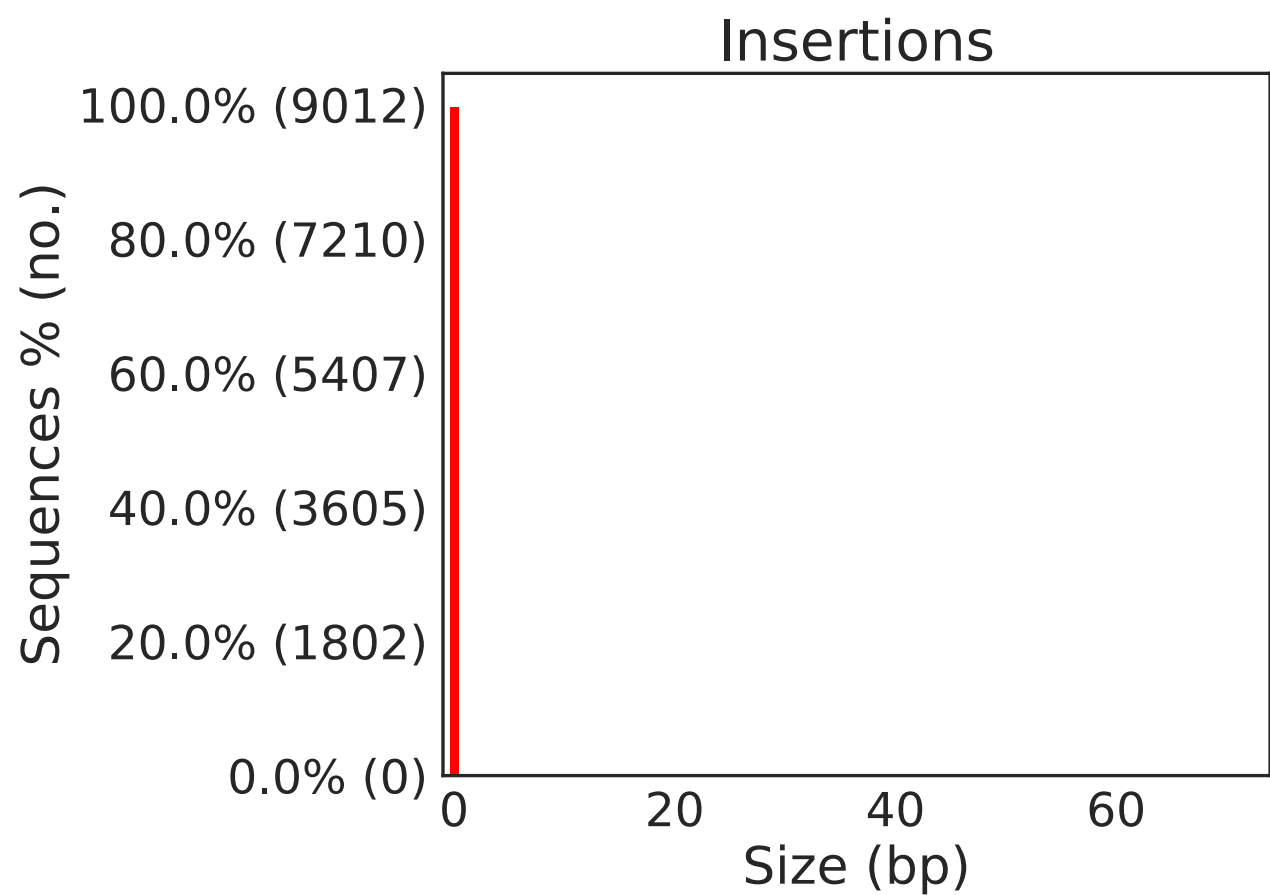


— Deletion
 — Non-deletion

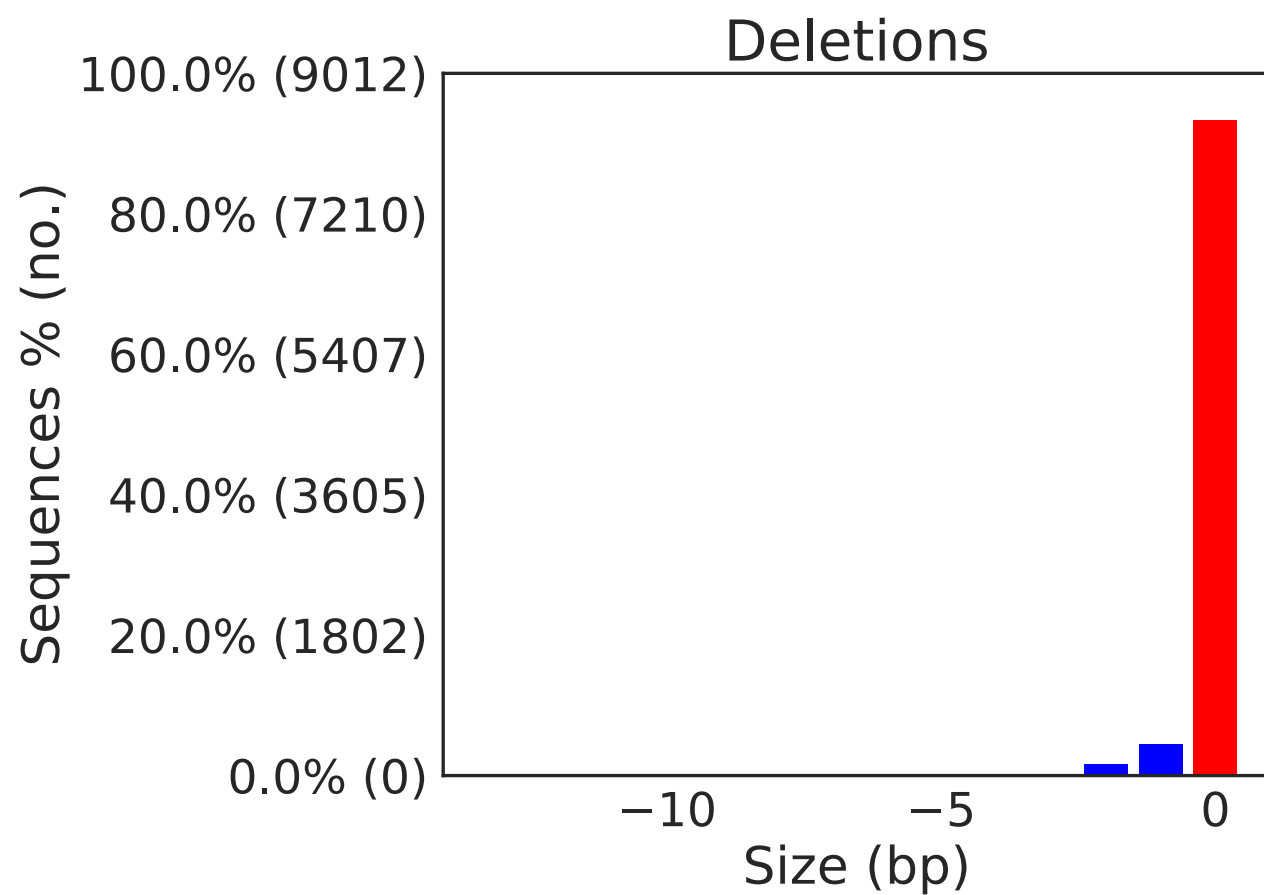
Tmc^{Bth/WT}, HypaCas9 + gRNA 1.1, Bth allele

bold Substitutions
 Insertions
 - Deletions
 - - - Predicted cleavage position

A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	G	G	G	G	A	A	G	T	T	C	T	G	T	C	C	C	A	C	C	C	T	G	T	Reference	
A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	G	G	G	G	A	A	G	T	T	C	T	G	T	C	C	C	A	C	C	C	T	G	T	84.94% (7655 reads)	
A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	-	G	G	G	A	A	G	T	T	C	T	G	T	C	C	C	A	C	C	C	T	G	T	4.59% (414 reads)	
A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	G	G	G	-	A	A	G	T	T	C	T	G	T	C	C	C	A	C	C	C	T	G	T	4.25% (383 reads)	
A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	G	G	G	-	-	A	A	G	T	T	C	T	G	T	C	C	C	A	C	C	C	T	G	T	1.20% (108 reads)
A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	-	-	G	G	A	A	G	T	T	C	T	G	T	C	C	C	A	C	C	C	T	G	T	0.22% (20 reads)	



█ Insertion
█ Non-insertion

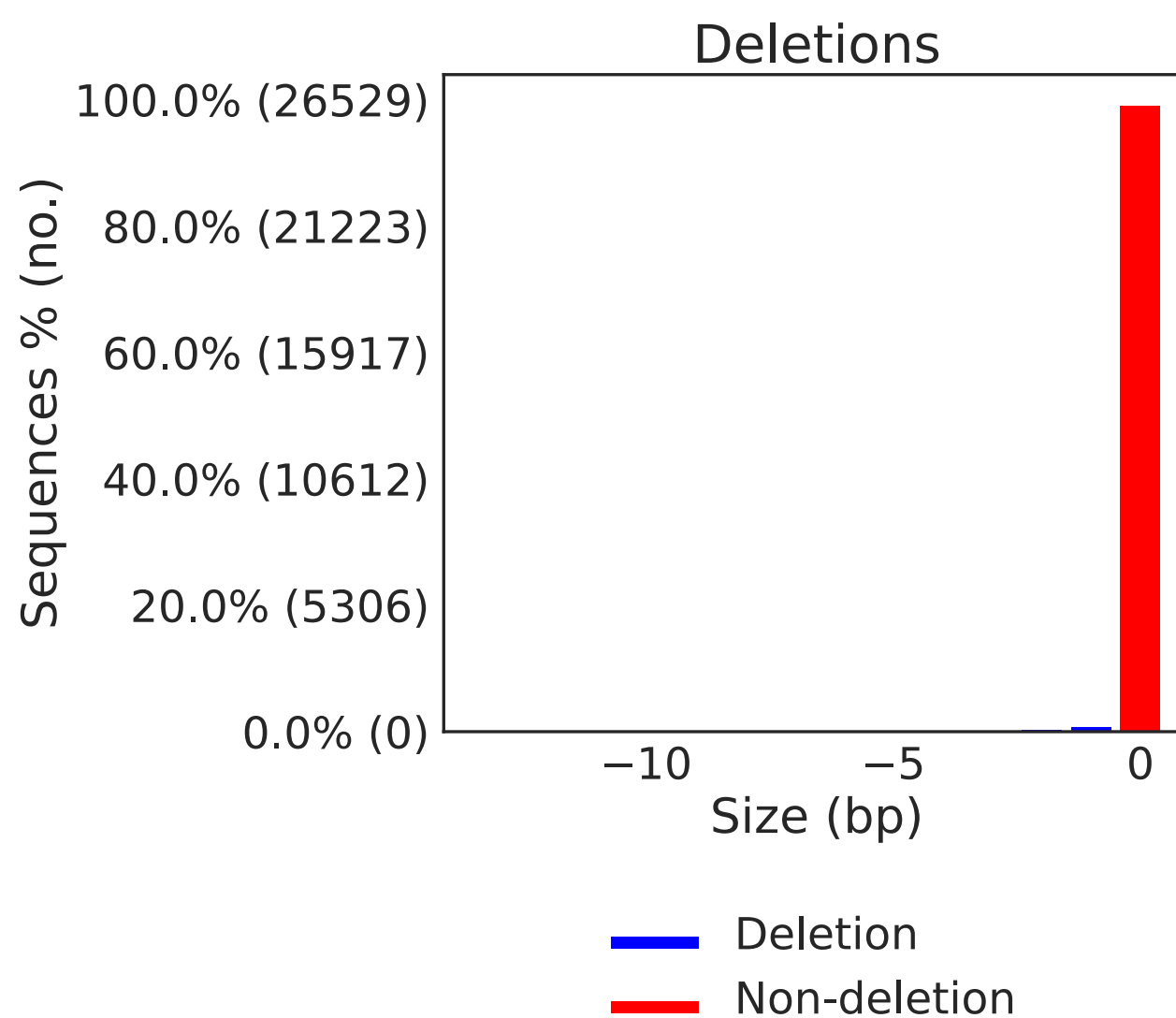
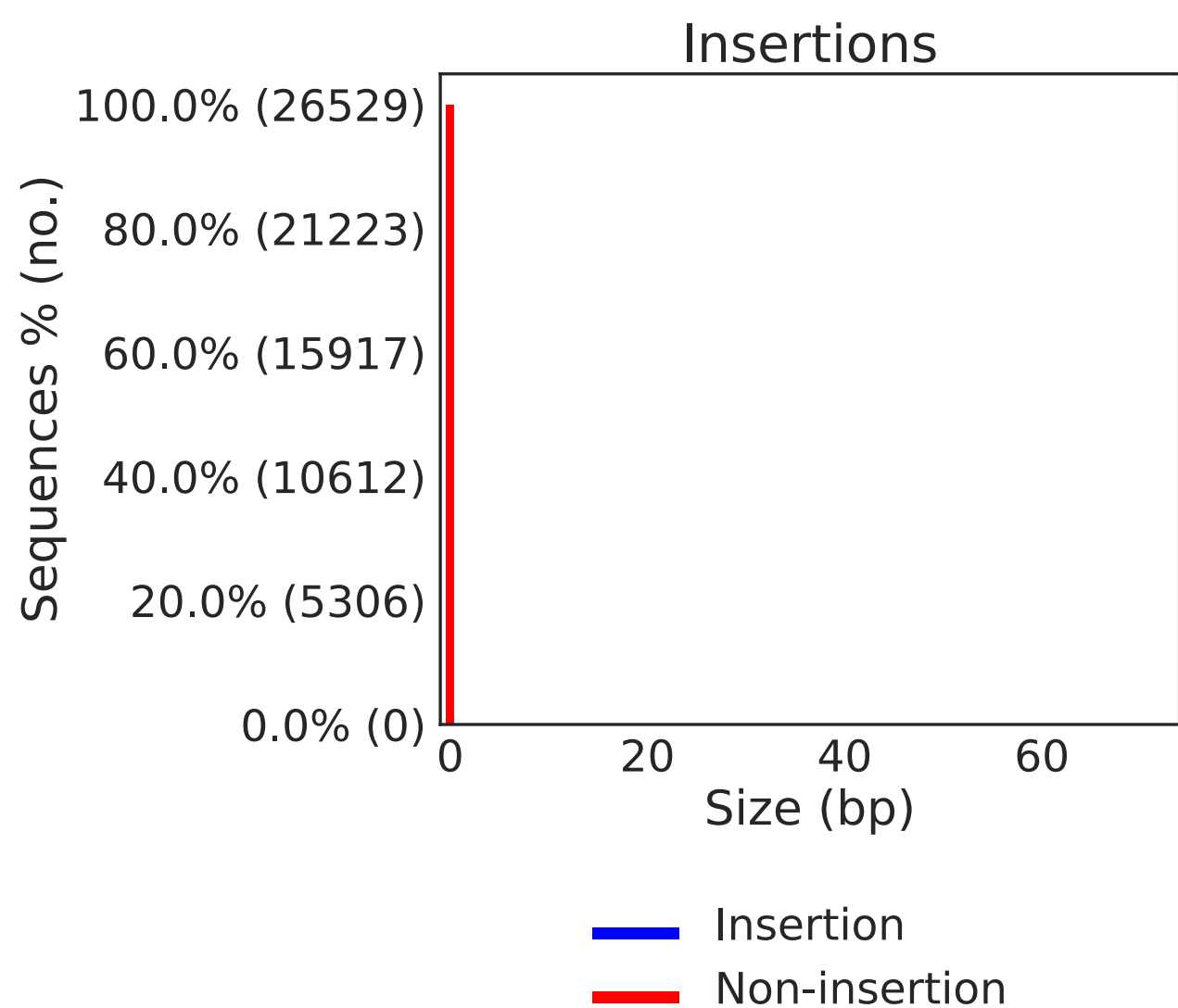


█ Deletion
█ Non-deletion

Tmc^{Bth/WT}, HypaCas9 + gRNA 1.1, WT allele

bold Substitutions
 Insertions
 - Deletions
 - - - Predicted cleavage position

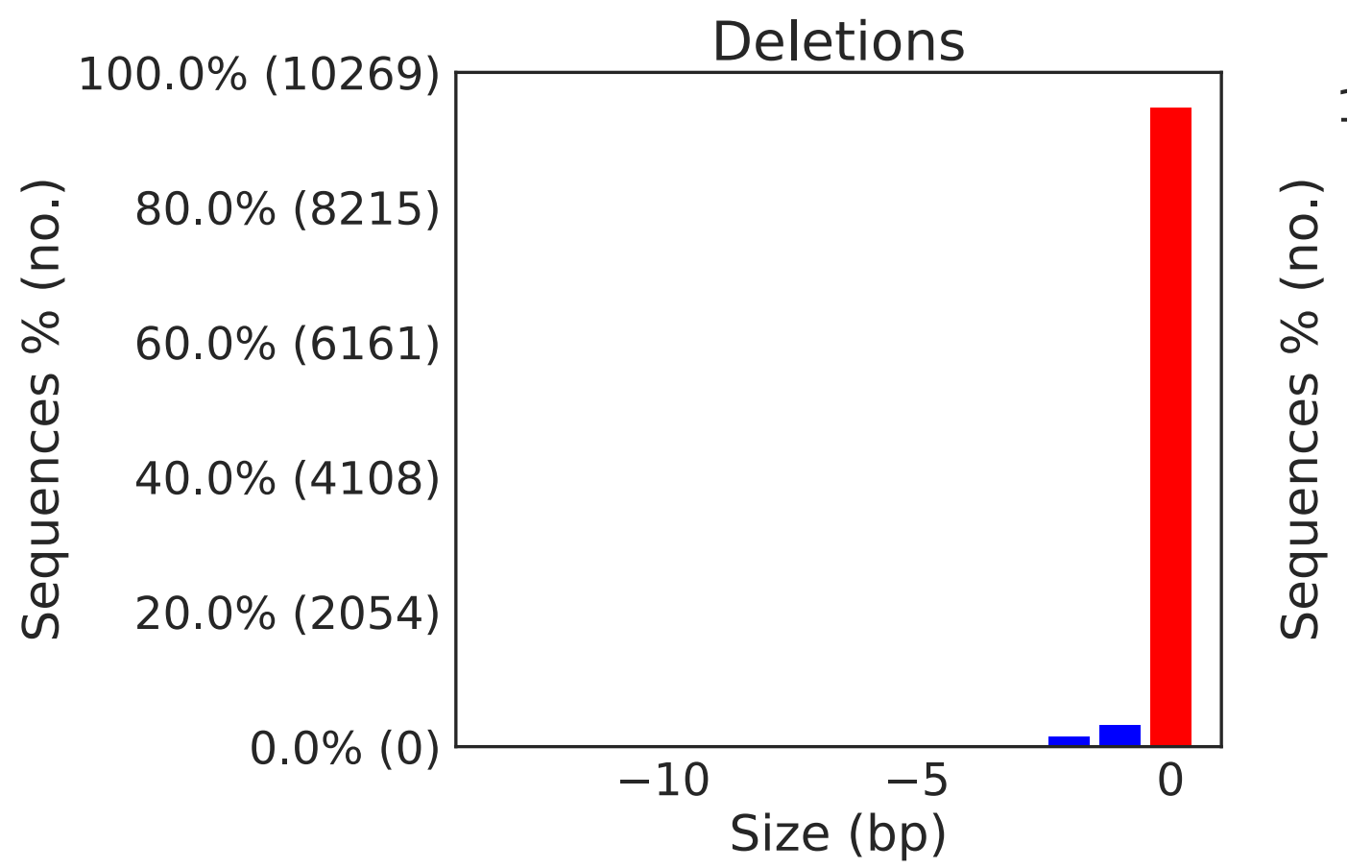
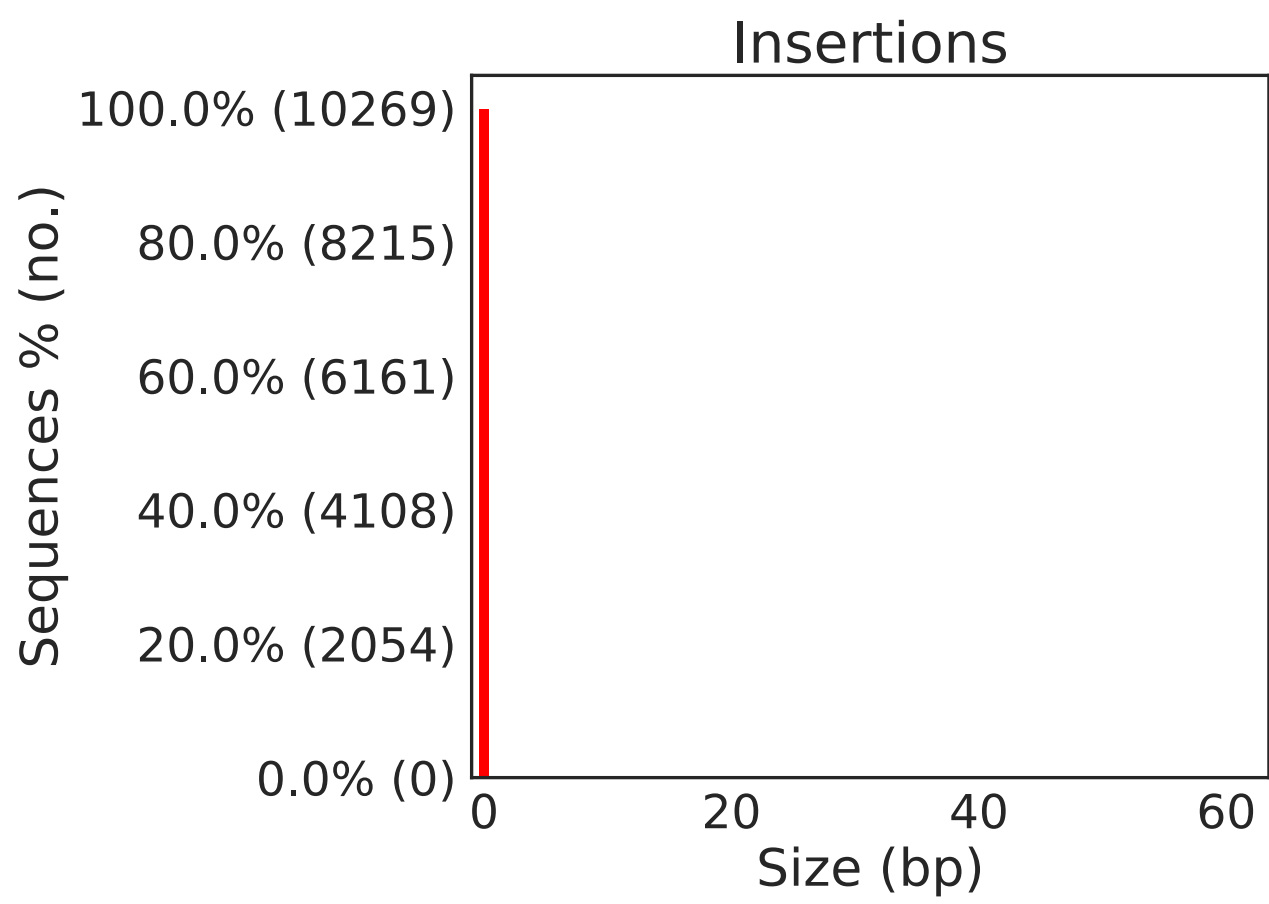
A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	G	G	G	G	A	A	G	T	T	C	T	G	T	C	C	C	A	C	C	C	T	G	T	Reference
A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	G	G	G	G	A	T	G	T	T	C	T	G	T	C	C	C	A	C	C	C	T	G	T	94.72% (25129 reads)
A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	G	G	G	G	A	T	G	T	T	C	T	G	T	C	C	C	A	C	C	C	T	G	T	0.64% (169 reads)
A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	-	G	G	G	A	T	G	T	T	C	T	G	T	C	C	C	A	C	C	C	T	G	T	0.62% (164 reads)



