

N-13-1 KWMTBOMO11394

G T T T C T G G G C A G G G C C G T C G T C A C C G T A C G C G T C C C G T T T - Reference
sgRNA

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

N-16-1 KWMTBOMO04918

CCCCGATGAAAGACGACCAACGGGGCCGACCCAGTCGATCCACG-Reference
sgRNA

C	G	G	A	G	A	G	G	C	G	G	C	A	C	C	A	G	T	C	G	A	T	A	A	A	G	19.30%	11368 reads
C	C	G	A	G	A	G	G	A	C	A	C	G	G	-	C	G	A	C	C	A	T	G	T	A	C	4.193%	(296 reads)
C	C	G	A	G	A	G	G	A	C	A	C	G	G	-	O	A	C	C	A	T	G	T	A	C	4.888%	2876 reads	
C	C	G	A	G	A	G	G	A	C	A	C	G	G	-	O	A	C	C	A	T	G	T	A	C	4.065%	330 reads	
C	C	G	A	G	A	G	G	A	C	A	C	G	G	-	C	A	T	G	T	A	C	G	T	A	3.756%	2218 reads	
C	C	G	A	G	A	G	G	A	C	A	C	G	G	-	C	A	T	G	T	A	C	G	T	A	3.524%	1670 reads	
C	C	G	A	G	A	G	G	A	C	A	C	G	G	-	C	G	G	T	C	A	T	G	T	A	2.665%	1569 reads	
C	C	G	A	G	A	G	G	A	C	A	C	G	G	-	A	C	C	A	T	G	T	A	C	2.379%	1397 reads		
C	C	G	A	G	A	G	G	A	C	A	C	G	G	-	A	T	C	G	T	A	C	G	T	A	2.059%	1147 reads	
C	C	G	A	G	A	G	G	A	C	A	C	G	G	-	C	G	C	T	A	C	G	T	A	C	1.622%	953 reads	
C	C	G	A	G	A	G	G	A	C	A	C	G	G	-	C	A	T	G	T	A	C	G	T	A	1.48%	869 reads	
C	C	G	A	G	A	G	G	A	C	A	C	G	G	-	A	C	C	A	T	G	T	A	C	1.455%	855 reads		
C	C	G	A	G	A	G	G	A	C	A	C	G	G	-	C	G	C	T	A	C	G	T	A	1.356%	796 reads		
C	C	G	A	G	A	G	G	A	C	A	C	G	G	-	G	A	T	C	G	A	T	C	G	A	1.272%	721 reads	
C	C	G	A	G	A	G	G	A	C	A	C	G	G	-	G	T	C	G	A	T	C	G	A	1.252%	700 reads		
C	C	G	A	G	A	G	G	A	C	A	C	G	G	-	G	T	C	G	A	T	C	G	A	1.055%	620 reads		
C	C	G	A	G	A	G	G	A	C	A	C	G	G	-	T	C	G	A	T	C	G	A	0.951%	561 reads			
C	C	G	A	G	A	G	G	A	C	A	C	G	G	-	T	C	G	A	T	C	G	A	0.949%	555 reads			
C	C	G	A	G	A	G	G	A	C	A	C	G	G	-	C	G	C	T	A	C	G	T	A	0.939%	527 reads		
C	C	G	A	G	A	G	G	A	C	A	C	G	G	-	C	A	T	G	T	A	C	G	T	A	0.777%	452 reads	
C	C	G	A	G	A	G	G	A	C	A	C	G	G	-	C	A	G	T	G	A	T	C	G	A	0.765%	445 reads	
C	C	G	A	G	A	G	G	A	C	A	C	G	G	-	G	A	T	C	G	A	T	C	G	A	0.755%	442 reads	
C	C	G	A	G	A	G	G	A	C	A	C	G	G	-	C	G	C	T	A	C	G	T	A	0.755%	440 reads		
C	C	G	A	G	A	G	G	A	C	A	C	G	G	-	C	A	T	G	T	A	C	G	T	A	0.644%	379 reads	
C	C	G	A	G	A	G	G	A	C	A	C	G	G	-	C	G	C	T	A	C	G	T	A	0.644%	378 reads		
C	C	G	A	G	A	G	G	A	C	A	C	G	G	-	C	A	T	G	T	A	C	G	T	A	0.609%	352 reads	
C	C	G	A	G	A	G	G	A	C	A	C	G	G	-	C	G	C	T	A	C	G	T	A	0.579%	335 reads		
C	C	G	A	G	A	G	G	A	C	A	C	G	G	-	A	G	T	C	G	A	T	C	G	A	0.569%	330 reads	
C	C	G	A	G	A	G	G	A	C	A	C	G	G	-	C	A	T	G	T	A	C	G	T	A	0.555%	325 reads	
C	C	G	A	G	A	G	G	A	C	A	C	G	G	-	C	G	C	T	A	C	G	T	A	0.519%	302 reads		
C	C	G	A	G	A	G	G	A	C	A	C	G	G	-	O	A	C	C	A	T	G	T	A	0.455%	267 reads		
C	C	G	A	G	A	G	G	A	C	A	C	G	G	-	C	G	G	T	C	A	T	G	A	0.433%	252 reads		
C	C	G	A	G	A	G	G	A	C	A	C	G	G	-	C	G	C	T	A	C	G	T	A	0.414%	240 reads		
C	C	G	A	G	A	G	G	A	C	A	C	G	G	-	C	G	C	T	A	C	G	T	A	0.395%	236 reads		
C	C	G	A	G	A	G	G	A	C	A	C	G	G	-	C	A	T	G	T	A	C	G	T	A	0.379%	220 reads	
C	C	G	A	G	A	G	G	A	C	A	C	G	G	-	O	A	C	C	A	T	G	T	A	0.355%	205 reads		
C	C	G	A	G	A	G	G	A	C	A	C	G	G	-	T	G	T	C	G	A	T	C	G	A	0.34%	202 reads	
C	C	G	A	G	A	G	G	A	C	A	C	G	G	-	T	G	T	C	G	A	T	C	G	A	0.32%	191 reads	

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

N-24-1 KWMTBOMO07119

TTCTATTTATCTAACCTATAATGTTATTTAACACAGTTT-Reference
sgRNA

T	C	T	A	T	T	A	T	T	A	T	A	T	T	G	T	T	T	T	A	A	C	A	G	T	T	26	35%	(1241 reads)
T	C	T	A	T	T	A	T	T	A	T	A	T	T	A	A	C	A	G	T	T	28	35%	(759 reads)					
T	C	T	A	T	T	A	T	T	A	T	A	T	T	A	A	C	A	G	T	T	4	4.35%	(205 reads)					
T	C	T	A	T	T	A	T	T	A	T	A	T	T	A	A	C	A	G	T	T	4	4.10%	(193 reads)					
T	C	T	A	T	T	A	T	T	A	T	A	T	T	A	A	C	A	G	T	T	3	3.63%	(193 reads)					
T	C	T	A	T	T	A	T	T	A	T	A	T	T	A	A	C	A	G	T	T	2	2.52%	(128 reads)					
T	C	T	A	T	T	A	T	T	A	T	A	T	T	A	A	C	A	G	T	T	2	2.31%	(109 reads)					
T	C	T	A	T	T	A	T	T	A	T	A	T	T	A	A	C	A	G	T	T	2	2.09%	(109 reads)					
T	C	T	A	T	T	A	T	T	A	T	A	T	T	A	A	C	A	G	T	T	2	2.00%	(94 reads)					
T	C	T	A	T	T	A	T	T	A	T	A	T	T	A	A	C	A	G	T	T	1	1.78%	(84 reads)					
T	C	T	A	T	T	A	T	T	A	T	A	T	T	A	A	C	A	G	T	T	1	1.42%	(67 reads)					
T	C	T	A	T	T	A	T	T	A	T	A	T	T	A	A	C	A	G	T	T	1	1.38%	(65 reads)					
T	C	T	A	T	T	A	T	T	A	T	A	T	T	A	A	C	A	G	T	T	1	1.35%	(65 reads)					
T	C	T	A	T	T	A	T	T	A	T	A	T	T	A	A	C	A	G	T	T	1	1.32%	(62 reads)					
T	C	T	A	T	T	A	T	T	A	T	A	T	T	A	A	C	A	G	T	T	1	1.08%	(51 reads)					
T	C	T	A	T	T	A	T	T	A	T	A	T	T	A	A	C	A	G	T	T	1	0.98%	(46 reads)					
T	C	T	A	T	T	A	T	T	A	T	A	T	T	A	A	C	A	G	T	T	1	0.87%	(41 reads)					
T	C	T	A	T	T	A	T	T	A	T	A	T	T	A	A	C	A	G	T	T	1	0.79%	(37 reads)					
T	C	T	A	T	T	A	T	T	A	T	A	T	T	A	A	C	A	G	T	T	1	0.76%	(36 reads)					
T	C	T	A	T	T	A	T	T	A	T	A	T	T	A	A	C	A	G	T	T	1	0.66%	(31 reads)					
T	C	T	A	T	T	A	T	T	A	T	A	T	T	A	A	C	A	G	T	T	1	0.55%	(26 reads)					
T	C	T	A	T	T	A	T	T	A	T	A	T	T	A	A	C	A	G	T	T	1	0.45%	(20 reads)					
T	C	T	A	T	T	A	T	T	A	T	A	T	T	A	A	C	A	G	T	T	1	0.45%	(21 reads)					
T	C	T	A	T	T	A	T	T	A	T	A	T	T	A	A	C	A	G	T	T	1	0.40%	(19 reads)					
T	C	T	A	T	T	A	T	T	A	T	A	T	T	A	A	C	A	G	T	T	1	0.38%	(18 reads)					
T	C	T	A	T	T	A	T	T	A	T	A	T	T	A	A	C	A	G	T	T	1	0.36%	(17 reads)					
T	C	T	A	T	T	A	T	T	A	T	A	T	T	A	A	C	A	G	T	T	1	0.34%	(16 reads)					
T	C	T	A	T	T	A	T	T	A	T	A	T	T	A	A	C	A	G	T	T	1	0.34%	(16 reads)					
T	C	T	A	T	T	A	T	T	A	T	A	T	T	A	A	C	A	G	T	T	1	0.32%	(15 reads)					
T	C	T	A	T	T	A	T	T	A	T	A	T	T	A	A	C	A	G	T	T	1	0.30%	(14 reads)					
T	C	T	A	T	T	A	T	T	A	T	A	T	T	A	A	C	A	G	T	T	1	0.30%	(14 reads)					
T	C	T	A	T	T	A	T	T	A	T	A	T	T	A	A	C	A	G	T	T	1	0.25%	(12 reads)					
T	C	T	A	T	T	A	T	T	A	T	A	T	T	A	A	C	A	G	T	T	1	0.23%	(11 reads)					
T	C	T	A	T	T	A	T	T	A	T	A	T	T	A	A	C	A	G	T	T	1	0.23%	(11 reads)					
T	C	T	A	T	T	A	T	T	A	T	A	T	T	A	A	C	A	G	T	T	1	0.21%	(10 reads)					
T	C	T	A	T	T	A	T	T	A	T	A	T	T	A	A	C	A	G	T	T	1	0.21%	(10 reads)					

