

NGS seq_Result

EL4 111mut cell line

Clone (#120, 126)

Cas-Analyzer

A JavaScript-based instant assessment tool for high-throughput sequencing data for genome edited cells.

Thanks to the improvements in the newest JavaScript engines in the most recent web browsers, the JavaScript based internal algorithm of Cas-Analyzer completely runs on the client-side so that large amounts of sequencing data do not need to be uploaded to the server. Currently, Cas-Analyzer supports various single nucleases (SpCas9, StCas9, NmCas9, SaCas9, CjCas9, and AsCpf1/LbCpf1) and paired nucleases (ZFNs, TALENs, Cas9 nickases, and dCas9-FokI nucleases).

Citation info: [Park J. et al. Cas-Analyzer: an online tool for assessing genome editing results using NGS data. *Bioinformatics* 33, 286-288 \(2017\).](#)

For the ones who would like to clarify the errors derived from DNA polymerase during PCR or sequencing process, comparison of treated sample and negative control (e.g. untreated sample) is recommended.

Please input your data in below form, or [download an example data here](#).

Sequencing Data

File Type:

Single-end read or fastq-joined file

Single Read File (fastq or gzipped fastq):

파일 선택 29.fastqjoin

Basic Information

Full reference sequence (5' to 3'):

Cacccttagagcagaaccccaaatctccctgggacttagcttatgtcactgaacacatttaccaacccccctctctacagcgtggtttctaaggttctttccaccggaagctacgacaaaaggaaatgtatgggtgggagggtctgaggagagtgttcagggttctgacagactacaccagagaaagaagcaagcaccatgtttgaaa

Nuclease Type:

Single nuclease

Select Nuclease:

SpCas9 from *Streptococcus pyogenes*: 5'-NGG-3'

Target DNA sequence (5' to 3', without PAM sequence):

Gtttctaaggtctttccac

(Optional) Donor DNA sequence for homology directed repair (HDR) (5' to 3')

ccctctctacagcgtggtttctaaggtcttgacaccggaagctacgacaaaaggaaatgtatgggtgggagggtctgaggagagtgggtcagggt

Analysis Parameters

Comparison range (R) [?]

70

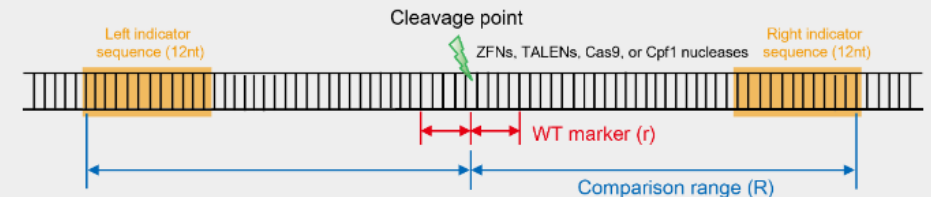
☐ or use both ends

Minimum frequency (n) [?]

1

☒ (Optional) WT marker (r) [?]

