

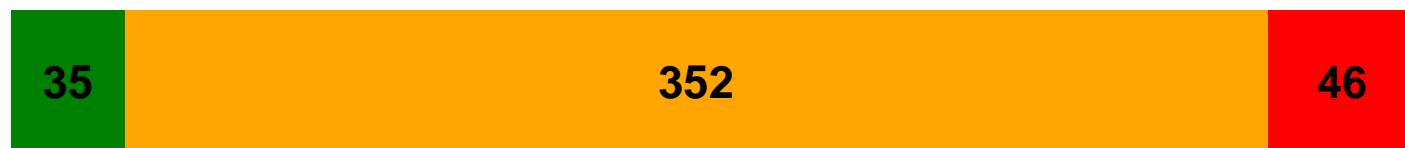
60X coverage, run 8

filter criterion

DNM candidates



DP_{min}



AB_{min}



GQ



AB_{max}



reassembly



■ DNMs
■ miscalled variants
■ sequencing errors

0.00 0.25 0.50 0.75 1.00
proportion