- Substitutions
- Insertions
- Deletions
- Predicted cleavage positions

N-24-1 KWMTBOMO12000

ACATTTCTAGCATCCGCTTCACGTCCGCTCTATTTCC-Reference
sgRNA

bold Substitutions
 Insertions
 Deletions

N-24-2 KWMTBOMO12000

ACATTTCTAGCATCCGCTTCACTGTCCGCCTCTATTTCC-Reference
DNA

sgRNA

bold Substitutions

Insertions

- Deletions

----- Predicted cleavage position

N-54-2 KWMTBOMO00711

CGAATTGGTCTTCGAGAATTCAAGGGTTCATGCCGCCCTC-Reference
sgRNA

bold Substitutions

Insertions

Deletions

----- Predicted cleavage position

N-44 KWMTBOMO07119

TTCTATTTATCTAACCTATAATGTATTTAACACAGTTT-Reference

sgRNA

C	T	A	T	T	T	A	A	C	C	T	A	A	T	G	T	A	T	T	T	A	A	C	A	G	T	T	33.36%	(6749 reads)	
T	T	C	A	T	T	T	A	C	T	A	T	A	-	T	G	T	A	T	T	T	A	A	C	A	G	T	T	14.17%	(2867 reads)
T	T	C	A	T	T	T	A	C	T	A	T	A	-	T	G	T	A	T	T	T	A	A	C	A	G	T	T	3.53%	(15 reads)
T	T	C	A	T	T	T	A	C	T	A	T	A	-	T	G	T	A	T	T	T	A	A	C	A	G	T	T	7.00%	(16 reads)
T	T	C	A	T	T	T	A	C	T	A	T	A	-	T	G	T	A	T	T	T	A	A	C	A	G	T	T	3.32%	(672 reads)
T	T	C	A	T	T	T	A	C	T	A	T	A	-	T	G	T	A	T	T	T	A	A	C	A	G	T	T	2.84%	(575 reads)
T	T	C	A	T	T	T	A	C	T	A	T	A	-	T	G	T	A	T	T	T	A	A	C	A	G	T	T	2.4%	(536 reads)
T	T	C	A	T	T	T	A	C	T	A	T	A	-	T	G	T	A	T	T	T	A	A	C	A	G	T	T	2.41%	(393 reads)
T	T	C	A	T	T	T	A	C	T	A	T	A	-	T	G	T	A	T	T	T	A	A	C	A	G	T	T	1.83%	(370 reads)
T	T	C	A	T	T	T	A	C	T	A	T	A	-	T	G	T	A	T	T	T	A	A	C	A	G	T	T	1.78%	(361 reads)
T	T	C	A	T	T	T	A	C	T	A	T	A	-	T	G	T	A	T	T	T	A	A	C	A	G	T	T	1.76%	(359 reads)
T	T	C	A	T	T	T	A	C	T	A	T	A	-	T	G	T	A	T	T	T	A	A	C	A	G	T	T	1.58%	(319 reads)
T	T	C	A	T	T	T	A	C	T	A	T	A	-	T	G	T	A	T	T	T	A	A	C	A	G	T	T	1.54%	(312 reads)
T	T	C	A	T	T	T	A	C	T	A	T	A	-	T	G	T	A	T	T	T	A	A	C	A	G	T	T	1.46%	(297 reads)
T	T	C	A	T	T	T	A	C	T	A	T	A	-	T	G	T	A	T	T	T	A	A	C	A	G	T	T	1.44%	(240 reads)
T	T	C	A	T	T	T	A	C	T	A	T	A	-	T	G	T	A	T	T	T	A	A	C	A	G	T	T	1.12%	(227 reads)
T	T	C	A	T	T	T	A	C	T	A	T	A	-	T	G	T	A	T	T	T	A	A	C	A	G	T	T	0.07%	(217 reads)
T	T	C	A	T	T	T	A	C	T	A	T	A	-	T	G	T	A	T	T	T	A	A	C	A	G	T	T	0.06%	(197 reads)
T	T	C	A	T	T	T	A	C	T	A	T	A	-	T	G	T	A	T	T	T	A	A	C	A	G	T	T	0.06%	(174 reads)
T	T	C	A	T	T	T	A	C	T	A	T	A	-	T	G	T	A	T	T	T	A	A	C	A	G	T	T	0.79%	(160 reads)
T	T	C	A	T	T	T	A	C	T	A	T	A	-	T	G	T	A	T	T	T	A	A	C	A	G	T	T	1.57%	(159 reads)
T	T	C	A	T	T	T	A	C	T	A	T	A	-	T	G	T	A	T	T	T	A	A	C	A	G	T	T	0.64%	(159 reads)
T	T	C	A	T	T	T	A	C	T	A	T	A	-	T	G	T	A	T	T	T	A	A	C	A	G	T	T	0.64%	(129 reads)
T	T	C	A	T	T	T	A	C	T	A	T	A	-	T	G	T	A	T	T	T	A	A	C	A	G	T	T	0.48%	(98 reads)
T	T	C	A	T	T	T	A	C	T	A	T	A	-	T	G	T	A	T	T	T	A	A	C	A	G	T	T	0.48%	(97 reads)
T	T	C	A	T	T	T	A	C	T	A	T	A	-	T	G	T	A	T	T	T	A	A	C	A	G	T	T	0.46%	(94 reads)
T	T	C	A	T	T	T	A	C	T	A	T	A	-	T	G	T	A	T	T	T	A	A	C	A	G	T	T	0.46%	(93 reads)
T	T	C	A	T	T	T	A	C	T	A	T	A	-	T	G	T	A	T	T	T	A	A	C	A	G	T	T	0.40%	(81 reads)
T	T	C	A	T	T	T	A	C	T	A	T	A	-	T	G	T	A	T	T	T	A	A	C	A	G	T	T	0.39%	(78 reads)
T	T	C	A	T	T	T	A	C	T	A	T	A	-	T	G	T	A	T	T	T	A	A	C	A	G	T	T	0.37%	(74 reads)
T	T	C	A	T	T	T	A	C	T	A	T	A	-	T	G	T	A	T	T	T	A	A	C	A	G	T	T	0.35%	(70 reads)
T	T	C	A	T	T	T	A	C	T	A	T	A	-	T	G	T	A	T	T	T	A	A	C	A	G	T	T	0.33%	(67 reads)
T	T	C	A	T	T	T	A	C	T	A	T	A	-	T	G	T	A	T	T	T	A	A	C	A	G	T	T	0.33%	(66 reads)
T	T	C	A	T	T	T	A	C	T	A	T	A	-	T	G	T	A	T	T	T	A	A	C	A	G	T	T	0.30%	(61 reads)
T	T	C	A	T	T	T	A	C	T	A	T	A	-	T	G	T	A	T	T	T	A	A	C	A	G	T	T	0.30%	(61 reads)
T	T	C	A	T	T	T	A	C	T	A	T	A	-	T	G	T	A	T	T	T	A	A	C	A	G	T	T	0.27%	(54 reads)
T	T	C	A	T	T	T	A	C	T	A	T	A	-	T	G	T	A	T	T	T	A	A	C	A	G	T	T	0.26%	(52 reads)
T	T	C	A	T	T	T	A	C	T	A	T	A	-	T	G	T	A	T	T	T	A	A	C	A	G	T	T	0.26%	(46 reads)
T	T	C	A	T	T	T	A	C	T	A	T	A	-	T	G	T	A	T	T	T	A	A	C	A	G	T	T	0.21%	(43 reads)