Tmc^{Bth/WT}, SpCas9-HF1 + gRNA 1.1, Bth allele

bold Substitutions
 Insertions
 - Deletions
 - - - Predicted cleavage position

A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	G	G	G	G	A	A	G	T	T	C	T	G	T	C	C	C	A	C	C	C	T	G	T	Reference
A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	G	G	G	G	A	A	G	T	T	C	T	G	T	C	C	C	A	C	C	C	T	G	T	87.66% (9002 reads)
A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	-	G	G	G	A	A	G	T	T	C	T	G	T	C	C	C	A	C	C	C	T	G	T	3.51% (360 reads)
A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	G	G	G	-	A	A	G	T	T	C	T	G	T	C	C	C	A	C	C	C	T	G	T	3.22% (331 reads)
A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	G	G	G	-	-	A	G	T	T	C	T	G	T	C	C	C	A	C	C	C	T	G	T	0.96% (99 reads)
A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	G	G	-	-	A	A	G	T	T	C	T	G	T	C	C	C	A	C	C	C	T	G	T	0.21% (22 reads)
A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	-	-	G	G	A	A	G	T	T	C	T	G	T	C	C	C	A	C	C	C	T	G	T	0.20% (21 reads)



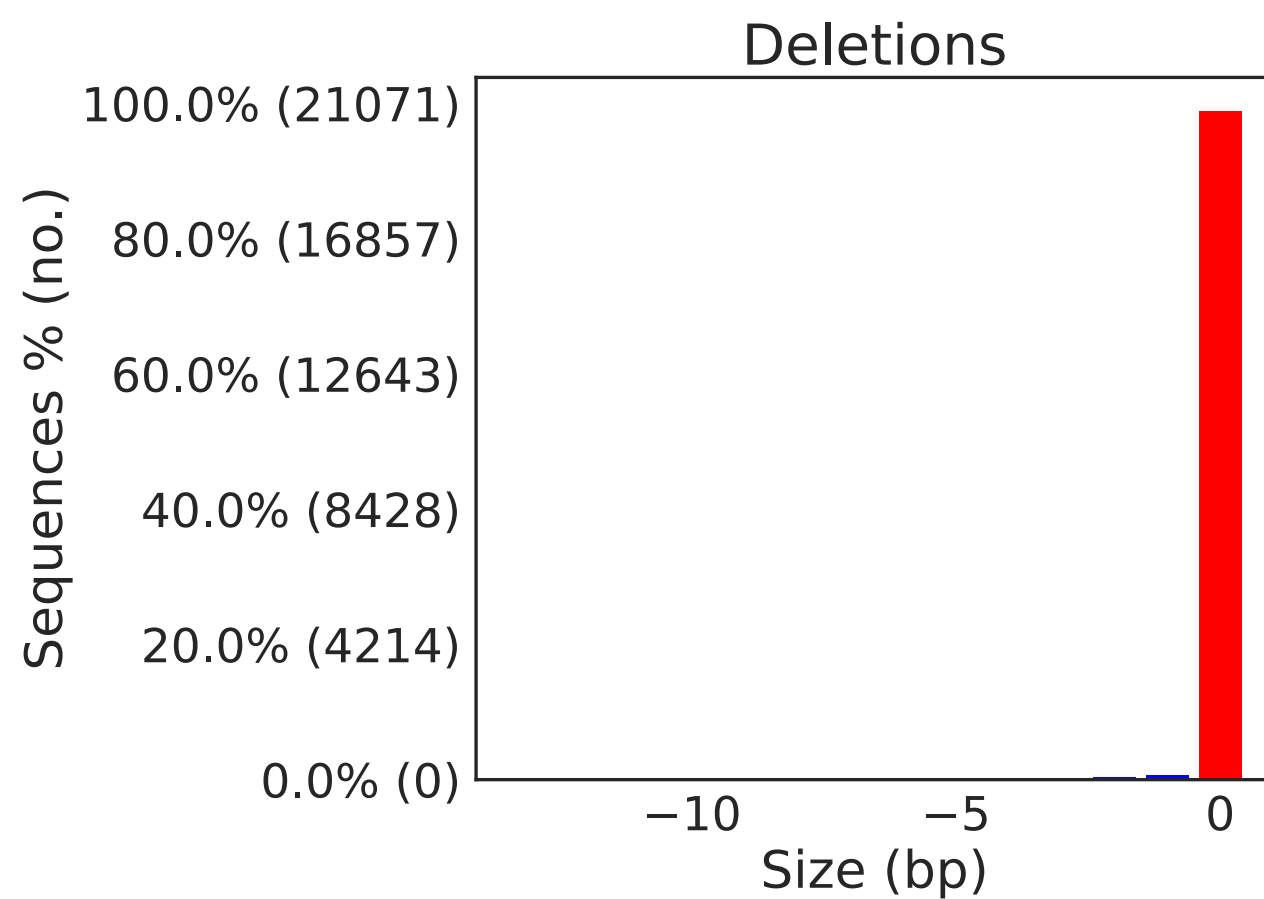
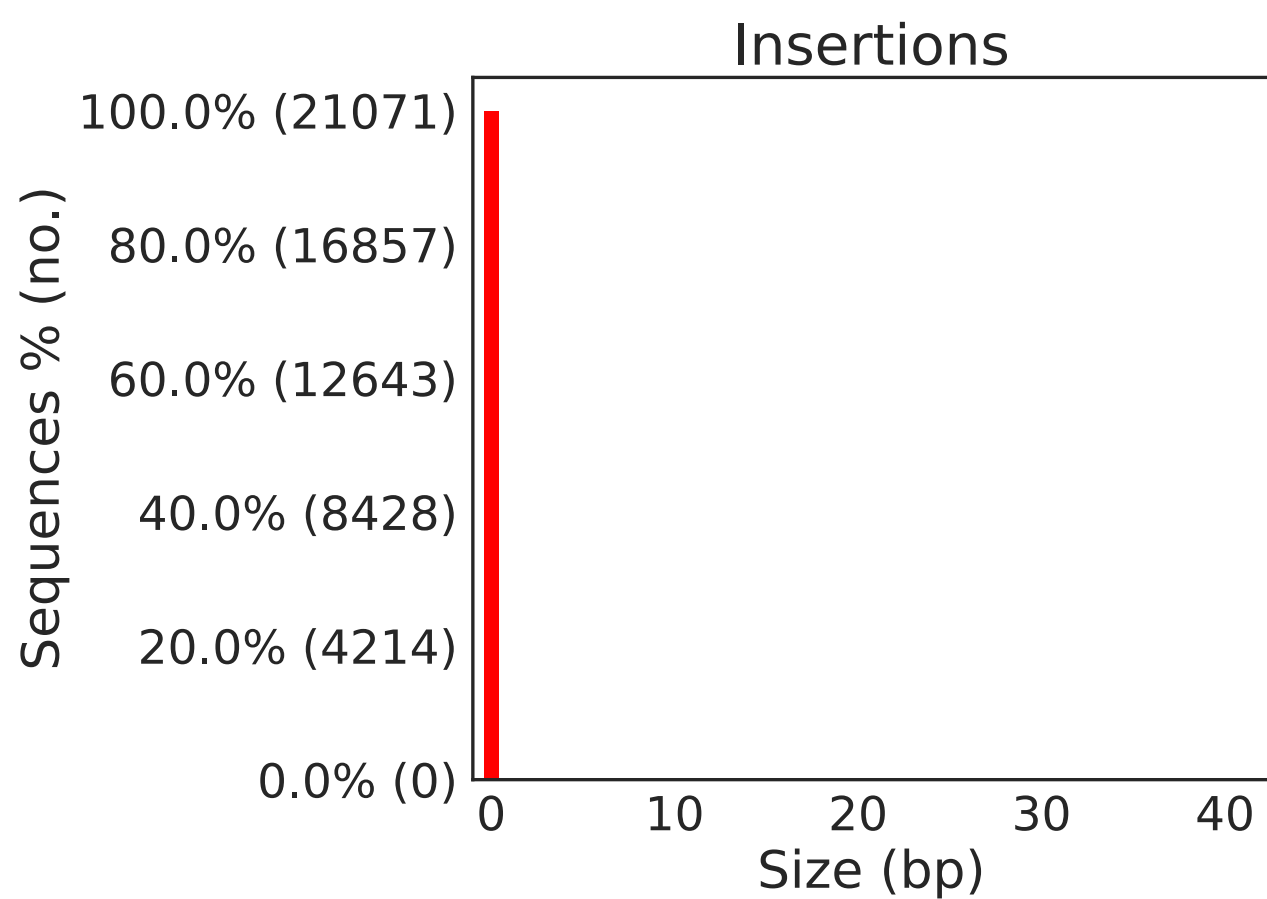
█ Insertion
█ Non-insertion

█ Deletion
█ Non-deletion

Tmc^{Bth/WT}, SpCas9-HF1 + gRNA 1.1, WT allele

bold Substitutions
 Insertions
 - Deletions
 - - - Predicted cleavage position

A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	G	G	G	G	A	A	G	T	T	C	T	G	T	C	C	C	A	C	C	C	T	G	T	Reference	
A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	G	G	G	G	G	A	A	G	T	T	C	T	G	T	C	C	C	A	C	C	C	T	G	T	94.96% (20010 reads)
A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	G	G	G	G	G	A	A	G	T	T	C	T	G	T	C	C	C	A	C	C	C	T	G	T	0.66% (140 reads)
A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	G	G	G	G	G	A	A	G	T	T	C	T	G	T	C	C	C	A	C	C	C	T	G	T	0.64% (135 reads)



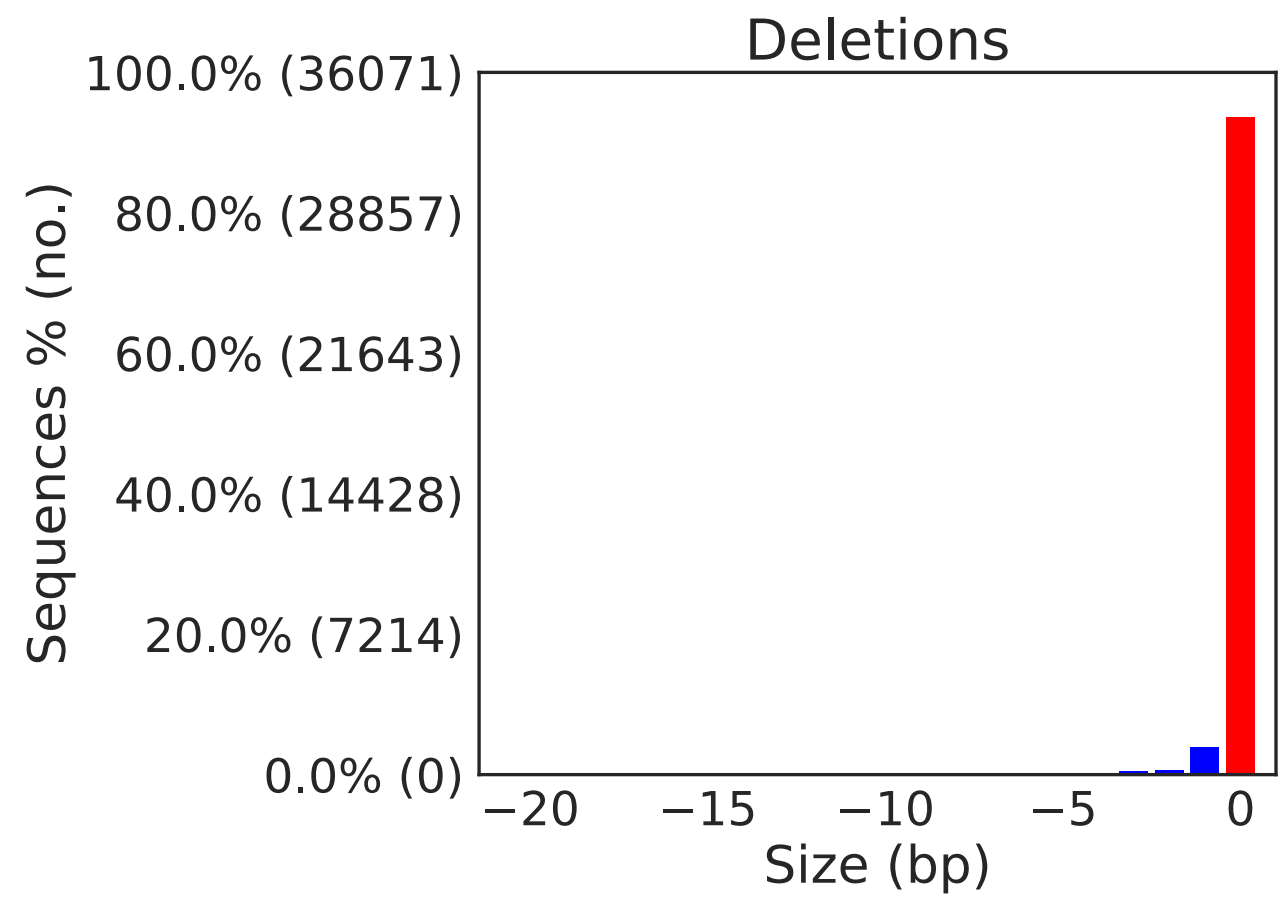
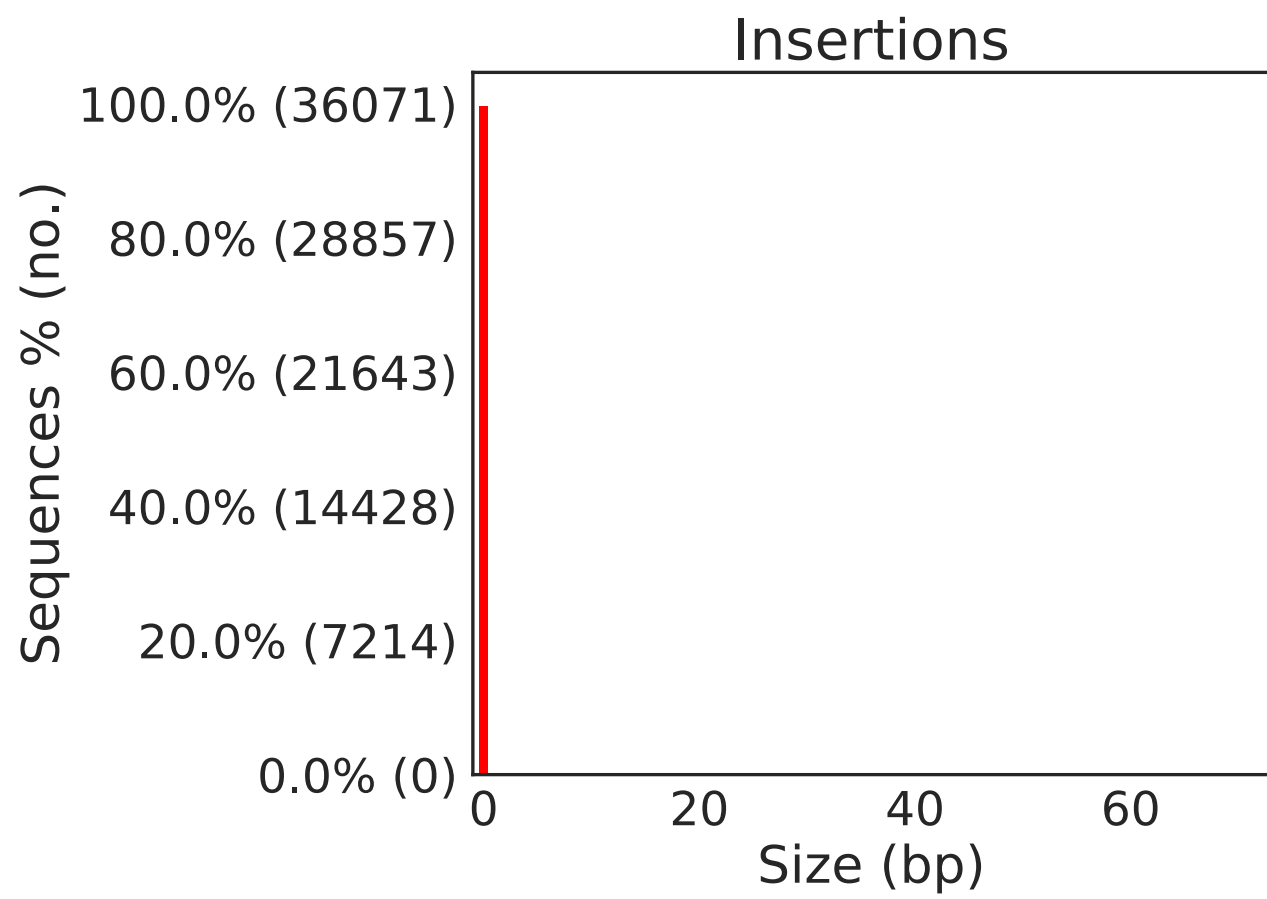
— Insertion
— Non-insertion

— Deletion
— Non-deletion

Tmc^{Bth/WT}, SaCas9^{KKH} + gRNA 4.1, Bth allele

bold Substitutions
 Insertions
 - Deletions
 - - - Predicted cleavage position

G	A	A	C	A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	G	G	G	G	A	A	G	T	T	C	T	G	T	C	C	C	A	C	C	Reference
G	A	A	C	A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	G	G	G	G	A	A	G	T	T	C	T	G	T	C	C	C	A	C	C	91.17% (32886 reads)
G	A	A	C	A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	-	G	G	G	G	A	A	G	T	T	C	T	G	T	C	C	C	A	C	C	2.90% (1047 reads)
G	A	A	C	A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	-	T	G	G	G	G	A	A	G	T	T	C	T	G	T	C	C	C	A	C	C	0.45% (161 reads)
G	A	A	C	A	T	G	G	T	A	A	T	G	T	C	C	C	T	-	C	T	G	G	G	G	A	A	G	T	T	C	T	G	T	C	C	C	A	C	C	0.44% (159 reads)
G	A	A	C	A	T	G	G	T	A	A	T	G	T	C	C	C	T	-	-	-	G	G	G	G	A	A	G	T	T	C	T	G	T	C	C	C	A	C	C	0.42% (150 reads)
G	A	A	C	A	T	G	G	T	A	A	T	G	T	C	-	-	-	C	C	T	G	G	G	G	A	A	G	T	T	C	T	G	T	C	C	C	A	C	C	0.39% (142 reads)
G	A	A	C	A	T	G	G	T	A	A	T	G	T	C	C	C	T	-	-	T	G	G	G	G	A	A	G	T	T	C	T	G	T	C	C	C	A	C	C	0.27% (98 reads)
G	A	A	C	A	T	G	G	T	A	A	T	G	T	C	C	C	T	-	-	-	G	G	G	G	A	A	G	T	T	C	T	G	T	C	C	C	A	C	C	0.24% (86 reads)



