GAGTAGGTGGACTATGCAGTCAATGGACGAACTGCCGCTA- Reference

sgRNA

GAGTAGGTGGACTATGCAGTCAATGGACGAACTGCCGCTA- 48.28% (87273 reads)
AGTTAGGTGGACTCTGCAGTCAATGGACGAACTGCCGCTA- 35.94% (64969 reads)
AGATAGGTGGACTATGCAGTCAATGGACGAACTGCCGCTA- 4.95% (8944 reads)
AGAGAGGTGGACTCTGCAGTCAATGGACGAACTGCCGCTA- 0.41% (742 reads)
GAGTAGGTGGACTAT------CAATGGACGAACTGCCGCTA- 0.40% (718 reads)
AGATAGGTGGACTATGCAGTCAATGGACGAACTTCCGCTA- 0.36% (657 reads)
GAGTAGGTGGACTATGCAGTTCAATGGACGAACTGCCGCT- 0.33% (595 reads)
AGTTAGGTGGACTATGCAGTCAATGGACGAACTGCCGCTA- 0.27% (483 reads)
GAGTAGGTGGACTATGCAG-CAATGGACGAACTGCCGCTA- 0.23% (422 reads)
GAGTAGGTGGACTCTGCAGTCAATGGACGAACTGCCGCTA- 0.21% (377 reads)

bold   Substitutions

☐   Insertions

-    Deletions

------   Predicted cleavage position