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 — Reference

sgRNA

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 — 66.58% (209409 reads)
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 — 6.87% (21594 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 — 6.70% (21064 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 — 4.71% (14825 reads)
A G A **G** 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 — 0.37% (1171 reads)
A G A 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 — 0.33% (1047 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 — 0.32% (1012 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 — 0.26% (823 reads)
A G A T A G G T G G A C T A T - - - - - T C A A T G G A C G A A C T G C C G C T A — 0.26% (823 reads)
A G A T A G G T G G A C T A T G C A G T C A **C** T G G A C G A A C T G C C G C T A — 0.25% (779 reads)
A G A 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 — 0.22% (680 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 **G** C T G C C G C T A — 0.21% (672 reads)
A G A T A G G T G G **G** 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 — 0.20% (633 reads)

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