

A	G	T	A	G	C	C	C	C	G	A	C	T	C	T	T	G	T	A	C	G	G	T	C	G	G	C	A	T	C	T	G	A	G	A	C	C	A	G	Reference		
sgRNA																																									
A	G	T	A	G	C	C	C	C	G	A	C	T	C	T	T	G	T	A	C	T	G	G	T	C	G	G	C	A	T	C	T	G	A	G	A	C	C	A	G	96.71% (206 reads)	
A	G	T	A	G	C	C	C	C	G	A	C	T	C	T	T	G	T	A	C	G	G	T	C	G	G	C	A	T	C	T	G	A	G	A	C	C	A	G	1.41% (3 reads)		
A	G	T	A	G	C	C	A	C	G	A	C	T	C	T	T	G	T	A	C	T	G	G	T	C	G	G	C	A	T	C	T	G	A	G	A	C	C	A	G	0.47% (1 reads)	
A	G	T	A	G	C	C	C	A	G	A	C	T	C	T	T	G	T	A	C	T	G	G	T	C	G	G	C	A	T	C	T	G	A	G	A	C	C	A	G	0.47% (1 reads)	
A	G	T	A	G	C	C	C	C	G	A	C	T	C	T	T	G	T	A	C	T	G	G	T	C	G	G	C	A	T	C	T	G	A	G	A	C	C	-	A	G	0.47% (1 reads)
A	G	T	A	G	C	C	C	C	G	A	C	T	C	T	T	G	T	A	C	T	G	G	T	C	G	G	C	A	T	C	T	G	A	G	A	C	C	A	G	0.47% (1 reads)	

**bold** Substitutions

  Insertions

- Deletions

----- Predicted cleavage position