Reference: `C T A G T T T T C T C G C A C T T A A G C T C T G G T T C A G A C A G A A A C G -`

sgRNA

Sequence	Percentage (reads)
C T A G T T T T C T C G C A C T T A A G C T C T G G T T C A G A C A G A A A C G -	84.84% (33901 reads)
C T A G T T **G** T C T C G C A C T T A A G C T C T G G T T C A G A C A G A A A C G -	0.50% (198 reads)
C T A G T T T T C T C G C A C T T A A G C T C T G G **T** T C A G A C A G A A A C G -	0.43% (173 reads)
C T A **T** T T T T C T C G C A C T T A A G C T C T G G T T C A G A C A G A A A C G -	0.35% (141 reads)
C T A G T T T T C T C T **T** C A C T T A A G C T C T G G T T C A G A C A G A A A C G -	0.35% (141 reads)
C T A G T **G** T T C T C G C A C T T A A G C T C T G G T T C A G A C A G A A A C G -	0.33% (130 reads)
A T A G T T T T C T C G C A C T T A A G C T C T G G T T C A G A C A G A A A C G -	0.31% (125 reads)
C T A G T T T T C T C G C A C T T A A **T** C T C T G G T T C A G A C A G A A A C G -	0.26% (104 reads)
C T A G T **C** T T C T C G C A C T T A A G C T C T G G T T C A G A C A G A A A C G -	0.26% (104 reads)
C T A G T T T T C T C G C A C T T A A G C T C T G G T T C A G A C A G A A A C **T** -	0.25% (100 reads)
C T A G T T T T C T C G C A C T T A A G C T C **T** G T T C A G A C A G A A A C G -	0.25% (100 reads)
C T A G T T T T C T C G C A C T T A A G C T C T G G **C** T C A G A C A G A A A C G -	0.25% (98 reads)
C T A G T T T T C T C G C A C T T A A G C T C T G G T T C A G A C A G A **G** A C G -	0.23% (90 reads)
C T A G T T T T C T C G C A C T T A A G C T C T G G T T C A G A C **G** G A A A C G -	0.22% (88 reads)
C T A G T T T T C T C G C A C T T A A G C T C T G G T T C A G **G** C A G A A A C G -	0.22% (88 reads)
C T A G T T T T C T C G C A C T T A A G C T C T G G T T C A G A C A **T** A A A C G -	0.22% (87 reads)
C T A G T T T T C T C G C A C T T A A G C T C T G G T T C A G A C A G **G** A A C G -	0.21% (84 reads)
C T A G T T T T C **C** C G C A C T T A A G C T C T G G T T C A G A C A G A A A C G -	0.20% (80 reads)

bold   Substitutions

☐   Insertions

-   Deletions

-------   Predicted cleavage position