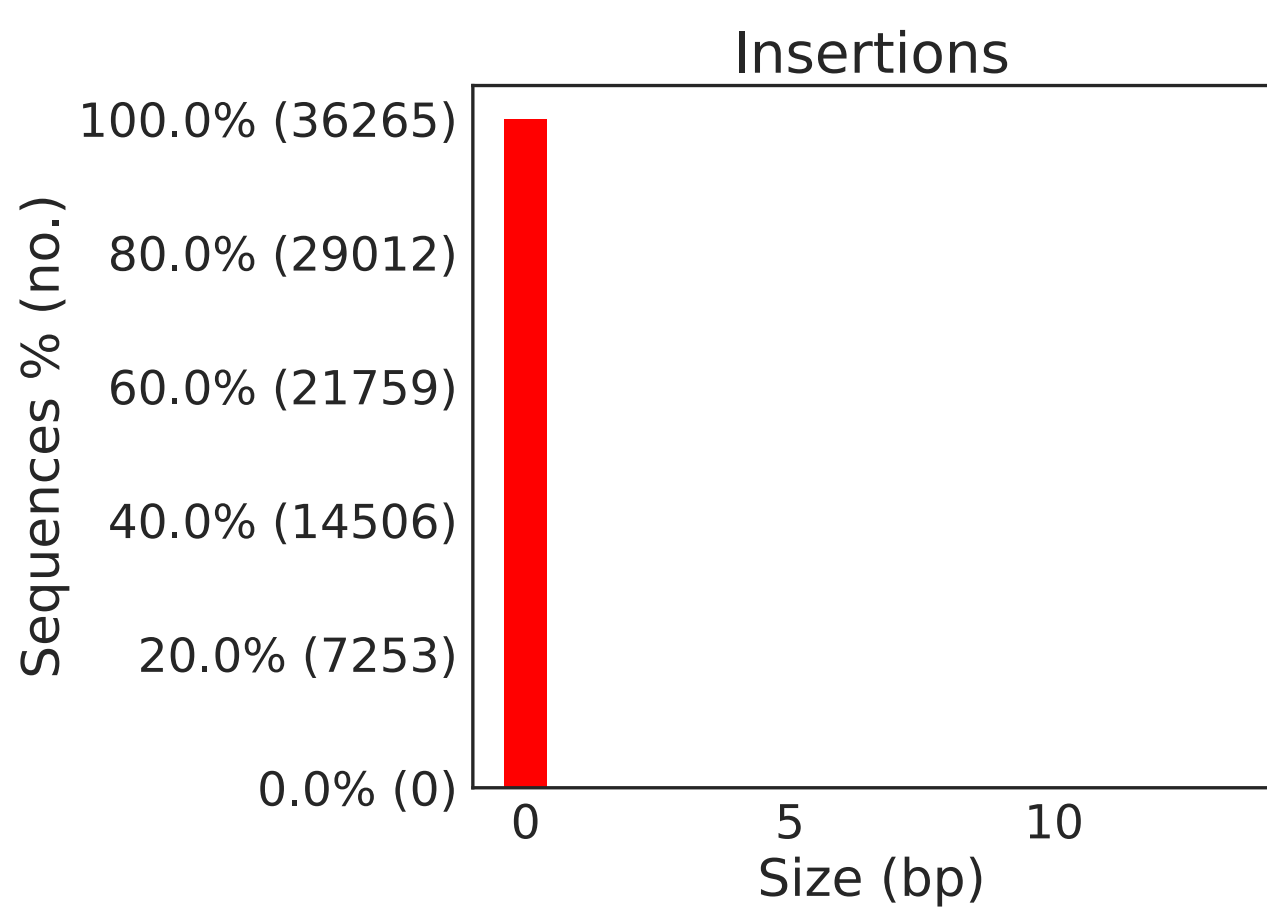
█ Insertion
█ Non-insertion

█ Deletion
█ Non-deletion

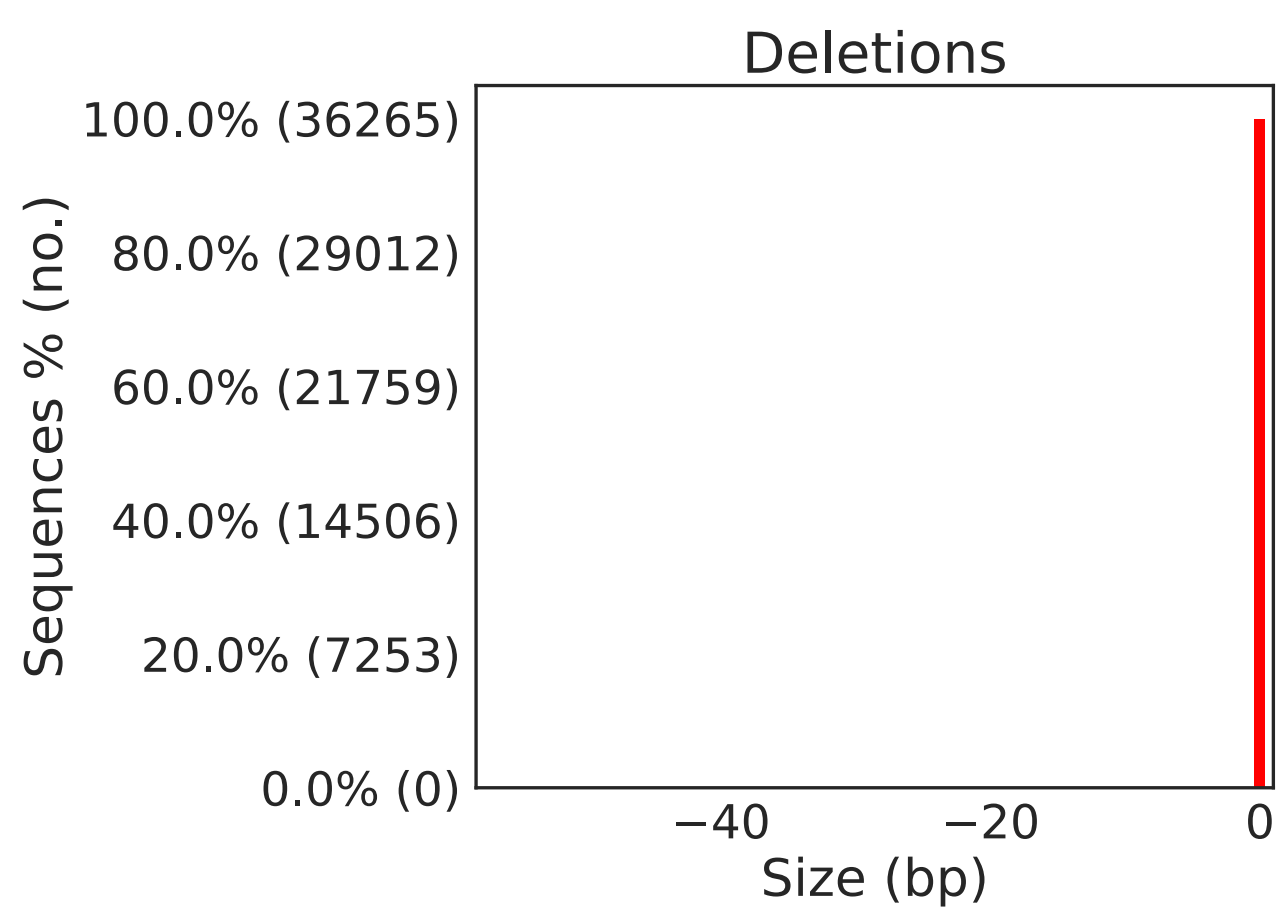
Tmc^{Bth/WT}, SaCas9^{KKH} + gRNA 4.1, WT allele

bold Substitutions
 Insertions
 - Deletions
 - - - Predicted cleavage position

G A A C A T G G T A A T G T C C C T C C T G G G G A A G T T C T G T C C C A C C Reference
 G A A C A T G G T A A T G T C C C T C C **T** G G G G A **T** G T T C T G T C C C A C C 98.31% (35652 reads)



Insertion
 Non-insertion

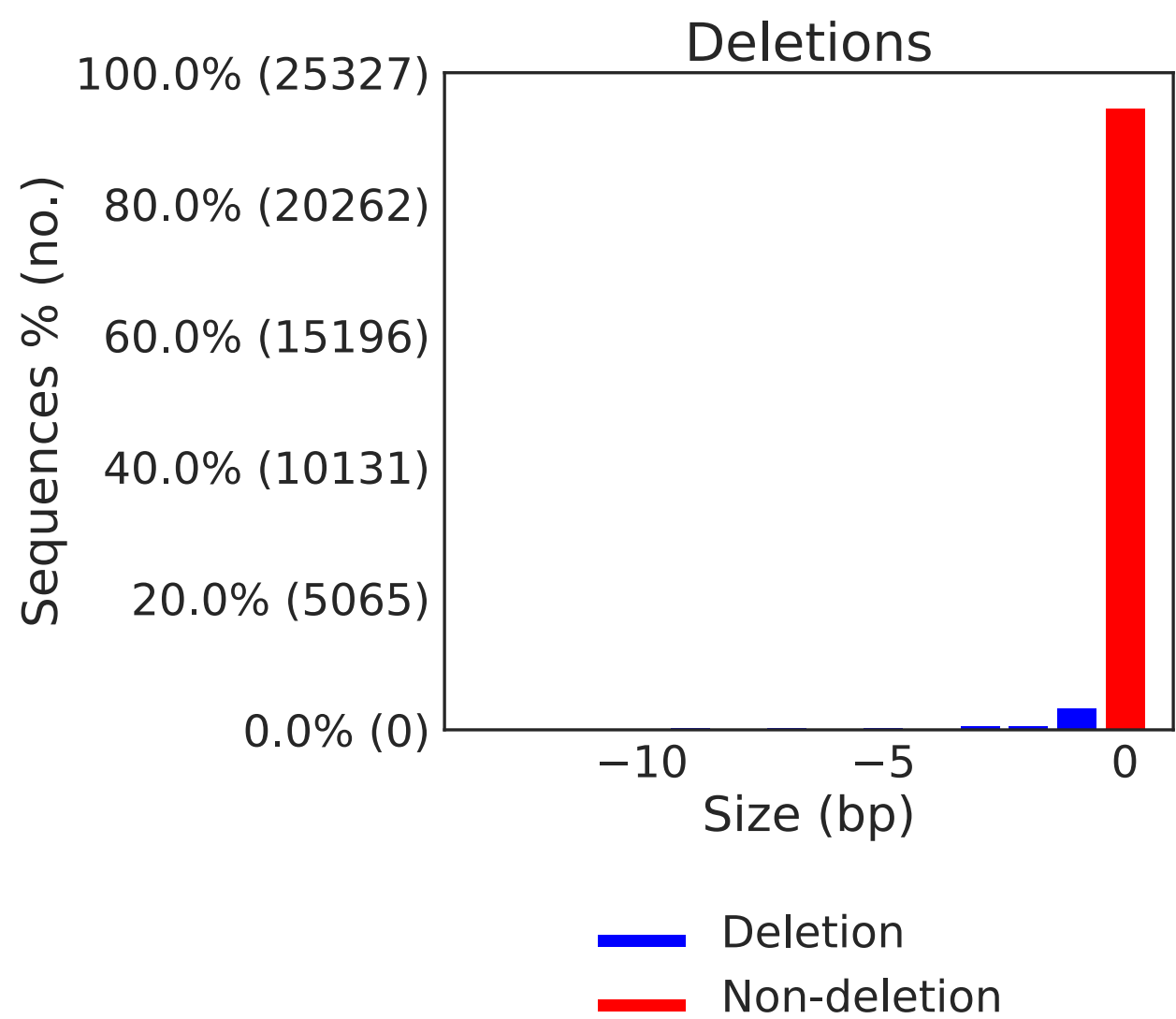
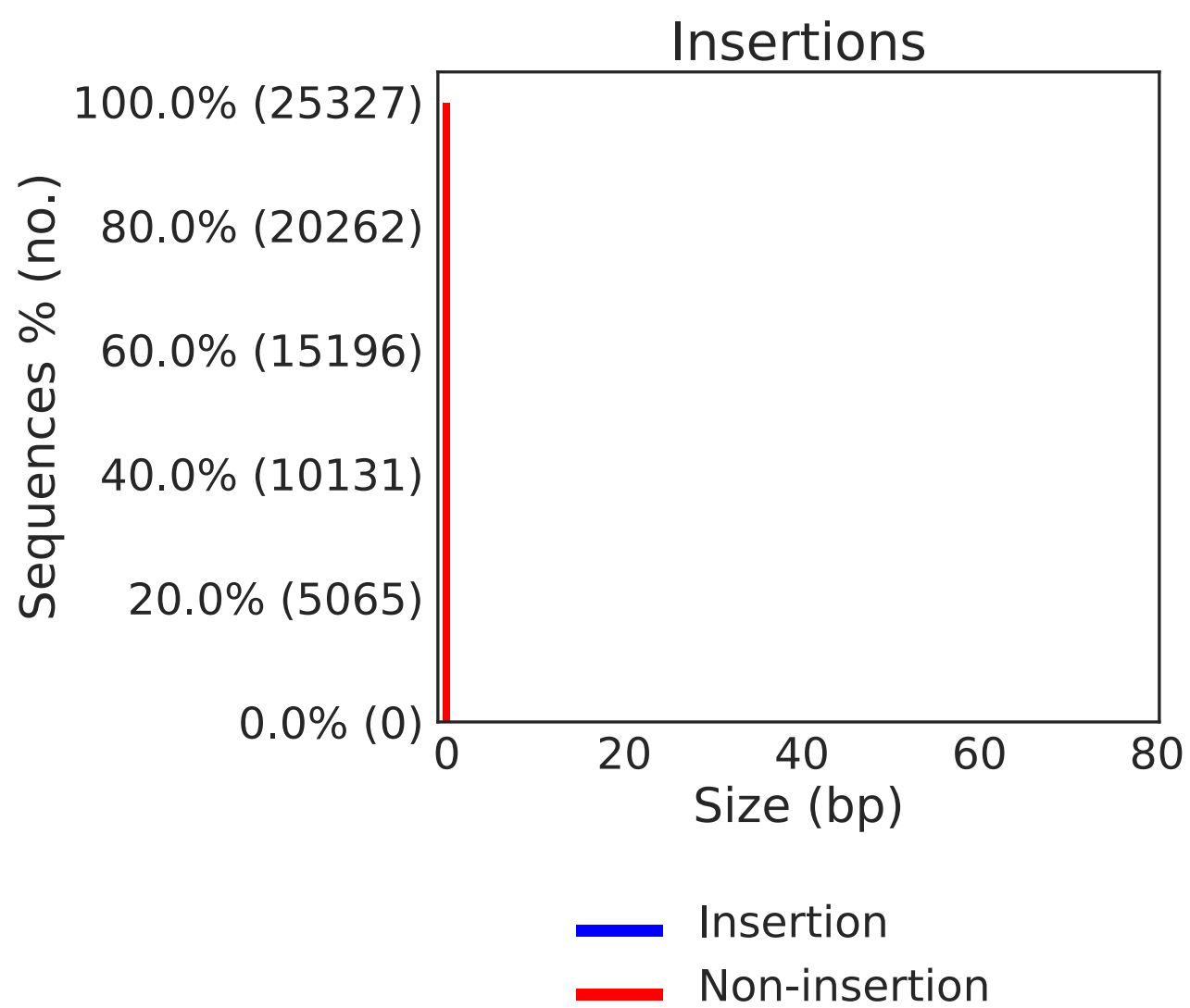


Deletion
 Non-deletion

Tmc^{Bth/WT}, SpCas9^{KKH} + gRNA 4.2, Bth allele

bold Substitutions
 Insertions
 - Deletions
 - - - Predicted cleavage position

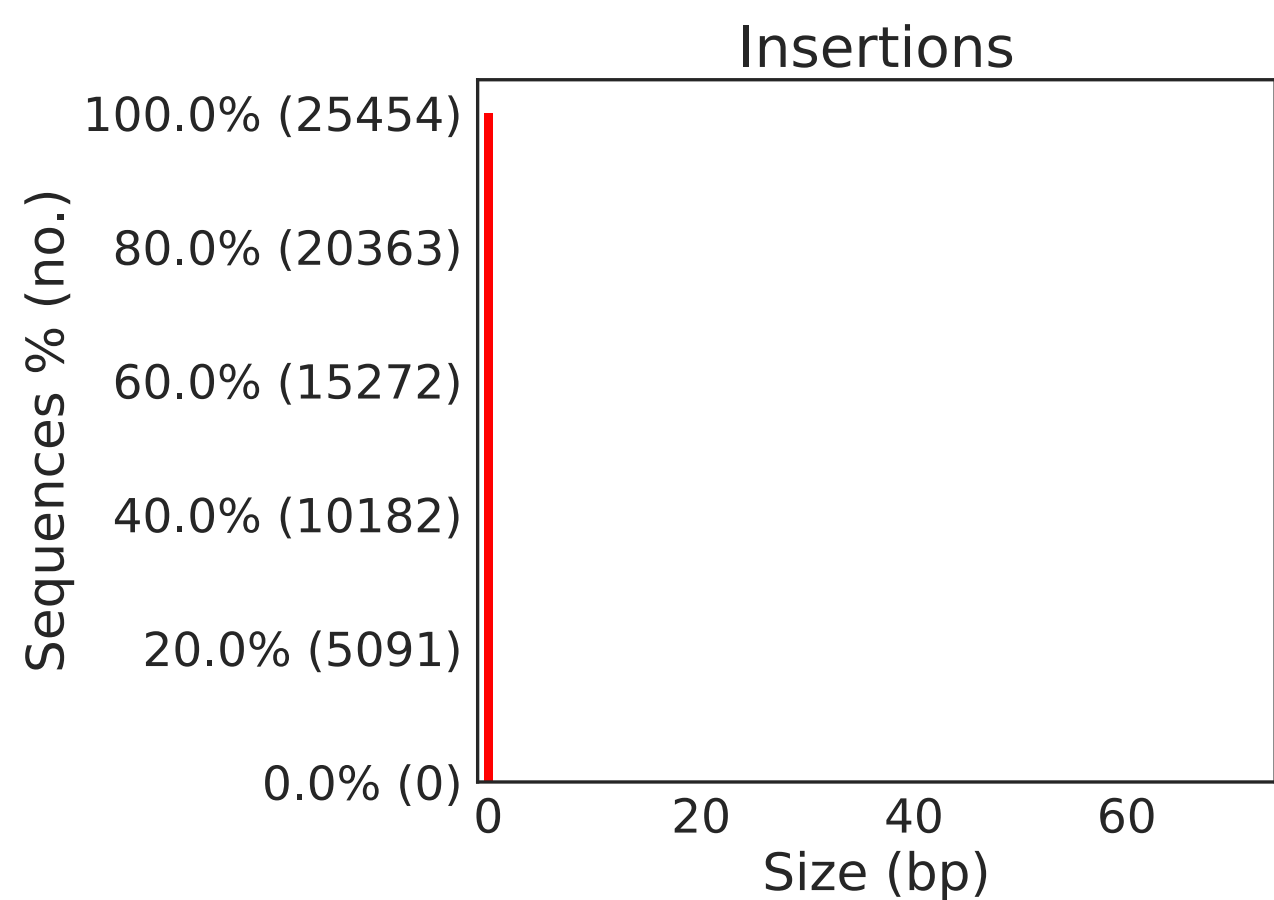
G	A	A	C	A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	G	G	G	G	A	A	G	T	T	C	T	G	T	C	C	C	A	C	C	Reference
G	A	A	C	A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	G	G	G	G	A	A	G	T	T	C	T	G	T	C	C	C	A	C	C	92.13% (23333 reads)
G	A	A	C	A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	-	G	G	G	G	A	A	G	T	T	C	T	G	T	C	C	C	A	C	C	2.40% (609 reads)
G	A	A	C	A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	-	T	G	G	G	G	A	A	G	T	T	C	T	G	T	C	C	C	A	C	C	0.40% (102 reads)
G	A	A	C	A	T	G	G	T	A	A	T	G	T	C	C	C	T	-	-	-	G	G	G	G	A	A	G	T	T	C	T	G	T	C	C	C	A	C	C	0.38% (95 reads)
G	A	A	C	A	T	G	G	T	A	A	T	G	T	C	C	C	T	-	C	T	G	G	G	G	A	A	G	T	T	C	T	G	T	C	C	C	A	C	C	0.33% (83 reads)
G	A	A	C	A	T	G	G	T	A	A	T	G	T	C	-	-	-	C	C	T	G	G	G	G	A	A	G	T	T	C	T	G	T	C	C	C	A	C	C	0.31% (79 reads)
G	A	A	C	A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	-	-	G	G	G	A	A	G	T	T	C	T	G	T	C	C	C	A	C	C	0.25% (63 reads)
G	A	A	C	A	T	G	G	T	A	A	T	G	T	C	C	C	T	-	-	T	G	G	G	G	A	A	G	T	T	C	T	G	T	C	C	C	A	C	C	0.23% (58 reads)



