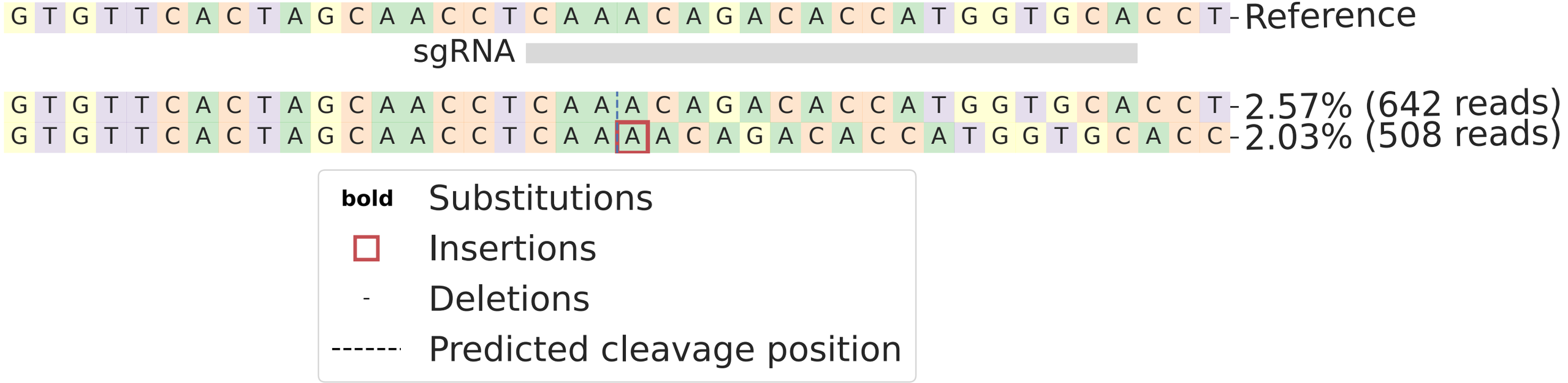
G T G T T C A C T A G C A A C C T C A A A C A G A C A C C A T G G T G C A C C T - Reference
sgRNA
G T G T T C A C T A G C A A C C T C A A A C A G A C A C C A T G G T G C A C C T - 2.57% (642 reads)
G T G T T C A C T A G C A A C C T C A A A C A G A C A C C A T G G T G C A C C - 2.03% (508 reads)
bold Substitutions
Insertions
- Deletions
------- Predicted cleavage position