


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

C	A	T	G	G	A	A	T	C	C	C	T	T	C	T	G	C	A	G	C	A	C	C	T	G	G	A	T	C	G	C	T	T	T	T	C	C	G	A	G	- 93.00% (93 reads)
C	A	T	G	G	A	G	T	C	C	C	T	T	C	T	G	C	A	G	C	A	C	C	T	G	G	A	T	C	G	C	T	T	T	T	C	C	G	A	G	- 3.00% (3 reads)
C	A	T	G	G	A	A	T	C	C	C	T	T	C	G	G	C	A	G	C	A	C	C	T	G	G	A	T	C	G	C	T	T	T	T	C	C	G	A	G	- 1.00% (1 reads)
C	A	T	G	G	A	A	T	C	C	C	T	T	C	T	G	C	A	G	C	A	C	C	T	G	G	A	T	C	A	C	T	T	T	T	C	C	G	A	G	- 1.00% (1 reads)
C	A	T	G	G	A	A	T	C	C	C	T	T	C	T	G	C	A	G	C	A	C	C	T	G	G	C	T	C	G	C	T	T	T	T	C	C	G	A	G	- 1.00% (1 reads)
C	A	T	G	G	A	A	T	C	C	C	T	T	C	T	G	C	G	G	C	A	C	C	T	G	G	A	T	C	G	C	T	T	T	T	C	C	G	A	G	- 1.00% (1 reads)

bold Substitutions

 Insertions

- Deletions

----- Predicted cleavage position