TTTTGTGCCAGAGTCCTTCGATAGGGACAAGACAATTGCA-Reference sgRNA

TTTTGTGCCAGAGTCCTTCGATAGGGGACAAGACAATTGCA-89.68% (22813 reads) TTTTGTGCCAGAGTCCTTCGAATAGGGACAAGACAATTGC-0.70% (177 reads) TTTTGTGCCAGAGTCCTTCGATAGGGACAAGGCAATTGCA-0.29% (73 reads) c t t t g t g c c a g a g t c c t t c g a t a g g g a c a a g a c a a t t g c a - 0.28% (72 reads) TTTTGTGCCAGGGTCCTTCGATAGGGACAAGACAATTGCA-0.24% (61 reads) TTCTGTGCCAGAGTCCTTCGATAGGGACAAGACAATTGCA-0.24% (60 reads) TTTTGTGCCAGAGTCCCTCGATAGGGACAAGACAATTGCA-0.23% TTTTGTGCCAGAGCCCTTCGATAGGGACAAGACAATTGCA-0.23% (58 reads TTGCGCCAGAGTCCTTCGATAGGGACAAGACAATTGCA-0.22% (57 reads) TTTTGTGCCAGAGTCCTTCGATAGGGACAAGACAGTTGCA-0.21% (53 reads) TTGTGCCAGAGTCCTTCGATAGGGACAGGACAATTGCA-0.21% (53 reads) TTTTGTGCCAGAGTCCTTCGATAGGGACAAGACAAT cGCA-0.20% (51 reads)

bold Substitutions

☐ Insertions

- Deletions

----- Predicted cleavage position