


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

sgRNA

A A A A T C A G A G A T C A A C C A G **G** | **G** **G** A C C C C A T A T T G C C C A A G A - 84.89% (2900 reads)
A A A A T C A G A G A T C A A C C A G A | T T A C C C C A T A T T G C C C A A G A - 15.11% (516 reads)

bold Substitutions

 Insertions

- Deletions

----- Predicted cleavage position