5



Submit

#120 HDR frequency

Input Summary

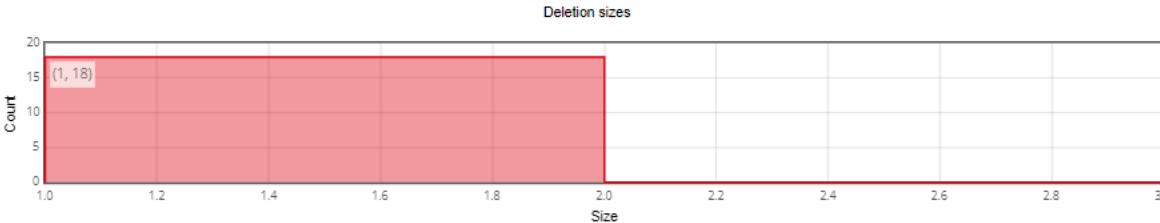
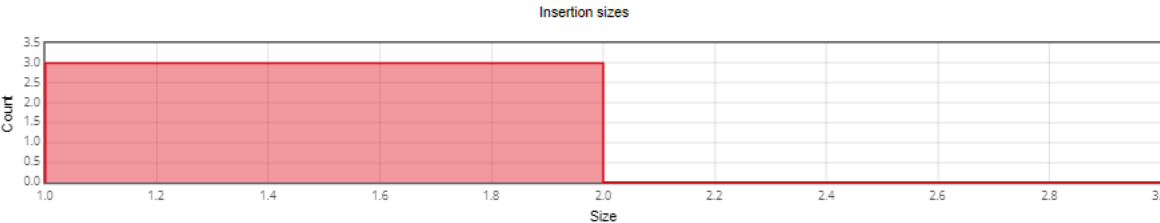
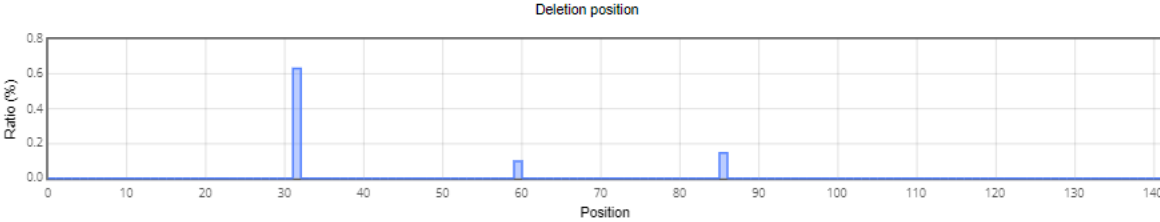
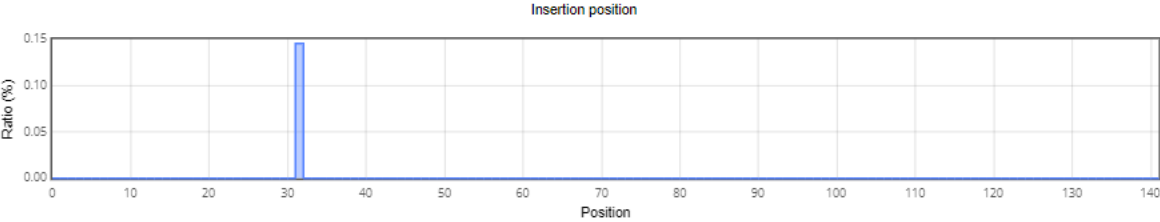
File name		
29.fastqjoin		
WT sequence (blue: indicator sequences at each ends of comparison range, green: crRNA sequence, red: WT marker sequence)		
CACCTTAGAGCAGAACCCAAATCTCCCTGGGGA CTTAGCTTATGTCAC TGAACACATTACCAACCCCTCTCTACAGCGTG GTTC TAAGG TTCTTCCACCG GAAGCTACGACAAAAGGAAATGTATGGGTGGGAGGGCTTGTGGGAGAGT GGTTCAGGGTTCTGA CACAGACTACACCCAGAGAAAGAGCAAGCACCATGTTGAAA		
crRNA sequence		
GTTTCTAAGGTTCTTCCAC		
Comparison range (R) [?]	Minimum frequency (n) [?]	WT marker (r) [?]
70	1	5

Run again with different values

Result Summary

Total Sequences	With both indicator sequences	More than minimum frequency	Insertions	Deletions	Indel frequency	HDR frequency
2717	2276	2062	3	18	21 (1.0%)	2036 (98.7%)

