


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	-	80.09% (138386 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	A	-	9.26% (16000 reads)
T	G	C	A	A	T	T	G	T	C	T	T	G	T	C	C	C	T	A	-	C	G	A	A	G	G	A	C	T	C	T	G	G	C	A	C	A	A	A	A	-	0.42% (734 reads)	
T	G	C	A	A	T	T	G	T	C	T	T	G	T	C	C	C	T	A	T	-	G	A	A	G	G	A	C	T	C	T	G	G	C	A	C	A	A	A	A	-	0.42% (723 reads)	
T	G	C	A	A	T	T	G	T	C	T	T	G	T	C	C	C	T	A	T	A	C	G	A	A	G	G	A	C	T	C	T	G	G	C	A	C	A	A	A	-	0.35% (604 reads)	
T	G	C	A	A	T	T	G	T	C	T	T	G	T	C	-	-	-	-	-	-	G	A	A	G	G	A	C	T	C	T	G	G	C	A	C	A	A	A	A	-	0.33% (570 reads)	
T	G	C	A	A	T	T	G	T	C	T	T	G	T	C	C	C	-	-	-	-	G	A	A	G	G	A	C	T	C	T	G	G	C	A	C	A	A	A	A	-	0.30% (526 reads)	
T	G	C	A	A	T	T	G	T	C	T	T	G	T	C	C	C	T	A	T	G	C	G	A	A	G	G	A	C	T	C	T	G	G	C	A	C	A	A	A	-	0.26% (443 reads)	

bold Substitutions

 Insertions

- Deletions

----- Predicted cleavage position