

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																																										
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	-	80.77% (92124 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	<b>T</b>	C	C	G	C	T	A	-	2.95% (3367 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	-	0.76% (870 reads)	
A	G	A	T	A	G	G	T	G	G	A	C	T	A	T	G	C	A	G	T	<b>T</b>	C	A	A	T	G	G	A	C	G	A	A	C	T	G	C	C	G	C	T	A	-	0.73% (828 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	-	0.52% (598 reads)	
A	G	A	<b>G</b>	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	-	0.35% (399 reads)	
A	G	<b>G</b>	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	-	0.31% (358 reads)	
A	G	A	T	A	G	G	T	G	G	A	C	T	A	T	G	C	A	G	T	C	A	<b>G</b>	T	G	G	A	C	G	A	A	C	T	G	C	C	G	C	T	A	-	0.27% (309 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	<b>G</b>	C	G	A	A	C	T	G	C	C	G	C	T	A	-	0.27% (305 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	<b>G</b>	A	C	T	G	C	C	G	C	T	A	-	0.26% (295 reads)	
<b>G</b>	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	-	0.26% (295 reads)	
A	G	A	T	A	G	G	T	G	G	A	C	T	A	T	G	C	A	G	T	C	A	<b>C</b>	T	G	G	A	C	G	A	A	C	T	G	C	C	G	C	T	A	-	0.26% (294 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	<b>G</b>	C	T	G	C	C	G	C	T	A	-	0.23% (267 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	-	0.22% (247 reads)	
A	G	A	T	A	G	G	T	G	G	A	C	T	A	T	G	C	A	G	<b>C</b>	C	A	A	T	G	G	A	C	G	A	A	C	T	G	C	C	G	C	T	A	-	0.21% (236 reads)	

**bold** Substitutions

Insertions

- Deletions

----- Predicted cleavage position