Insertions and Deletions



#120 Sequence information

Sequence Information

All WT and Substitutions Insertions Deletions ☐ Show HDR only

Download table

ID	Sequence	Length	Count	Type	HDR
1	CTTAGCTTATGCTACTGAACACATTTACCAACCCCCCTCTCTACAGCGTGGTTCTAAGGTTCTTCCACCGGAAGCTACGACAAAAGGAAATGTATGGGTGGGAGGGCTTGTGGGAGAGTGGTTCAGGGTTCTGA CTTAGCTTATGCTACTGAACACATTTACCAACCCCCCTCTCTACAGCGTGGTTCTAAGGTTCTTGACACCGGAAGCTACGACAAAAGGAAATGTATGGGTGGGAGGGCTTGTGGGAGAGTGGTTCAGGGTTCTGA	140	1769	WT or Sub	O
2	CTTAGCTTATGCTACTGAACACATTTACCAACCCCCCTCTCTACAGCGTGGTTCTAAGGTTCTTCCACCGGAAGCTACGACAAAAGGAAATGTATGGGTGGGAGGGCTTGTGGGAGAGTGGTTCAGGGTTCTGA CTTAGCTTATGCTACTGAACACATTTACCAA-CCCCCTCTCTACAGCGTGGTTCTAAGGTTCTTGACACCGGAAGCTACGACAAAAGGAAATGTATGGGTGGGAGGGCTTGTGGGAGAGTGGTTCAGGGTTCTGA	139	9	Del	O
3	CTTAGCTTATGCTACTGAACACATTTACCAACCCCCCTCTCTACAGCGTGGTTCTAAGGTTCTTCCACCGGAAGCTACGACAAAAGGAAATGTATGGGTGGGAGGGCTTGTGGGAGAGTGGTTCAGGGTTCTGA CTTAGCTTATGTCGCTGAACACATTTACCAACCCCCCTCTCTACAGCGTGGTTCTAAGGTTCTTGACACCGGAAGCTACGACAAAAGGAAATGTATGGGTGGGAGGGCTTGTGGGAGAGTGGTTCAGGGTTCTGA	140	7	WT or Sub	O
4	CTTAGCTTATGCTACTGAACACATTTACCAACCCCCCTCTCTACAGCGTGGTTCTAAGGTTCTTCCACCGGAAGCTACGACAAAAGGAAATGTATGGGTGGGAGGGCTTGTGGGAGAGTGGTTCAGGGTTCTGA CTTAGCTTATGGCACTGAACACATTTACCAACCCCCCTCTCTACAGCGTGGTTCTAAGGTTCTTGACACCGGAAGCTACGACAAAAGGAAATGTATGGGTGGGAGGGCTTGTGGGAGAGTGGTTCAGGGTTCTGA	140	7	WT or Sub	O
5	CTTAGCTTATGCTACTGAACACATTTACCAACCCCCCTCTCTACAGCGTGGTTCTAAGGTTCTTCCACCGGAAGCTACGACAAAAGGAAATGTATGGGTGGGAGGGCTTGTGGGAGAGTGGTTCAGGGTTCTGA CTTAGCTTATGCTACTGAACACATTTACCAACCCCCCTCTCTACAGCGTGGTTCTAAGGTTCTTGACACCGGAAGCTACGACAAAAGGAAATGTATGGGTGGGAGGGCTTGTGGGAGAGTGGTTCAGGGTTCTGA	140	6	WT or Sub	O
6	CTTAGCTTATGCTACTGAACACATTTACCAACCCCCCTCTCTACAGCGTGGTTCTAAGGTTCTTCCACCGGAAGCTACGACAAAAGGAAATGTATGGGTGGGAGGGCTTGTGGGAGAGTGGTTCAGGGTTCTGA CTTAGCTTATGCTACTGAACACATTTACCAACCCCCCTCTCTACAGCGTGGTTCTAAGGTTCTTGACACCGGAAGCTACGACAAAAGGAAATGTATGGGTGGGAGGGCTTGTGGGAGAGTGGTTCAGGGTTCTGA	140	6	WT or Sub	O
7	CTTAGCTTATGCTACTGAACACATTTACCAACCCCCCTCTCTACAGCGTGGTTCTAAGGTTCTTCCACCGGAAGCTACGACAAAAGGAAATGTATGGGTGGGAGGGCTTGTGGGAGAGTGGTTCAGGGTTCTGA CTTAGCTTATGCTACTGAACACATTTACCAACCCCCCTCTCTACAGCGTGGTTCTAAGGTTCTTGACACCGGAAGCTACGACAAAAGGAAATGTATGGGGGGGAGGGCTTGTGGGAGAGTGGTTCAGGGTTCTGA	140	6	WT or Sub	O
8	CTTAGCTTATGCTACTGAACACATTTACCAACCCCCCTCTCTACAGCGTGGTTCTAAGGTTCTTCCACCGGAAGCTACGACAAAAGGAAATGTATGGGTGGGAGGGCTTGTGGGAGAGTGGTTCAGGGTTCTGA CTTAGCTTGTCAGTGAACACATTTACCAACCCCCCTCTCTACAGCGTGGTTCTAAGGTTCTTGACACCGGAAGCTACGACAAAAGGAAATGTATGGGTGGGAGGGCTTGTGGGAGAGTGGTTCAGGGTTCTGA	140	6	WT or Sub	O
9	CTTAGCTTATGCTACTGAACACATTTACCAACCCCCCTCTCTACAGCGTGGTTCTAAGGTTCTTCCACCGGAAGCTACGACAAAAGGAAATGTATGGGTGGGAGGGCTTGTGGGAGAGTGGTTCAGGGTTCTGA CTTAGCTTATGTCAGTGAACACATTTACCAACCCCCCTCTCTACAGCGTGGTTCTAAGGTTCTTGACACCGGAAGCTACGACAAAAGGAAATGTATGGGTGGGAGGGCTTGTGGGAGAGTGGTTCAGGGTTCTGA	140	6	WT or Sub	O
10	CTTAGCTTATGCTACTGAACACATTTACCAACCCCCCTCTCTACAGCGTGGTTCTAAGGTTCTTCCACCGGAAGCTACGACAAAAGGAAATGTATGGGTGGGAGGGCTTGTGGGAGAGTGGTTCAGGGTTCTGA CTTAGCTTATGCTACTGAACACATTTACCAACCCCCCTCTCTACAGCGTGGTTCTAAGGTTCTTGACACCGGAAGCTACGACAAAAGGAAATGTATGGGTGGGAGGGCTTATGGGAGAGTGGTTCAGGGTTCTGA	140	5	WT or Sub	O

