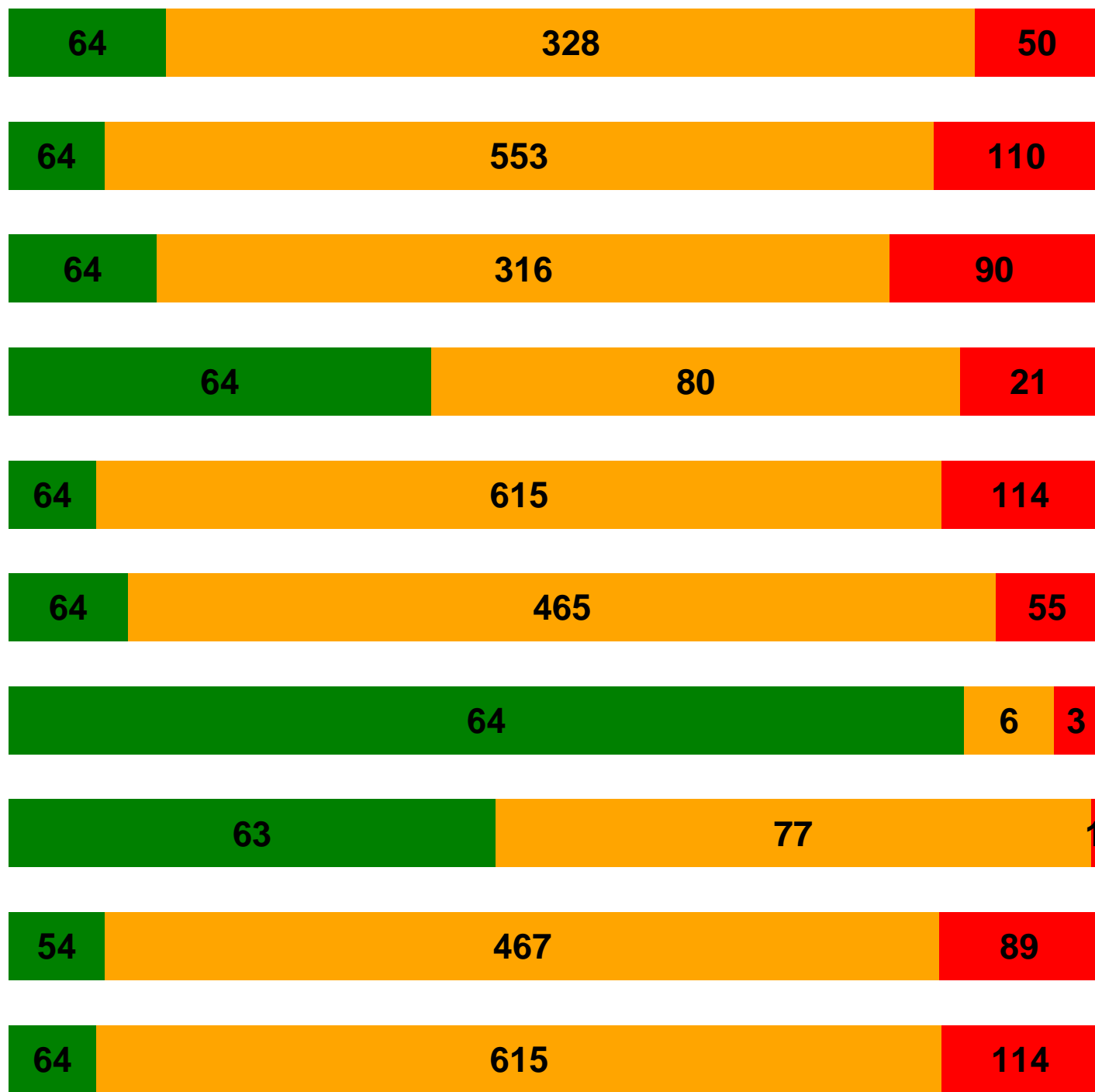


100X coverage, run 1

filter criterion



■ DNMs
■ miscalled variants
■ sequencing errors

0.00 0.25 0.50 0.75 1.00
proportion