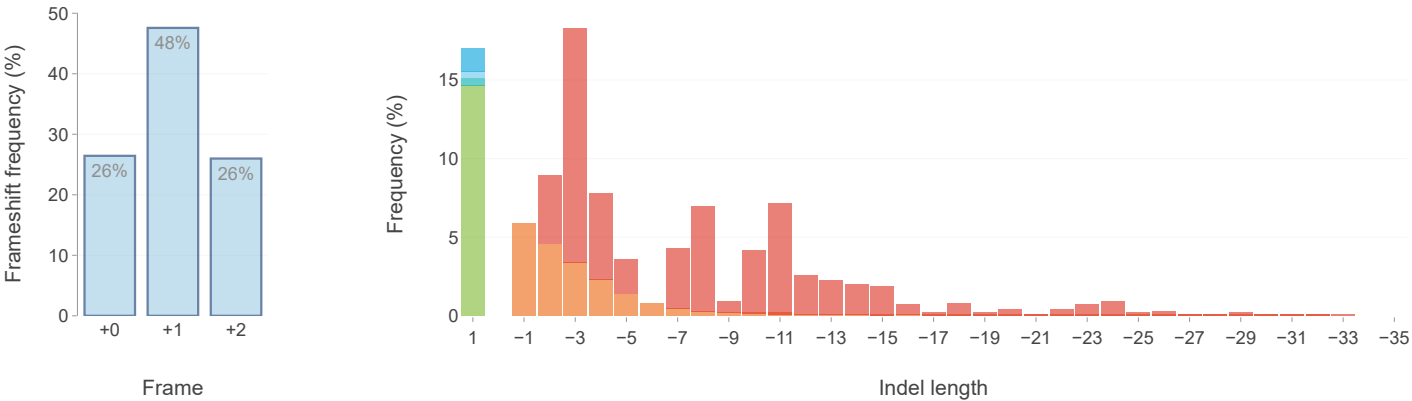


Summary of predictions at target site with gRNA: TTTACAGTATGACCGAACAA

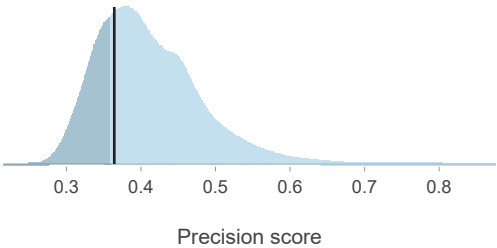
Alignment	Category	%
TCCTGGGCCTTTACAGTATGACCGAA CAATGGAGAGCCAGTGTCCCGAGTGTG	Reference	-
TCCTGGGCCTTTACAGTATGACCGAA ---TGGAGAGCCAGTGTCCCGAGTGTG	3-bp deletion	14.9
TCCTGGGCCTTTACAGTATGACCGAAACAATGGAGAGCCAGTGTCCCGAGTGTG	1-bp insertion	14.7
TCCTGGGCCTTTACAGTATG----- -----GAGAGCCAGTGTCCCGAGTGTG	11-bp deletion	7.1
TCCTGGGCCTTTACAGTATGACCGA- -----GAGCCAGTGTCCCGAGTGTG	8-bp deletion	5.7
TCCTGGGCCTTTACAGTATGACCG-- CAATGGAGAGCCAGTGTCCCGAGTGTG	2-bp deletion	4.6
TCCTGGGCCTTTACAGTATGACCGAA --ATGGAGAGCCAGTGTCCCGAGTGTG	2-bp deletion	4.4
TCCTGGGCCTTTACAGTATGACCGA- -----GCCAGTGTCCCGAGTGTG	10-bp deletion	3.5
TCCTGGGCCTTTACAGTATGACC--- CAATGGAGAGCCAGTGTCCCGAGTGTG	3-bp deletion	3.4
TCCTGGGCCTTTACAGTATGACCGAA -AATGGAGAGCCAGTGTCCCGAGTGTG	1-bp deletion	2.9
TCCTGGGCCTTTACAGTATGACCGA- CAATGGAGAGCCAGTGTCCCGAGTGTG	1-bp deletion	2.9

Indel length predictions



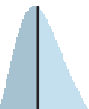
[Shareable link to your results](#)

Comparison to predictions at 13,273,449 SpCas9 target sites in human exons and introns

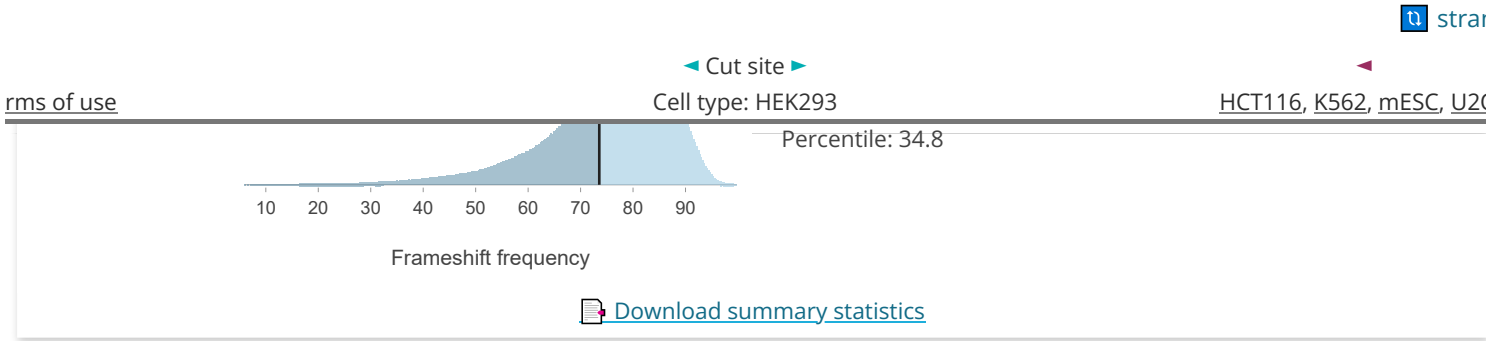


This target site has typical precision. [?](#)
Precision score: 0.36
Percentile: 26.2

