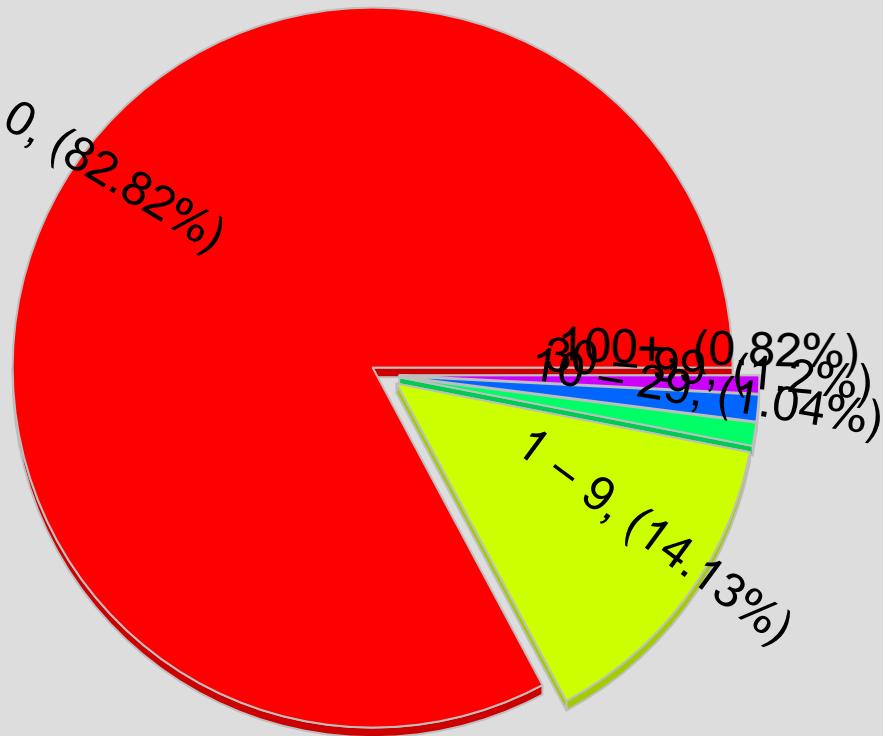
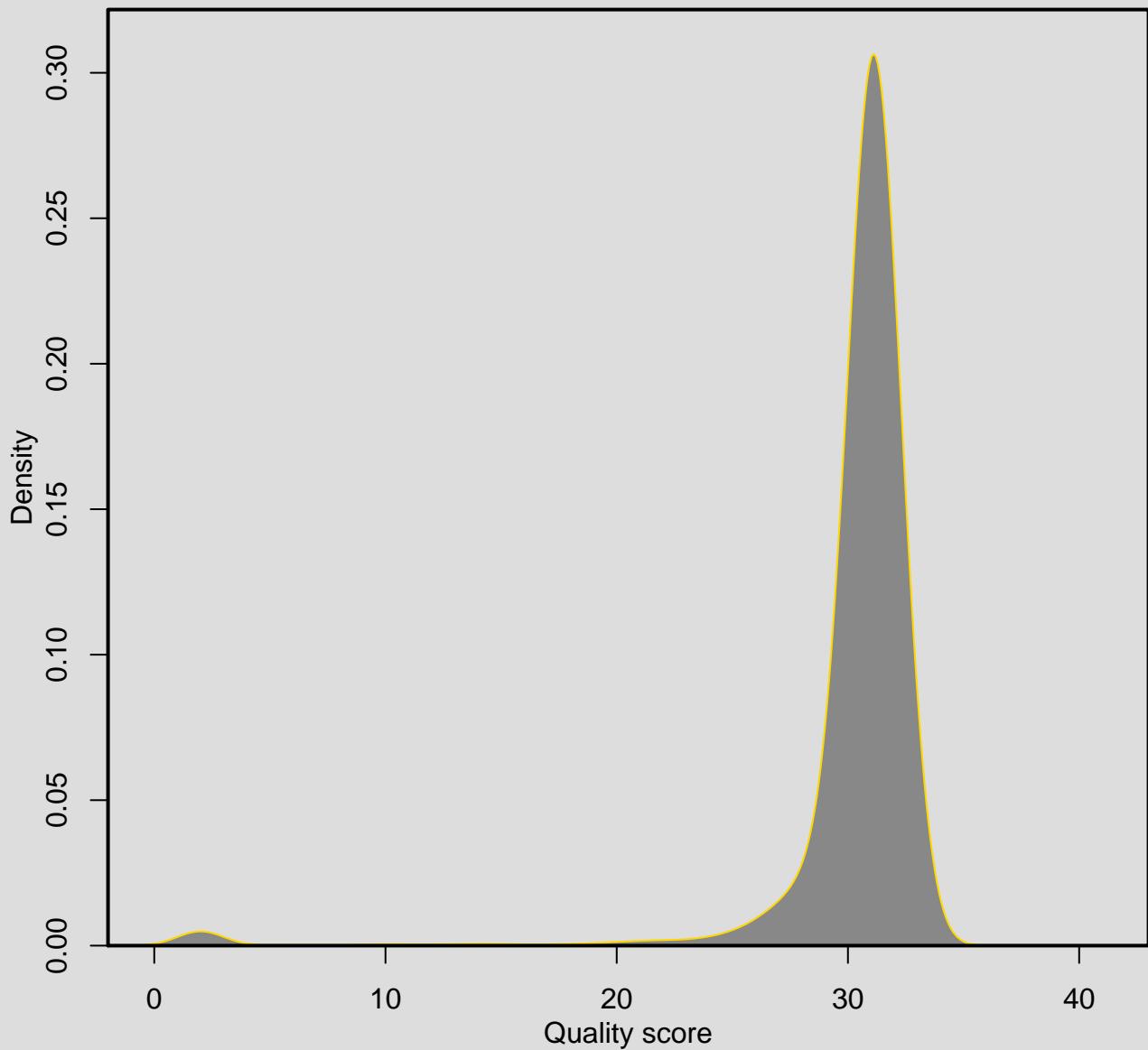


