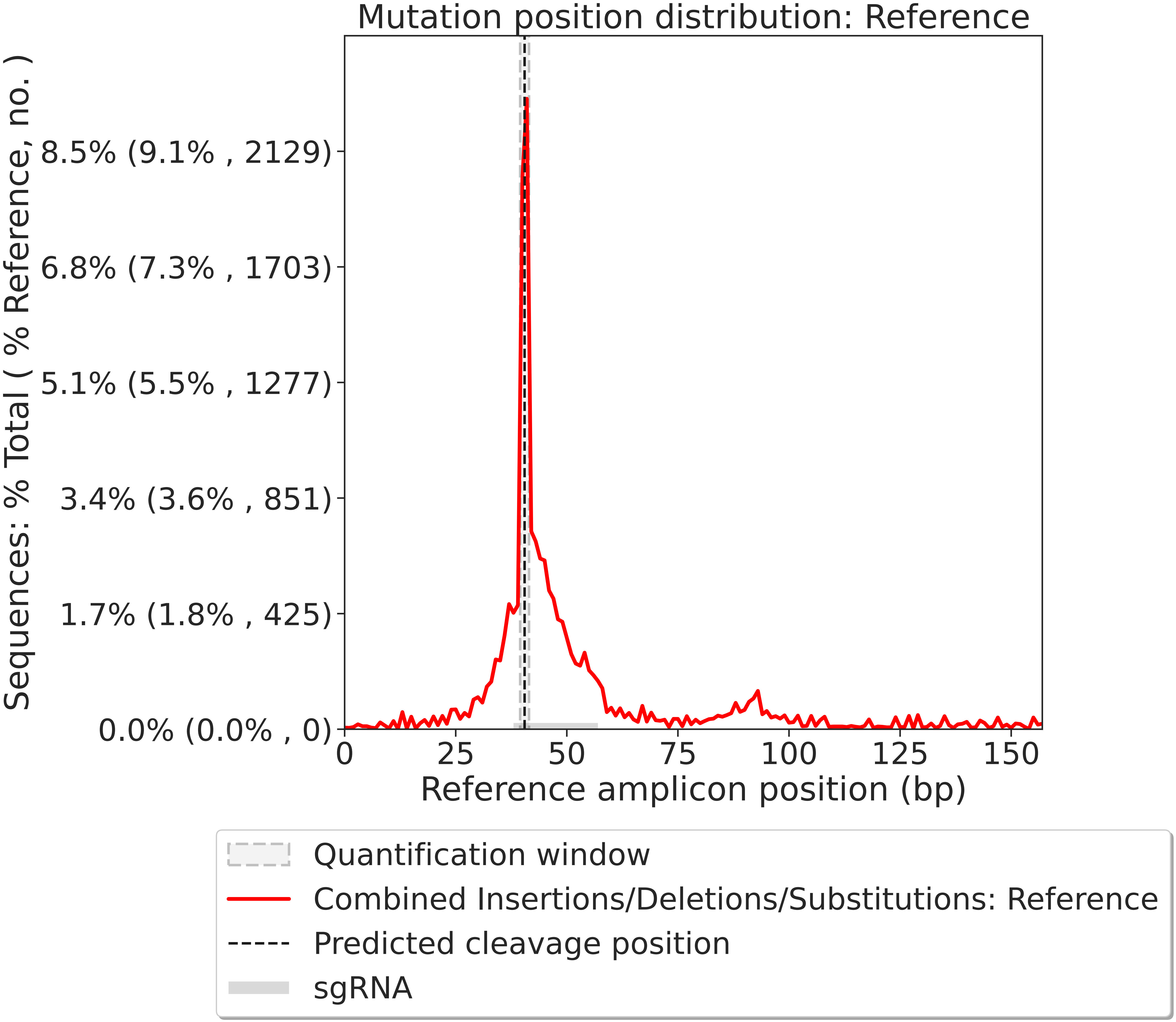
Mutation position distribution: Reference
Sequences: % Total (% Reference, no.)
8.5% (9.1% , 2129)
6.8% (7.3% , 1703)
5.1% (5.5% , 1277)
3.4% (3.6% , 851)
1.7% (1.8% , 425)
0.0% (0.0% , 0)
0
25
50
75
100
125
150
Reference amplicon position (bp)
Quantification window
Combined Insertions/Deletions/Substitutions: Reference
Predicted cleavage position
sgRNA