Please input your data in below form, or [download an example data here](#).

Sequencing Data

File Type:
Single-end read or fastq-joined file

Single Read File (fastq or gzipped fastq):
파일 선택 34.fastqjoin

Basic Information

Full reference sequence (5' to 3'):
Caccttagagcagaacccaaatctccctggggacttagcttatgtcactgaacacattaccaacccccctctctacagcgtggttcttaagggtcttccacggaagctacgacaaaaggaaatgtatgggtggggagggttgtgggagagtgttcagggttctgacacagactacccagagaaagaagagcaagcaccatgttgaaa

Nuclease Type:
Single nuclease

Select Nuclease:
SpCas9 from Streptococcus pyogenes: 5'-NGG-3'

Target DNA sequence (5' to 3', without PAM sequence):
Gtttctaaggtctttccac

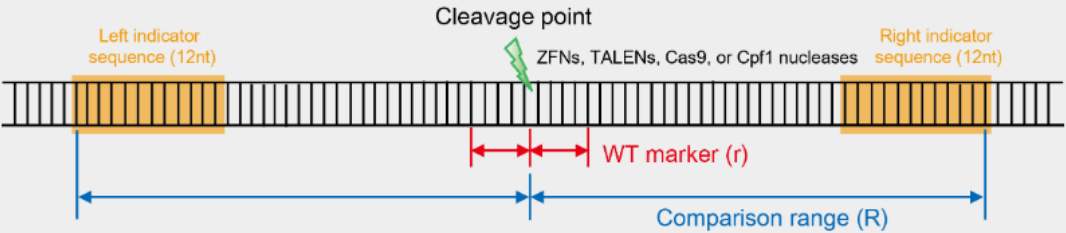
(Optional) Donor DNA sequence for homology directed repair (HDR) (5' to 3')
ccctctctacagcgtggttcttaagggtcttgacaccggaagctacgacaaaaggaaatgtatgggtggggagggtgtgtgggagagtgttcagggt

