

# Mutation position distribution: Reference

Sequences: % Total ( % Reference, no. )

37.0% (50.0% , 13384)

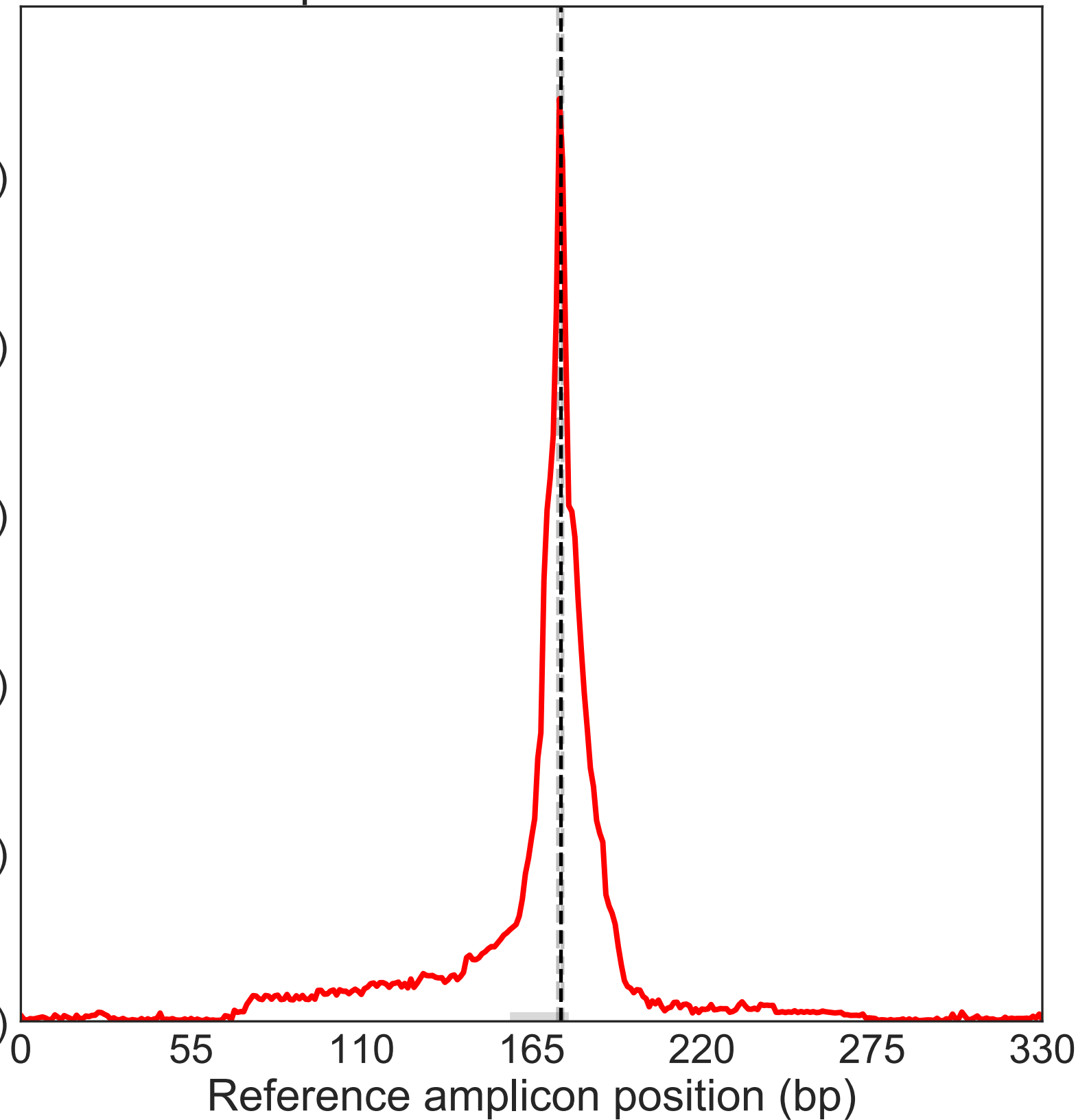
29.6% (40.0% , 10707)

22.2% (30.0% , 8030)

14.8% (20.0% , 5353)

7.4% (10.0% , 2676)

0.0% (0.0% , 0)



- Combined Insertions/Deletions/Substitutions: Reference
- Predicted cleavage position
- sgRNA
- Quantification window