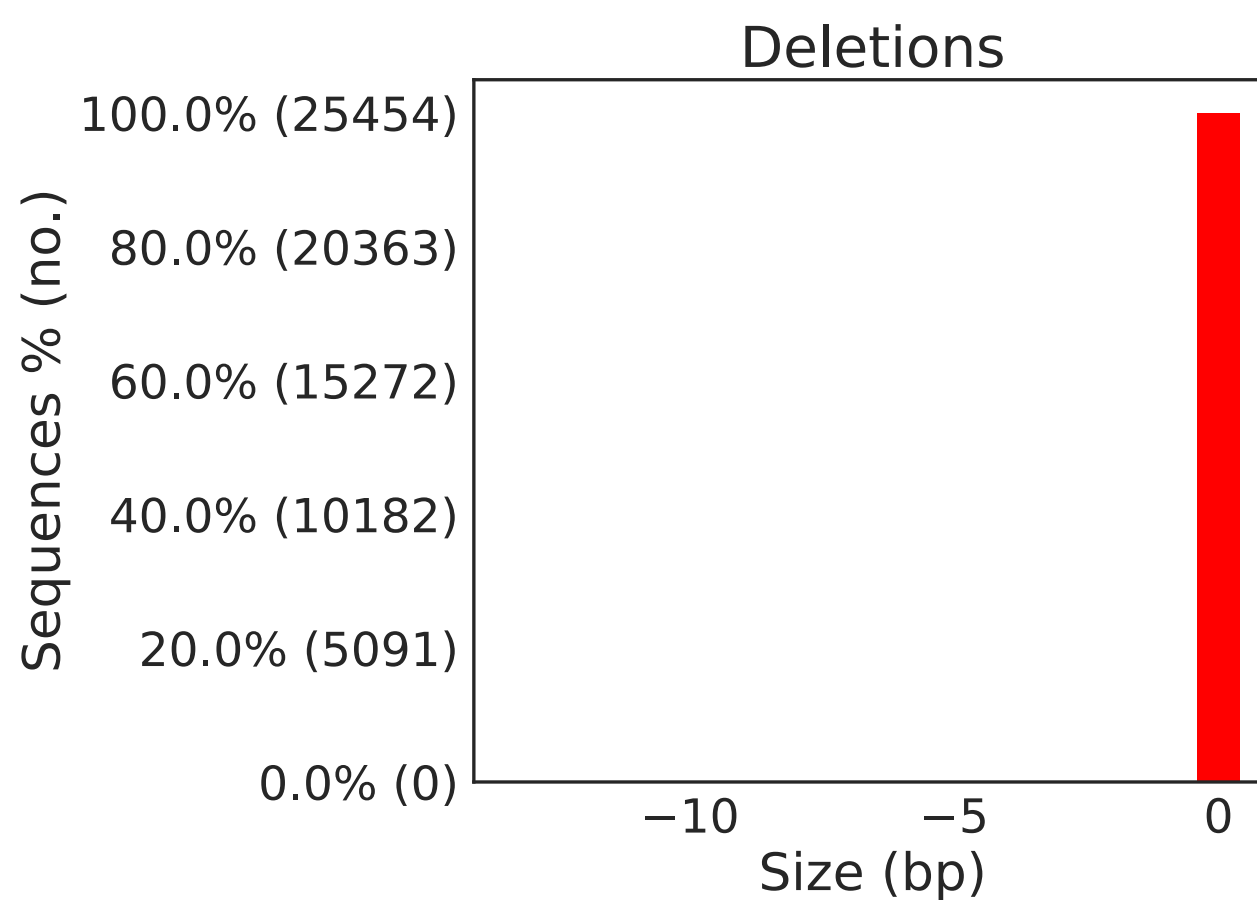
Tmc^{Bth/WT}, SaCas9^{KKH} + gRNA 4.2, WT allele

bold Substitutions
 Insertions
 - Deletions
 - - - Predicted cleavage position

G A A C A T G G T A A T G T C C C T C C T G G G G A A G T T C T G T C C C A C C Reference
 G A A C A T G G T A A T G T C C C T C C **T** G G G G A **T** G T T C T G T C C C A C C 98.20% (24996 reads)



— Insertion
— Non-insertion

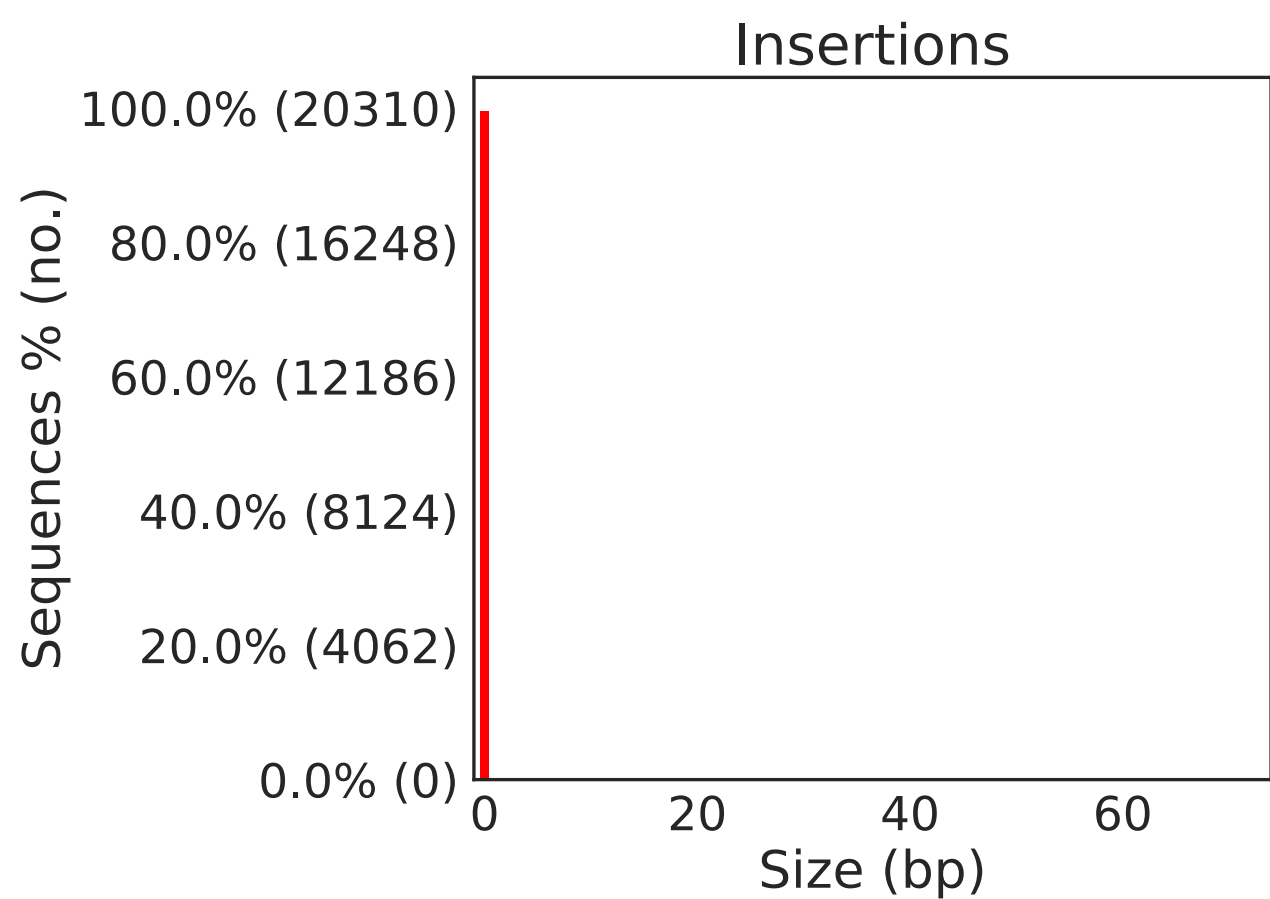


— Deletion
— Non-deletion

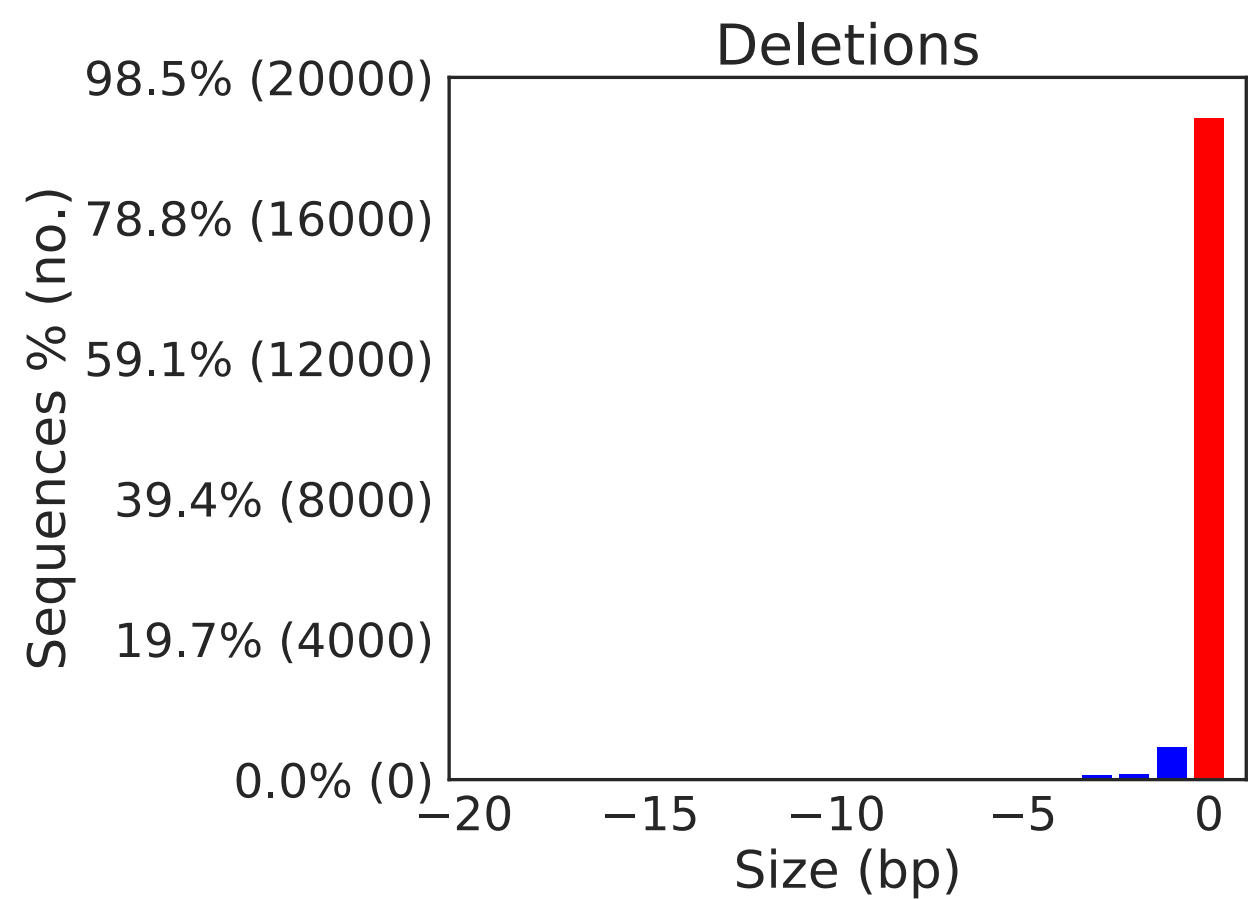
Tmc^{Bth/WT}, SaCas9^{KKH} + gRNA 4.3, Bth allele

bold Substitutions
 Insertions
 - Deletions
 - - - Predicted cleavage position

G	A	A	C	A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	G	G	G	G	A	A	G	T	T	C	T	G	T	C	C	C	A	C	C	Reference
G	A	A	C	A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	G	G	G	G	A	A	G	T	T	C	T	G	T	C	C	C	A	C	C	90.24% (18328 reads)
G	A	A	C	A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	-	G	G	G	G	A	A	G	T	T	C	T	G	T	C	C	C	A	C	C	3.32% (674 reads)
G	A	A	C	A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	-	T	G	G	G	G	A	A	G	T	T	C	T	G	T	C	C	C	A	C	C	0.62% (125 reads)
G	A	A	C	A	T	G	G	T	A	A	T	G	T	C	C	C	T	-	C	T	G	G	G	G	A	A	G	T	T	C	T	G	T	C	C	C	A	C	C	0.51% (104 reads)
G	A	A	C	A	T	G	G	T	A	A	T	G	T	C	C	C	T	-	-	-	G	G	G	G	A	A	G	T	T	C	T	G	T	C	C	C	A	C	C	0.51% (103 reads)
G	A	A	C	A	T	G	G	T	A	A	T	G	T	C	-	-	-	C	C	T	G	G	G	G	A	A	G	T	T	C	T	G	T	C	C	C	A	C	C	0.46% (93 reads)
G	A	A	C	A	T	G	G	T	A	A	T	G	T	C	C	C	T	-	-	T	G	G	G	G	A	A	G	T	T	C	T	G	T	C	C	C	A	C	C	0.40% (81 reads)
G	A	A	C	A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	-	-	G	G	G	A	A	G	T	T	C	T	G	T	C	C	C	A	C	C	0.22% (45 reads)



Insertion
 Non-insertion

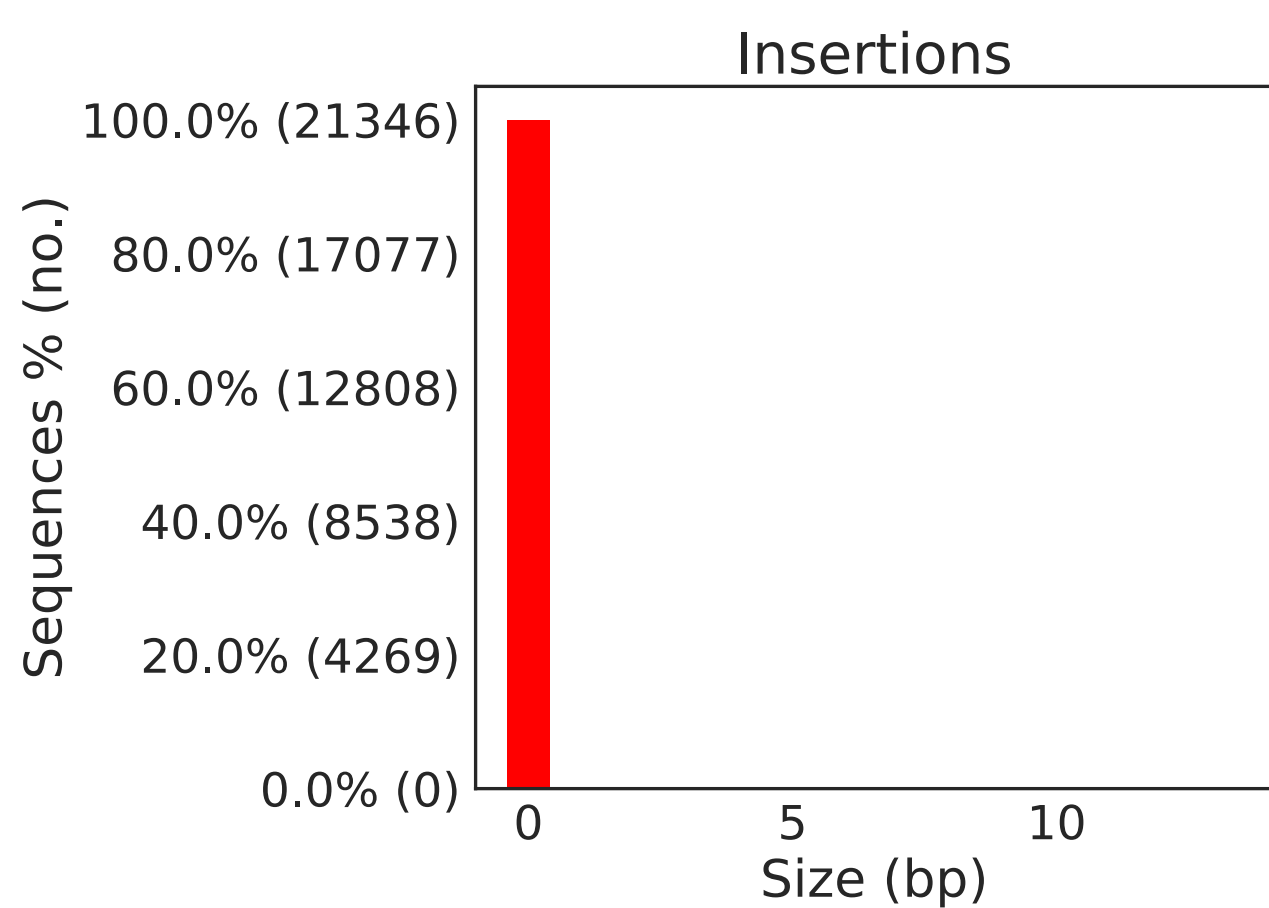


Deletion
 Non-deletion

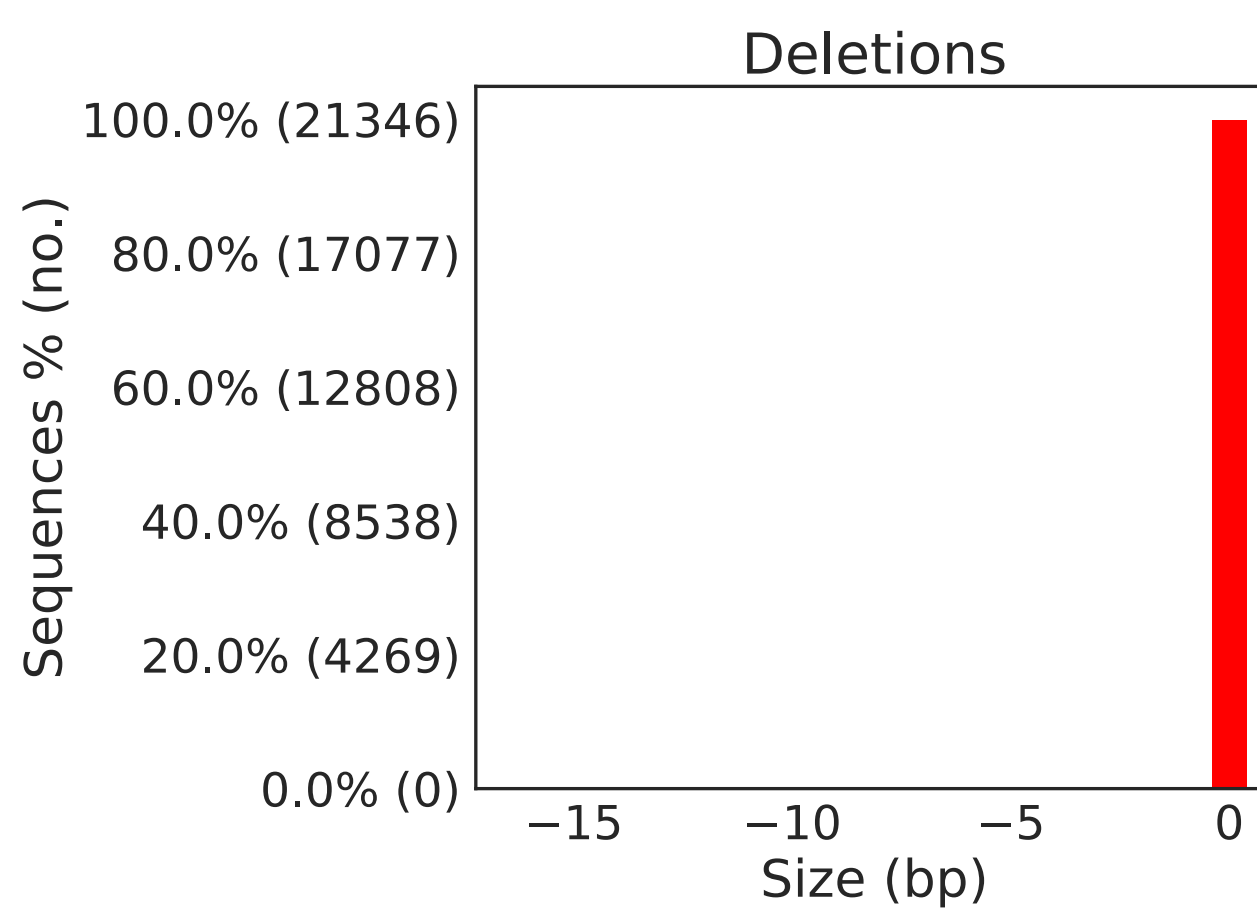
Tmc^{Bth/WT}, SaCas9^{KKH} + gRNA 4.3, WT allele

bold Substitutions
 Insertions
 - Deletions
 - - - Predicted cleavage position

G A A C A T G G T A A T G T C C C T C C T G G G G A A G T T C T G T C C C A C C Reference
 G A A C A T G G T A A T G T C C C T C C **T** G G G G A **T** G T T C T G T C C C A C C 98.14% (20950 reads)



