Mutation position distribution in all reads with reference to Reference 29.6% (10714) Sequences: % Total (no.) 23.7% (8571) 17.8% (6428) 11.9% (4285) 5.9% (2142) 0.0% (0) 55 110 165 220 275 330 Reference position (bp) Insertions **Deletions Substitutions** Predicted cleavage position sgRNA Quantification window