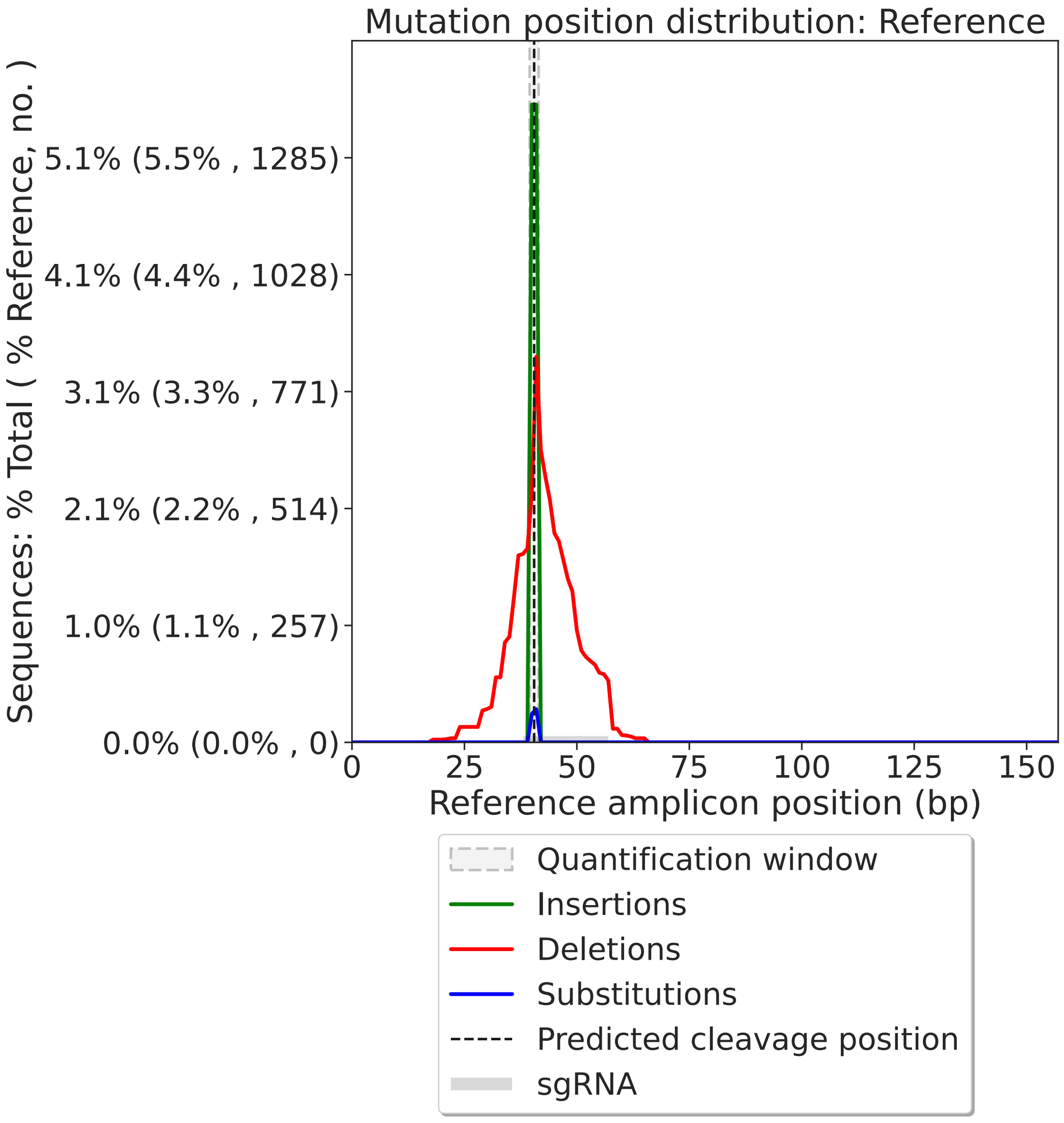
Mutation position distribution: Reference
Sequences: % Total (% Reference, no.)
5.1% (5.5% , 1285)
4.1% (4.4% , 1028)
3.1% (3.3% , 771)
2.1% (2.2% , 514)
1.0% (1.1% , 257)
0.0% (0.0% , 0)
0
25
50
75
100
125
150
Reference amplicon position (bp)
Quantification window
Insertions
Deletions
Substitutions
Predicted cleavage position
sgRNA