— Insertion
— Non-insertion

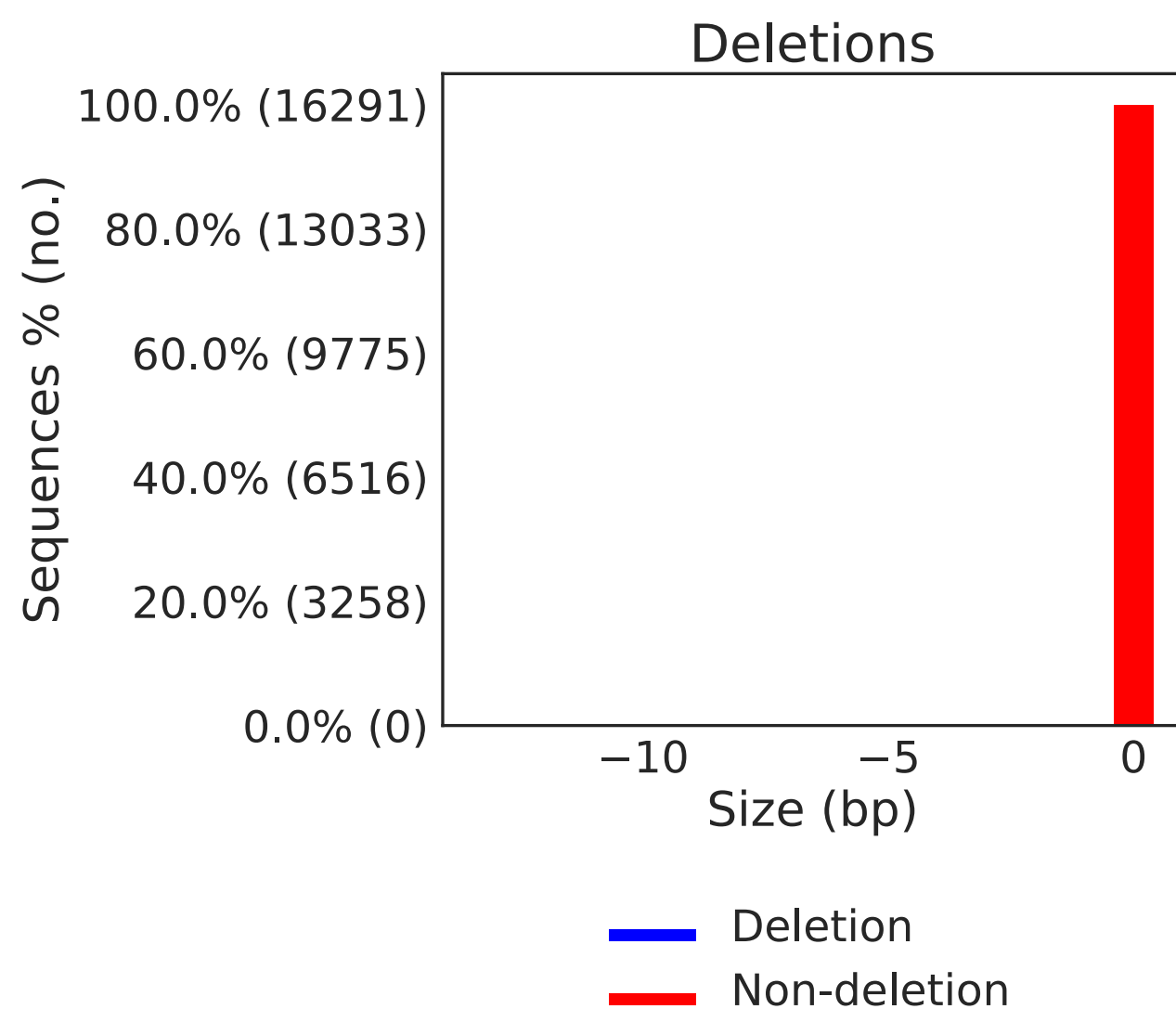
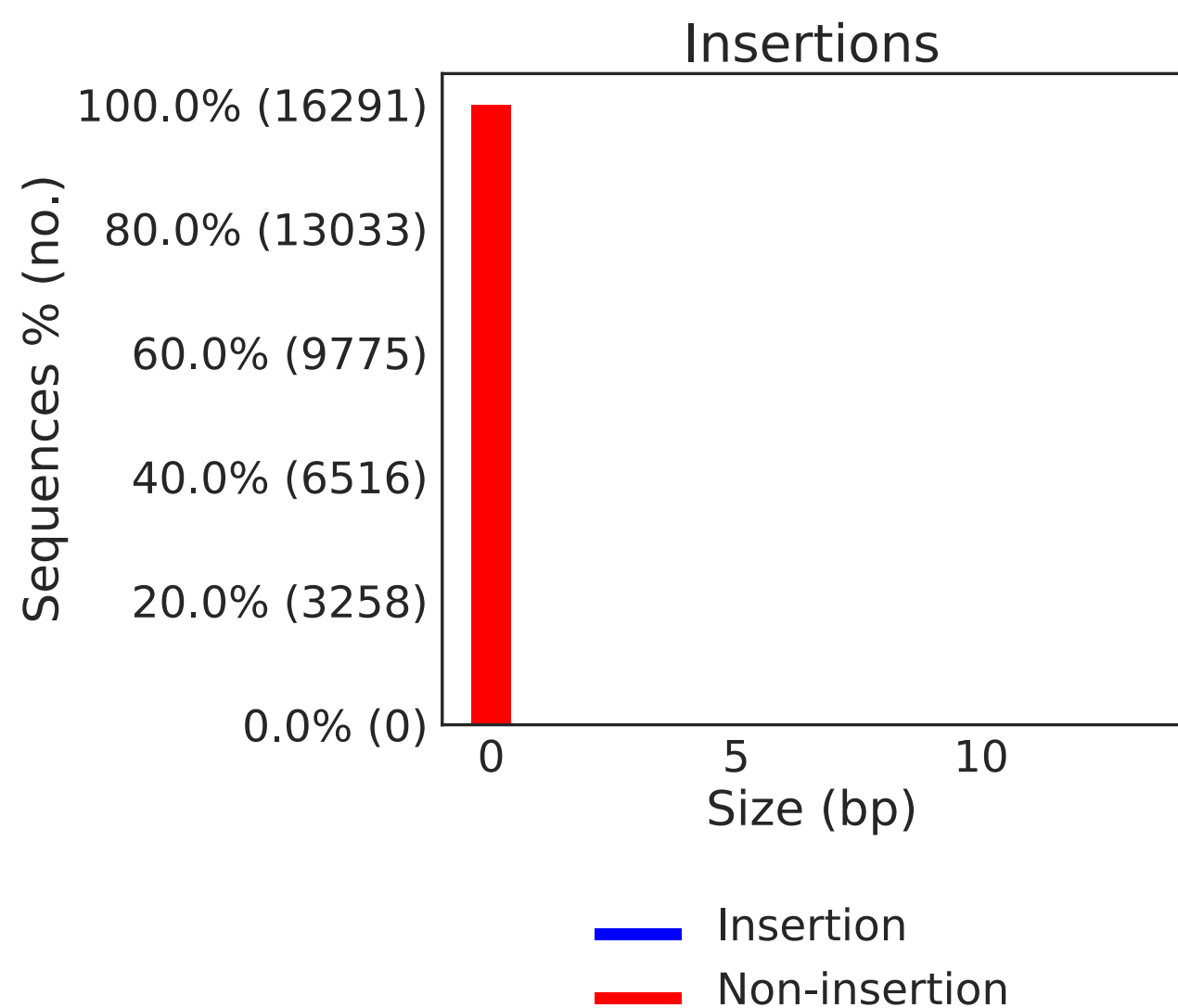


— Deletion
— Non-deletion

Tmc^{WT/WT}, SpCas9 only

bold Substitutions
 Insertions
 - Deletions
 - - - Predicted cleavage position

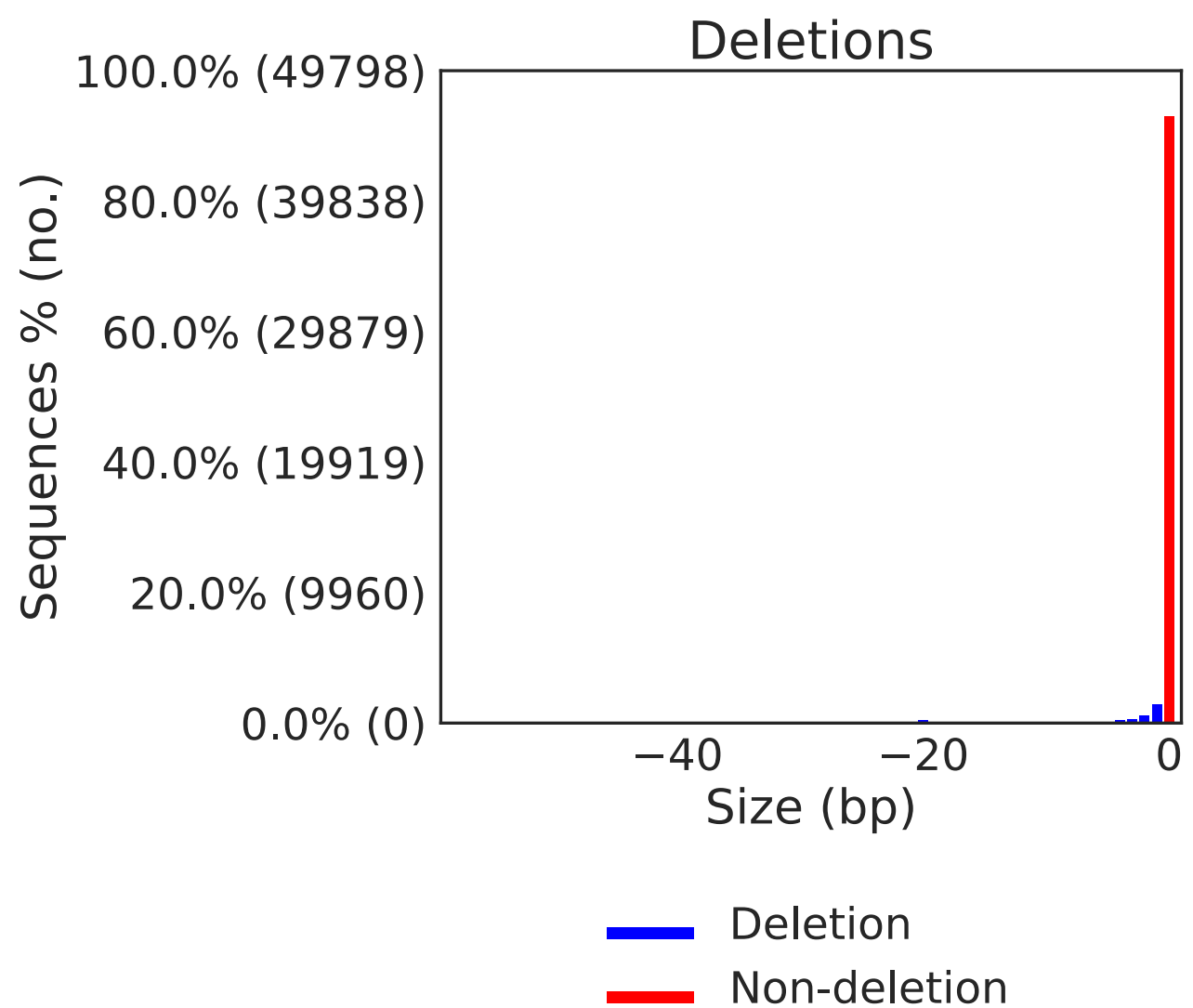
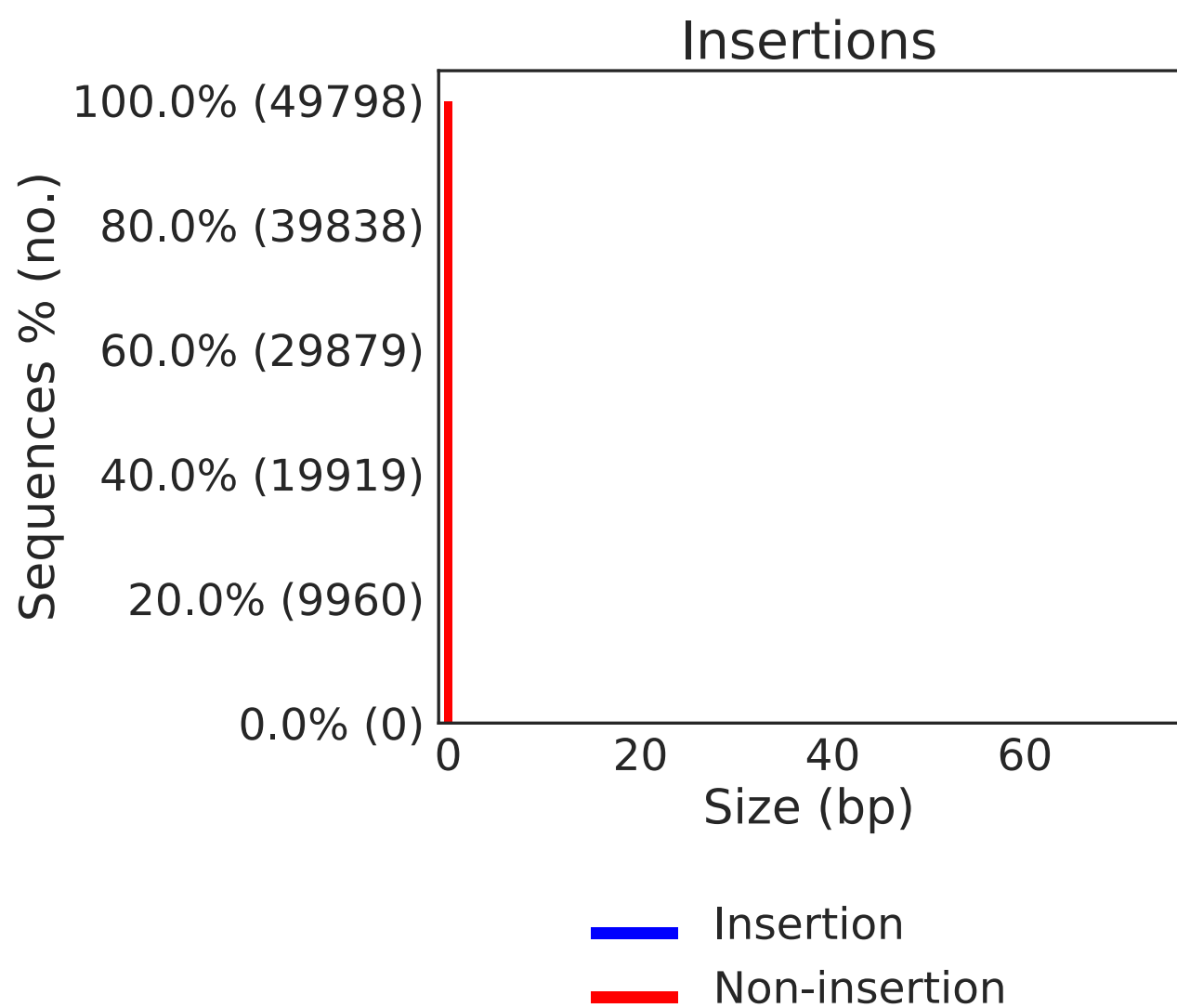
A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	G	G	G	G	A	A	G	T	T	C	T	G	T	C	C	C	A	C	C	C	T	G	T	Reference	
A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	G	G	G	G	G	A	T	G	T	T	C	T	G	T	C	C	C	A	C	C	C	T	G	T	96.81% (15771 reads)
A	T	G	G	A	A	A	T	G	T	C	C	C	T	C	C	T	G	G	G	G	G	A	T	G	T	T	C	T	G	T	C	C	C	A	C	C	C	T	G	T	0.48% (78 reads)
A	T	G	G	C	A	A	T	G	T	C	C	C	T	C	C	T	G	G	G	G	G	A	T	G	T	T	C	T	G	T	C	C	C	A	C	C	C	T	G	T	0.38% (62 reads)
A	T	G	G	G	A	A	T	G	T	C	C	C	T	C	C	T	G	G	G	G	G	A	T	G	T	T	C	T	G	T	C	C	C	A	C	C	C	T	G	T	0.36% (58 reads)



