CCAGTTTTCTCGCACTTAAGCTCTGGTTCGGACAGAAATA- Reference

sgRNA

CCAGTTTTCTCGCACTTAAGCTCTGGTTCGGACAGAAATA-78.63% (28765 reads)
CCAGTTTTCTCGCACTTAAG-TCTGGTTCGGACAGAAATA-1.34% (489 reads)
CCAGTTTTCTCGCACTTAA-CTCTGGTTCGGACAGAAATA-1.27% (466 reads)
CCAGTTTTCTCGCACT-----|--CTGGTTCGGACAGAAATA-1.08% (396 reads)
CCAGTTTTCTCGCACTTAAGCTCTGGTTCGGACAGAAA**C**A-0.62% (227 reads)
CCAGTTTTCTCGCACTTA--CTCTGGTTCGGACAGAAATA-0.61% (223 reads)
CCAGTTTTCTCGC-------CTCTGGTTCGGACAGAAATA-0.43% (159 reads)
CCAGTT**G**TCTCGCACTTAAGCTCTGGTTCGGACAGAAATA-0.41% (151 reads)
CCAGT**G**TCTCGCACTTAAGCTCTGGTTCGGACAGAAATA-0.40% (147 reads)
CCAGTTTTCTCGCAC-----CTCTGGTTCGGACAGAAATA-0.37% (136 reads)
CCAGTTTTCTCGCACTTAAGCTCTGGTT**T**GGA**T**C**GAAA**G**A-0.36% (131 reads)
CCAGTTTTCTCGCACTTAAG[A]CTCTGGTTCGGACAGAAAT-0.24% (86 reads)
CCAGTTTTCTCGCACTTAAG**C**CTGGTTCGGACAGAAATA-0.23% (85 reads)
CCAGTTTTCTCGCACTTAAGCTCTGGTTCGG**G**CAGAAATA-0.22% (82 reads)
CCAGT**C**TCTCGCACTTAAGCTCTGGTTCGGACAGAAATA-0.22% (82 reads)
CCAGTTTTCTCGCACTTAAGCTCTGGTTCGGAC**G**GAAATA-0.22% (81 reads)
CCAGTTTTCTCGCACTTAAGCTCTGGTTCGGACAGA**G**ATA-0.22% (80 reads)
CCAGTTTTCTCGCACTTAAGCTCTGGTTC**T**GACAGAAATA-0.21% (76 reads)
CCAGTTT**C**CTCGCACTTAAGCTCTGGTTCGGACAGAAATA-0.20% (74 reads)

bold	Substitutions
☐	Insertions
-	Deletions
------	Predicted cleavage position