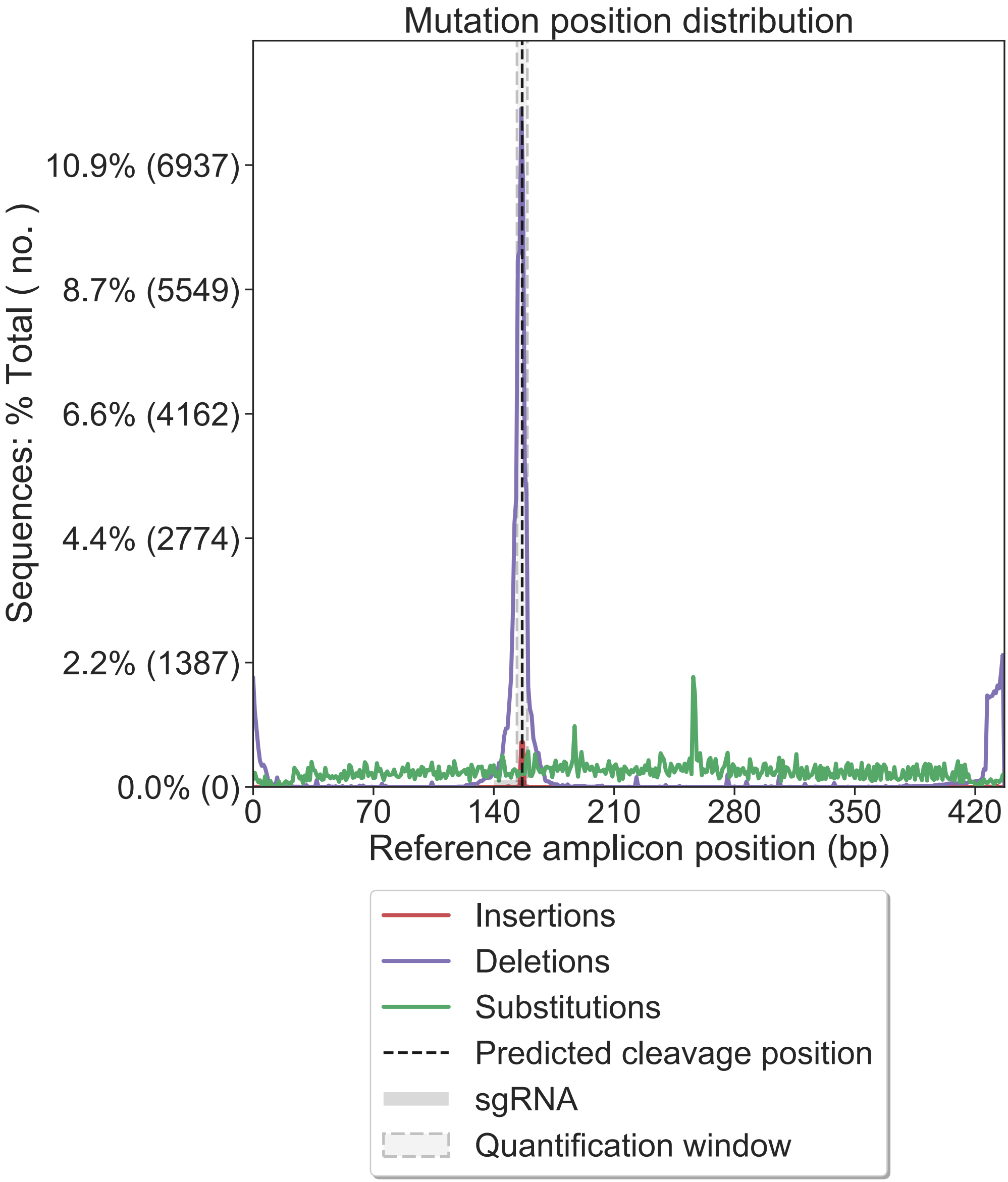
Mutation position distribution
Sequences: % Total (no.)
10.9% (6937)
8.7% (5549)
6.6% (4162)
4.4% (2774)
2.2% (1387)
0.0% (0)
0
70
140
210
280
350
420
Reference amplicon position (bp)
Insertions
Deletions
Substitutions
Predicted cleavage position
sgRNA
Quantification window