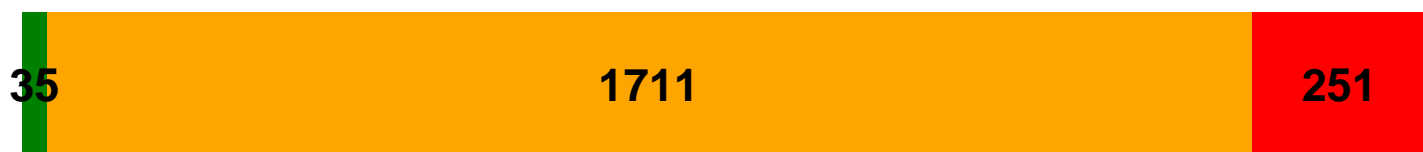


50X coverage, run 8

filter criterion

DNM candidates



DP_{min}



GQ



AB_{min}



reassembly



QUAL



DNMs
miscalled variants
sequencing errors

0.00

0.25

0.50

0.75

1.00

proportion