


T G C A A T T G T C T T G T C C C T A T C G A A G G A C T C T G G C A C A A A A - Reference
sgRNA

T	G	C	A	A	T	T	G	T	C	T	T	G	T	C	C	C	T	A	T	C	G	A	A	G	G	A	C	T	C	T	G	G	C	A	C	A	A	A	A	- 84.30% (101476 reads)
T	G	C	A	A	T	T	G	T	C	T	T	G	T	C	C	C	T	A	T	T	C	G	A	A	G	G	A	C	T	C	T	G	G	C	A	C	A	A	A	- 2.21% (2660 reads)
T	G	C	A	A	T	T	G	T	C	T	T	G	T	C	C	C	T	A	T	C	G	A	G	G	G	A	C	T	C	T	G	G	C	A	C	A	A	A	A	- 0.27% (324 reads)
T	G	C	A	A	T	T	G	T	C	T	T	G	T	C	C	C	T	A	T	T	G	A	A	G	G	A	C	T	C	T	G	G	C	A	C	A	A	A	A	- 0.26% (313 reads)
T	G	C	A	A	T	T	G	C	C	T	T	G	T	C	C	C	T	A	T	C	G	A	A	G	G	A	C	T	C	T	G	G	C	A	C	A	A	A	A	- 0.26% (310 reads)
T	G	C	A	A	T	T	G	T	C	C	T	G	T	C	C	C	T	A	T	C	G	A	A	G	G	A	C	T	C	T	G	G	C	A	C	A	A	A	A	- 0.21% (249 reads)
T	G	C	A	A	T	C	G	T	C	T	T	G	T	C	C	C	T	A	T	C	G	A	A	G	G	A	C	T	C	T	G	G	C	A	C	A	A	A	A	- 0.21% (247 reads)
T	G	C	A	A	T	T	G	T	C	T	T	G	C	C	C	C	T	A	T	C	G	A	A	G	G	A	C	T	C	T	G	G	C	A	C	A	A	A	A	- 0.21% (247 reads)

bold Substitutions

 Insertions

- Deletions

----- Predicted cleavage position