

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 C C G A G - 98.00% (98 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 G C T T T T G 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 T 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