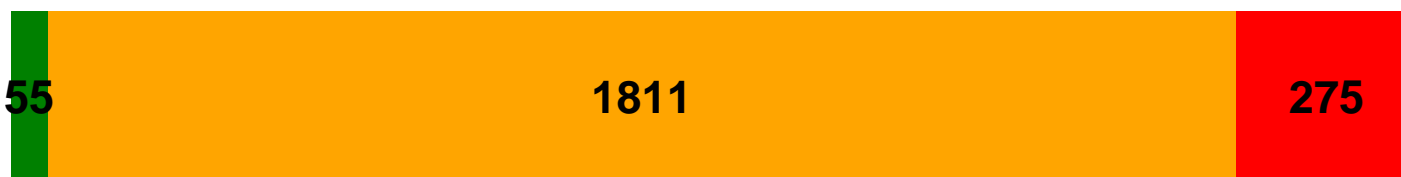


# 50X coverage, run 2

DNM candidates



GQ



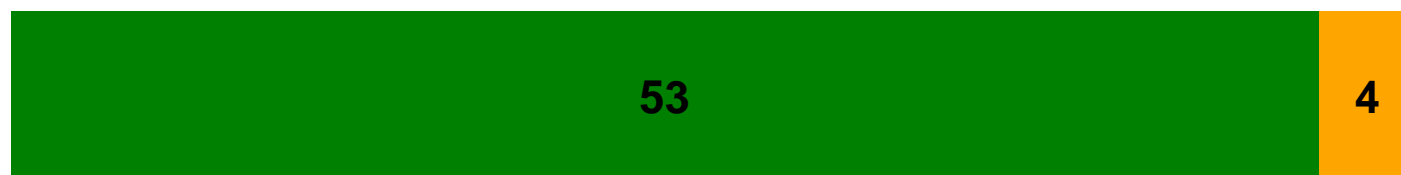
AB<sub>min</sub>



AB<sub>max</sub>



reassembly



■ DNMs  
■ miscalled variants  
■ sequencing errors

0.00 0.25 0.50 0.75 1.00  
proportion