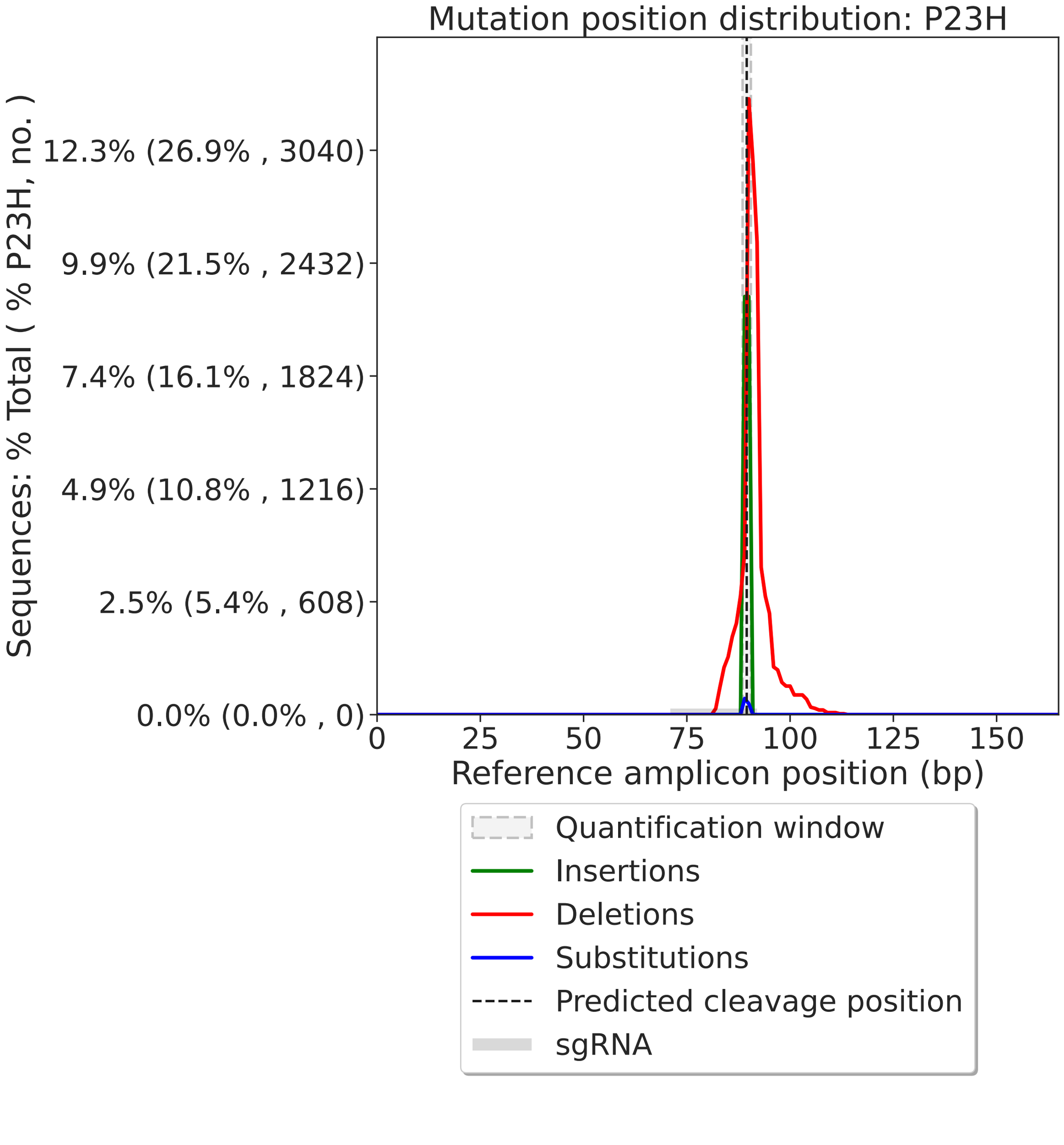
Mutation position distribution: P23H
Sequences: % Total (% P23H, no.)
12.3% (26.9% , 3040)
9.9% (21.5% , 2432)
7.4% (16.1% , 1824)
4.9% (10.8% , 1216)
2.5% (5.4% , 608)
0.0% (0.0% , 0)
0
25
50
75
100
125
150
Reference amplicon position (bp)
Quantification window
Insertions
Deletions
Substitutions
Predicted cleavage position
sgRNA