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

N-65-1 KWMTBOMO03319

ACTA**CTGCCATTGGGCCACCATACGGTGCACCGCTAACTA**-Reference
sgRNA

A	T	C	A	T	G	C	T	G	G	C	C	G	T	A	T	A	22.67%	(1830 reads)
A	T	C	A	T	G	C	T	G	G	C	C	G	T	A	T	A	18.07%	(1459 reads)
A	T	C	A	T	G	C	T	G	G	C	C	G	T	A	T	A	5.97%	(482 reads)
A	T	C	A	T	G	C	T	G	G	C	C	G	T	A	T	A	3.65%	(295 reads)
A	T	C	A	T	G	C	T	G	G	C	C	G	T	A	T	A	2.65%	(214 reads)
A	T	C	A	T	G	C	T	G	G	C	C	G	T	A	T	A	2.18%	(175 reads)
A	T	C	A	T	G	C	T	G	G	C	C	G	T	A	T	A	1.67%	(140 reads)
A	T	C	A	T	G	C	T	G	G	C	C	G	T	A	T	A	1.47%	(119 reads)
A	T	C	A	T	G	C	T	G	G	C	C	G	T	A	T	A	1.45%	(117 reads)
A	T	C	A	T	G	C	T	G	G	C	C	G	T	A	T	A	1.28%	(108 reads)
A	T	C	A	T	G	C	T	G	G	C	C	G	T	A	T	A	1.23%	(99 reads)
A	T	C	A	T	G	C	T	G	G	C	C	G	T	A	T	A	1.16%	(94 reads)
A	T	C	A	T	G	C	T	G	G	C	C	G	T	A	T	A	1.07%	(89 reads)
A	T	C	A	T	G	C	T	G	G	C	C	G	T	A	T	A	1.03%	(83 reads)
A	T	C	A	T	G	C	T	G	G	C	C	G	T	A	T	A	0.83%	(67 reads)
A	T	C	A	T	G	C	T	G	G	C	C	G	T	A	T	A	0.79%	(65 reads)
A	T	C	A	T	G	C	T	G	G	C	C	G	T	A	T	A	0.74%	(60 reads)
A	T	C	A	T	G	C	T	G	G	C	C	G	T	A	T	A	0.68%	(55 reads)
A	T	C	A	T	G	C	T	G	G	C	C	G	T	A	T	A	0.57%	(49 reads)
A	T	C	A	T	G	C	T	G	G	C	C	G	T	A	T	A	0.53%	(51 reads)
A	T	C	A	T	G	C	T	G	G	C	C	G	T	A	T	A	0.52%	(50 reads)
A	T	C	A	T	G	C	T	G	G	C	C	G	T	A	T	A	0.51%	(49 reads)
A	T	C	A	T	G	C	T	G	G	C	C	G	T	A	T	A	0.50%	(43 reads)
A	T	C	A	T	G	C	T	G	G	C	C	G	T	A	T	A	0.46%	(37 reads)
A	T	C	A	T	G	C	T	G	G	C	C	G	T	A	T	A	0.45%	(36 reads)
A	T	C	A	T	G	C	T	G	G	C	C	G	T	A	T	A	0.38%	(31 reads)
A	T	C	A	T	G	C	T	G	G	C	C	G	T	A	T	A	0.35%	(28 reads)
A	T	C	A	T	G	C	T	G	G	C	C	G	T	A	T	A	0.31%	(25 reads)
A	T	C	A	T	G	C	T	G	G	C	C	G	T	A	T	A	0.30%	(24 reads)
A	T	C	A	T	G	C	T	G	G	C	C	G	T	A	T	A	0.28%	(23 reads)
A	T	C	A	T	G	C	T	G	G	C	C	G	T	A	T	A	0.28%	(23 reads)
A	T	C	A	T	G	C	T	G	G	C	C	G	T	A	T	A	0.26%	(21 reads)
A	T	C	A	T	G	C	T	G	G	C	C	G	T	A	T	A	0.26%	(21 reads)
A	T	C	A	T	G	C	T	G	G	C	C	G	T	A	T	A	0.24%	(19 reads)
A	T	C	A	T	G	C	T	G	G	C	C	G	T	A	T	A	0.21%	(17 reads)

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

N-70-1 KWMTBOM001164

G C G A G T C C C T G G A C C C G A T G G G G G C G G G C C C G G A T G C A G - Reference
sgRNA

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

N-87-1 KWMTBOMO13064

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

N-75-2 KWMTBOMO14660

A C T G T G C G C C G A G T G T T G C G T G A C G G C C A C G G T A T G T T G T -Reference
sgRNA

A	T	G	T	G	C	G	C	A	G	T	T	T	T	6.77%	(1408 reads)
A	T	G	T	G	C	G	C	A	G	T	T	T	T	5.47%	(1137 reads)
A	T	G	T	G	C	G	C	A	G	T	T	T	T	4.72%	982 reads
A	T	G	T	G	C	G	C	A	G	T	T	T	T	4.05%	842 reads
A	T	G	T	G	C	G	C	A	G	T	T	T	T	3.53%	767 reads
A	T	G	T	G	C	G	C	A	G	T	T	T	T	3.14%	641 reads
A	T	G	T	G	C	G	C	A	G	T	T	T	T	2.89%	601 reads
A	T	G	T	G	C	G	C	A	G	T	T	T	T	2.36%	490 reads
A	T	G	T	G	C	G	C	A	G	T	T	T	T	2.10%	436 reads
A	T	G	T	G	C	G	C	A	G	T	T	T	T	1.96%	408 reads
A	T	G	T	G	C	G	C	A	G	T	T	T	T	1.71%	355 reads
A	T	G	T	G	C	G	C	A	G	T	T	T	T	1.57%	318 reads
A	T	G	T	G	C	G	C	A	G	T	T	T	T	1.48%	307 reads
A	T	G	T	G	C	G	C	A	G	T	T	T	T	1.47%	306 reads
A	T	G	T	G	C	G	C	A	G	T	T	T	T	1.38%	287 reads
A	T	G	T	G	C	G	C	A	G	T	T	T	T	1.12%	233 reads
A	T	G	T	G	C	G	C	A	G	T	T	T	T	1.08%	223 reads
A	T	G	T	G	C	G	C	A	G	T	T	T	T	1.02%	212 reads
A	T	G	T	G	C	G	C	A	G	T	T	T	T	0.81%	169 reads
A	T	G	T	G	C	G	C	A	G	T	T	T	T	0.79%	161 reads
A	T	G	T	G	C	G	C	A	G	T	T	T	T	0.75%	155 reads
A	T	G	T	G	C	G	C	A	G	T	T	T	T	0.73%	152 reads
A	T	G	T	G	C	G	C	A	G	T	T	T	T	0.65%	136 reads
A	T	G	T	G	C	G	C	A	G	T	T	T	T	0.64%	133 reads
A	T	G	T	G	C	G	C	A	G	T	T	T	T	0.56%	116 reads
A	T	G	T	G	C	G	C	A	G	T	T	T	T	0.51%	106 reads
A	T	G	T	G	C	G	C	A	G	T	T	T	T	0.46%	96 reads
A	T	G	T	G	C	G	C	A	G	T	T	T	T	0.44%	91 reads
A	T	G	T	G	C	G	C	A	G	T	T	T	T	0.42%	88 reads
A	T	G	T	G	C	G	C	A	G	T	T	T	T	0.39%	81 reads
A	T	G	T	G	C	G	C	A	G	T	T	T	T	0.33%	68 reads
A	T	G	T	G	C	G	C	A	G	T	T	T	T	0.32%	66 reads
A	T	G	T	G	C	G	C	A	G	T	T	T	T	0.30%	63 reads
A	T	G	T	G	C	G	C	A	G	T	T	T	T	0.25%	52 reads
A	T	G	T	G	C	G	C	A	G	T	T	T	T	0.24%	50 reads

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

N-93-2 KWMTBOMO02626

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

N-120-1 KWMTBOMO06146

A A C C A C C C A T T G G G G T A G G G A G G G G G C A A T T G C T G C C C A - Reference
sgRNA

C	C	C	C	C	C	T	G	G	G	A	T	T	T	G	C	A	23.29%	(3676 reads)	
A	C	C	C	C	C	T	G	G	G	A	T	T	T	G	C	C	9.13%	(1446 reads)	
A	C	C	C	C	C	T	G	G	G	A	T	T	T	G	C	C	7.47%	(1181 reads)	
A	C	C	C	C	C	A	T	G	G	G	A	T	T	T	G	C	C	6.01%	(966 reads)
A	C	C	C	C	C	A	T	G	G	G	A	T	T	T	G	C	C	5.58%	566 reads
A	C	C	C	C	C	T	G	G	G	A	T	T	T	G	C	C	3.08%	487 reads	
A	C	C	C	C	C	A	T	G	G	G	A	T	T	T	G	C	C	2.77%	438 reads
A	C	C	C	C	C	T	G	G	G	A	T	T	T	G	C	C	2.59%	331 reads	
A	C	C	C	C	C	T	G	G	G	A	T	T	T	G	C	C	1.90%	301 reads	
A	C	C	C	C	C	A	T	G	G	G	A	T	T	T	G	C	C	1.84%	286 reads
A	C	C	C	C	C	T	G	G	G	A	T	T	T	G	C	C	1.55%	245 reads	
A	C	C	C	C	C	A	T	G	G	G	A	T	T	T	G	C	C	1.52%	240 reads
A	C	C	C	C	C	T	G	G	G	A	T	T	T	G	C	C	1.47%	235 reads	
A	C	C	C	C	C	A	T	G	G	G	A	T	T	T	G	C	C	1.17%	17 reads
A	C	C	C	C	C	T	G	G	G	A	T	T	T	G	C	C	1.16%	184 reads	
A	C	C	C	C	C	A	T	G	G	G	A	T	T	T	G	C	C	0.95%	151 reads
A	C	C	C	C	C	T	G	G	G	A	T	T	T	G	C	C	0.88%	140 reads	
A	C	C	C	C	C	A	T	G	G	G	A	T	T	T	G	C	C	0.79%	125 reads
A	C	C	C	C	C	T	G	G	G	A	T	T	T	G	C	C	0.78%	115 reads	
A	C	C	C	C	C	A	T	G	G	G	A	T	T	T	G	C	C	0.70%	111 reads
A	C	C	C	C	C	T	G	G	G	A	T	T	T	G	C	C	0.64%	102 reads	
A	C	C	C	C	C	A	T	G	G	G	A	T	T	T	G	C	C	0.59%	95 reads
A	C	C	C	C	C	T	G	G	G	A	T	T	T	G	C	C	0.45%	72 reads	
A	C	C	C	C	C	A	T	G	G	G	A	T	T	T	G	C	C	0.44%	70 reads
A	C	C	C	C	C	T	G	G	G	A	T	T	T	G	C	C	0.44%	69 reads	
A	C	C	C	C	C	A	T	G	G	G	A	T	T	T	G	C	C	0.42%	67 reads
A	C	C	C	C	C	T	G	G	G	A	T	T	T	G	C	C	0.42%	67 reads	
A	C	C	C	C	C	A	T	G	G	G	A	T	T	T	G	C	C	0.40%	66 reads
A	C	C	C	C	C	T	G	G	G	A	T	T	T	G	C	C	0.47%	66 reads	
A	C	C	C	C	C	A	T	G	G	G	A	T	T	T	G	C	C	0.47%	66 reads
A	C	C	C	C	C	T	G	G	G	A	T	T	T	G	C	C	0.39%	61 reads	
A	C	C	C	C	C	A	T	G	G	G	A	T	T	T	G	C	C	0.39%	61 reads
A	C	C	C	C	C	T	G	G	G	A	T	T	T	G	C	C	0.35%	59 reads	
A	C	C	C	C	C	A	T	G	G	G	A	T	T	T	G	C	C	0.33%	53 reads
A	C	C	C	C	C	T	G	G	G	A	T	T	T	G	C	C	0.28%	45 reads	
A	C	C	C	C	C	A	T	G	G	G	A	T	T	T	G	C	C	0.25%	40 reads
A	C	C	C	C	C	T	G	G	G	A	T	T	T	G	C	C	0.24%	38 reads	
A	C	C	C	C	C	A	T	G	G	G	A	T	T	T	G	C	C	0.21%	33 reads
A	C	C	C	C	C	T	G	G	G	A	T	T	T	G	C	C	0.21%	33 reads	
A	C	C	C	C	C	A	T	G	G	G	A	T	T	T	G	C	C	0.20%	32 reads

