**Mutation position distribution**

- **Sequences:** % Total (no.)
  - 17.8% (3572)
  - 14.2% (2857)
  - 10.7% (2143)
  - 7.1% (1428)
  - 3.6% (714)
  - 0.0% (0)

**Reference amplicon position (bp):**

- **Insertions**
- **Deletions**
- **Substitutions**

**Legend:**
- Red: Insertions
- Blue: Deletions
- Green: Substitutions
- Gray: sgRNA
- Light gray: Quantification window