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CCAGTTTTCTCGCACTTAAGCTCTGGTTCGGACAGAAATA- Reference
sgRNA
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CCAGTTTTCTCGCACTTAAG|CTCTGGTTCGGACAGAAATA- 70.39% (32505 reads)
CCAGTTTTCTCGCACTTCAG|CTCTGGTTCGGACAGAAATA- 1.87% (864 reads)
CCAGTTTTCTCGCACTTAAG|CTCTGGTTCGGACAGAAACA- 1.52% (703 reads)
CCAGTTTTCTCGCACTTAAG|-TCTGGTTCGGACAGAAATA- 1.18% (546 reads)
CCAGTTTTCTCGCACTTAA-|CTCTGGTTCGGACAGAAATA- 1.11% (511 reads)
CCAGTTTTCTCTCACTTAAG|CTCTGGTTCGGACAGAAATA- 0.85% (394 reads)
CCAGTTGTCTCGCACTTAAG|CTCTGGTTCGGACAGAAATA- 0.79% (365 reads)
CCAGTTTTCTCGCACT----|--CTGGTTCGGACAGAAATA- 0.70% (323 reads)
CCAGTTTTCTCGCACTTAAG|CTCTGGTTCGGACAGAAAGA- 0.61% (282 reads)
CCAGTGTTCTCGCACTTAAG|CTCTGGTTCGGACAGAAATA- 0.57% (263 reads)
CCAGTTTTCTCGCACTTAAG|CTCTGGTTCTGACAGAAATA- 0.55% (256 reads)
CCAGTTTTCTCGCACTTAAG|CTCTGGTTCGGACAGACATA- 0.50% (233 reads)
CCAGTTTTCTCGCACTTAAG|CTCTGGGTCGGACAGAAATA- 0.40% (187 reads)
CCAGTTTTCTCGCACTTAAG|CTCTGGTTCGGACAGAACTA- 0.40% (187 reads)
CCAGTTTTCTCGCACTTA--|CTCTGGTTCGGACAGAAATA- 0.36% (164 reads)
CCAGTTTTCTCGCACTTAAG|CTCTTGTTCGGACAGAAATA- 0.31% (143 reads)
CCAGTTTTCTCGCACTGAAG|CTCTGGTTCGGACAGAAATA- 0.28% (128 reads)
CCAGTTTTCTCGCTCTTAAG|CTCTGGTTCGGACAGAAATA- 0.26% (118 reads)
CCAGTTTTCTCGCACTTAAG|CTCTGGTTCGGACAGATATA- 0.24% (109 reads)
CCAGTTTTCTCGCAC----|-CTCTGGTTCGGACAGAAATA- 0.22% (103 reads)
CCAGTTTTCTCGCACTTAAT|CTCTGGTTCGGACAGAAATA- 0.21% (97 reads)
CAAGTTTTCTCGCACTTAAG|CTCTGGTTCGGACAGAAATA- 0.20% (94 reads)
CCAGATTTCTCGCACTTAAG|CTCTGGTTCGGACAGAAATA- 0.20% (94 reads)
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bold	Substitutions
□	Insertions
-	Deletions
------	Predicted cleavage position