CTAGTTTTCTCGCACTTAAGCTCTGGTTCAGACAGAAACG-Reference sgRNA

CTAGTTTTCTCGCACTTAAGCTTCTGGTTCAGACAGAAACG-84.41% (8439 reads)
CTAGTTGTCTCGCACTTAAGCTTCTGGTTCAGACAGAAACG-1.30% (130 reads) CTAGTGTTCTCGCACTTAAGCTTCTGGTTCAGACAGAAACG-0.77% (77 reads) CTAGTTTTCTCGCACTTCAGCTTCAGACAGAAACG-0.32% (32 reads) CTAGTTTTCTCGCACTTAAGCTCTTGTTCAGACAGAAACG-0.30% (30 reads) ctagarttctcgcacttaagctctggttcagacagaaacg-0.30% (30 reads) CTAGTTTTCTCGCACTTAAGCTTCTGGCTCAGACAGAAACG-0.24% (24 reads) CTAGTTTTCTCGCACTTAATICTCTGGTTCAGACAGAAACG-0.24% (24 reads) CTAGTTTTCTCTCACTTAAGCTCTGGTTCAGACAGAAACG-0.24% (24 reads) CTAGTTTTCTCGCACTTAAGCTTCTGGTTCAGACAGAAGCG-0.24% (24 reads) CTAGTTTTCTCGCACATAAGCTCTGGTTCAGACAGAAACG-0.24% (24 reads) ctagttttctcgcacttaagcttctggttcagacagaatcg-0.23% (23 reads) CTAGTTTTCTCGCACTTAAGCTCTGGTTCAGACAGAGACG-0.22% (22 reads) CTAGTCTTCGCACTTAAGCTTCTGGTTCAGACAGAAACG-0.20% (20 reads)

bold Substitutions

- Insertions
- Deletions
- ----- Predicted cleavage position