A G T A G C C C C G A C T C T T G T A C G G T C G G C A T C T G A G A C C A G T **Reference**

sgRNA

A G T A G C C C C G A C T C T T G T A **G** G G - - - G C A T C T G A G A C C A G T	53.97% (170 reads)
A G T A G C C C C G A C T C T T G - - - - - - - - - - - - - - - - A G A C C A G T	44.76% (141 reads)
A G T A G C C C C G A C T **A** T T G T A **G** G G - - - G C A T C T G A G A C C A G T	0.32% (1 reads)
A G T A G C C C C G A C T C T T G T A **G** G G - - - G C A T C **A** G A G A C C A G T	0.32% (1 reads)
A G T A G C C C C G A C T C T T G T A **G** G G **A** C - - - A T C T G A G A C C A G T	0.32% (1 reads)
A G T A G C C **T** C G A C T C T T G T A **G** G G - - - G C A T C T G A G A C C A G T	0.32% (1 reads)

bold Substitutions

□ Insertions

- Deletions

----- Predicted cleavage position