G A G T A G G T G G A C T A T G C A G T C A A T G G A C G A A C T G C C G C T A — Reference

sgRNA

G A G T A G G T G G A C T A T G C A G T C A A T G G A C G A A C T G C C G C T A — 48.06% (19456 reads)
A G T T A G G T G G A C T **C** T G C A G T C A A T G G A C G A A C T G C C G C T A — 34.91% (14132 reads)
A G A T A G G T G G A C T A T G C A G T C A A T G G A C G A A C T G C C G C T A — 5.76% (2332 reads)
A G A T A G G T G G A C T A T G C A G T C A A T G G A C G A A C T **T** C C G C T A — 0.72% (290 reads)
A G T T A G G T G G A C T A T G C A G T C A A T G G A C G A A C T G C C G C T A — 0.51% (208 reads)
G A G T A G G T G G A C T A T G C A G T T C A A T G G A C G A A C T G C C G C T — 0.46% (185 reads)
G A G T A G G T G G A C T A T - - - - - - C A A T G G A C G A A C T G C C G C T A — 0.41% (164 reads)
G A G T A G G T G G A C T **C** T G C A G T C A A T G G A C G A A C T G C C G C T A — 0.32% (131 reads)
A G **A** G A G G T G G A C T **C** T G C A G T C A A T G G A C G A A C T G C C G C T A — 0.32% (128 reads)
G A G T A G G T G G A C T A T G C A G - C A A T G G A C G A A C T G C C G C T A — 0.22% (88 reads)

bold   Substitutions

☐   Insertions

-    Deletions

------   Predicted cleavage position