Tmc^{WT/WT}, SpCas9 + gRNA 1.1

bold Substitutions
 Insertions
 - Deletions
 - - - Predicted cleavage position

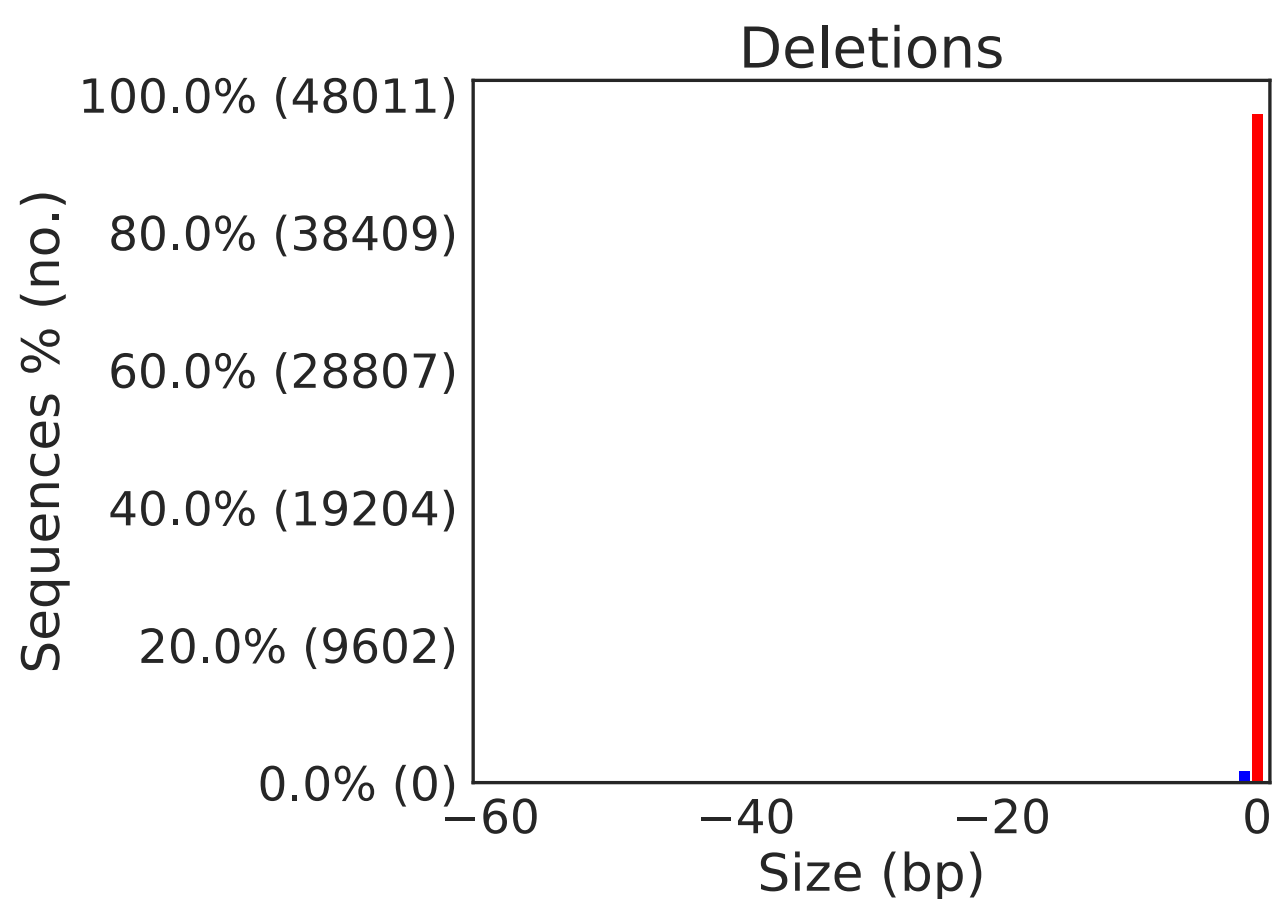
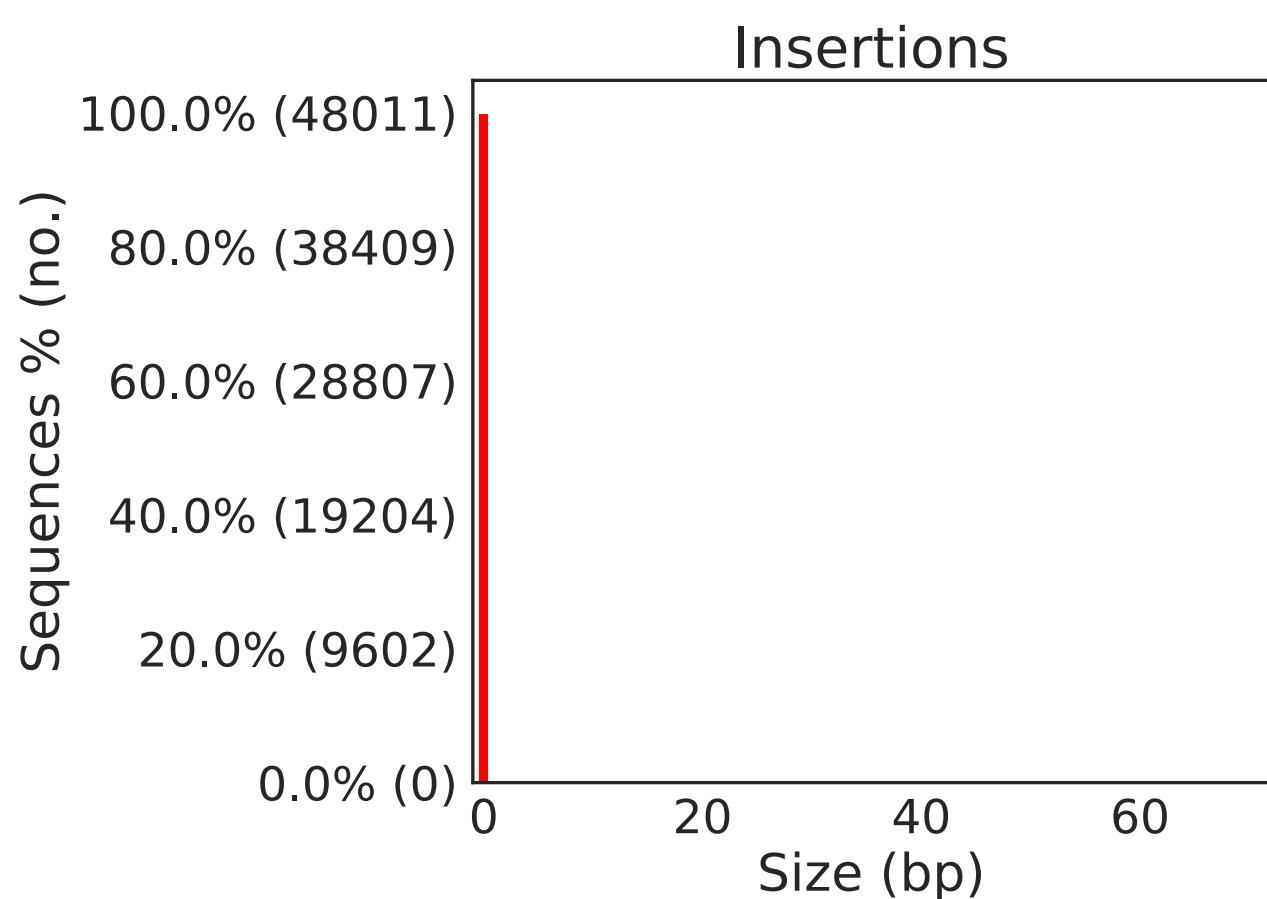
A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	G	G	G	G	A	A	G	T	T	C	T	G	T	C	C	C	A	C	C	C	T	G	T	Reference		
A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	G	G	G	G	A	T	G	T	T	C	T	G	T	C	C	C	A	C	C	C	T	G	T	86.61% (43129 reads)		
A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	-	G	G	G	A	T	G	T	T	C	T	G	T	C	C	C	A	C	C	C	T	G	T	2.74% (1363 reads)		
A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	G	G	G	-	A	T	G	T	T	C	T	G	T	C	C	C	A	C	C	C	T	G	T	2.73% (1357 reads)		
A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	G	G	G	T	-	-	G	T	T	C	T	G	T	C	C	C	A	C	C	C	T	G	T	0.41% (206 reads)		
A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	G	G	G	-	-	T	G	T	T	C	T	G	T	C	C	C	A	C	C	C	T	G	T	0.37% (185 reads)		
A	T	G	G	T	A	A	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	T	G	T	C	C	C	A	C	C	C	T	G	T	0.20% (102 reads)
A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	G	G	G	-	-	-	G	T	T	C	T	G	T	C	C	C	A	C	C	C	T	G	T	0.20% (101 reads)		
A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	G	G	G	G	-	-	-	T	T	C	T	G	T	C	C	C	A	C	C	C	T	G	T	0.20% (101 reads)		
A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	G	G	G	G	-	-	-	T	T	C	T	G	T	C	C	C	A	C	C	C	T	G	T	0.20% (100 reads)		



Tmc^{WT/WT}, SpCas9 + gRNA 2.1

bold Substitutions
 Insertions
 - Deletions
 - - - Predicted cleavage position

A	A	C	A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	G	G	G	G	A	A	G	T	T	C	T	G	T	C	C	C	A	C	C	C	Reference
A	A	C	A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	G	G	G	G	A	T	G	T	T	C	T	G	T	C	C	C	A	C	C	C	92.58% (44449 reads)
A	A	C	A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	G	G	G	G	A	T	G	T	T	C	T	G	T	C	C	C	A	C	C	C	0.80% (383 reads)
A	A	C	A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	G	G	G	G	A	T	G	T	T	C	T	G	T	C	C	C	A	C	C	C	0.77% (372 reads)
A	A	C	A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	G	G	G	G	A	T	G	T	T	C	T	G	T	C	C	C	A	C	C	C	0.77% (370 reads)



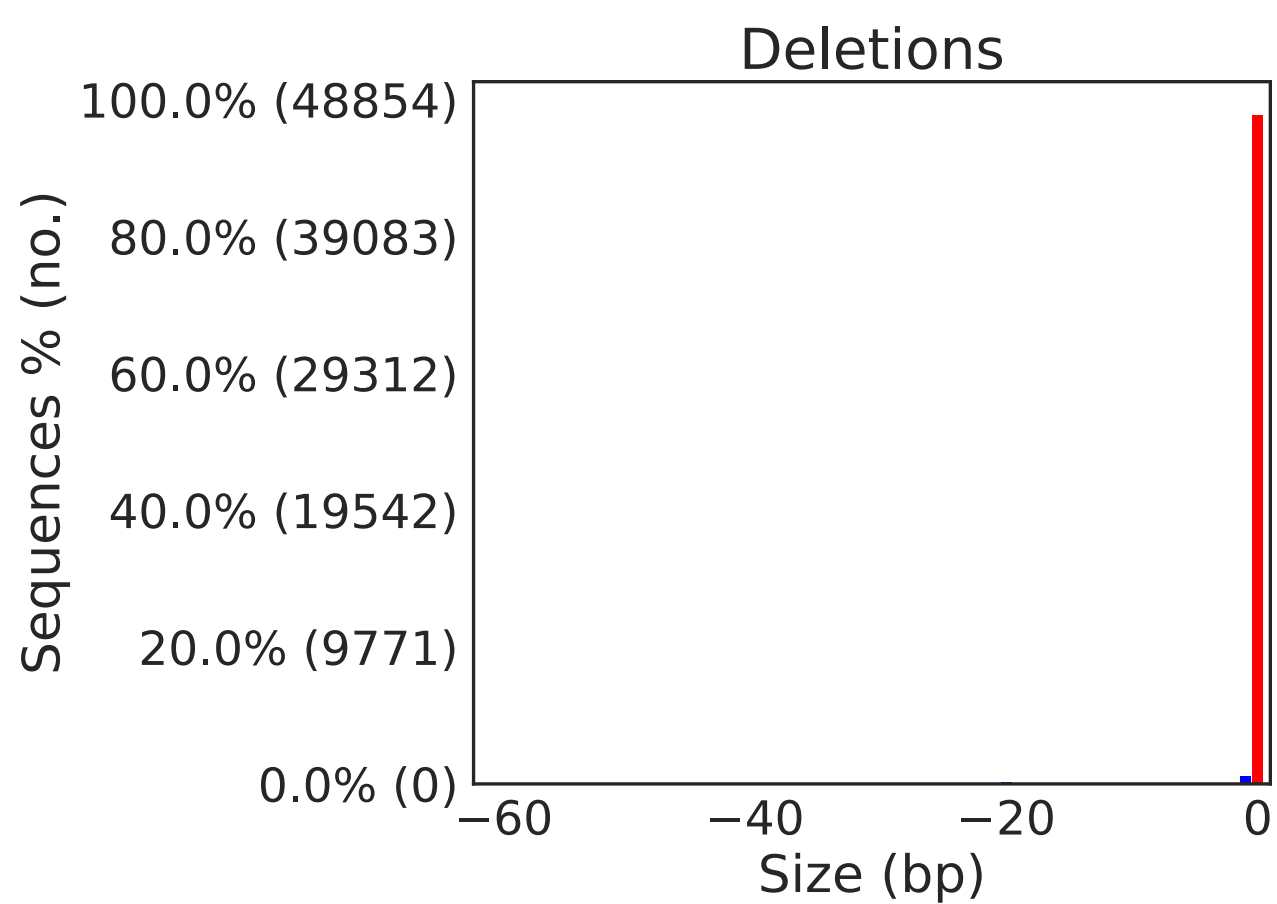
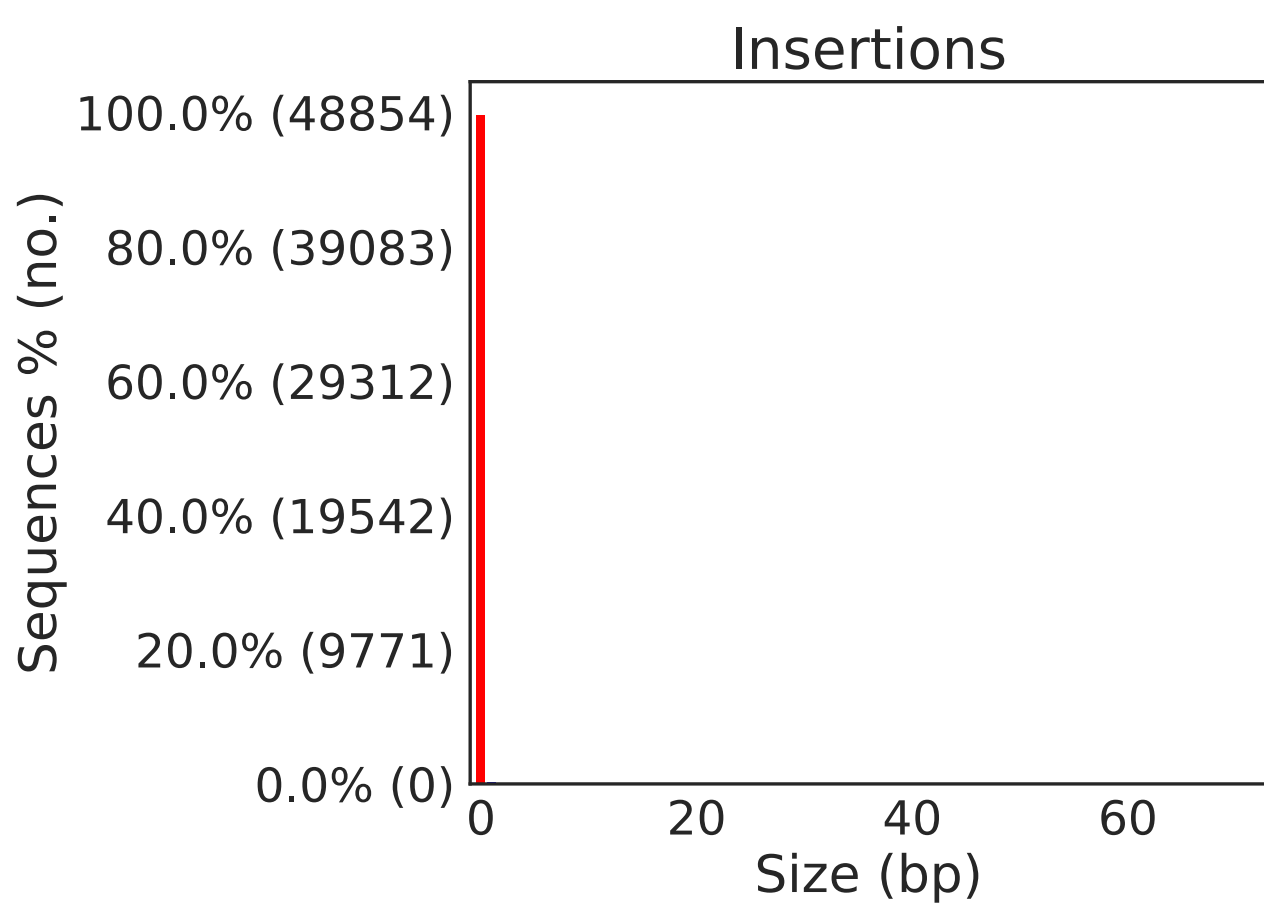
— Insertion
 — Non-insertion

— Deletion
 — Non-deletion

Tmc^{WT/WT}, SpCas9 + gRNA 2.4

bold Substitutions
 Insertions
 - Deletions
 - - - Predicted cleavage position

A	A	C	A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	G	G	G	G	A	A	G	T	T	C	T	G	T	C	C	C	A	C	C	C	Reference
A	A	C	A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	G	G	G	G	A	T	G	T	T	C	T	G	T	C	C	C	A	C	C	C	93.02% (45443 reads)
A	A	C	A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	G	G	G	-	A	T	G	T	T	C	T	G	T	C	C	C	A	C	C	C	0.64% (311 reads)
A	A	C	A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	-	G	G	G	A	T	G	T	T	C	T	G	T	C	C	C	A	C	C	C	0.61% (297 reads)
A	A	C	A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	-	G	G	G	G	A	T	G	T	T	C	T	G	T	C	C	C	A	C	C	C	0.44% (215 reads)



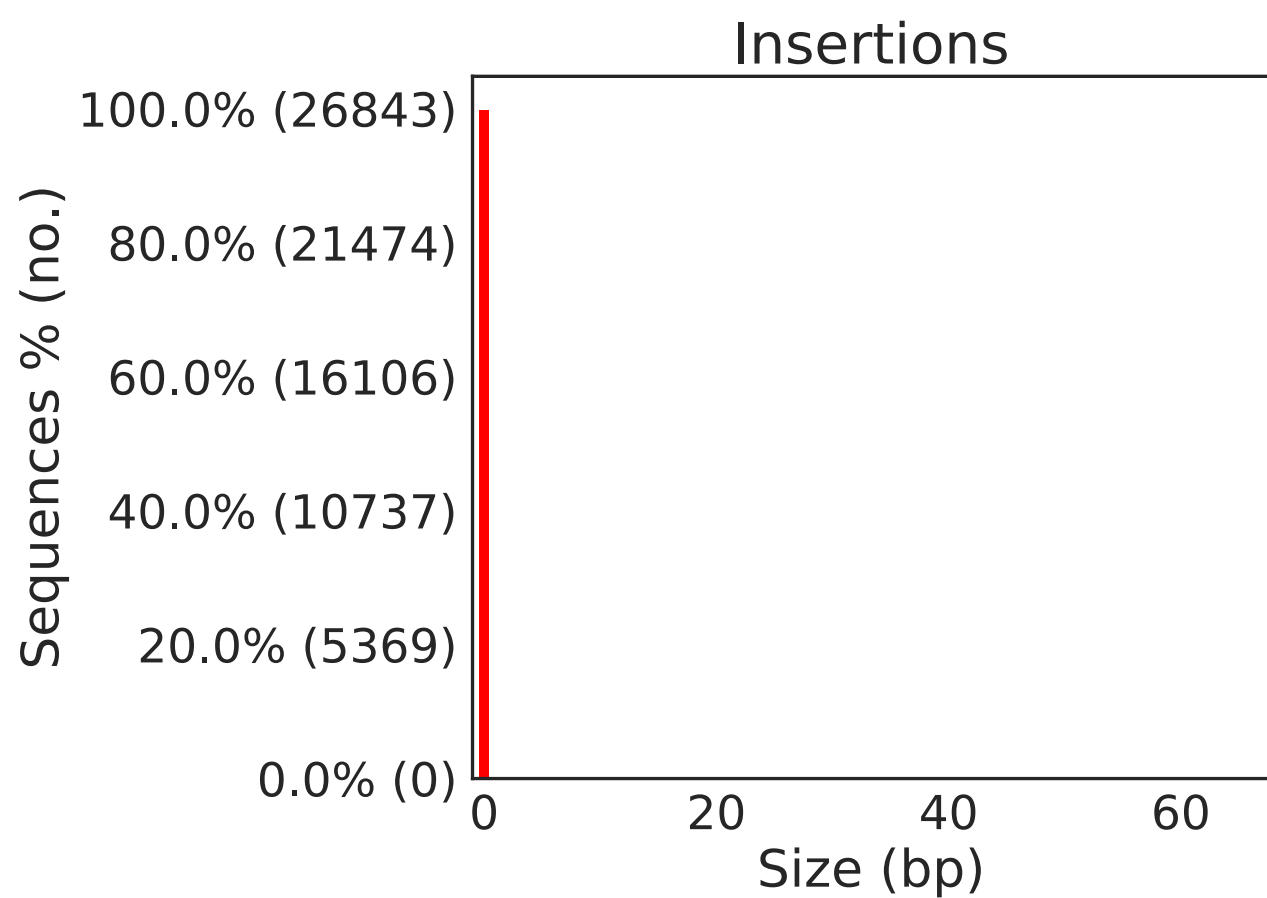
— Insertion
— Non-insertion

— Deletion
— Non-deletion

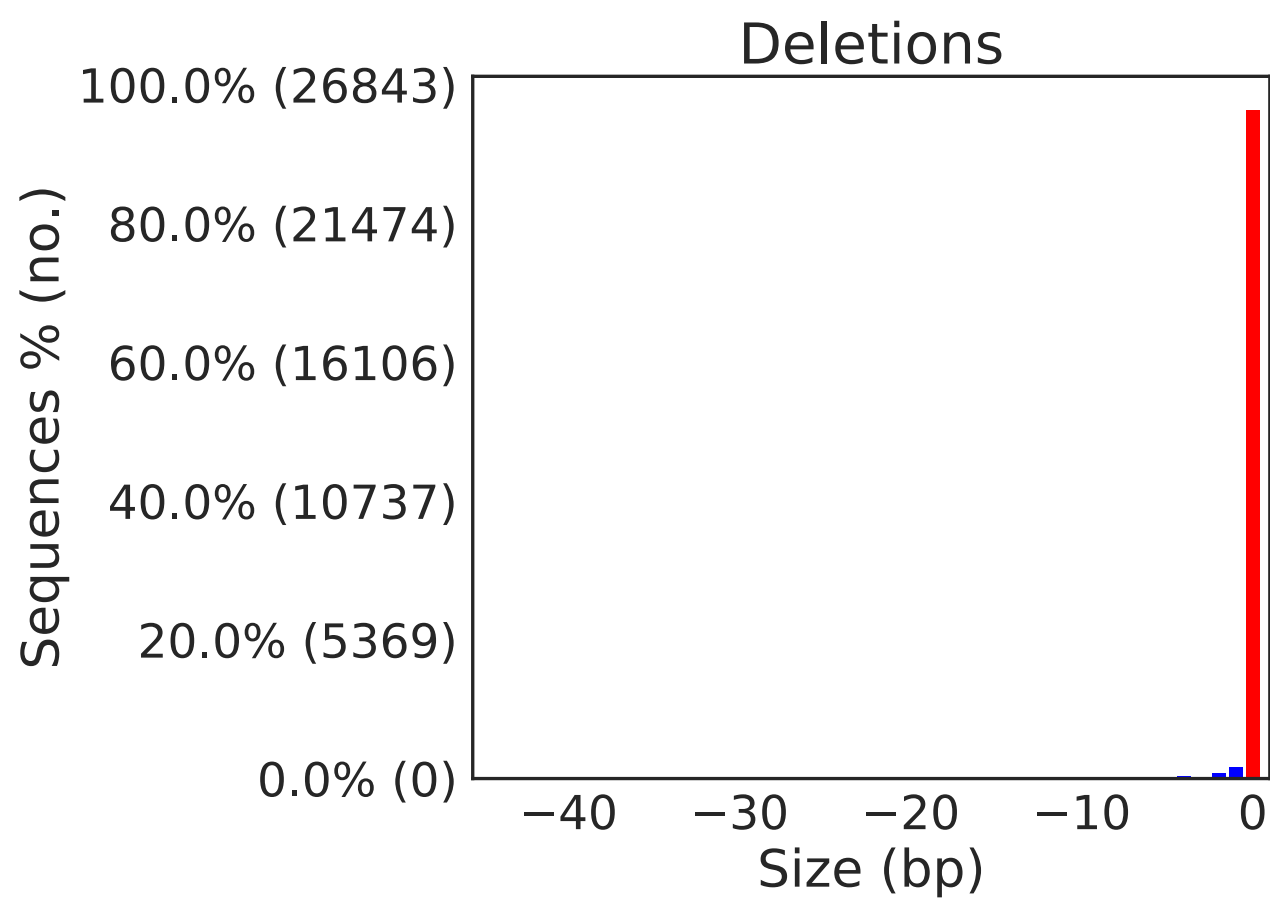
Tmc^{WT/WT}, eSpCas9 + gRNA 1.1

bold Substitutions
 Insertions
 - Deletions
 - - - Predicted cleavage position

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A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	-	G	G	G	G	A	T	G	T	T	C	T	G	T	C	C	C	A	C	C	C	T	G	T	1.56% (419 reads)
A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	G	G	G	-	A	T	G	T	T	C	T	G	T	C	C	C	A	C	C	C	T	G	T	1.52% (408 reads)	
A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	G	G	G	T	-	-	G	T	T	C	T	G	T	C	C	C	A	C	C	C	T	G	T	0.26% (70 reads)	
A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	G	G	G	-	-	T	G	T	T	C	T	G	T	C	C	C	A	C	C	C	T	G	T	0.25% (66 reads)	



