AGTAGCCCCGACTCTTGTACGGTCGGCATCTGAGACCAGT Reference

sgRNA

AGTAGCCCCGACTC-------GGTCGGCATCTGAGACCAGT 54.68% (111 reads)
AGTAGCCCCGACTCTTG**AG**----GGCATCTGAGACCAGT 42.36% (86 reads)
AGTAGCCCCGACTCTT-TA**G**----GGCATCTGAGACCAGT 0.99% (2 reads)
AGTAGC**AT**C**A**A---------------TCTGAGAC**T**AGT 0.49% (1 reads)
AGTAGCCCCGACTC-------GGTCGG**T**ATCTGAGACCAGT 0.49% (1 reads)
AGTAGCCCCGACTCTTGTACGGTCGGCATCTGAGACCAGT 0.49% (1 reads)
TGTAGCCCCGACTC-------GGTCGGCATCTGAGACCAGT 0.49% (1 reads)

bold   Substitutions

☐   Insertions

-   Deletions

-----   Predicted cleavage position