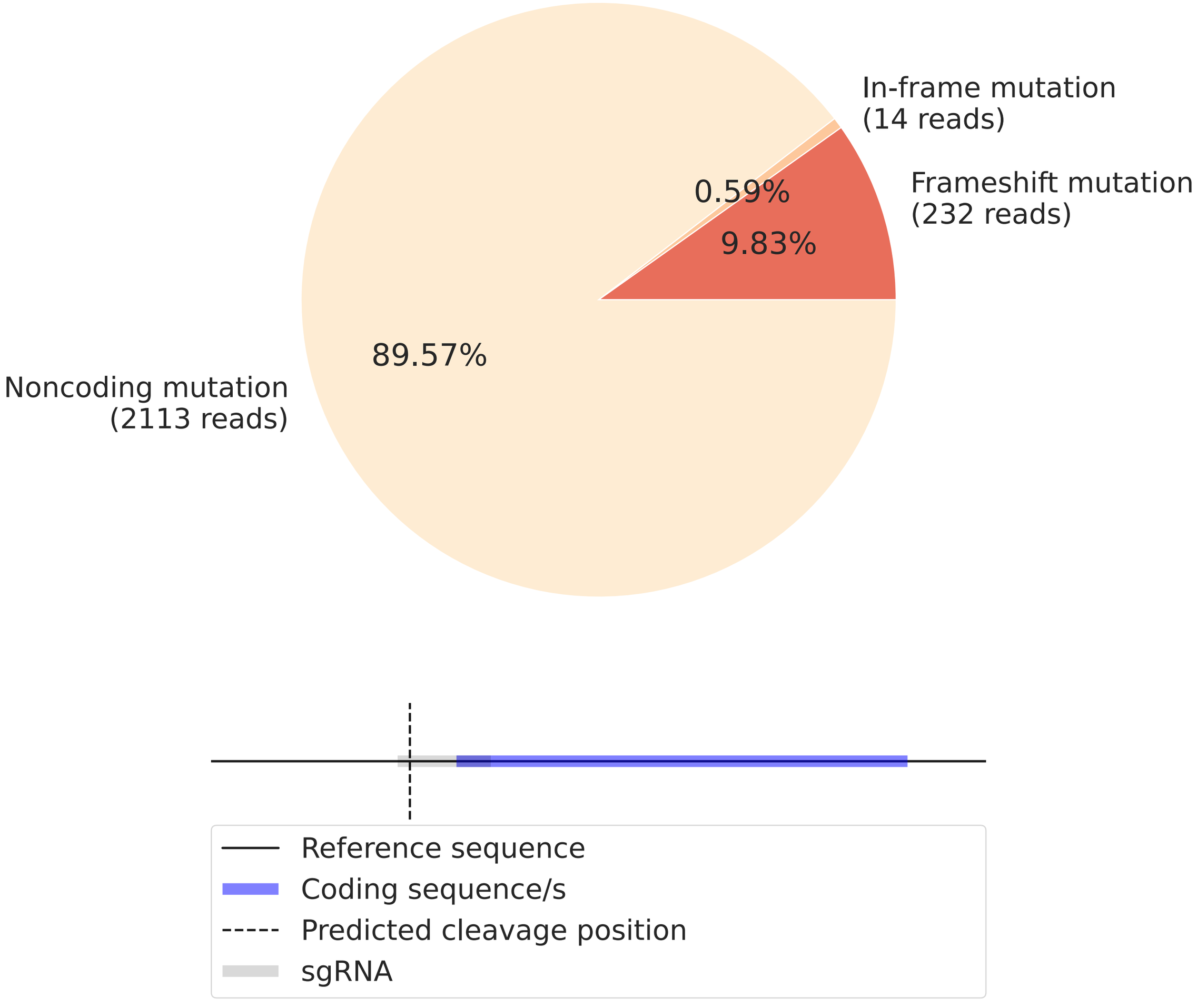
In-frame mutation
(14 reads)
0.59%
Frameshift mutation
(232 reads)
9.83%
89.57%
Noncoding mutation
(2113 reads)
Reference sequence
Coding sequence/s
Predicted cleavage position
sgRNA