Analysis Parameters

Comparison range (R) [?]
70 or use both ends

Minimum frequency (n) [?]
1

☒ (Optional) WT marker (r) [?]
5



Submit

#126

HDR frequency

Input Summary

File name

34.fastqjoin

WT sequence

(blue: indicator sequences at each ends of comparison range, green: crRNA sequence, red: WT marker sequence)

CACCTTAGAGCAGAACCCAAATCTCCCTGGGGA**CTTAGCTTATGTC**ACTGAACACATTACCAACCCCCCTCTCTCTACAGCGT**GTTTCTAAGGTTCTTCCAC**CGAAGCTACGACAAAAGGAAATGTATGGTGGGGAGGGCTTGTGGGAGAGT**GGTTCAGGGTTCTGA**CACAGACTACACCCAGAGAAAAGAGCAAGCACCATGTTGAAA

crRNA sequence

GTTTCTAAGGTTCTTCCAC

Comparison range (R) [\[?\]](#)

Minimum frequency (n) [\[?\]](#)

WT marker (r) [\[?\]](#)

70

1

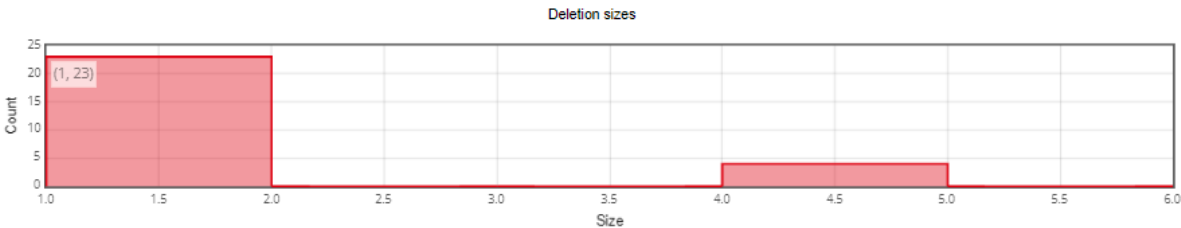
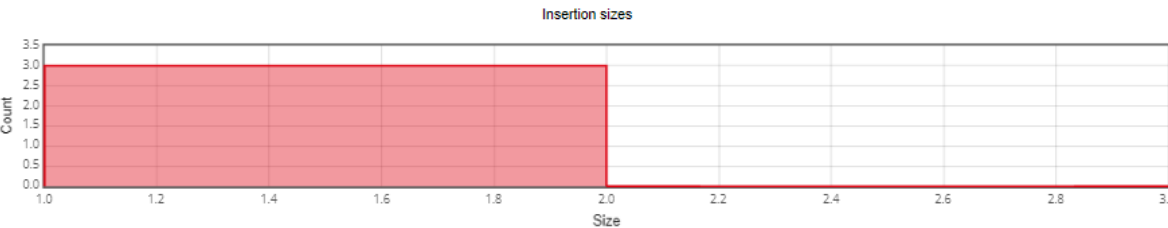
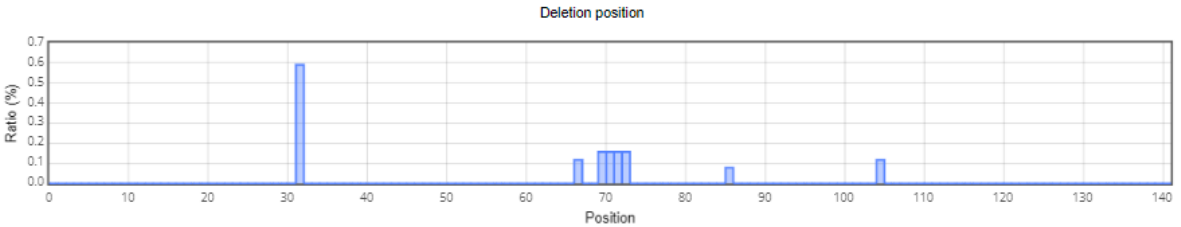
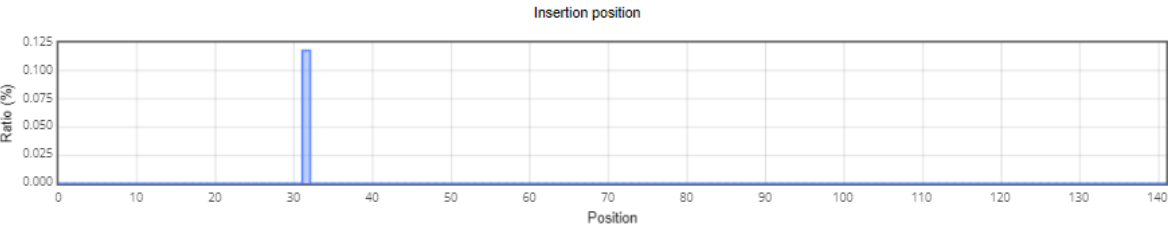
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Run again with different values

