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 - 81.00% (81 reads)
C A T G G A A T **T** **T** 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 - 6.00% (6 reads)
C A T G G A A T **T** 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 - 5.00% (5 reads)
C A T G G A A T C C **T** 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 - 2.00% (2 reads)
C A T G G A A **G** 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 - 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 G C T T T T C C G A **C** - 1.00% (1 reads)
C A T G G A A T C **T** 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 - 1.00% (1 reads)
C A T G G A A T C **T** **T** 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 - 1.00% (1 reads)
C A T G G A A T **T** **T** **T** 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 - 1.00% (1 reads)
C A T G G A **C** 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 - 1.00% (1 reads)

bold   Substitutions

☐   Insertions

-   Deletions

------   Predicted cleavage position