

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

sgRNA

T G C A A T T G T C T T G T C C C T A T C G A A G G A C T C T G G C A C A A A A - 74.10% (60912 reads)  
T G C A A T T G T C T T G T C C C T A T **T** C G A A G G A C T C T G G C A C A A A A - 17.59% (14459 reads)

**bold**

Substitutions

Insertions

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Deletions

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Predicted cleavage position