Mutation position distribution: P23H

Sequences: % Total (% P23H, no.)
- 12.3% (26.9%, 3040)
- 9.9% (21.5%, 2432)
- 7.4% (16.1%, 1824)
- 4.9% (10.8%, 1216)
- 2.5% (5.4%, 608)

Reference amplicon position (bp)

- Insertions
- Deletions
- Substitutions
- Predicted cleavage position
- sgRNA
- Quantification window