bold Substitutions

Insertions

Deletion Predictor

----- Predicted cleavage position

N-130-2 KWMTBOM006044

C A G A T C G G A T A G G T C G T G A C A T G T G G G G C G C C G C T C C A A C C - Reference
sgRNA

AGGTC ... CA

bold Substitu
□ Insertion

□ Insertion - Deletion

----- Predicted cleavage position

N-152-1 KWMTBOMO11590

TTTTTTATAAGTCATCCATGTTAGGTGGGGCCAAATGGCATA-Reference
sgRNA

T	T	T	T	A	T	G	T	C	T	C	A	T	G	T	-	M	G	T	G	G	C	C	A	A	T	G	C	A	T	-	72.40%	(756 reads)								
T	T	T	T	A	T	G	T	C	T	C	A	T	G	T	-	-	G	G	C	C	A	A	T	G	C	A	T	-	72.21%	(729 reads)										
T	T	T	T	A	T	G	T	C	T	C	A	T	G	T	-	-	-	G	G	C	C	A	A	T	G	C	A	T	-	1.98%	(205 reads)									
T	T	T	T	A	T	G	T	C	T	C	A	T	G	T	-	-	-	-	G	G	C	C	A	A	T	G	C	A	T	-	1.95%	(202 reads)								
T	T	T	T	A	T	G	T	C	T	C	A	T	G	T	-	-	-	-	-	G	G	C	C	A	A	T	G	C	A	T	-	1.69%	(175 reads)							
T	T	T	T	A	T	G	T	C	T	C	A	T	G	T	-	-	-	-	-	-	G	G	C	C	A	A	T	G	C	A	T	-	0.99%	(93 reads)						
T	T	T	T	A	T	G	T	C	T	C	A	T	G	T	-	-	-	-	-	-	-	G	G	C	C	A	A	T	G	C	A	T	-	0.90%	(93 reads)					
T	T	T	T	A	T	G	T	C	T	C	A	T	G	T	-	-	-	-	-	-	-	-	G	G	C	C	A	A	T	G	C	A	T	-	0.65%	(67 reads)				
T	T	T	T	A	T	G	T	C	T	C	A	T	G	T	-	-	-	-	-	-	-	-	-	G	G	C	C	A	A	T	G	C	A	T	-	0.63%	(65 reads)			
T	T	T	T	A	T	G	T	C	T	C	A	T	G	T	-	-	-	-	-	-	-	-	-	-	G	G	C	C	A	A	T	G	C	A	T	-	0.54%	(56 reads)		
T	T	T	T	A	T	G	T	C	T	C	A	T	G	T	-	-	-	-	-	-	-	-	-	-	-	G	G	C	C	A	A	T	G	C	A	T	-	0.49%	(51 reads)	
T	T	T	T	A	T	G	T	C	T	C	A	T	G	T	-	-	-	-	-	-	-	-	-	-	-	G	G	C	C	A	A	T	G	C	A	T	-	0.49%	(51 reads)	
T	T	T	T	A	T	G	T	C	T	C	A	T	G	T	-	-	-	-	-	-	-	-	-	-	-	G	G	C	C	A	A	T	G	C	A	T	-	0.49%	(51 reads)	
T	T	T	T	A	T	G	T	C	T	C	A	T	G	T	-	-	-	-	-	-	-	-	-	-	-	G	G	C	C	A	A	T	G	C	A	T	-	0.49%	(51 reads)	
T	T	T	T	A	T	G	T	C	T	C	A	T	G	T	-	-	-	-	-	-	-	-	-	-	-	G	G	C	C	A	A	T	G	C	A	T	-	0.38%	(39 reads)	
T	T	T	T	A	T	G	T	C	T	C	A	T	G	T	-	-	-	-	-	-	-	-	-	-	-	-	G	G	C	C	A	A	T	G	C	A	T	-	0.36%	(39 reads)
T	T	T	T	A	T	G	T	C	T	C	A	T	G	T	-	-	-	-	-	-	-	-	-	-	-	-	G	G	C	C	A	A	T	G	C	A	T	-	0.35%	(39 reads)
T	T	T	T	A	T	G	T	C	T	C	A	T	G	T	-	-	-	-	-	-	-	-	-	-	-	-	G	G	C	C	A	A	T	G	C	A	T	-	0.30%	(31 reads)
T	T	T	T	A	T	G	T	C	T	C	A	T	G	T	-	-	-	-	-	-	-	-	-	-	-	-	G	G	C	C	A	A	T	G	C	A	T	-	0.29%	(30 reads)
T	T	T	T	A	T	G	T	C	T	C	A	T	G	T	-	-	-	-	-	-	-	-	-	-	-	-	G	G	C	C	A	A	T	G	C	A	T	-	0.28%	(29 reads)
T	T	T	T	A	T	G	T	C	T	C	A	T	G	T	-	-	-	-	-	-	-	-	-	-	-	-	G	G	C	C	A	A	T	G	C	A	T	-	0.26%	(27 reads)
T	T	T	T	A	T	G	T	C	T	C	A	T	G	T	-	-	-	-	-	-	-	-	-	-	-	-	G	G	C	C	A	A	T	G	C	A	T	-	0.21%	(22 reads)
T	T	T	T	A	T	G	T	C	T	C	A	T	G	T	-	-	-	-	-	-	-	-	-	-	-	-	G	G	C	C	A	A	T	G	C	A	T	-	0.20%	(21 reads)

bold Substitutions

Insertion
Deletion

- Deletion
---- Predictor

----- Predicted cleavage position

N-152-1 KWMTBOMO15293

CTGCTGCACTCGAACCTTCCCTGAGGTATAAACGCCAAT-Reference
sgRNA

T	G	C	T	G	A	C	T	T	C	G	A	G	T	T	A	A	G	C	C	A	T	-11.45%	(21545 reads)
T	G	C	T	G	A	C	T	T	C	G	A	G	T	T	A	A	G	C	C	A	T	-16.48%	(8565 reads)
T	G	C	T	G	A	C	T	T	C	G	A	G	T	T	A	A	G	C	C	A	T	-4.10%	(2132 reads)
T	G	C	T	G	A	C	T	T	C	G	A	G	T	T	A	A	G	C	C	A	T	-7.15%	(1930 reads)
T	G	C	T	G	A	C	T	T	C	G	A	G	T	T	A	A	G	C	C	A	T	-5.55%	(223 reads)
T	G	C	T	G	A	C	T	T	C	G	A	G	T	T	A	A	G	C	C	A	T	-1.80%	(936 reads)
T	G	C	T	G	A	C	T	T	C	G	A	G	T	T	A	A	G	C	C	A	T	-1.63%	(848 reads)
T	G	C	T	G	A	C	T	T	C	G	A	G	T	T	A	A	G	C	C	A	T	-1.52%	(788 reads)
T	G	C	T	G	A	C	T	T	C	G	A	G	T	T	A	A	G	C	C	A	T	-1.42%	(739 reads)
T	G	C	T	G	A	C	T	T	C	G	A	G	T	T	A	A	G	C	C	A	T	-1.35%	(600 reads)
T	G	C	T	G	A	C	T	T	C	G	A	G	T	T	A	A	G	C	C	A	T	-1.11%	(579 reads)
T	G	C	T	G	A	C	T	T	C	G	A	G	T	T	A	A	G	C	C	A	T	-0.11%	(525 reads)
T	G	C	T	G	A	C	T	T	C	G	A	G	T	T	A	A	G	C	C	A	T	-0.08%	(496 reads)
T	G	C	T	G	A	C	T	T	C	G	A	G	T	T	A	A	G	C	C	A	T	-0.01%	(423 reads)
T	G	C	T	G	A	C	T	T	C	G	A	G	T	T	A	A	G	C	C	A	T	-0.80%	(418 reads)
T	G	C	T	G	A	C	T	T	C	G	A	G	T	T	A	A	G	C	C	A	T	-0.79%	(411 reads)
T	G	C	T	G	A	C	T	T	C	G	A	G	T	T	A	A	G	C	C	A	T	-0.79%	(369 reads)
T	G	C	T	G	A	C	T	T	C	G	A	G	T	T	A	A	G	C	C	A	T	-0.75%	(367 reads)
T	G	C	T	G	A	C	T	T	C	G	A	G	T	T	A	A	G	C	C	A	T	-0.64%	(335 reads)
T	G	C	T	G	A	C	T	T	C	G	A	G	T	T	A	A	G	C	C	A	T	-0.61%	(315 reads)
T	G	C	T	G	A	C	T	T	C	G	A	G	T	T	A	A	G	C	C	A	T	-0.56%	(291 reads)
T	G	C	T	G	A	C	T	T	C	G	A	G	T	T	A	A	G	C	C	A	T	-0.55%	(286 reads)
T	G	C	T	G	A	C	T	T	C	G	A	G	T	T	A	A	G	C	C	A	T	-0.52%	(272 reads)
T	G	C	T	G	A	C	T	T	C	G	A	G	T	T	A	A	G	C	C	A	T	-0.48%	(251 reads)
T	G	C	T	G	A	C	T	T	C	G	A	G	T	T	A	A	G	C	C	A	T	-0.44%	(230 reads)
T	G	C	T	G	A	C	T	T	C	G	A	G	T	T	A	A	G	C	C	A	T	-0.43%	(223 reads)
T	G	C	T	G	A	C	T	T	C	G	A	G	T	T	A	A	G	C	C	A	T	-0.35%	(183 reads)
T	G	C	T	G	A	C	T	T	C	G	A	G	T	T	A	A	G	C	C	A	T	-0.32%	(164 reads)
T	G	C	T	G	A	C	T	T	C	G	A	G	T	T	A	A	G	C	C	A	T	-0.28%	(145 reads)
T	G	C	T	G	A	C	T	T	C	G	A	G	T	T	A	A	G	C	C	A	T	-0.23%	(120 reads)

