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TAGCGACATTCATAACAGAGACATGGTAACGAGATCTGTT-Reference
sgRNA

TAGCGACATTCATAACAGAG|ACATGGTAACGAGATCTGTT-36.26% (3470 reads)
TAGCGACATTCATAACAGA-|-CATGGTAACGAGATCTGTT-9.43% (902 reads)
TAGCGACATTCATAACA---|---TGGTAACGAGATCTGTT-4.78% (457 reads)
TAGCGACATTCATAACA---|-CATGGTAACGAGATCTGTT-4.41% (422 reads)
TAGCGACATTCATAA-----|ACATGGTAACGAGATCTGTT-3.67% (351 reads)
TAGCGACATTCATAACAGAG|-CATGGTAACGAGATCTGTT-3.06% (293 reads)
TAGCGACATTCAT-------|---GGTAACGAGATCTGTT-2.32% (222 reads)
TAGCGACATTCATA------|-CATGGTAACGAGATCTGTT-2.06% (197 reads)
TAGCGACATTCATAACAGA-|ACATGGTAACGAGATCTGTT-1.45% (139 reads)
TAGCGACAT-----------|---GGTAACGAGATCTGTT-1.36% (130 reads)
TAGCGACATTCATAACAGAG|-------------ATCTGTT-1.26% (121 reads)
TAGCGACATTCATAACA---|ACATGGTAACGAGATCTGTT-0.66% (63 reads)
TAGCGACATTCATAAC----|-CATGGTAACGAGATCTGTT-0.65% (62 reads)
TAGCGACATTCA--------|-CATGGTAACGAGATCTGTT-0.65% (62 reads)
TAGCGACATTCATAA-----|---TGGTAACGAGATCTGTT-0.57% (55 reads)
TAGCGACATTCATAACAGAG|--ATGGTAACGAGATCTGTT-0.56% (54 reads)
TAGCGACATTCATAAC----|----------GAGATCTGTT-0.50% (48 reads)
TAGCGACATTCATAACAGA-|---TGGTAACGAGATCTGTT-0.43% (41 reads)
TAGCGACATTCATA-----G|ACATGGTAACGAGATCTGTT-0.38% (36 reads)
TAGCGACATTCATA------|---TGGTAACGAGATCTGTT-0.36% (34 reads)
TAGCGACATTCAT------G|ACATGGTAACGAGATCTGTT-0.36% (34 reads)
TAGCGACATTCATAACAGAG|------TAACGAGATCTGTT-0.32% (31 reads)
TAGCGACATTCATAACAGAG|-----GTAACGAGATCTGTT-0.31% (30 reads)
TAGCGACATTCATAACAGAG|---TGGTAACGAGATCTGTT-0.29% (28 reads)
TAGCGACATTCATAAC----|----GGTAACGAGATCTGTT-0.26% (25 reads)
TAGAGACATTCATAACAGAG|ACATGGTAACGAGATCTGTT-0.22% (21 reads)
T-------------------|-------------------T-0.22% (21 reads)
GAGCGACATTCATAACAGAG|ACATGGTAACGAGATCTGTT-0.21% (20 reads)
TAGCGACATTCATAACAGAG|ACAT*T*GTAACGAGATCTGTT-0.21% (20 reads)
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bold	Substitutions
□	Insertions
-	Deletions
------	Predicted cleavage position