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TTTTGTGCCAGAGTCCTTCGATAGGGACAAGACAATTGCA- Reference
sgRNA

TTTTGTGCCAGAGTCCTTCGATAGGGACAAGACAATTGCA- 25.91% (20820 reads)
TTTTGTGCCAGAGTCCTTCGAATAGGGACAAGACAATTGC- 12.58% (10112 reads)
TTTTGTGCCAGAGTCCTTCGCATAGGGACAAGACAATTGC- 12.25% (9848 reads)
TTTTGTGCCAGAGTCCTTCGTATAGGGACAAGACAATTGC- 4.92% (3952 reads)
TTTTGTGCCAGAGTCCTTC-ATAGGGACAAGACAATTGCA- 3.91% (3140 reads)
TTTTGTGCCAGAGTCC----ATAGGGACAAGACAATTGCA- 2.36% (1896 reads)
TTTTGTGCCAGAGTCCTTCG----GGACAAGACAATTGCA- 2.17% (1743 reads)
TTTTGTGCCAGAGTCCTTCG-TAGGGACAAGACAATTGCA- 1.96% (1578 reads)
TTTTGTGCCAGAGA-----GATAGGGACAAGACAATTGCA- 1.82% (1460 reads)
TTTTGTGCCAGAG-------ATAGGGACAAGACAATTGCA- 1.57% (1261 reads)
TTTTGTGCCAGAGTCCTTCGGATAGGGACAAGACAATTGC- 1.44% (1157 reads)
TTTTGTGCCAGAGTCCTTC--AGGGACAAGACAATTGCA- 1.36% (1090 reads)
TTTTGTGCCAGAGTC-----ATAGGGACAAGACAATTGCA- 1.29% (1036 reads)
TTTTGTGCCAGAGTCCTT----AGGGACAAGACAATTGCA- 1.02% (818 reads)
TTTTGTGCCAGAGTCC---GATAGGGACAAGACAATTGCA- 0.98% (789 reads)
TTTTGTGCCAGAGTCCTT--ATAGGGACAAGACAATTGCA- 0.90% (723 reads)
TTTTGTGCCAGAGTCCT---ATAGGGACAAGACAATTGCA- 0.76% (609 reads)
TTTTGTGCCAGAGTCCT----AGGGACAAGACAATTGCA- 0.71% (570 reads)
----------------------GGGACAAGACAATTGCA- 0.64% (515 reads)
TTTTGTGCCAGAGTC----GATAGGGACAAGACAATTGCA- 0.63% (507 reads)
TTTTGTGCCAGA-------T-AGGGACAAGACAATTGCA- 0.59% (472 reads)
TTTTGTGCCAGA-------ATAGGGACAAGACAATTGCA- 0.50% (405 reads)
TTTTGTGCCAGAGTCCTTC--TAGGGACAAGACAATTGCA- 0.50% (403 reads)
TTTTGTGCCAGAGT------ATAGGGACAAGACAATTGCA- 0.40% (321 reads)
TTTTGTGCCAGAGT------AGGGACAAGACAATTGCA- 0.34% (276 reads)
TTTTGTGCCAGAGT-----GATAGGGACAAGACAATTGCA- 0.34% (272 reads)
TTTTGTGCCAGAGTCCTTCG--AGGGACAAGACAATTGCA- 0.33% (262 reads)
TTTTGTGCCAGAGTC-----AGGGACAAGACAATTGCA- 0.27% (219 reads)
TTTTGTGCCAGAGTCCTT-GATAGGGACAAGACAATTGCA- 0.27% (215 reads)
TTTTGTGCCAGAGTCCT--GATAGGGACAAGACAATTGCA- 0.27% (214 reads)
TTTTGTGCCAGA-------------------CAATTGCA- 0.24% (194 reads)
TTTTGTGCCAGAGTCC----AGGGACAAGACAATTGCA- 0.24% (192 reads)
TTTTGTGCCAGAGTCCTTCG---GGGACAAGACAATTGCA- 0.23% (187 reads)
TTTTGTGCCAG---------GGGACAAGACAATTGCA- 0.22% (175 reads)
TTTTGTGCCAGAGTCCTTCG----------ACAATTGCA- 0.21% (168 reads)
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bold	Substitutions
□	Insertions
-	Deletions
------	Predicted cleavage position