— Insertion
— Non-insertion

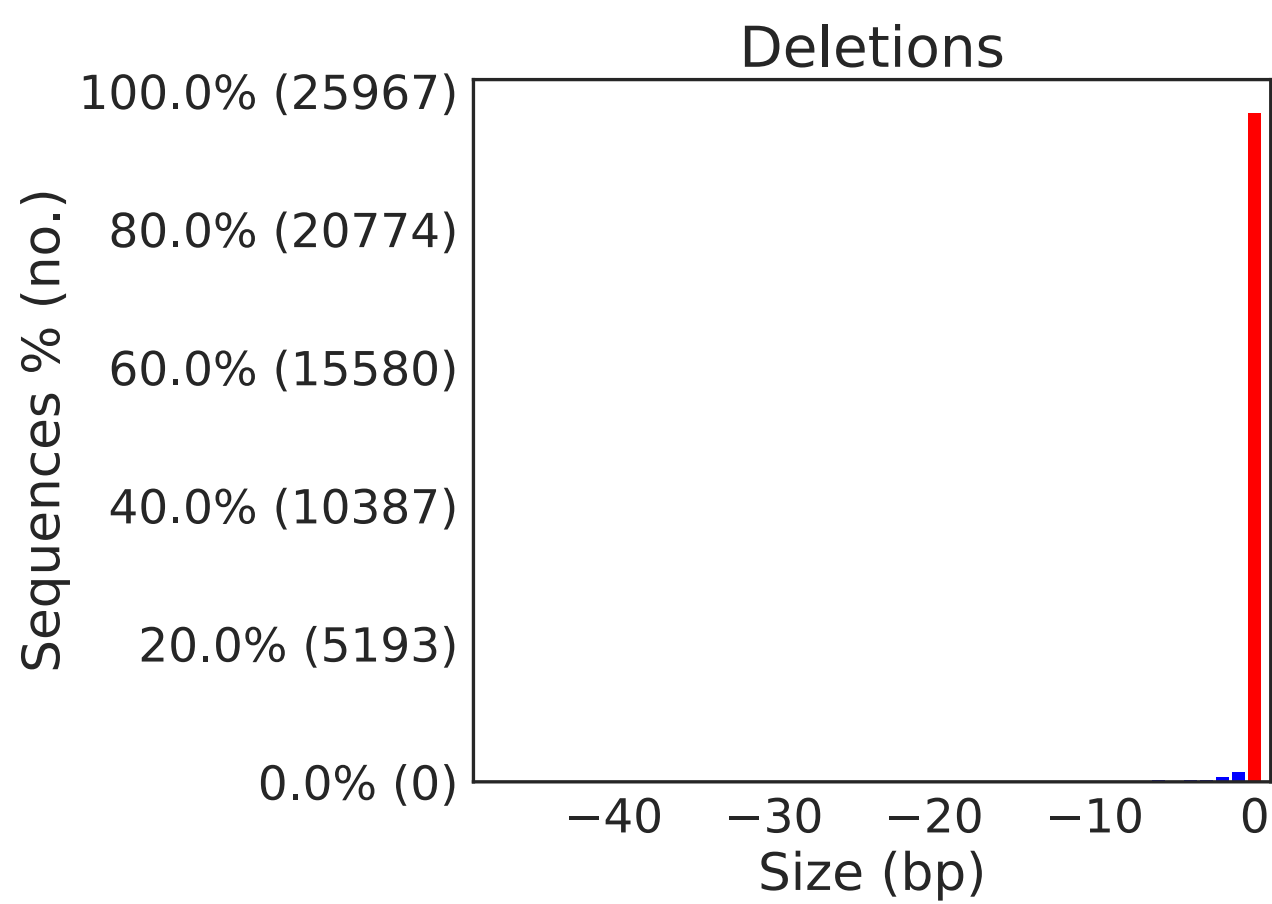
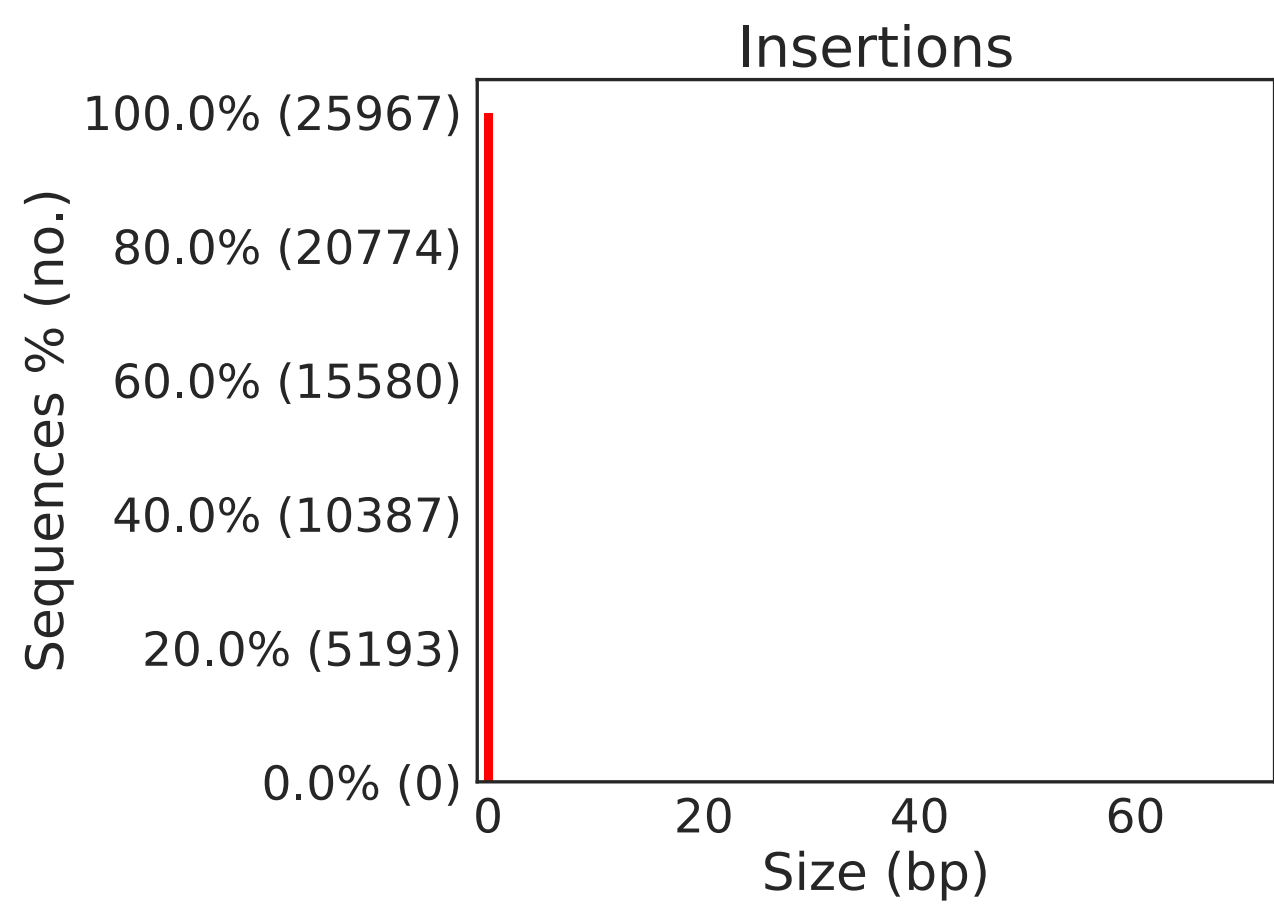


— Deletion
— Non-deletion

Tmc^{WT/WT}, HypaCas9 + gRNA 1.1

bold Substitutions
 Insertions
 - Deletions
 - - - Predicted cleavage position

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A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	-	G	G	G	G	A	T	G	T	T	C	T	G	T	C	C	C	A	C	C	C	T	G	T	1.32% (344 reads)
A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	G	G	G	G	-	A	T	G	T	T	C	T	G	T	C	C	C	A	C	C	C	T	G	T	1.30% (338 reads)



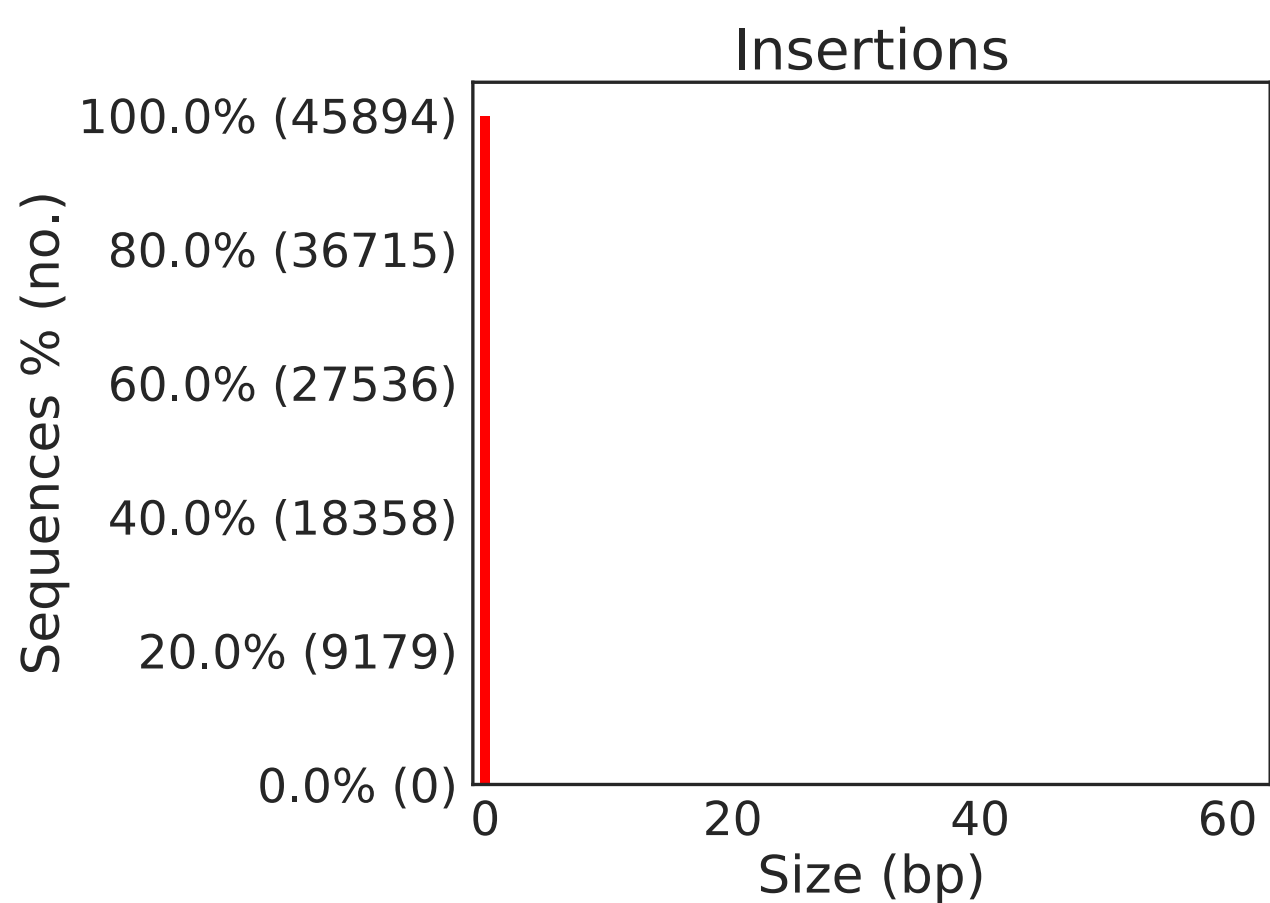
█ Insertion
█ Non-insertion

█ Deletion
█ Non-deletion

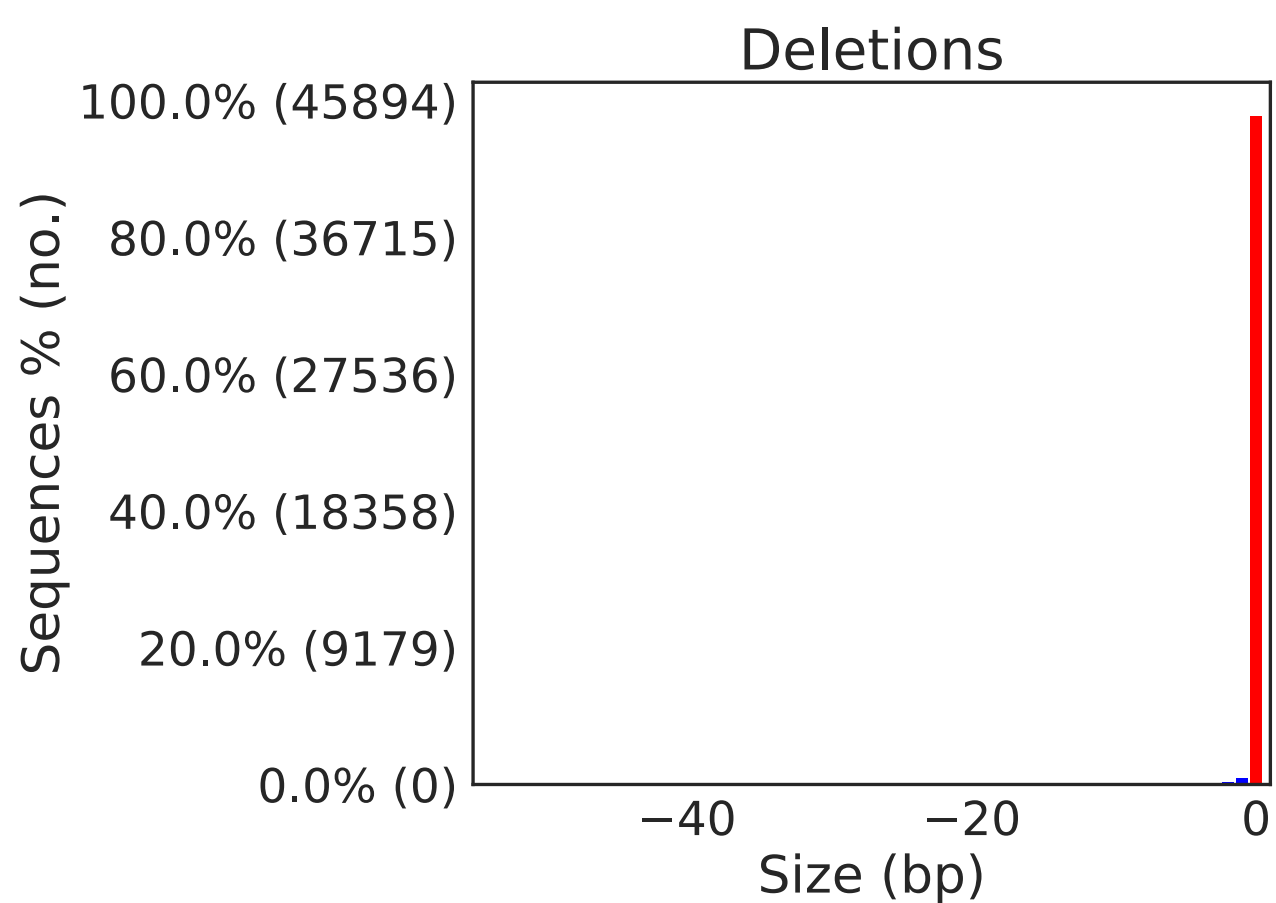
Tmc^{WT/WT}, SpCas9-HF1 + gRNA 1.1

bold Substitutions
 Insertions
 - Deletions
 - - - Predicted cleavage position

A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	G	G	G	G	A	A	G	T	T	C	T	G	T	C	C	C	A	C	C	C	T	G	T	Reference	
A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	G	G	G	G	G	A	T	G	T	T	C	T	G	T	C	C	C	A	C	C	C	T	G	T	92.89% (42631 reads)
A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	-	G	G	G	G	A	T	G	T	T	C	T	G	T	C	C	C	A	C	C	C	T	G	T	1.08% (497 reads)
A	T	G	G	T	A	A	T	G	T	C	C	C	T	C	C	T	G	G	G	G	-	A	T	G	T	T	C	T	G	T	C	C	C	A	C	C	C	T	G	T	0.98% (452 reads)



