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AATCAACTCTCAAAGCCGTAATGGCAAGATTCAGAAAA-Reference sgRNA
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AATCAACTCTCAAAAGCCGTAATGGCAAGATTCAGAAAA-72.14% (21642 reads)
AATCAACTCTCAAAGCC-TAATGGCAAGATTCAGAAAA-5.78% (1735 reads)
AATCAACTCTCAAAGCCGTTAAATGGCAAGATTCAGAAA-4.31% (1294 reads)
AATCAACTCTCAAAGCCGTAATGTCAAGATTCAGAAAA-0.95% (284 reads)
AATCAACTCTCAAAGCCGTAATGGCAAGAGTCAGAAAA-0.80% (241 reads)
ACTCAACTCTCAAAGCCGTAATGGCAAGATTCAGAAAA-0.49% (146 reads
AATCAACTCTCAAAGCCGTAATGGCAAGATTCATAAAA-0.44% (133 reads)
catcaactctctcaaagccgtaatggcaagattcagaaaa-0.43% (129 reads)
AATAAACTCTCTCAAAGCCGTAATGGCAAGATTCAGAAAA-0.36% (109 reads)
AATCAACTCTCAAAGACGTAATGGCAAGATTCAGAAAA-0.34% (101 reads)
AATCAACTCTCAAAGCAGTAATGGCAAGATTCAGAAAA-0.23% (68 reads)
AATCAACTCTCAAAGCCGTAATGGAAAGATTCAGAAAA-0.21% (62 reads)
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bold Substitutions

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