

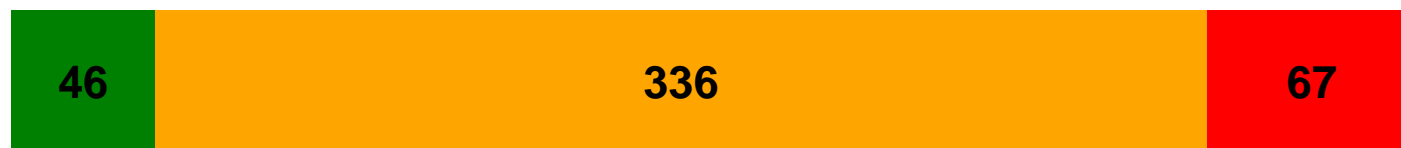
60X coverage, run 3

filter criterion

DNM candidates



DP_{min}



GQ



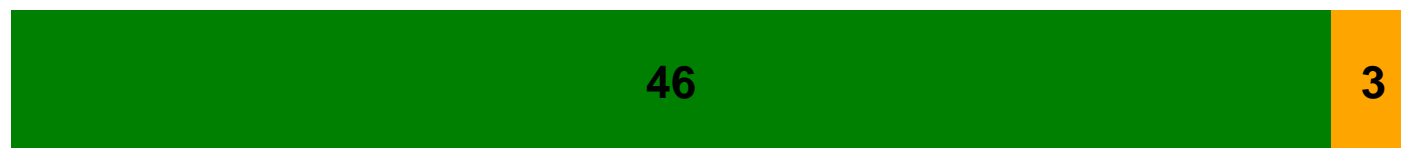
AB_{min}



DP_{max}



reassembly



■ DNMs
■ miscalled variants
■ sequencing errors

0.00

0.25

0.50

0.75

1.00

proportion