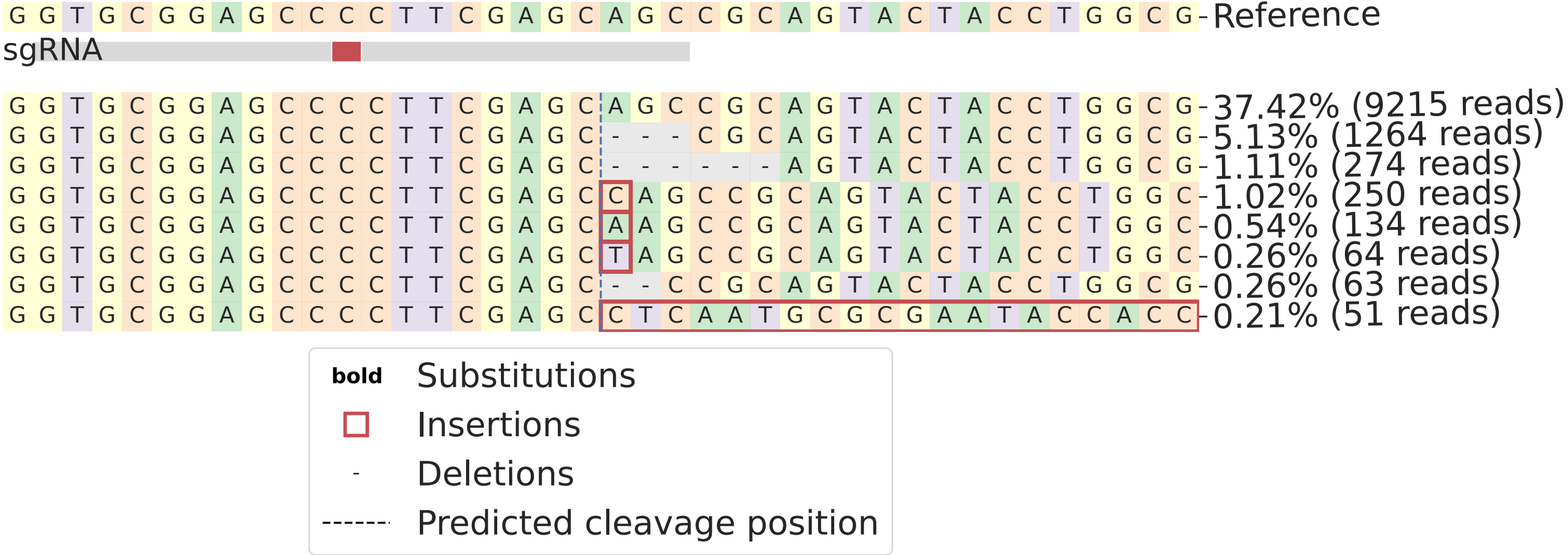
GGTGCGGAGCCCCTTCGAGCAGCCGCAGTACTACCTGGCG- Reference
sgRNA
GGTGCGGAGCCCCTTCGAGCAGCCGCAGTACTACCTGGCG- 37.42% (9215 reads)
GGTGCGGAGCCCCTTCGAGC---CGCAGTACTACCTGGCG- 5.13% (1264 reads)
GGTGCGGAGCCCCTTCGAGC------AGTACTACCTGGCG- 1.11% (274 reads)
GGTGCGGAGCCCCTTCGAGCCAGCCGCAGTACTACCTGGC- 1.02% (250 reads)
GGTGCGGAGCCCCTTCGAGCAAGCCGCAGTACTACCTGGC- 0.54% (134 reads)
GGTGCGGAGCCCCTTCGAGCTAGCCGCAGTACTACCTGGC- 0.26% (64 reads)
GGTGCGGAGCCCCTTCGAGC--CCGCAGTACTACCTGGCG- 0.26% (63 reads)
GGTGCGGAGCCCCTTCGAGCCTCAATGCGCGAATACCACC- 0.21% (51 reads)
bold Substitutions
Insertions
- Deletions
Predicted cleavage position