

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

A	G	T	A	G	C	C	C	C	G	A	C	T	C	T	T	G	T	-	-	-	-	-	C	G	G	C	A	T	C	T	G	A	G	A	C	C	A	G	T	52.91% (273 reads)
A	G	T	A	G	C	C	C	C	G	A	C	T	C	T	T	G	T	A	C	G	G	T	C	G	G	C	A	T	C	T	G	A	G	A	C	C	A	G	T	45.93% (237 reads)
A	G	T	A	G	C	C	C	C	G	A	C	T	C	T	T	G	T	A	C	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0.58% (3 reads)	

**bold** Substitutions

Insertions

- Deletions

----- Predicted cleavage position