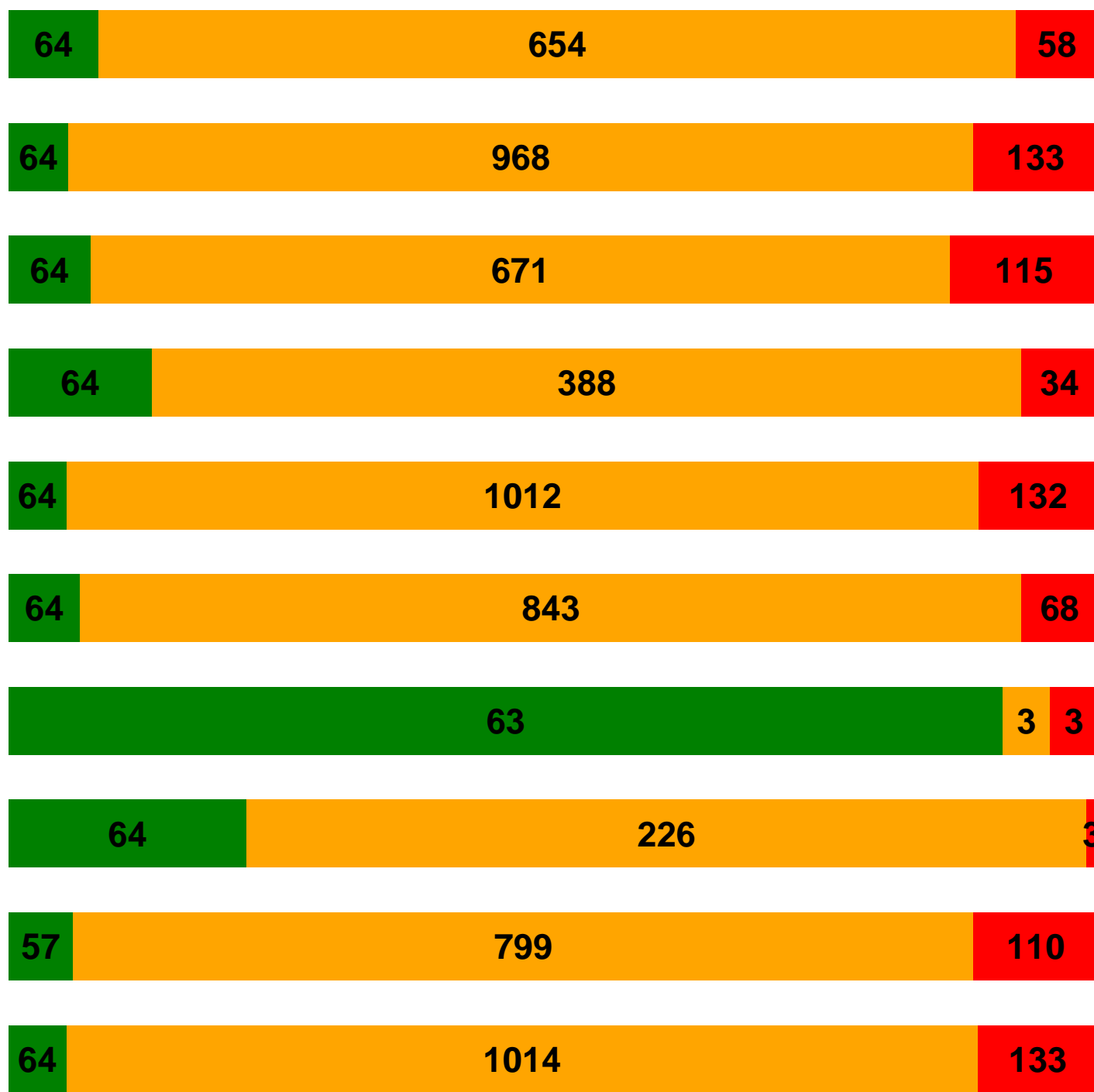


# 60X coverage, run 1

filter criterion



■ DNMs  
■ miscalled variants  
■ sequencing errors

0.00 0.25 0.50 0.75 1.00  
proportion