

G A G G G C A A A G A G A C C G G G C C G C G G G A G G G C C A A G G A A A G G G T A C Reference
sgRNA

G A G G G C A **G** A G A G A C C G G G C C G |C **T** G A G G G C C A A G G A A A A G G T A C 57.14% (3902 reads)
G A G G G C **G** A A G A G A C C G G G C C G |C **T** G A G G G C C A A G G A A A A G G T A C 41.10% (2807 reads)
G A G G G C A A A A G A G A C C G G G C C G |C G G A G G G C C A A G G A A A A G G T A C 0.21% (14 reads)

bold Substitutions

Insertions

- Deletions

----- Predicted cleavage position