Result Summary

Total Sequences	With both indicator sequences	More than minimum frequency	Insertions	Deletions	Indel frequency	HDR frequency
4280	2769	2544	3	27	30 (1.2%)	2410 (94.7%)

Insertions and Deletions



#126 Sequence information

Sequence Information

All

WT and Substitutions

Insertions

Deletions

☐ Show HDR only

Download table

ID	Sequence	Length	Count	Type	HDR
1	CTTAGCTTATGCTCACTGAACACATTTACCAACCCCCCTCTCTACAGCGTGGTTTCTAAGGTTCTTTCCACCGGAAGCTACGACAAAAGGAAATGTATGGGTGGGGAGGGCTTGTGGGAGAGTGTTTCAGGGTTCTGA CTTAGCTTATGCTCACTGAACACATTTACCAACCCCCCTCTCTACAGCGTGGTTTCTAAGGTTCTTGACACCGGAAGCTACGACAAAAGGAAATGTATGGGTGGGGAGGGCTTGTGGGAGAGTGTTTCAGGGTTCTGA	140	2074	WT or Sub	O
2	CTTAGCTTATGCTCACTGAACACATTTACCAACCCCCCTCTCTACAGCGTGGTTTCTAAGGTTCTTTCCACCGGAAGCTACGACAAAAGGAAATGTATGGGTGGGGAGGGCTTGTGGGAGAGTGTTTCAGGGTTCTGA CTTAGCTTATGCTCACTGAACACATTTACCAACCCCCCTCTCTACAGCGTGGTTTCTAAGGTTCTTTCCACCGGAAGCTACGACAAAAGGAAATGTATGGGTGGGGAGGGCTTGTGGGAGAGTGTTTCAGGGTTCTGA	140	106	WT or Sub	X
3	CTTAGCTTATGCTCACTGAACACATTTACCAACCCCCCTCTCTACAGCGTGGTTTCTAAGGTTCTTTCCACCGGAAGCTACGACAAAAGGAAATGTATGGGTGGGGAGGGCTTGTGGGAGAGTGTTTCAGGGTTCTGA CTTAGCTTATGCTCACTGAACACATTTACCAACCCCCCTCTCTACAGCGTGGTTTCTAAGGTTCTTGACACCGGAAGCTACGACAAAAGGAAATGTATGGGTGGGGAGGGCTTGTGGGAGAGTGTTTCAGGGTTCTGA	140	10	WT or Sub	O
4	CTTAGCTTATGCTCACTGAACACATTTACCAACCCCCCTCTCTACAGCGTGGTTTCTAAGGTTCTTTCCACCGGAAGCTACGACAAAAGGAAATGTATGGGTGGGGAGGGCTTGTGGGAGAGTGTTTCAGGGTTCTGA CTTAGCTTATGCTCACTGAACACATTTACCAACCCCCCTCTCTACAGCGTGGTTTCTAAGGTTCTTGACACCGGAAGCTACGACAAAAGGAAATGTATGGGTGGGGAGGGCTTGTGGGAGAGTGTTTCAGGGTTCTGA	140	10	WT or Sub	O
