

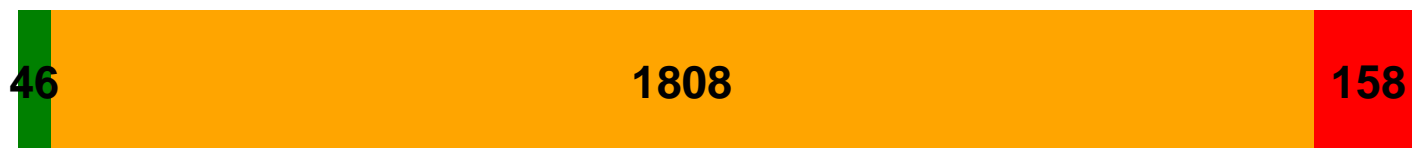
30X coverage, run 7

filter criterion

DNM candidates



DP_{min}



AB_{min}



GQ



GATK_{BestPractices}



reassembly



DNMs
miscalled variants
sequencing errors

0.00 0.25 0.50 0.75 1.00
proportion