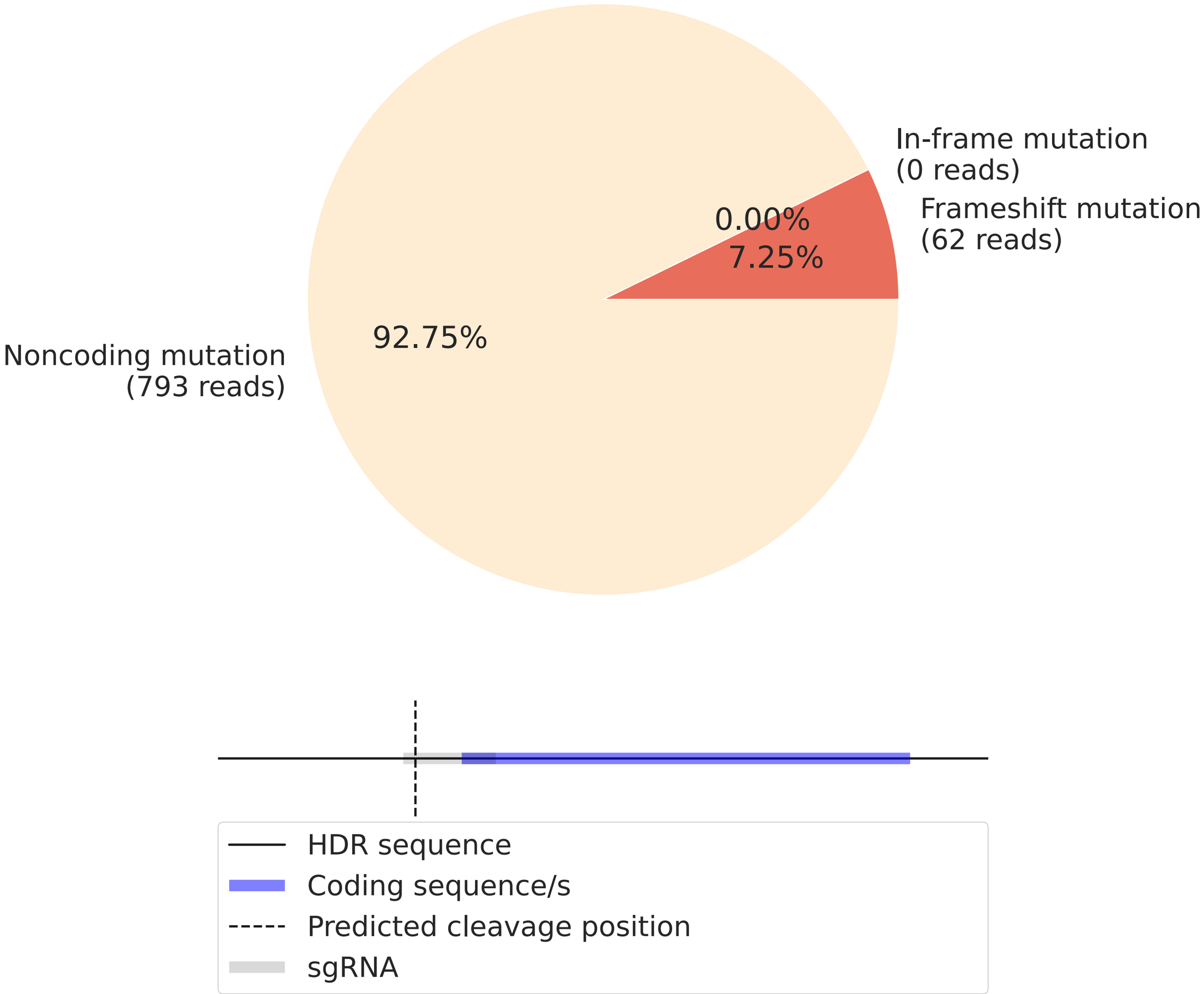
In-frame mutation
(0 reads)
Frameshift mutation
(62 reads)
0.00%
7.25%
92.75%
Noncoding mutation
(793 reads)
HDR sequence
Coding sequence/s
Predicted cleavage position
sgRNA