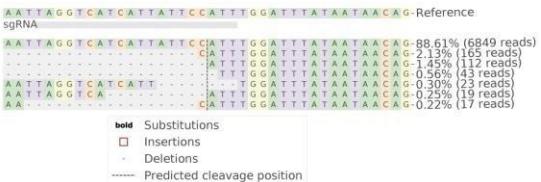
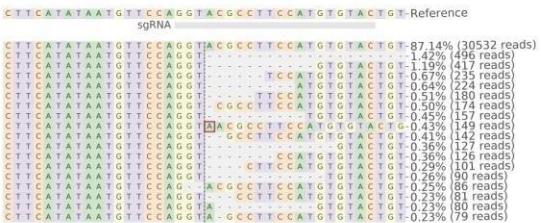
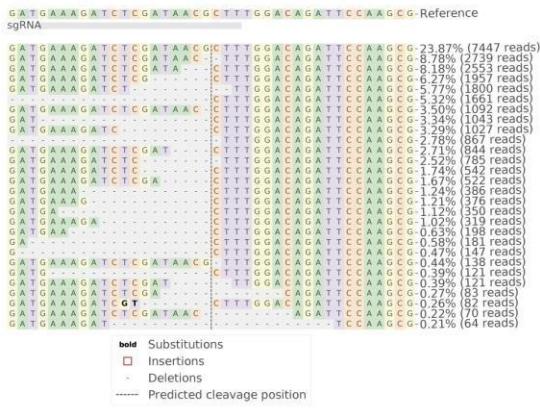
bold Substitutions

- Insertions
- Deletions

- Deletion
---- Predicted

Predicted cleavage position

N-152-1 KWMTBOMO13293



N-195-2 KWMTBOMO01805

CTTGTTCATTCACACAGATGATGGCAAGCTTTGGCCAA-Reference
sgRNA

T	G	T	T	C	A	T	C	A	G	T	T	G	C	A	A	16.23%	(4973 reads)
C	T	G	T	C	A	T	T	C	A	G	T	T	G	C	A	16.03%	(4876 reads)
C	T	G	T	C	A	T	T	C	A	G	T	T	G	C	A	6.28%	(1911 reads)
C	T	G	T	C	A	T	T	C	A	G	T	T	G	C	A	5.21%	(1133 reads)
C	T	G	T	C	A	T	T	C	A	G	T	T	G	C	A	3.12%	(948 reads)
C	T	G	T	C	A	T	T	C	A	G	T	T	G	C	A	2.77%	(843 reads)
C	T	G	T	C	A	T	T	C	A	G	T	T	G	C	A	2.47%	(782 reads)
C	T	G	T	C	A	T	T	C	A	G	T	T	G	C	A	1.84%	(560 reads)
C	T	G	T	C	A	T	T	C	A	G	T	T	G	C	A	1.62%	(494 reads)
C	T	G	T	C	A	T	T	C	A	G	T	T	G	C	A	1.37%	(417 reads)
C	T	G	T	C	A	T	T	C	A	G	T	T	G	C	A	1.20%	(365 reads)
C	T	G	T	C	A	T	T	C	A	G	T	T	G	C	A	1.05%	(354 reads)
C	T	G	T	C	A	T	T	C	A	G	T	T	G	C	A	1.00%	(334 reads)
C	T	G	T	C	A	T	T	C	A	G	T	T	G	C	A	1.10%	(334 reads)
C	T	G	T	C	A	T	T	C	A	G	T	T	G	C	A	0.96%	(293 reads)
C	T	G	T	C	A	T	T	C	A	G	T	T	G	C	A	0.89%	(270 reads)
C	T	G	T	C	A	T	T	C	A	G	T	T	G	C	A	0.80%	(243 reads)
C	T	G	T	C	A	T	T	C	A	G	T	T	G	C	A	0.64%	(191 reads)
C	T	G	T	C	A	T	T	C	A	G	T	T	G	C	A	0.61%	(105 reads)
C	T	G	T	C	A	T	T	C	A	G	T	T	G	C	A	0.60%	(102 reads)
C	T	G	T	C	A	T	T	C	A	G	T	T	G	C	A	0.57%	(102 reads)
C	T	G	T	C	A	T	T	C	A	G	T	T	G	C	A	0.55%	(161 reads)
C	T	G	T	C	A	T	T	C	A	G	T	T	G	C	A	0.49%	(161 reads)
C	T	G	T	C	A	T	T	C	A	G	T	T	G	C	A	0.48%	(146 reads)
C	T	G	T	C	A	T	T	C	A	G	T	T	G	C	A	0.44%	(134 reads)
C	T	G	T	C	A	T	T	C	A	G	T	T	G	C	A	0.42%	(127 reads)
C	T	G	T	C	A	T	T	C	A	G	T	T	G	C	A	0.41%	(126 reads)
C	T	G	T	C	A	T	T	C	A	G	T	T	G	C	A	0.41%	(124 reads)
C	T	G	T	C	A	T	T	C	A	G	T	T	G	C	A	0.38%	(117 reads)
C	T	G	T	C	A	T	T	C	A	G	T	T	G	C	A	0.36%	(108 reads)
C	T	G	T	C	A	T	T	C	A	G	T	T	G	C	A	0.33%	(100 reads)
C	T	G	T	C	A	T	T	C	A	G	T	T	G	C	A	0.30%	(92 reads)
C	T	G	T	C	A	T	T	C	A	G	T	T	G	C	A	0.29%	(89 reads)
C	T	G	T	C	A	T	T	C	A	G	T	T	G	C	A	0.26%	(79 reads)
C	T	G	T	C	A	T	T	C	A	G	T	T	G	C	A	0.25%	(76 reads)
C	T	G	T	C	A	T	T	C	A	G	T	T	G	C	A	0.22%	(69 reads)
C	T	G	T	C	A	T	T	C	A	G	T	T	G	C	A	0.21%	(63 reads)

bold Substitutions

- Insertions
- Deletions
- Predicted cleavage position

N-221-2 KWMTBOMO05783

GGCGATTACCTTGTAAATCGTAGGTGGTGAAAAACCAAA-Reference

sgRNA	Sequence	Reads
G	G C A T T A C C T T G T T T A A T	67.97% (7596 reads)
G	G C G A T T A C C T T G T T T A A T	8.19% (915 reads)
G	G C G A T T A C C T T G T T T A A T	2.47% (276 reads)
G	G C G A T T A C C T T G T T T A A T	2.12% (237 reads)
G	G C G A T T A C C T T G T T T A A T	1.17% (131 reads)
G	G C G A T T A C C T T G T T T A A T	0.89% (99 reads)
G	G C G A T T A C C T T G T T T A A T	0.86% (96 reads)
G	G C G A T T A C C T T G T T T A A T	0.78% (87 reads)
G	G C G A T T A C C T T G T T T A A T	0.65% (73 reads)
G	G C G A T T A C C T T G T T T A A T	0.57% (64 reads)
G	G C G A T T A C C T T G T T T A A T	0.52% (58 reads)
G	G C G A T T A C C T T G T T T A A T	0.43% (48 reads)
G	G C G A T T A C C T T G T T T A A T	0.37% (41 reads)
G	G C G A T T A C C T T G T T T A A T	0.36% (40 reads)
G	G C G A T T A C C T T G T T T A A T	0.33% (35 reads)
G	G C G A T T A C C T T G T T T A A T	0.27% (30 reads)
G	G C G A T T A C C T T G T T T A A T	0.23% (28 reads)

