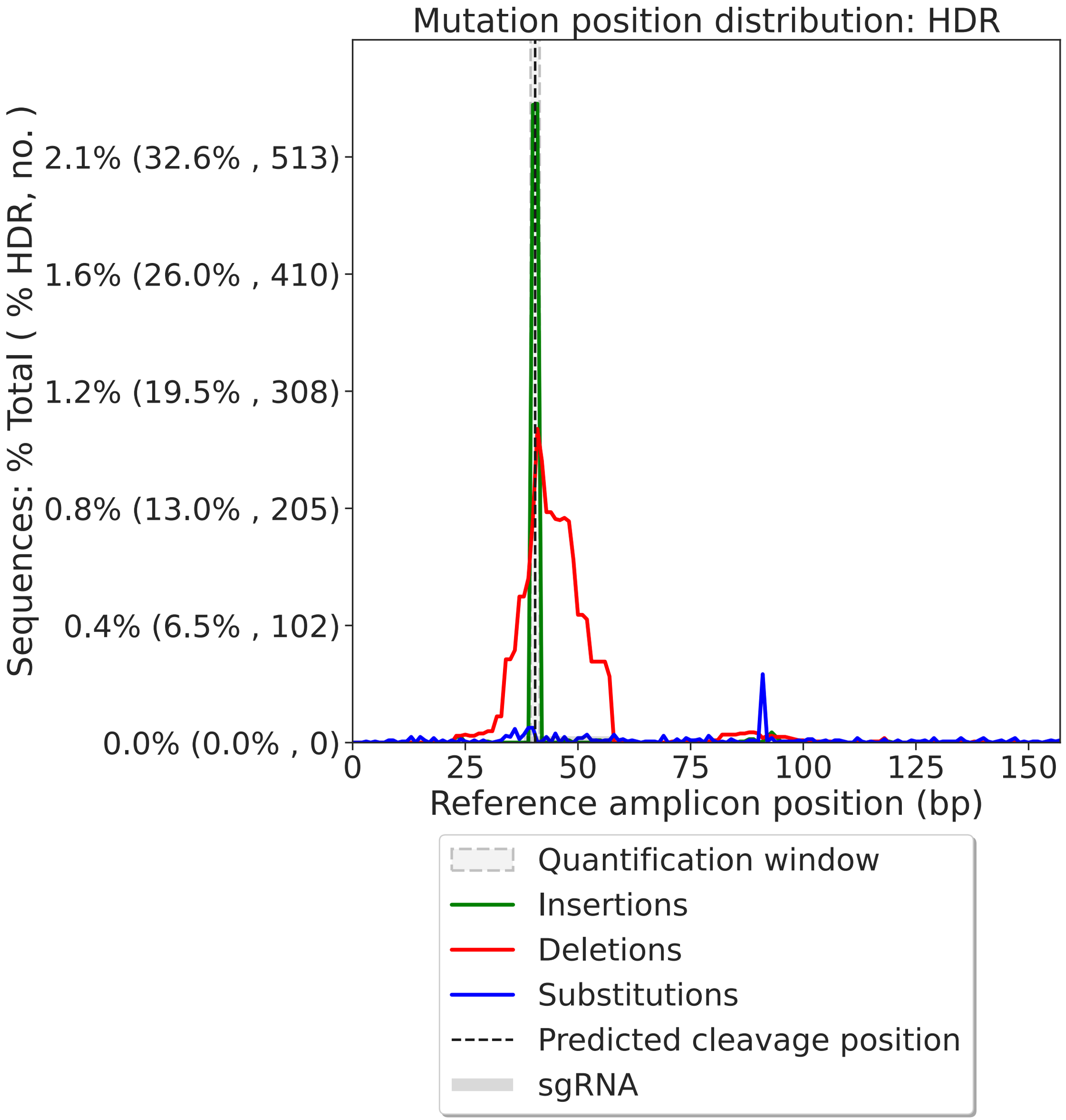
Mutation position distribution: HDR
Sequences: % Total (% HDR, no.)
2.1% (32.6% , 513)
1.6% (26.0% , 410)
1.2% (19.5% , 308)
0.8% (13.0% , 205)
0.4% (6.5% , 102)
0.0% (0.0% , 0)
0
25
50
75
100
125
150
Reference amplicon position (bp)
Quantification window
Insertions
Deletions
Substitutions
Predicted cleavage position
sgRNA