

A T A T A A A C T G A G T T C C C A T G T T T T G C T T A A T G G T T G A G T T - Reference
PE nicking sgRNA

A T A T A A A C T G A G T T C C C A T **G** T T T T G C T T A A T G G T T G A G T T - 1.28% (320 reads)

- bold** Substitutions
- Insertions
- Deletions
- Predicted cleavage position