bold Substitutions

- Insertions
- Deletions
- Predicted cleavage position

N-204-1 KWMTBOMO06524

CATCTCCGAGAGCGAGGCCCTAGCAGGGCTATAGCCGTGAA-Reference
sgRNA

A	T	C	T	C	C	G	A	G	C	G	A	C	T	A	G	A	G	G	C	T	T	A	G	C	G	T	A	A	13.80%	(10563 reads)	
C	A	T	C	T	C	G	A	G	A	G	-	-	-	A	G	C	A	G	G	C	T	T	A	G	C	G	T	A	A	8.47%	(6485 reads)
C	A	T	C	T	C	G	A	G	A	G	-	-	-	A	G	C	A	G	G	C	T	T	A	G	C	G	T	A	A	4.73%	(3619 reads)
C	A	T	C	T	C	G	A	G	A	G	-	-	-	A	G	C	A	G	G	C	T	T	A	G	C	G	T	A	A	4.74%	(3624 reads)
C	A	T	C	T	C	G	A	G	A	G	-	-	-	A	G	C	A	G	G	C	T	T	A	G	C	G	T	A	A	4.19%	(3207 reads)
C	A	T	C	T	C	G	A	G	A	G	-	-	-	A	G	C	A	G	G	C	T	T	A	G	C	G	T	A	A	3.84%	(2940 reads)
C	A	T	C	T	C	G	A	G	A	G	-	-	-	A	G	C	A	G	G	C	T	T	A	G	C	G	T	A	A	3.49%	(2669 reads)
C	A	T	C	T	C	G	A	G	A	G	-	-	-	A	G	C	A	G	G	C	T	T	A	G	C	G	T	A	A	3.36%	(2517 reads)
C	A	T	C	T	C	G	A	G	A	G	-	-	-	A	G	C	A	G	G	C	T	T	A	G	C	G	T	A	A	2.78%	(1749 reads)
C	A	T	C	T	C	G	A	G	A	G	-	-	-	A	G	C	A	G	G	C	T	T	A	G	C	G	T	A	A	2.77%	(1741 reads)
C	A	T	C	T	C	G	A	G	A	G	-	-	-	A	G	C	A	G	G	C	T	T	A	G	C	G	T	A	A	2.07%	(1585 reads)
C	A	T	C	T	C	G	A	G	A	G	-	-	-	A	G	C	A	G	G	C	T	T	A	G	C	G	T	A	A	1.98%	(1513 reads)
C	A	T	C	T	C	G	A	G	A	G	-	-	-	A	G	C	A	G	G	C	T	T	A	G	C	G	T	A	A	1.87%	(1432 reads)
C	A	T	C	T	C	G	A	G	A	G	-	-	-	A	G	C	A	G	G	C	T	T	A	G	C	G	T	A	A	1.76%	(1309 reads)
C	A	T	C	T	C	G	A	G	A	G	-	-	-	A	G	C	A	G	G	C	T	T	A	G	C	G	T	A	A	1.72%	(917 reads)
C	A	T	C	T	C	G	A	G	A	G	-	-	-	A	G	C	A	G	G	C	T	T	A	G	C	G	T	A	A	1.19%	(912 reads)
C	A	T	C	T	C	G	A	G	A	G	-	-	-	A	G	C	A	G	G	C	T	T	A	G	C	G	T	A	A	1.2%	(858 reads)
C	A	T	C	T	C	G	A	G	A	G	-	-	-	A	G	C	A	G	G	C	T	T	A	G	C	G	T	A	A	0.84%	(643 reads)
C	A	T	C	T	C	G	A	G	A	G	-	-	-	A	G	C	A	G	G	C	T	T	A	G	C	G	T	A	A	0.82%	(627 reads)
C	A	T	C	T	C	G	A	G	A	G	-	-	-	A	G	C	A	G	G	C	T	T	A	G	C	G	T	A	A	0.80%	(611 reads)
C	A	T	C	T	C	G	A	G	A	G	-	-	-	A	G	C	A	G	G	C	T	T	A	G	C	G	T	A	A	0.80%	(609 reads)
C	A	T	C	T	C	G	A	G	A	G	-	-	-	A	G	C	A	G	G	C	T	T	A	G	C	G	T	A	A	0.66%	(505 reads)
C	A	T	C	T	C	G	A	G	A	G	-	-	-	A	G	C	A	G	G	C	T	T	A	G	C	G	T	A	A	0.64%	(488 reads)
C	A	T	C	T	C	G	A	G	A	G	-	-	-	A	G	C	A	G	G	C	T	T	A	G	C	G	T	A	A	0.61%	(467 reads)
C	A	T	C	T	C	G	A	G	A	G	-	-	-	A	G	C	A	G	G	C	T	T	A	G	C	G	T	A	A	0.59%	(449 reads)
C	A	T	C	T	C	G	A	G	A	G	-	-	-	A	G	C	A	G	G	C	T	T	A	G	C	G	T	A	A	0.49%	(378 reads)
C	A	T	C	T	C	G	A	G	A	G	-	-	-	A	G	C	A	G	G	C	T	T	A	G	C	G	T	A	A	0.48%	(366 reads)
C	A	T	C	T	C	G	A	G	A	G	-	-	-	A	G	C	A	G	G	C	T	T	A	G	C	G	T	A	A	0.47%	(359 reads)
C	A	T	C	T	C	G	A	G	A	G	-	-	-	A	G	C	A	G	G	C	T	T	A	G	C	G	T	A	A	0.44%	(336 reads)
C	A	T	C	T	C	G	A	G	A	G	-	-	-	A	G	C	A	G	G	C	T	T	A	G	C	G	T	A	A	0.41%	(317 reads)
C	A	T	C	T	C	G	A	G	A	G	-	-	-	A	G	C	A	G	G	C	T	T	A	G	C	G	T	A	A	0.41%	(315 reads)
C	A	T	C	T	C	G	A	G	A	G	-	-	-	A	G	C	A	G	G	C	T	T	A	G	C	G	T	A	A	0.30%	(258 reads)
C	A	T	C	T	C	G	A	G	A	G	-	-	-	A	G	C	A	G	G	C	T	T	A	G	C	G	T	A	A	0.28%	(217 reads)
C	A	T	C	T	C	G	A	G	A	G	-	-	-	A	G	C	A	G	G	C	T	T	A	G	C	G	T	A	A	0.28%	(215 reads)
C	A	T	C	T	C	G	A	G	A	G	-	-	-	A	G	C	A	G	G	C	T	T	A	G	C	G	T	A	A	0.26%	(199 reads)
C	A	T	C	T	C	G	A	G	A	G	-	-	-	A	G	C	A	G	G	C	T	T	A	G	C	G	T	A	A	0.25%	(193 reads)
C	A	T	C	T	C	G	A	G	A	G	-	-	-	A	G	C	A	G	G	C	T	T	A	G	C	G	T	A	A	0.21%	(160 reads)

bold Substitutions

- Insertions
- Deletions
- Predicted cleavage position

N-223 KWMTBOMO11741

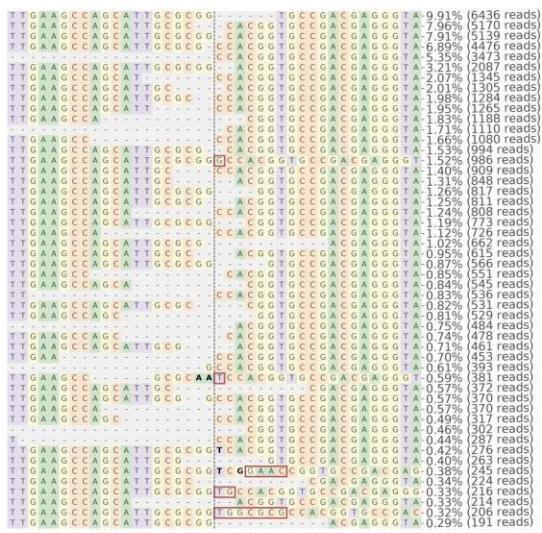
ATGTAAC TGAGAAGCCTCC TTCAAGTATTGAAGGGATTGC-Reference

