

30X coverage, run 7

filter criterion

DNM candidates

46

3634

435

GQ

35

73

15

AB_{min}

35

69

5

AB_{max}

35

68

5

reassembly

35

3

1

QUAL

35

3

DNMs
miscalled variants
sequencing errors

0.00

0.25

0.50

0.75

1.00

proportion