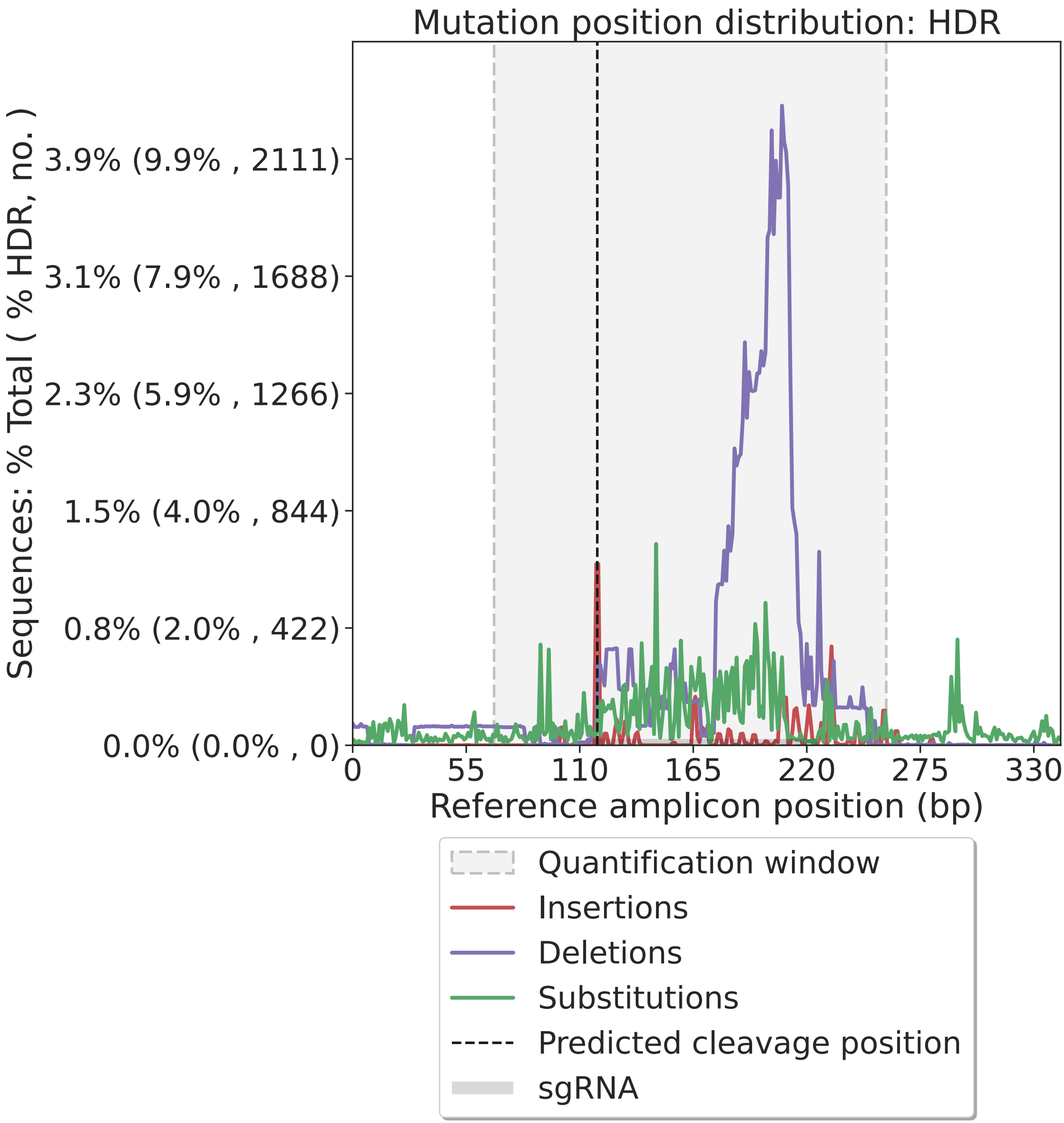
Mutation position distribution: HDR
Sequences: % Total (% HDR, no.)
3.9% (9.9% , 2111)
3.1% (7.9% , 1688)
2.3% (5.9% , 1266)
1.5% (4.0% , 844)
0.8% (2.0% , 422)
0.0% (0.0% , 0)
0
55
110
165
220
275
330
Reference amplicon position (bp)
Quantification window
Insertions
Deletions
Substitutions
Predicted cleavage position
sgRNA