[undo](#)



This target site has typical microhomology strength. [?](#)
Microhomology strength score: 0.53



All predictions of 1-bp insertion and 1- to 60-bp deletion events

Display indel type: ☒ 1-bp insertions ☒ Microhomology deletions ☒ Microhomology-less deletions

Sort by: Indel length

Frequency range: 0.05% 0.5% 1% 5% 10% 25% 50% 100%

Indel length range: +1 bp -1 bp -5 bp -10 bp -15 bp -20 bp -25 bp -30 bp -35 bp

[Download table of inDelphi genotype predictions](#)

	Indel len.	MH len.	Freq.
TCCTGGGCCTTTACAGTATGACCGAA CAATGGAGAGCCAGTGTCCCGGAGTG	+1 bp	----	1.47%
TCCTGGGCCTTTACAGTATGACCGAAATCAATGGAGAGCCAGTGTCCCGGAGTG	+1 bp	----	14.66%
TCCTGGGCCTTTACAGTATGACCGAA--AATGGAGAGCCAGTGTCCCGGAGTG	-1 bp	0 nt	2.94%
TCCTGGGCCTTTACAGTATGACCGAA-CAATGGAGAGCCAGTGTCCCGGAGTG	-1 bp	0 nt	2.94%
TCCTGGGCCTTTACAGTATGACCGAA--ATGGAGAGCCAGTGTCCCGGAGTG	-2 bp	1 nt	4.38%
TCCTGGGCCTTTACAGTATGACCG--CAATGGAGAGCCAGTGTCCCGGAGTG	-2 bp	0 nt	4.56%
TCCTGGGCCTTTACAGTATGACCG---CAATGGAGAGCCAGTGTCCCGGAGTG	-3 bp	0 nt	3.41%
TCCTGGGCCTTTACAGTATGACCGAA---TGGAGAGCCAGTGTCCCGGAGTG	-3 bp	2 nt	14.90%
TCCTGGGCCTTTACAGTATGACCGAA----GGAGAGCCAGTGTCCCGGAGTG	-4 bp	0 nt	2.31%
TCCTGGGCCTTTACAGTATGACCG---AATGGAGAGCCAGTGTCCCGGAGTG	-4 bp	1 nt	2.84%
TCCTGGGCCTTTACAGTATGACCGA---TGGAGAGCCAGTGTCCCGGAGTG	-4 bp	1 nt	2.65%
TCCTGGGCCTTTACAGTATGAC---AATGGAGAGCCAGTGTCCCGGAGTG	-5 bp	1 nt	2.21%
TCCTGGGCCTTTACAGTATGACCGAA----GAGAGCCAGTGTCCCGGAGTG	-5 bp	0 nt	0.69%
TCCTGGGCCTTTACAGTATGACCGAA-----GAGCCAGTGTCCCGGAGTG	-7 bp	1 nt	1.25%
TCCTGGGCCTTTACAGTATGACCG------GAGAGCCAGTGTCCCGGAGTG	-7 bp	1 nt	1.34%
TCCTGGGCCTTTACAGTATGA-----ATGGAGAGCCAGTGTCCCGGAGTG	-7 bp	1 nt	1.25%
TCCTGGGCCTTTACAGTATGACCGA-----GAGCCAGTGTCCCGGAGTG	-8 bp	2 nt	5.71%
TCCTGGGCCTTTACAGTATGA-----TGGAGAGCCAGTGTCCCGGAGTG	-8 bp	1 nt	0.98%
TCCTGGGCCTTTACAGTATGACCGAA-----GCCAGTGTCCCGGAGTG	-9 bp	1 nt	0.76%
TCCTGGGCCTTTACAGTATGACCGA-----GCCAGTGTCCCGGAGTG	-10 bp	2 nt	3.46%
TCCTGGGCCTTTACAGTA-----ATGGAGAGCCAGTGTCCCGGAGTG	-10 bp	1 nt	0.59%
TCCTGGGCCTTTACAGTATG-----GAGAGCCAGTGTCCCGGAGTG	-11 bp	3 nt	7.09%
TCCTGGGCCTTTACAGTATGA-----GAGCCAGTGTCCCGGAGTG	-12 bp	2 nt	2.10%
TCCTGGGCCTTTACA-----ATGGAGAGCCAGTGTCCCGGAGTG	-13 bp	2 nt	1.64%
TCCTGGGCCTTTACAGTATGA-----GCCAGTGTCCCGGAGTG	-14 bp	2 nt	1.27%
TCCTGGGCCTTTACAGTATGAC---AGTGTCCCGGAGTG	-15 bp	2 nt	1.36%
TCCTGGGCCTTTACAGTATGACCG---GAGTG	-23 bp	3 nt	0.71%
TCCTGGGCCTTTACAGT-----GTCCCGGAGTG	-24 bp	4 nt	0.72%

0

5

10

15

Frequency (%)