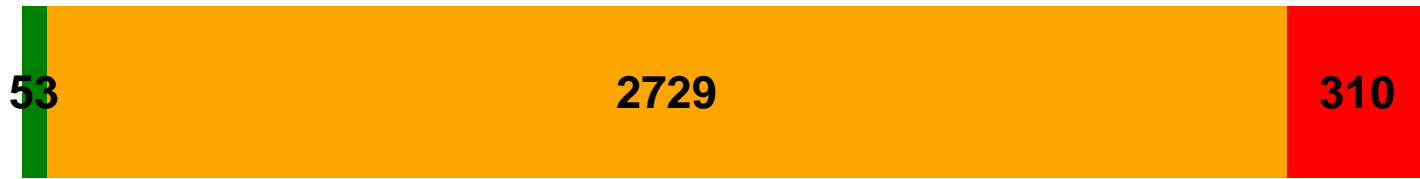


# 40X coverage, run 9

filter criterion

DNM candidates



DP<sub>min</sub>



GQ



AB<sub>min</sub>



reassembly



■ DNMs  
■ miscalled variants  
■ sequencing errors

0.00

0.25

0.50

0.75

1.00

proportion