— Insertion
— Non-insertion

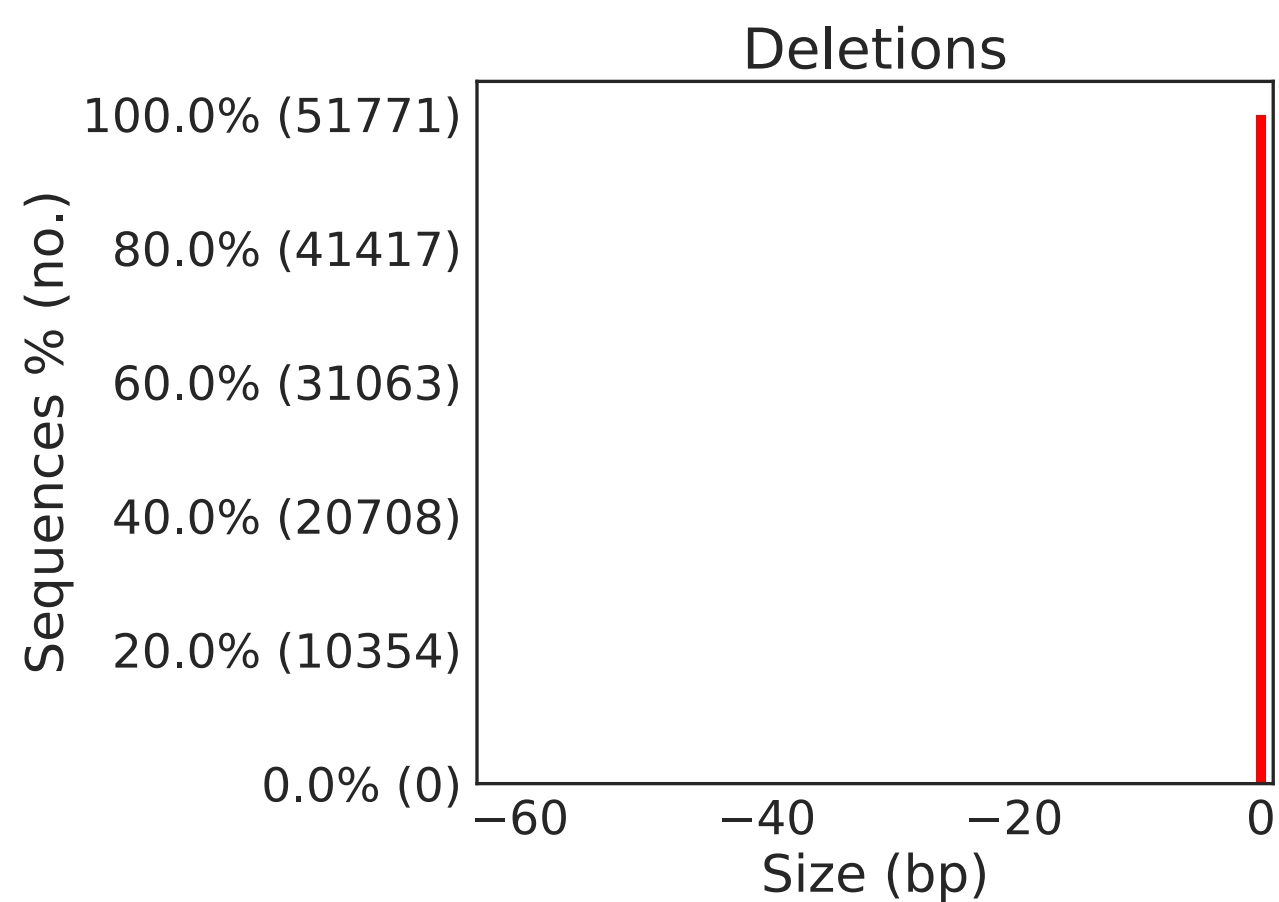
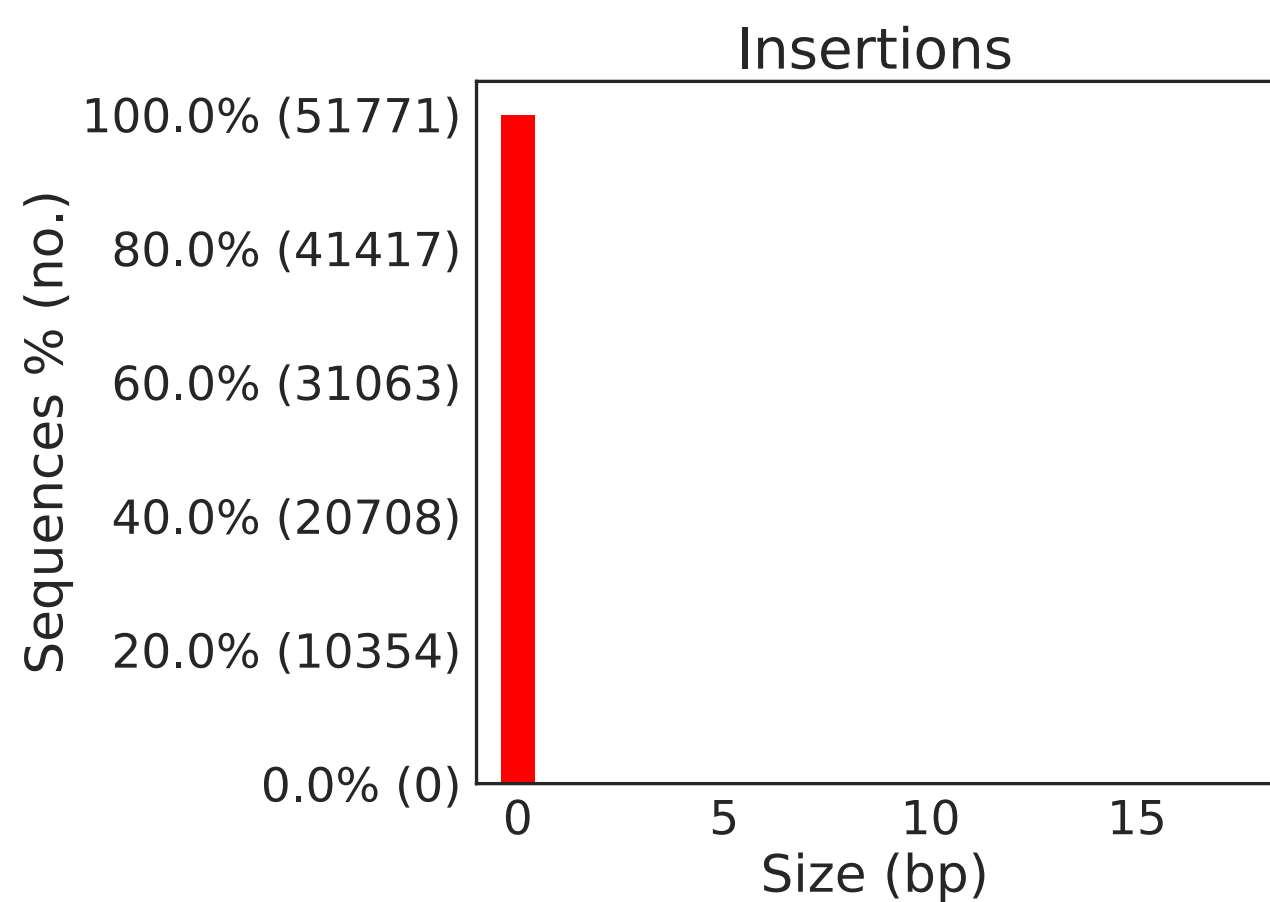


— Deletion
— Non-deletion

Tmc^{WT/WT}, SaCas9^{KKH} + gRNA 4.1

bold Substitutions
 Insertions
 - Deletions
 - - - Predicted cleavage position

G A A C A T G G T A A T G T C C C T C C T G G G G A A G T T C T G T C C C A C C Reference
 G A A C A T G G T A A T G T C C C T C C **T** G G G G A **T** G T T C T G T C C C A C C 96.30% (49854 reads)



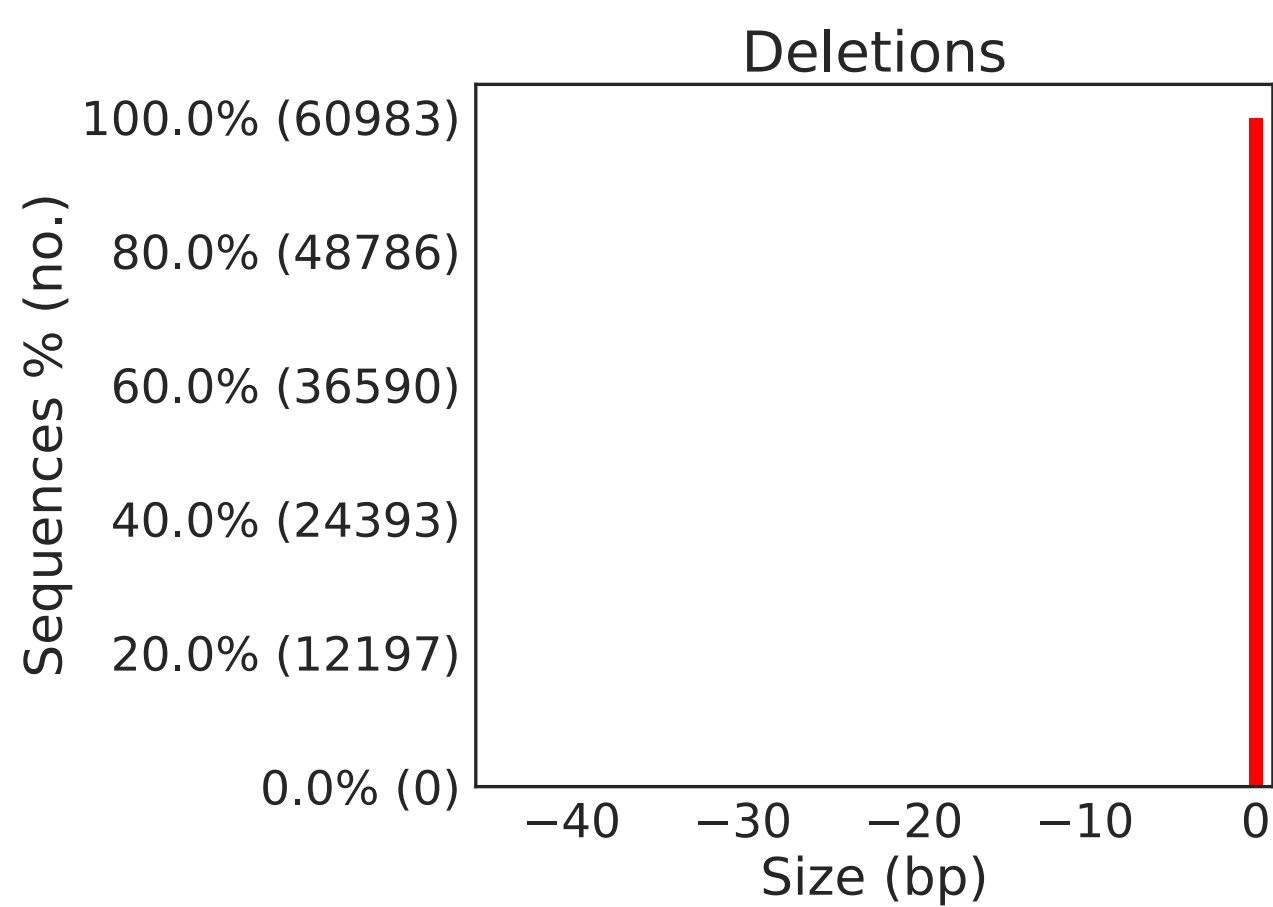
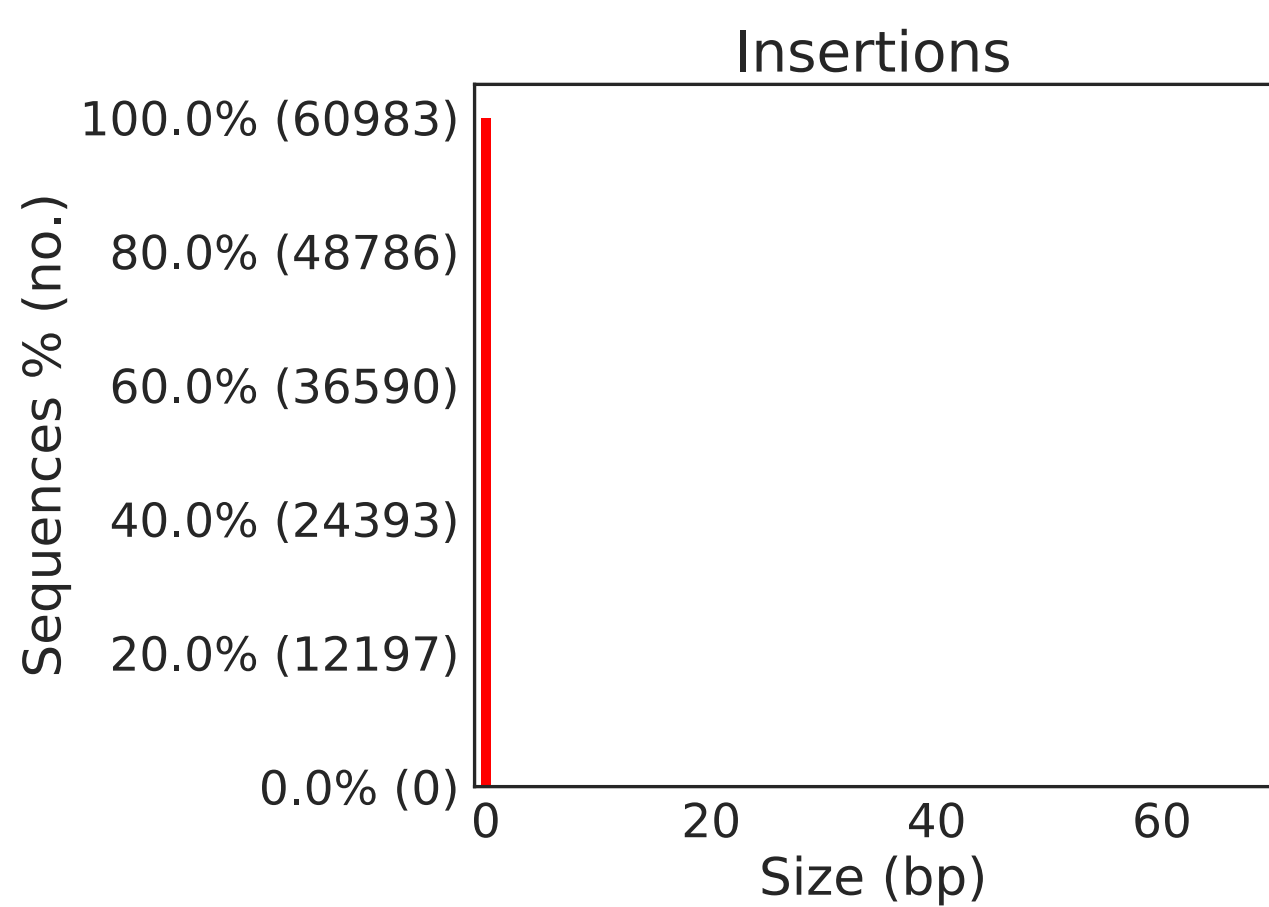
— Insertion
 — Non-insertion

— Deletion
 — Non-deletion

Tmc^{WT/WT}, SaCas9^{KKH} + gRNA 4.2

bold Substitutions
 Insertions
 - Deletions
 - - - Predicted cleavage position

G A A C A T G G T A A T G T C C C T C C T G G G G A A G T T C T G T C C C A C C Reference
 G A A C A T G G T A A T G T C C C T C C **T** G G G G A **T** G T T C T G T C C C A C C 96.39% (58783 reads)



— Insertion
— Non-insertion

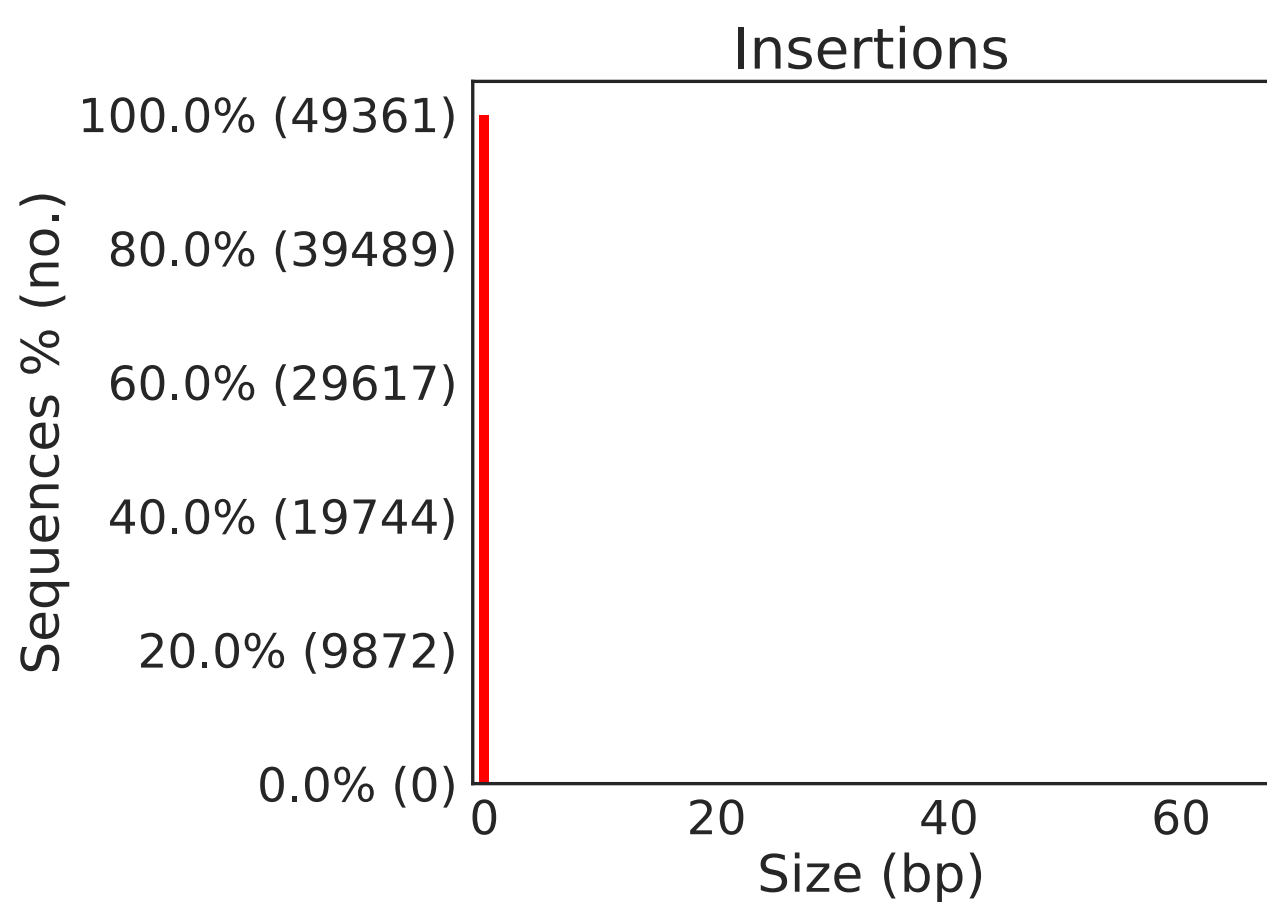
— Deletion
— Non-deletion

Tmc^{WT/WT}, SaCas9^{KKH} + gRNA 4.3

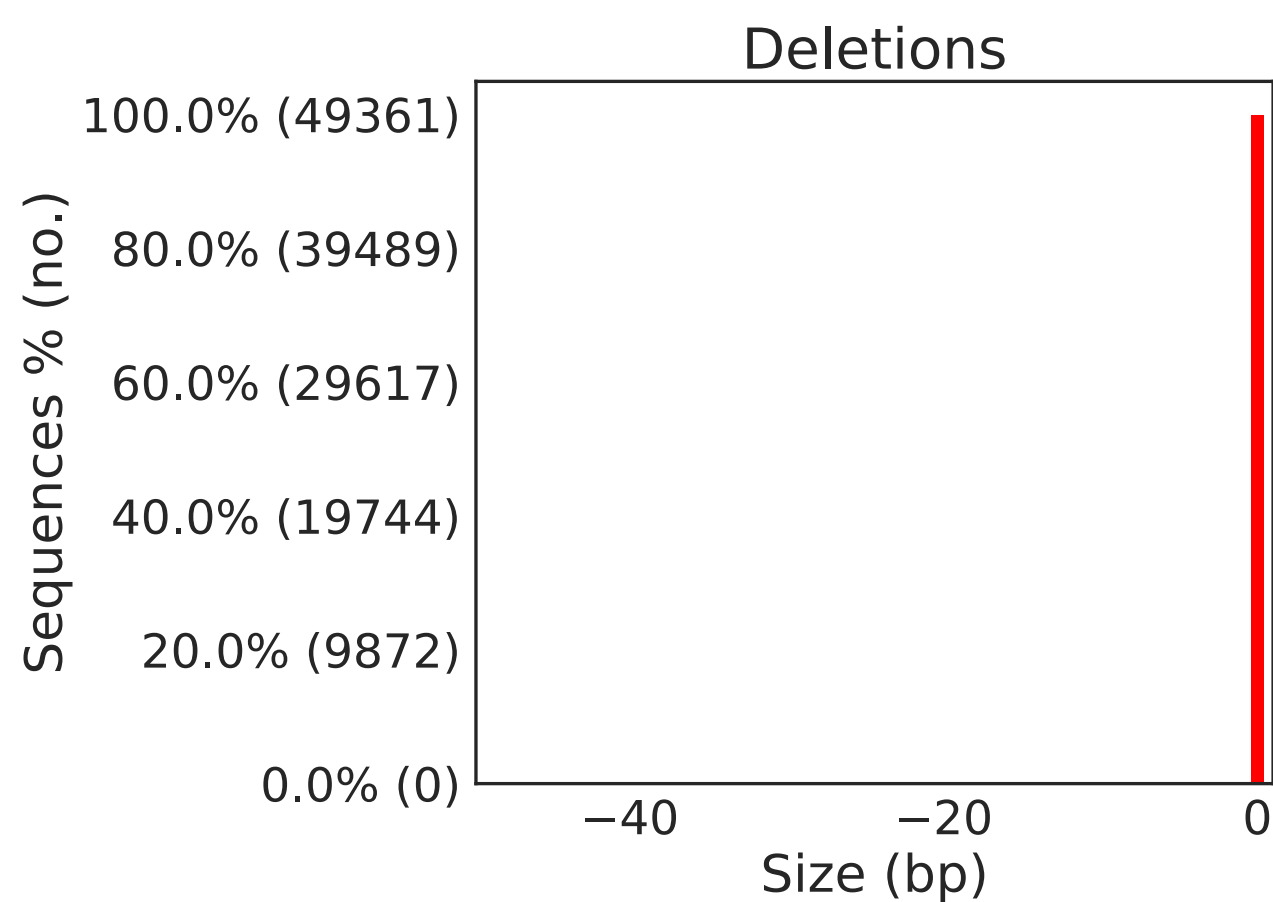
- bold** Substitutions
- Insertions
- Deletions
- - - Predicted cleavage position

G A A C A T G G T A A T G T C C C T C C T G G G G A A G T T C T G T C C C A C C Reference

G A A C A T G G T A A T G T C C C T C C T G G G G A **T** G T T C T G T C C C A C C 96.03% (47401 reads)



- Insertion
- Non-insertion



- Deletion
- Non-deletion

**Supplementary Data Set 4. Sequencing result from pBG201 (pAAV-CMV-NLS(SV40)-
SaCas9(E782K/N968K/R1015H)-NLS(nucleoplasmin)-3xHA-bGHpA0-U6-BsaI-sgRNA)**

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