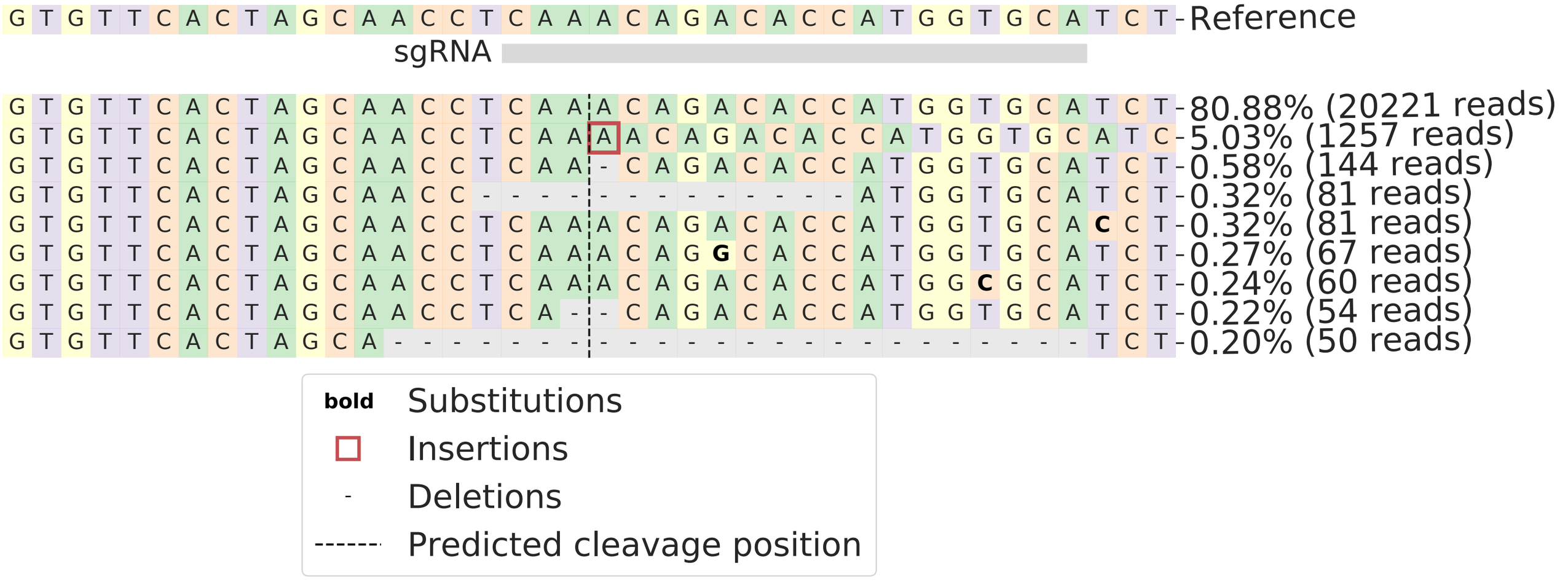
GTGTTCACTAGCAACCTCAAACAGACACCATGGTGCATCT-Reference
sgRNA
GTGTTCACTAGCAACCTCAAACAGACACCATGGTGCATCT-80.88% (20221 reads)
GTGTTCACTAGCAACCTCAAAACAGACACCATGGTGCATC-5.03% (1257 reads)
GTGTTCACTAGCAACCTCAA-CAGACACCATGGTGCATCT-0.58% (144 reads)
GTGTTCACTAGCAACC----------ATGGTGCATCT-0.32% (81 reads)
GTGTTCACTAGCAACCTCAAACAGACACCATGGTGCACCT-0.32% (81 reads)
GTGTTCACTAGCAACCTCAAACAGGCACCATGGTGCATCT-0.27% (67 reads)
GTGTTCACTAGCAACCTCAAACAGACACCATGGCGCATCT-0.24% (60 reads)
GTGTTCACTAGCAACCTCA--CAGACACCATGGTGCATCT-0.22% (54 reads)
GTGTTCACTAGCA----------ATGCT-0.20% (50 reads)
bold
Substitutions
Insertions
-
Deletions
Predicted cleavage position