5	CTTAGCTTATGCTCACTGAACACATTTACCAACCCCCCTCTCTACAGCGTGGTTTCTAAGGTTCTTTCCACCGGAAGCTACGACAAAAGGAAATGTATGGGTGGGGAGGGCTTGTGGGAGAGTGTTTCAGGGTTCTGA CTTAGCTTATGCTCACTGAACACATTTACCAA-CCCCCTCTCTACAGCGTGGTTTCTAAGGTTCTTGACACCGGAAGCTACGACAAAAGGAAATGTATGGGTGGGGAGGGCTTGTGGGAGAGTGTTTCAGGGTTCTGA	139	9	Del	O
6	CTTAGCTTATGCTCACTGAACACATTTACCAACCCCCCTCTCTACAGCGTGGTTTCTAAGGTTCTTTCCACCGGAAGCTACGACAAAAGGAAATGTATGGGTGGGGAGGGCTTGTGGGAGAGTGTTTCAGGGTTCTGA CTTAGCTTATGGCAGTGAACACATTTACCAACCCCCCTCTCTACAGCGTGGTTTCTAAGGTTCTTGACACCGGAAGCTACGACAAAAGGAAATGTATGGGTGGGGAGGGCTTGTGGGAGAGTGTTTCAGGGTTCTGA	140	8	WT or Sub	O
7	CTTAGCTTATGCTCACTGAACACATTTACCAACCCCCCTCTCTACAGCGTGGTTTCTAAGGTTCTTTCCACCGGAAGCTACGACAAAAGGAAATGTATGGGTGGGGAGGGCTTGTGGGAGAGTGTTTCAGGGTTCTGA CTTAGCTTATGCTCACTGAACACATTTACCAACCCCCCTCTCTACAGCGTGGTTTCTAAGGTTCTTGACACCGGAAGCTACGACAAAAGGAAATGTATGGGGGGGAGGGCTTGTGGGAGAGTGTTTCAGGGTTCTGA	140	7	WT or Sub	O
8	CTTAGCTTATGCTCACTGAACACATTTACCAACCCCCCTCTCTACAGCGTGGTTTCTAAGGTTCTTTCCACCGGAAGCTACGACAAAAGGAAATGTATGGGTGGGGAGGGCTTGTGGGAGAGTGTTTCAGGGTTCTGA CTTAGCTTATGTCAGTGAACACATTTACCAACCCCCCTCTCTACAGCGTGGTTTCTAAGGTTCTTGACACCGGAAGCTACGACAAAAGGAAATGTATGGGTGGGGAGGGCTTGTGGGAGAGTGTTTCAGGGTTCTGA	140	7	WT or Sub	O
9	CTTAGCTTATGCTCACTGAACACATTTACCAACCCCCCTCTCTACAGCGTGGTTTCTAAGGTTCTTTCCACCGGAAGCTACGACAAAAGGAAATGTATGGGTGGGGAGGGCTTGTGGGAGAGTGTTTCAGGGTTCTGA CTTAGCTTATGCTCACTGAACACATTTACCAACCCCCCTCTCTACAGCGTGGTTTCTAAGGTTCTTGACACCGGAAGCTACGACAAAAGGAAATGTATGGGTGGGGAGGGCTTGTGGGAGAGTGTTTCAGGGTTCTGA	140	6	WT or Sub	O
10	CTTAGCTTATGCTCACTGAACACATTTACCAACCCCCCTCTCTACAGCGTGGTTTCTAAGGTTCTTTCCACCGGAAGCTACGACAAAAGGAAATGTATGGGTGGGGAGGGCTTGTGGGAGAGTGTTTCAGGGTTCTGA CTTAGCTTATGCTCACTGAACACATTTACCAACCCCCCTCTCTACAGCGTGGTTTCTAAGGTTCTTGACACCGGAAGCTACGACAAAAGGAAATGTATGTGTGGGGAGGGCTTGTGGGAGAGTGTTTCAGGGTTCTGA	140	6	WT or Sub	O