

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

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

bold Substitutions

Insertions

- Deletions

----- Predicted cleavage position