Mutation position distribution: P23H

Reference amplicon position (bp)

0.0% (0.0%, 0)
2.5% (5.4%, 608)
4.9% (10.8%, 1216)
7.4% (16.1%, 1824)
9.9% (21.5%, 2432)
12.3% (26.9%, 3040)

Sequences: % Total (% P23H, no.)

Insertions
Deletions
Substitutions
Predicted cleavage position
sgRNA
Quantification window