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

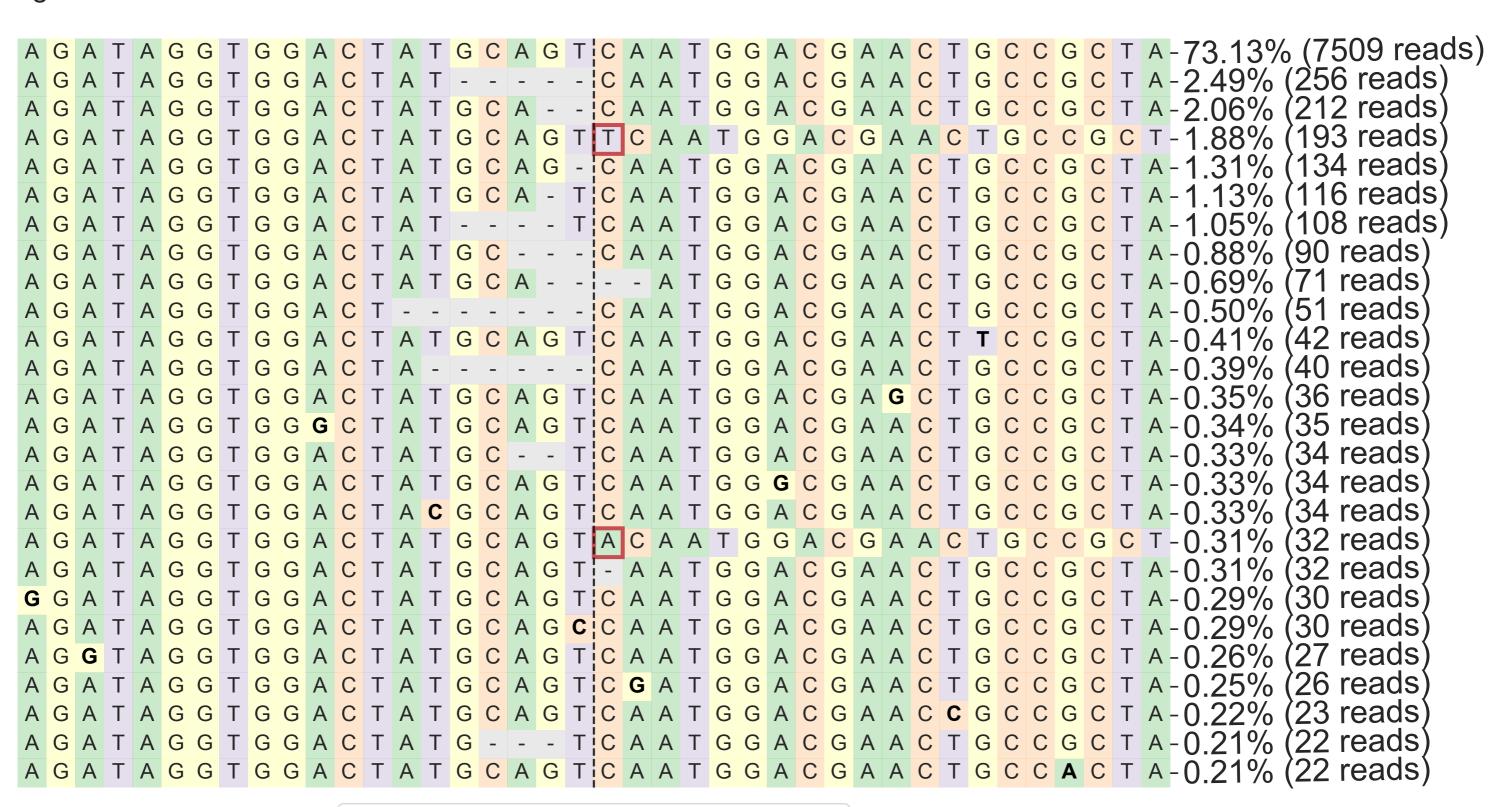| Sequence	Percentage (reads)
A G A T A G G T G G A C T A T G C A G T C A A T G G A C G A A C T G C C G C T A	73.13% (7509 reads)
A G A T A G G T G G A C T A T - - - - - C A A T G G A C G A A C T G C C G C T A	2.49% (256 reads)
A G A T A G G T G G A C T A T G C A - - C A A T G G A C G A A C T G C C G C T A	2.06% (212 reads)
A G A 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	1.88% (193 reads)
A G A 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	1.31% (134 reads)
A G A T A G G T G G A C T A T G C A - T C A A T G G A C G A A C T G C C G C T A	1.13% (116 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	1.05% (108 reads)
A G A T A G G T G G A C T A T G C - - - C A A T G G A C G A A C T G C C G C T A	0.88% (90 reads)
A G A T A G G T G G A C T A T G C A - - - - A T G G A C G A A C T G C C G C T A	0.69% (71 reads)
A G A T A G G T G G A C T - - - - - - C A A T G G A C G A A C T G C C G C T A	0.50% (51 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	0.41% (42 reads)
A G A T A G G T G G A C T A - - - - - - C A A T G G A C G A A C T G C C G C T A	0.39% (40 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 **G** C T G C C G C T A	0.35% (36 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	0.34% (35 reads)
A G A T A G G T G G A C T A T G C - - T C A A T G G A C G A A C T G C C G C T A	0.33% (34 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 **G** C G A A C T G C C G C T A	0.33% (34 reads)
A G A T A G G T G G A C T A **C** 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	0.33% (34 reads)
A G A T A G G T G G A C T A T G C A G T **A** C A A T G G A C G A A C T G C C G C T	0.31% (32 reads)
A G A T A G G T G G A C T A T G C A G T - A A T G G A C G A A C T G C C G C T A	0.31% (32 reads)
G 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	0.29% (30 reads)
A G A T A G G T G G A C T A T G C A G **C** C A A T G G A C G A A C T G C C G C T A	0.29% (30 reads)
A G **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	0.26% (27 reads)
A G A T A G G T G G A C T A T G C A G T C **G** A T G G A C G A A C T G C C G C T A	0.25% (26 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 **C** G C C G C T A	0.22% (23 reads)
A G A T A G G T G G A C T A T G - - - T C A A T G G A C G A A C T G C C G C T A	0.21% (22 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 **A** C T A	0.21% (22 reads)

bold Substitutions

□ Insertions

- Deletions

------ Predicted cleavage position