bold Substitutions

- Insertions
- Deletions

N-233 KWMTBOMO09983

TTGAAAGCCAGCATTGCGCGGCA CGT GCGGACCGAGGGTA-Reference
sgRNA



bold Substitutions

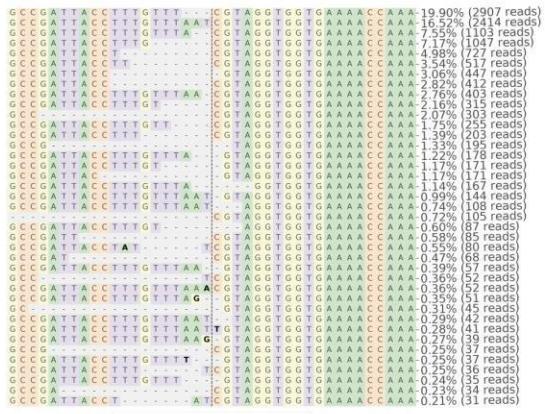
□ Insertions

- Deletions

----- Predicted cleavage position

N-241-2 KWMTBOMO05783

GCGGATTACCTTTTTAATCGTAGGTGGTGAAAACCAAA-Reference
sgRNA



bold Substitutions

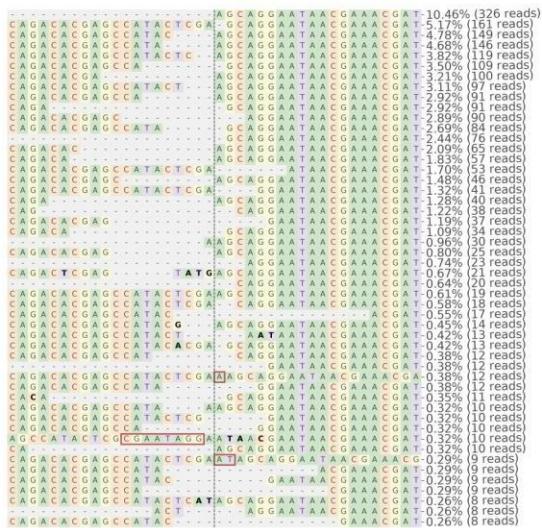
□ Insertions

- Deletions

----- Predicted cleavage position

N-257-1 KWMTBOMO04687_promoter

CAGACACGAGCCATACTCGAAGAATAACGAAACGAT-Reference
sgRNA



bold Substitutions

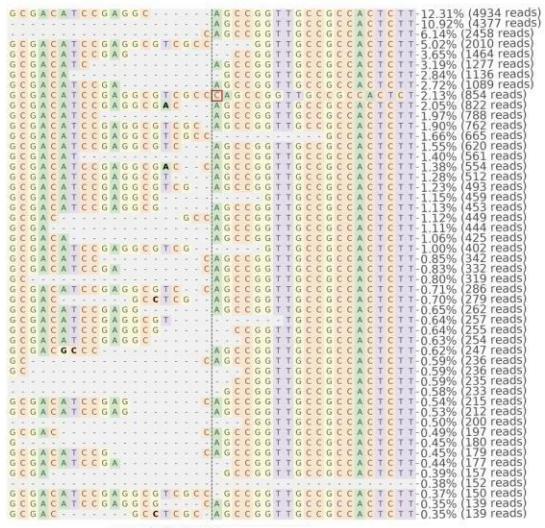
□ Insertions

- Deletions

----- Predicted cleavage position

N-268-2 KWMTBOMO02712

GCGACATCCGGGGTCCCGACCGCGTTGCGCACCTT-Reference
sgRNA



bold Substitutions

□ Insertions

- Deletions

----- Predicted cleavage position

N-280-3 KWMTBOMO12902

CGCTGAGAACCTTCCAGCAGTCATTTAAACTTCCAAA-Reference
sgRNA

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

N-292-1 KWMTBOMO04687

GAAGC AAGCAGTCCGCTGTCCCTGAACAACTCTGGACAG-Reference
sgRNA

G	A	G	C	A	A	G	A	T	G	C	T	G	T	-	A	C	A	T	C	T	G	G	A	18.7%	(5759 reads)			
G	A	G	C	A	A	G	A	T	G	C	T	G	T	-	T	G	A	C	A	T	C	G	G	A	13.7%	(4318 reads)		
G	A	G	C	A	A	G	A	T	G	C	T	G	T	-	T	G	A	C	A	T	C	G	G	A	8.62%	(2712 reads)		
G	A	G	C	A	A	G	A	T	G	C	T	G	T	-	C	T	G	A	C	A	T	C	G	G	A	7.42%	(2344 reads)	
G	A	G	C	A	A	G	A	T	G	C	T	G	T	-	G	C	A	C	A	T	C	T	G	G	A	3.74%	(1116 reads)	
G	A	G	C	A	A	G	A	T	G	C	T	G	T	-	T	G	A	C	A	T	C	T	G	G	A	3.77%	(872 reads)	
G	A	G	C	A	A	G	A	T	G	C	T	G	T	-	T	G	A	C	A	T	C	T	G	G	A	2.63%	(827 reads)	
G	A	G	C	A	A	G	A	T	G	C	T	G	T	-	C	T	G	A	C	A	T	C	T	G	G	A	2.39%	(752 reads)
G	A	G	C	A	A	G	A	T	G	C	T	G	T	-	T	G	A	C	A	T	C	T	G	G	A	2.04%	(691 reads)	
G	A	G	C	A	A	G	A	T	G	C	T	G	T	-	C	T	G	A	C	A	T	C	T	G	G	A	1.94%	(609 reads)
G	A	G	C	A	A	G	A	T	G	C	T	G	T	-	A	C	A	T	C	T	G	G	A	1.60%	(502 reads)			
G	A	G	C	A	A	G	A	T	G	C	T	G	T	-	C	T	G	A	C	A	T	C	T	G	G	A	1.45%	(456 reads)
G	A	G	C	A	A	G	A	T	G	C	T	G	T	-	A	C	A	T	C	T	G	G	A	1.13%	(357 reads)			
G	A	G	C	A	A	G	A	T	G	C	T	G	T	-	C	T	G	A	C	A	T	C	T	G	G	A	0.95%	(300 reads)
G	A	G	C	A	A	G	A	T	G	C	T	G	T	-	T	C	G	A	C	A	T	C	T	G	G	A	0.90%	(295 reads)
G	A	G	C	A	A	G	A	T	G	C	T	G	T	-	C	T	G	A	C	A	T	C	T	G	G	A	0.72%	(226 reads)
G	A	G	C	A	A	G	A	T	G	C	T	G	T	-	A	C	A	T	C	T	G	G	A	0.72%	(225 reads)			
G	A	G	C	A	A	G	A	T	G	C	T	G	T	-	C	T	G	A	C	A	T	C	T	G	G	A	0.69%	(204 reads)
G	A	G	C	A	A	G	A	T	G	C	T	G	T	-	A	C	A	T	C	T	G	G	A	0.64%	(201 reads)			
G	A	G	C	A	A	G	A	T	G	C	T	G	T	-	C	T	G	A	C	A	T	C	T	G	G	A	0.60%	(189 reads)
G	A	G	C	A	A	G	A	T	G	C	T	G	T	-	A	C	A	T	C	T	G	G	A	0.54%	(184 reads)			
G	A	G	C	A	A	G	A	T	G	C	T	G	T	-	C	T	G	A	C	A	T	C	T	G	G	A	0.5%	(162 reads)
G	A	G	C	A	A	G	A	T	G	C	T	G	T	-	C	T	G	A	C	A	T	C	T	G	G	A	0.47%	(149 reads)
G	A	G	C	A	A	G	A	T	G	C	T	G	T	-	C	T	G	A	C	A	T	C	T	G	G	A	0.44%	(138 reads)
G	A	G	C	A	A	G	A	T	G	C	T	G	T	-	C	T	G	A	C	A	T	C	T	G	G	A	0.42%	(132 reads)
G	A	G	C	A	A	G	A	T	G	C	T	G	T	-	C	T	G	A	C	A	T	C	T	G	G	A	0.39%	(123 reads)
G	A	G	C	A	A	G	A	T	G	C	T	G	T	-	A	C	A	T	C	T	G	G	A	0.38%	(120 reads)			
G	A	G	C	A	A	G	A	T	G	C	T	G	T	-	C	T	G	A	C	A	T	C	T	G	G	A	0.36%	(114 reads)
G	A	G	C	A	A	G	A	T	G	C	T	G	T	-	C	T	G	A	C	A	T	C	T	G	G	A	0.36%	(114 reads)
G	A	G	C	A	A	G	A	T	G	C	T	G	T	-	A	C	A	T	C	T	G	G	A	0.34%	(108 reads)			
G	A	G	C	A	A	G	A	T	G	C	T	G	T	-	C	T	G	A	C	A	T	C	T	G	G	A	0.33%	(103 reads)
G	A	G	C	A	A	G	A	T	G	C	T	G	T	-	T	C	G	A	C	A	T	C	T	G	G	A	0.32%	(102 reads)
G	A	G	C	A	A	G	A	T	G	C	T	G	T	-	C	T	G	A	C	A	T	C	T	G	G	A	0.31%	(98 reads)
G	A	G	C	A	A	G	A	T	G	C	T	G	T	-	C	A	G	A	C	A	T	C	T	G	G	A	0.31%	(96 reads)
G	A	G	C	A	A	G	A	T	G	C	T	G	T	-	C	T	G	A	C	A	T	C	T	G	G	A	0.28%	(88 reads)
G	A	G	C	A	A	G	A	T	G	C	T	G	T	-	C	T	G	A	C	A	T	C	T	G	G	A	0.27%	(85 reads)
G	A	G	C	A	A	G	A	T	G	C	T	G	T	-	A	C	G	A	C	A	T	C	T	G	G	A	0.24%	(77 reads)
G	A	G	C	A	A	G	A	T	G	C	T	G	T	-	T	C	G	A	C	A	T	C	T	G	G	A	0.24%	(74 reads)
G	A	G	C	A	A	G	A	T	G	C	T	G	T	-	C	T	G	A	C	A	T	C	T	G	G	A	0.22%	(70 reads)
G	A	G	C	A	A	G	A	T	G	C	T	G	T	-	G	C	A	C	A	T	C	T	G	G	A	0.22%	(69 reads)	
G	A	G	C	A	A	G	A	T	G	C	T	G	T	-	C	T	G	A	C	A	T	C	T	G	G	A	0.20%	(64 reads)

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

N-296-1 KWMTBOMO03436

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

G	A	A	G	G	G	G	G	A	G	A	G	12.31%	(4671 reads)
G	A	A	C	T	C	G	G	T	G	T	G	7.59%	(2879 reads)
G	A	A	C	T	C	G	G	T	G	T	G	7.77%	(1812 reads)
G	A	A	C	T	C	G	G	T	G	T	G	3.14%	(1191 reads)
G	A	A	C	T	C	G	G	T	G	T	G	2.89%	(1048 reads)
G	A	A	C	T	C	G	G	T	G	T	G	2.66%	(1010 reads)
G	A	A	C	T	C	G	G	T	G	T	G	2.66%	(1010 reads)
G	A	A	C	T	C	G	G	T	G	T	G	2.08%	(791 reads)
G	A	A	C	T	C	G	G	T	G	T	G	1.96%	(744 reads)
G	A	A	C	T	C	G	G	T	G	T	G	1.78%	(678 reads)
G	A	A	C	T	C	G	G	T	G	T	G	1.53%	(582 reads)
G	A	A	C	T	C	G	G	T	G	T	G	1.52%	(576 reads)
G	A	A	C	T	C	G	G	T	G	T	G	1.44%	(565 reads)
G	A	A	C	T	C	G	G	T	G	T	G	1.44%	(564 reads)
G	A	A	C	T	C	G	G	T	G	T	G	1.39%	(527 reads)
G	A	A	C	T	C	G	G	T	G	T	G	1.05%	(399 reads)
G	A	A	C	T	C	G	G	T	G	T	G	1.00%	(379 reads)
G	A	A	C	T	C	G	G	T	G	T	G	0.98%	(371 reads)
G	A	A	C	T	C	G	G	T	G	T	G	0.88%	(333 reads)
G	A	A	C	T	C	G	G	T	G	T	G	0.72%	(275 reads)
G	A	A	C	T	C	G	G	T	G	T	G	0.63%	(200 reads)
G	A	A	C	T	C	G	G	T	G	T	G	0.53%	(200 reads)
G	A	A	C	T	C	G	G	T	G	T	G	0.50%	(188 reads)
G	A	A	C	T	C	G	G	T	G	T	G	0.48%	(184 reads)
G	A	A	C	T	C	G	G	T	G	T	G	0.47%	(178 reads)
G	A	A	C	T	C	G	G	T	G	T	G	0.44%	(167 reads)
G	A	A	C	T	C	G	G	T	G	T	G	0.36%	(138 reads)
G	A	A	C	T	C	G	G	T	G	T	G	0.35%	(130 reads)
G	A	A	C	T	C	G	G	T	G	T	G	0.32%	(128 reads)
G	A	A	C	T	C	G	G	T	G	T	G	0.32%	(123 reads)
G	A	A	C	T	C	G	G	T	G	T	G	0.32%	(123 reads)
G	A	A	C	T	C	G	G	T	G	T	G	0.26%	(98 reads)
G	A	A	C	T	C	G	G	T	G	T	G	0.25%	(93 reads)
G	A	A	C	T	C	G	G	T	G	T	G	0.24%	(92 reads)
G	A	A	C	T	C	G	G	T	G	T	G	0.24%	(91 reads)
G	A	A	C	T	C	G	G	T	G	T	G	0.23%	(87 reads)

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

N-297-2 KWMTBOMO08464

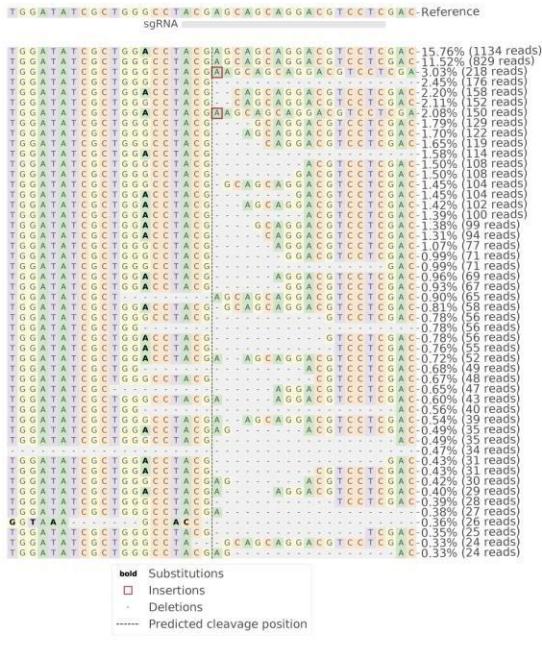
TTGACTTGCATAATCGCCCTGGCTGGCCATGTCCTTCAAG Reference
sgRNA

