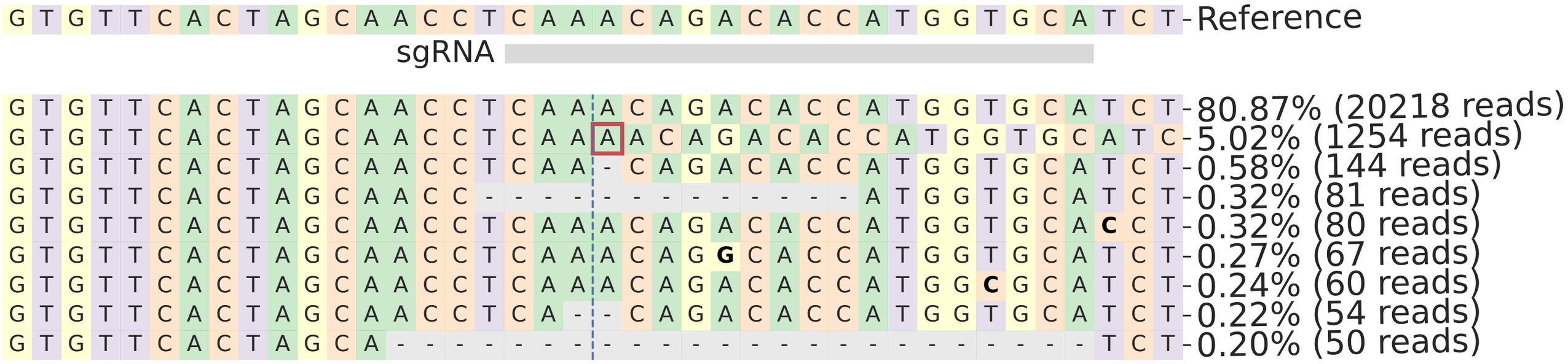
GTGTTCACTAGCAACCTCAAACAGACACCATGGTGCATCT-Reference
sgRNA
GTGTTCACTAGCAACCTCAAACAGACACCATGGTGCATCT-80.87% (20218 reads)
GTGTTCACTAGCAACCTCAAAACAGACACCATGGTGCATC-5.02% (1254 reads)
GTGTTCACTAGCAACCTCAA-CAGACACCATGGTGCATCT-0.58% (144 reads)
GTGTTCACTAGCAACC----------ATGGTGCATCT-0.32% (81 reads)
GTGTTCACTAGCAACCTCAAACAGACACCATGGTGCACCT-0.32% (80 reads)
GTGTTCACTAGCAACCTCAAACAGGCACCATGGTGCATCT-0.27% (67 reads)
GTGTTCACTAGCAACCTCAAACAGACACCATGGCGCATCT-0.24% (60 reads)
GTGTTCACTAGCAACCTCA--CAGACACCATGGTGCATCT-0.22% (54 reads)
GTGTTCACTAGCA----------TCT-0.20% (50 reads)
bold Substitutions
Insertions
- Deletions
Predicted cleavage position