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GGTGCGGAGCCACTTCGAGCAGCCGCAGTACTACCTGGCG- Reference
sgRNA

GGTGCGGAGCCACTTCGAGCAGCCGCAGTACTACCTGGCG- 18.49% (4553 reads)
GGTGCGGAGCCACTTCGAGC---CGCAGTACTACCTGGCG- 6.61% (1629 reads)
GGTGCGGAGCCACTTCGAGCAAGCCGCAGTACTACCTGGC- 2.76% (679 reads)
GGTGCGGAGCCACTTCGAGCCAGCCGCAGTACTACCTGGC- 2.14% (527 reads)
GGTGCGGAGCCACTTCGAGC--CCGCAGTACTACCTGGCG- 1.41% (346 reads)
GGTGCGGAGCCACTTCGAGCTAGCCGCAGTACTACCTGGC- 1.34% (329 reads)
GGTGCGGAGCCACTTCGAGC-GCCGCAGTACTACCTGGCG- 1.10% (270 reads)
GGTGCGGAGCCACTTCGAGC------AGTACTACCTGGCG- 0.98% (242 reads)
GGTGCGGAGCCACTTCGAG-AGCCGCAGTACTACCTGGCG- 0.63% (155 reads)
GGTGCGGAGCCACTTCGA--AGCCGCAGTACTACCTGGCG- 0.52% (127 reads)
GGTGCGGAGCCACTTCGAGC----GCAGTACTACCTGGCG- 0.52% (127 reads)
GGTGCGGAGCCACT------AGCCGCAGTACTACCTGGCG- 0.37% (90 reads)
GGTGCGGAGCCAC-------AGCCGCAGTACTACCTGGCG- 0.32% (78 reads)
GGTGCGGAGCCACTTCGAGCCCAGCCGCAGTACTACCTGG- 0.30% (74 reads)
GGTGCGGAGCCACTTCGAGCA-CCGCAGTACTACCTGGCG- 0.26% (64 reads)
GGTGCGGAGCCACTTCGAGCAAAGCCGCAGTACTACCTGG- 0.25% (62 reads)
GGTGCGGAGCCACTTCGAGC----CAGTACTACCTGGCG- 0.21% (52 reads)
GGTGCGGAGCCACTTCG---CCGCAGTACTACCTGGCG- 0.21% (51 reads)
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bold	Substitutions
□	Insertions
-	Deletions
------	Predicted cleavage position