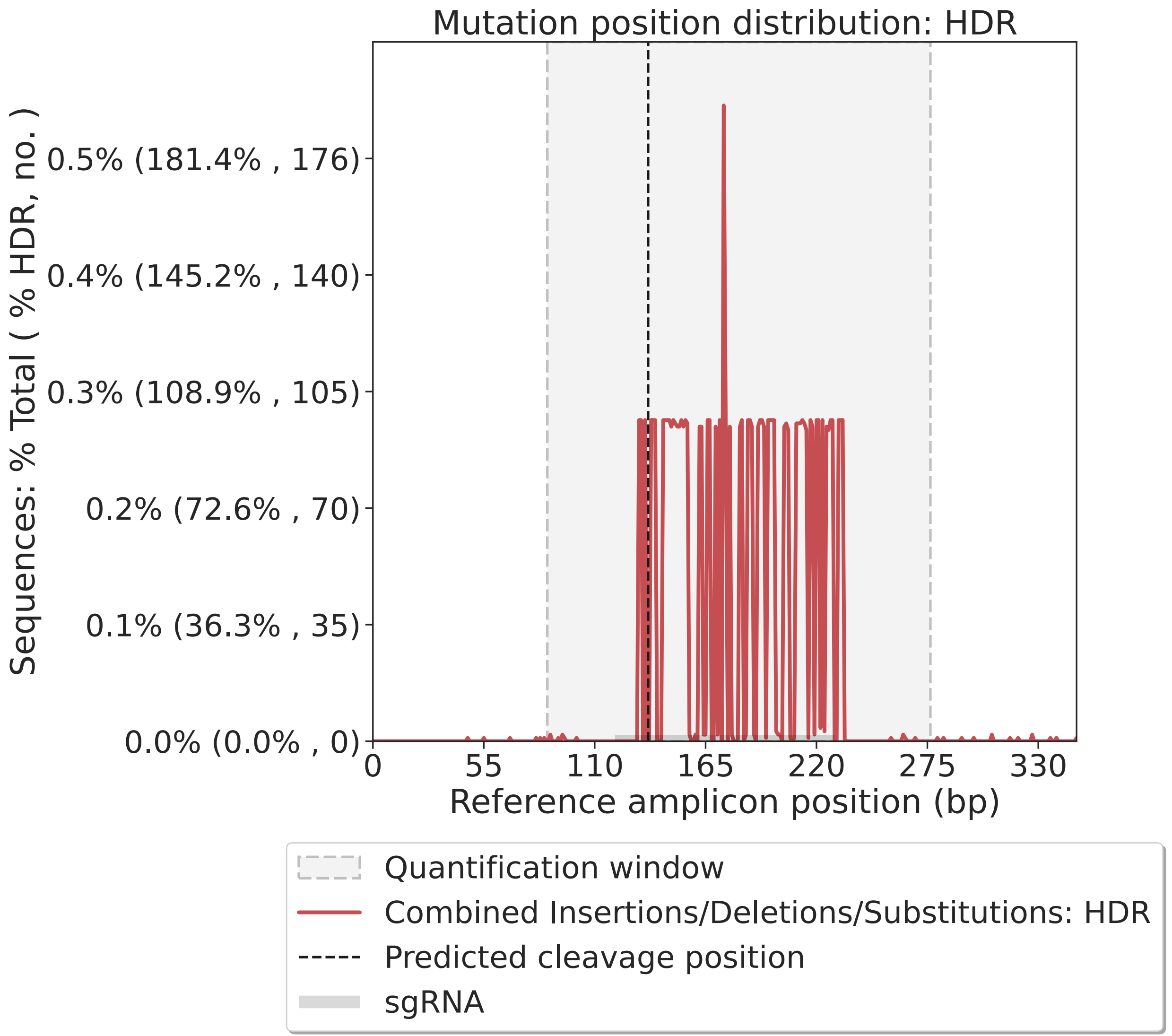
Mutation position distribution: HDR
Sequences: % Total (% HDR, no.)
0.5% (181.4% , 176)
0.4% (145.2% , 140)
0.3% (108.9% , 105)
0.2% (72.6% , 70)
0.1% (36.3% , 35)
0.0% (0.0% , 0)
0
55
110
165
220
275
330
Reference amplicon position (bp)
Quantification window
Combined Insertions/Deletions/Substitutions: HDR
Predicted cleavage position
sgRNA