T	G	A	C	T	G	C	C	T	G	T	G	C	A	G	A	G	17.7%	(4891 reads)
T	T	G	A	C	T	G	C	A	T	G	C	T	T	C	T	A	4.17%	(1181 reads)
T	T	G	A	C	T	G	C	C	A	T	G	C	T	T	C	A	4.12%	(1167 reads)
T	T	G	A	C	T	G	C	C	A	T	G	C	T	T	C	A	3.45%	(978 reads)
T	T	G	A	C	T	G	C	C	A	T	G	C	T	T	C	A	3.38%	(957 reads)
T	T	G	A	C	T	G	C	C	A	T	G	C	T	T	C	A	3.42%	(957 reads)
T	T	G	A	C	T	G	C	C	A	T	G	C	T	T	C	A	3.45%	(957 reads)
T	T	G	A	C	T	G	C	C	A	T	G	C	T	T	C	A	1.96%	(554 reads)
T	T	G	A	C	T	G	C	C	A	T	G	C	T	T	C	A	1.84%	(522 reads)
T	T	G	A	C	T	G	C	C	A	T	G	C	T	T	C	A	1.81%	(512 reads)
T	T	G	A	C	T	G	C	C	A	T	G	C	T	T	C	A	1.67%	(474 reads)
T	T	G	A	C	T	G	C	C	A	T	G	C	T	T	C	A	1.46%	(414 reads)
T	T	G	A	C	T	G	C	C	A	T	G	C	T	T	C	A	1.44%	(409 reads)
T	T	G	A	C	T	G	C	C	A	T	G	C	T	T	C	A	1.36%	(385 reads)
T	T	G	A	C	T	G	C	C	A	T	G	C	T	T	C	A	1.13%	(319 reads)
T	T	G	A	C	T	G	C	C	A	T	G	C	T	T	C	A	1.11%	(315 reads)
T	T	G	A	C	T	G	C	C	A	T	G	C	T	T	C	A	0.90%	(256 reads)
T	T	G	A	C	T	G	C	C	A	T	G	C	T	T	C	A	0.82%	(233 reads)
T	T	G	A	C	T	G	C	C	A	T	G	C	T	T	C	A	0.82%	(233 reads)
T	T	G	A	C	T	G	C	C	A	T	G	C	T	T	C	A	0.74%	(209 reads)
T	T	G	A	C	T	G	C	C	A	T	G	C	T	T	C	A	0.64%	(182 reads)
T	T	G	A	C	T	G	C	C	A	T	G	C	T	T	C	A	0.61%	(172 reads)
T	T	G	A	C	T	G	C	C	A	T	G	C	T	T	C	A	0.59%	(167 reads)
T	T	G	A	C	T	G	C	C	A	T	G	C	T	T	C	A	0.59%	(166 reads)
T	T	G	A	C	T	G	C	C	A	T	G	C	T	T	C	A	0.56%	(160 reads)
T	T	G	A	C	T	G	C	C	A	T	G	C	T	T	C	A	0.55%	(157 reads)
T	T	G	A	C	T	G	C	C	A	T	G	C	T	T	C	A	0.52%	(153 reads)
T	T	G	A	C	T	G	C	C	A	T	G	C	T	T	C	A	0.54%	(153 reads)
T	T	G	A	C	T	G	C	C	A	T	G	C	T	T	C	A	0.53%	(146 reads)
T	T	G	A	C	T	G	C	C	A	T	G	C	T	T	C	A	0.47%	(132 reads)
T	T	G	A	C	T	G	C	C	A	T	G	C	T	T	C	A	0.46%	(131 reads)
T	T	G	A	C	T	G	C	C	A	T	G	C	T	T	C	A	0.37%	(105 reads)
T	T	G	A	C	T	G	C	C	A	T	G	C	T	T	C	A	0.35%	(95 reads)
T	T	G	A	C	T	G	C	C	A	T	G	C	T	T	C	A	0.33%	(94 reads)
T	T	G	A	C	T	G	C	C	A	T	G	C	T	T	C	A	0.31%	(88 reads)
T	T	G	A	C	T	G	C	C	A	T	G	C	T	T	C	A	0.29%	(75 reads)

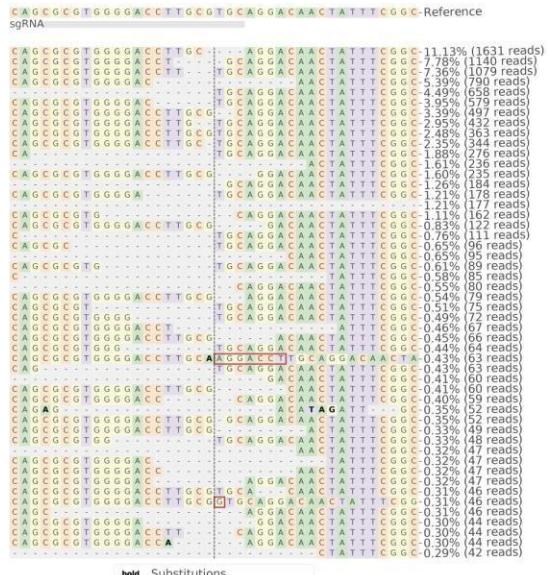
- Substitutions
- Insertions
- Deletions

----- Predicted cleavage position

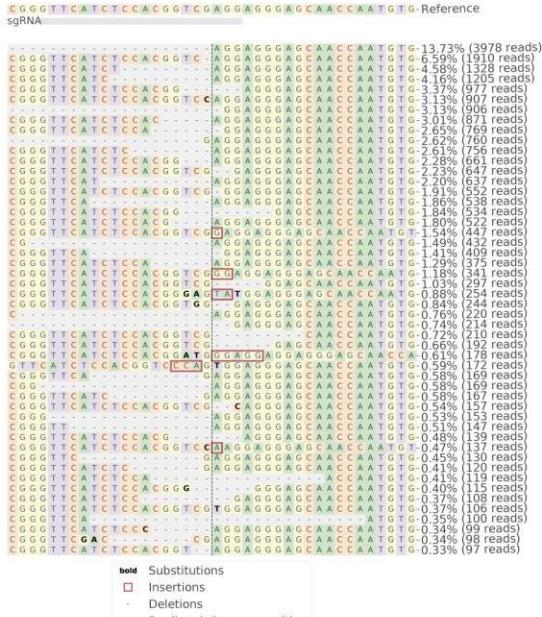
N-297-2 KWMTBOMO13971



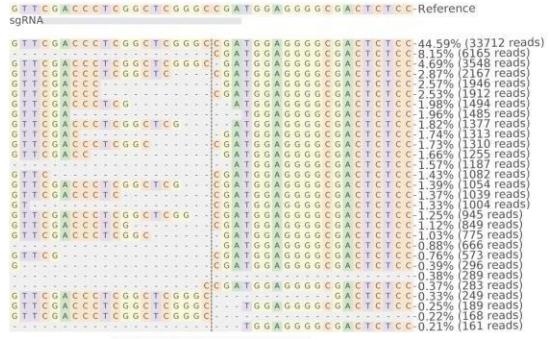
N-300-1 KWMTBOMO1641



N-353-1 KWMTBOMO08448



N-371-2 KWMTBOMO07554



bold Substitutions

□ Insertions

- Deletions

----- Predicted cleavage position

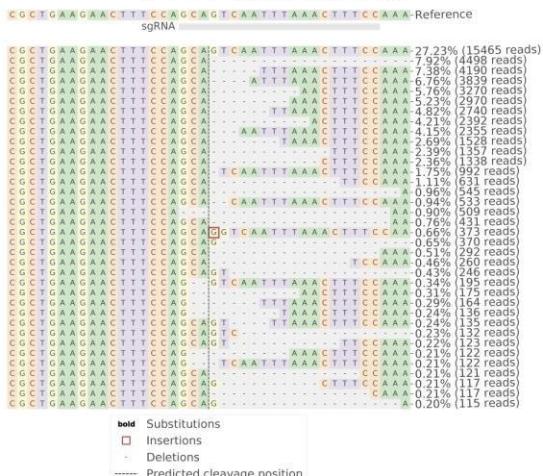
bold Substitutions

□ Insertions

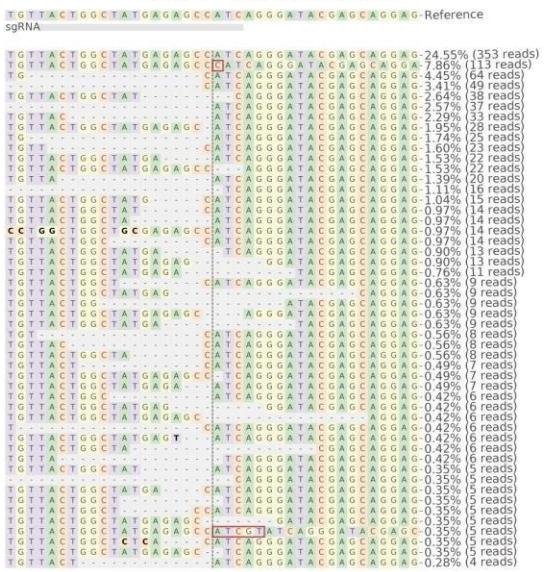
- Deletions

----- Predicted cleavage position

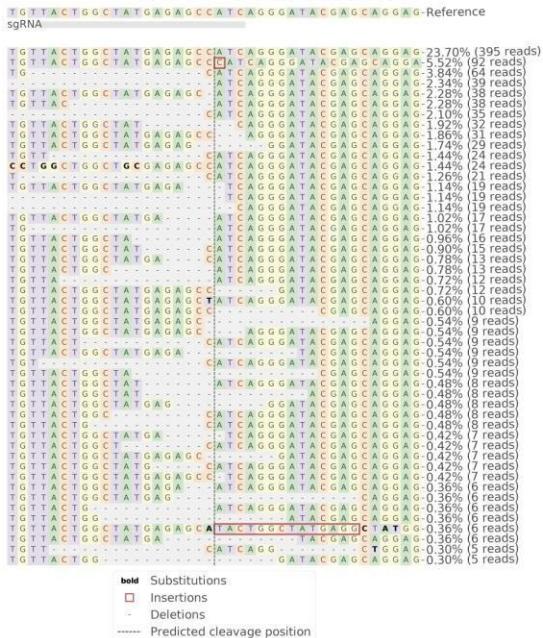
N-371-2 KWMTBOMO12902



N-371-2 KWMTBOMO1543



N-371-1 KWMTBOMO01543



Supplemental Fig S8. The editing efficiency at target sites of 33 F1 lines. The top of sequence alignment plot shows the sgRNA and its target gene sequences, the sequences and frequency of edited alleles is shown below.