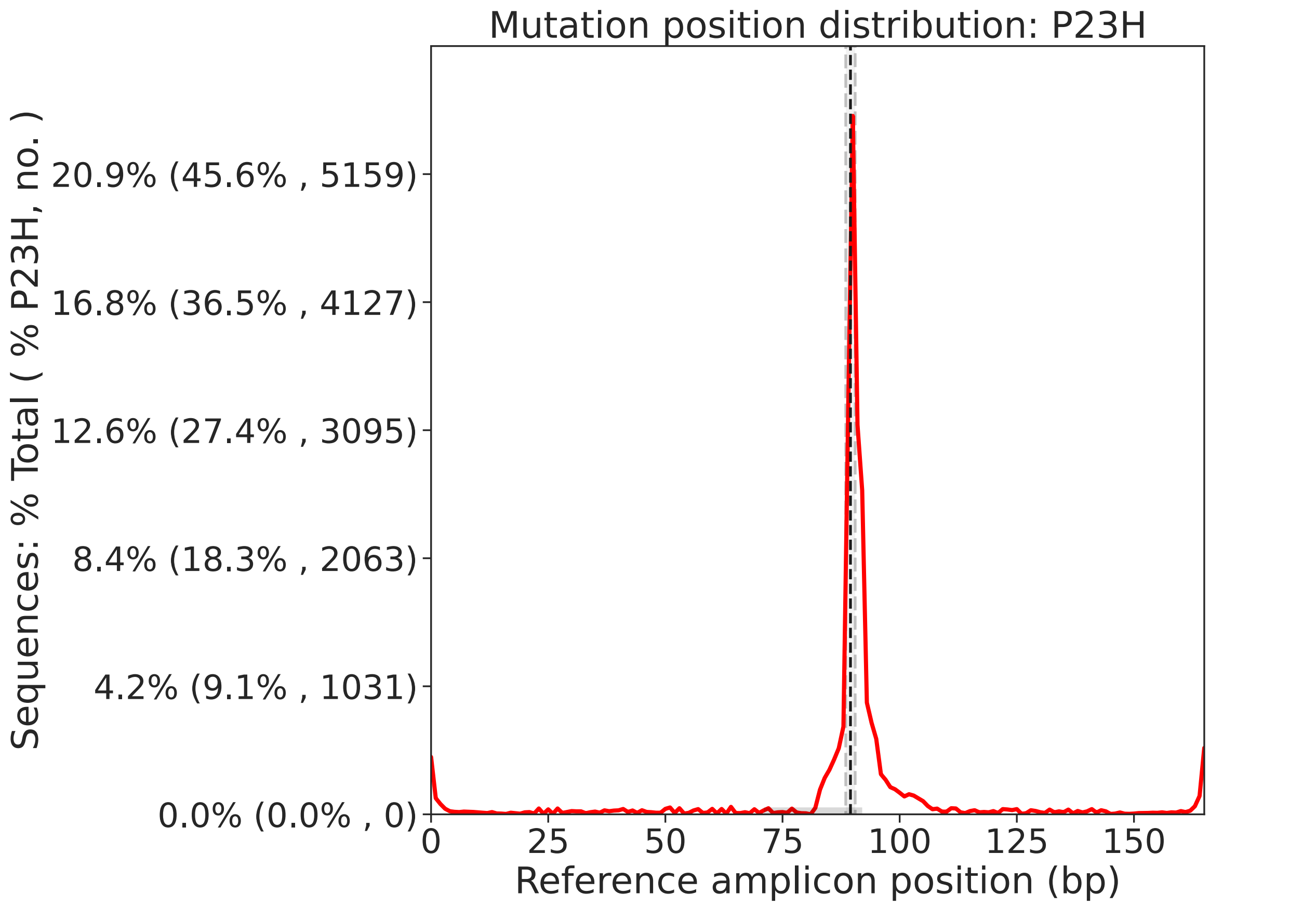
Mutation position distribution: P23H
Sequences: % Total (% P23H, no.)
20.9% (45.6% , 5159)
16.8% (36.5% , 4127)
12.6% (27.4% , 3095)
8.4% (18.3% , 2063)
4.2% (9.1% , 1031)
0.0% (0.0% , 0)
0
25
50
75
100
125
150
Reference amplicon position (bp)
Quantification window
Combined Insertions/Deletions/Substitutions: P23H
Predicted cleavage position
sgRNA