


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

sgRNA

T	T	T	T	G	T	G	C	C	A	G	A	G	T	C	C	T	T	C	G	A	T	A	G	G	G	A	C	A	A	G	A	C	A	A	T	T	G	C	A	-	90.88% (27072 reads)
T	T	T	T	G	T	G	C	C	A	G	A	G	T	C	C	-	-	-	-	A	T	A	G	G	G	A	C	A	A	G	A	C	A	A	T	T	G	C	A	-	0.39% (116 reads)
T	T	T	T	G	T	G	C	C	A	G	A	G	T	C	C	T	T	C	G	A	A	T	A	G	G	G	A	C	A	A	G	A	C	A	A	T	T	G	C	-	0.30% (89 reads)
T	T	T	T	G	T	G	C	C	A	G	A	G	T	C	C	T	T	C	G	A	T	A	G	G	G	A	C	A	A	G	G	C	A	A	T	T	G	C	A	-	0.29% (87 reads)
T	T	T	T	G	T	G	C	C	A	G	A	G	T	C	C	T	T	C	G	G	A	T	A	G	G	G	A	C	A	A	G	A	C	A	A	T	T	G	C	-	0.27% (79 reads)

bold Substitutions

 Insertions

- Deletions

----- Predicted cleavage position