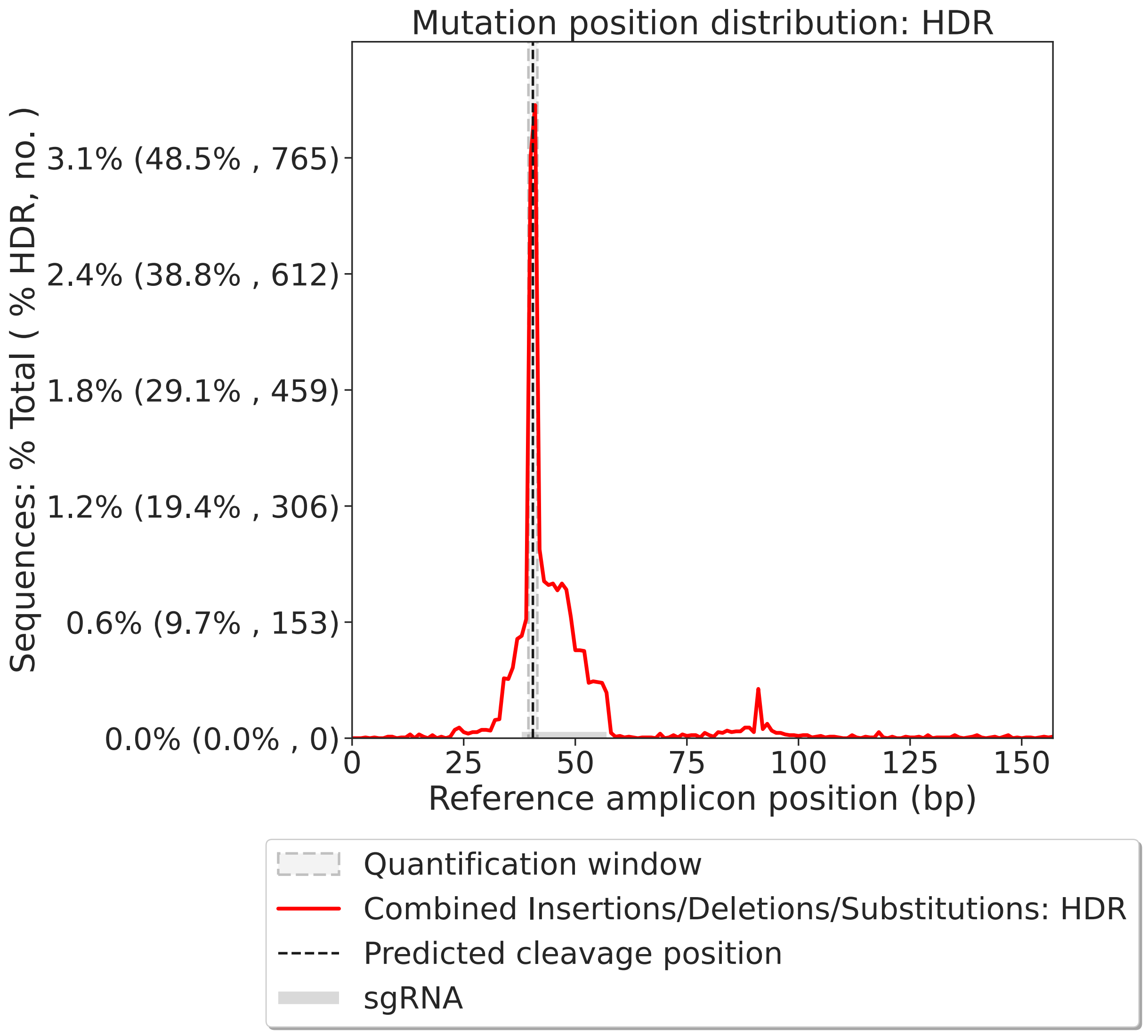
Mutation position distribution: HDR
Sequences: % Total (% HDR, no.)
3.1% (48.5% , 765)
2.4% (38.8% , 612)
1.8% (29.1% , 459)
1.2% (19.4% , 306)
0.6% (9.7% , 153)
0.0% (0.0% , 0)
0
25
50
75
100
125
150
Reference amplicon position (bp)
Quantification window
Combined Insertions/Deletions/Substitutions: HDR
Predicted cleavage position
sgRNA