TGCAATTGTCTTGTCCCTATCGAAGGACTCTGGCACAAAA-Reference sgRNA

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TGCAATTGTCTTGTCCCTATCGAAGGACTCTGGCACAAAA-79.02% (79129 reads)
TGCAATTGTCTTGTCCCTATTCGAAGGACTCTGGCACAAA-3.71% (3720 reads)
TGCAATTGTCTTGTCCTTATCGAAGGACTCTGGCACAAAA-0.47% (473 reads)
TGCAATTGTCTTGTCCCT------CTGGCACAAAA-0.30% (301 reads)
TGCAATTGCCTTATCGAAGGACTCTGGCACAAAA-0.29% (286 reads)
TGCAATTGTCTTGTCCCTAT - - - - GACTCTGGCACAAAA-0.26% (261 reads)
TGCAATTGTCTTGTCCCTATI-GAAGGACTCTGGCACAAAA-0.26% (260 reads)
TGCAATTGTCTTGTCCC----GAAGGACTCTGGCACAAAA-0.24% (243 reads)
TGCAATTGTCTTGTCCCTAT-----CTCTGGCACAAAA-0.21% (212 reads)
TGCAATTGTCTTGTCCCTATCGAGGGACTCTGGCACAAAA-0.21% (211 reads
TGCAATTGTCTTGCCCCTATCGAAGGACTCTGGCACAAAA-0.21% (206 reads)
TGCAATTGTCTTG------ACTCTGGCACAAAA-0.20% (205 reads)
TGCAATTGTCTTGTCCCTATCGAAGGACCCTTGGCACAAAA-0.20% (201 reads)
```

**bold** Substitutions

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