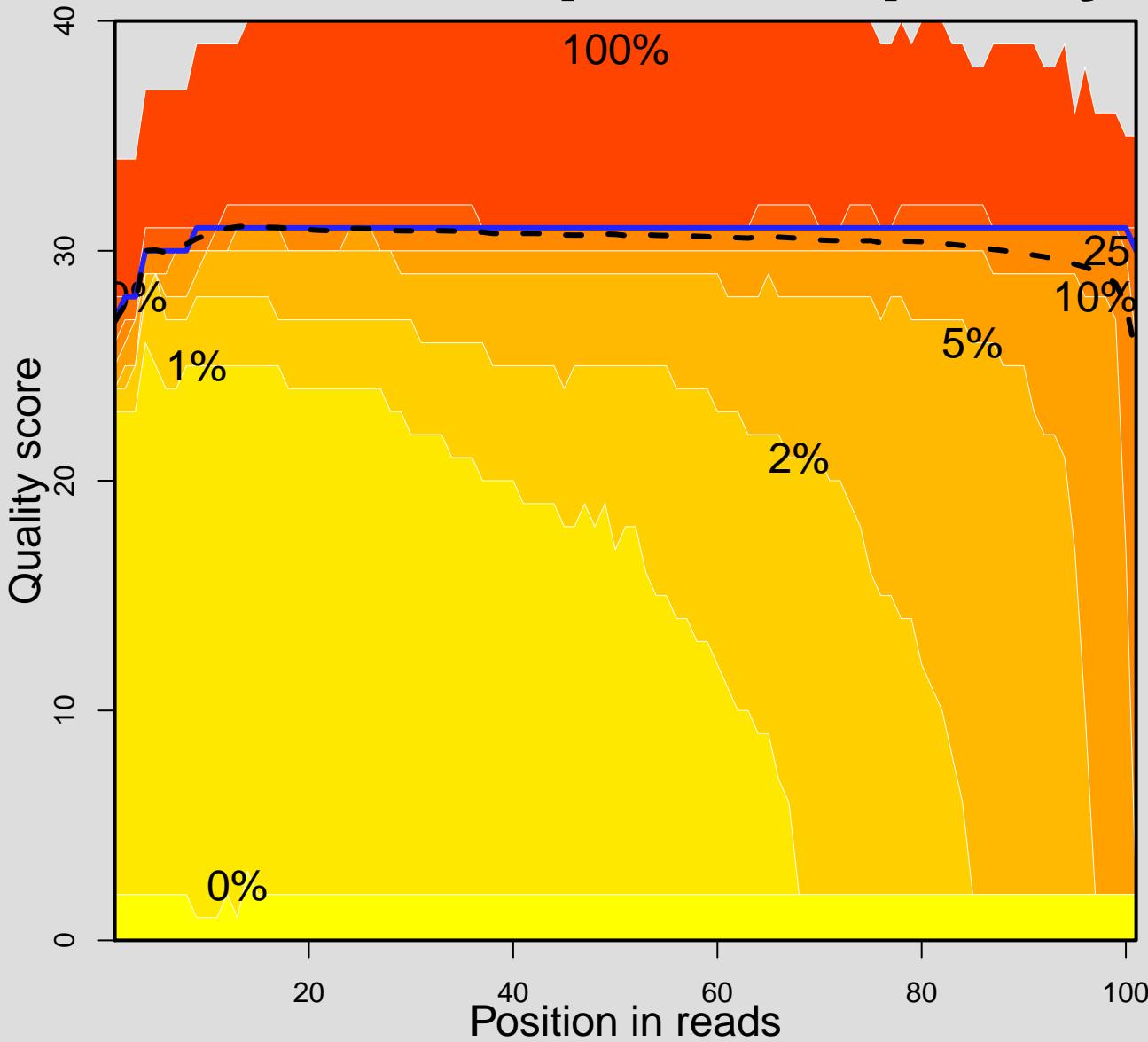
Whole genome depth



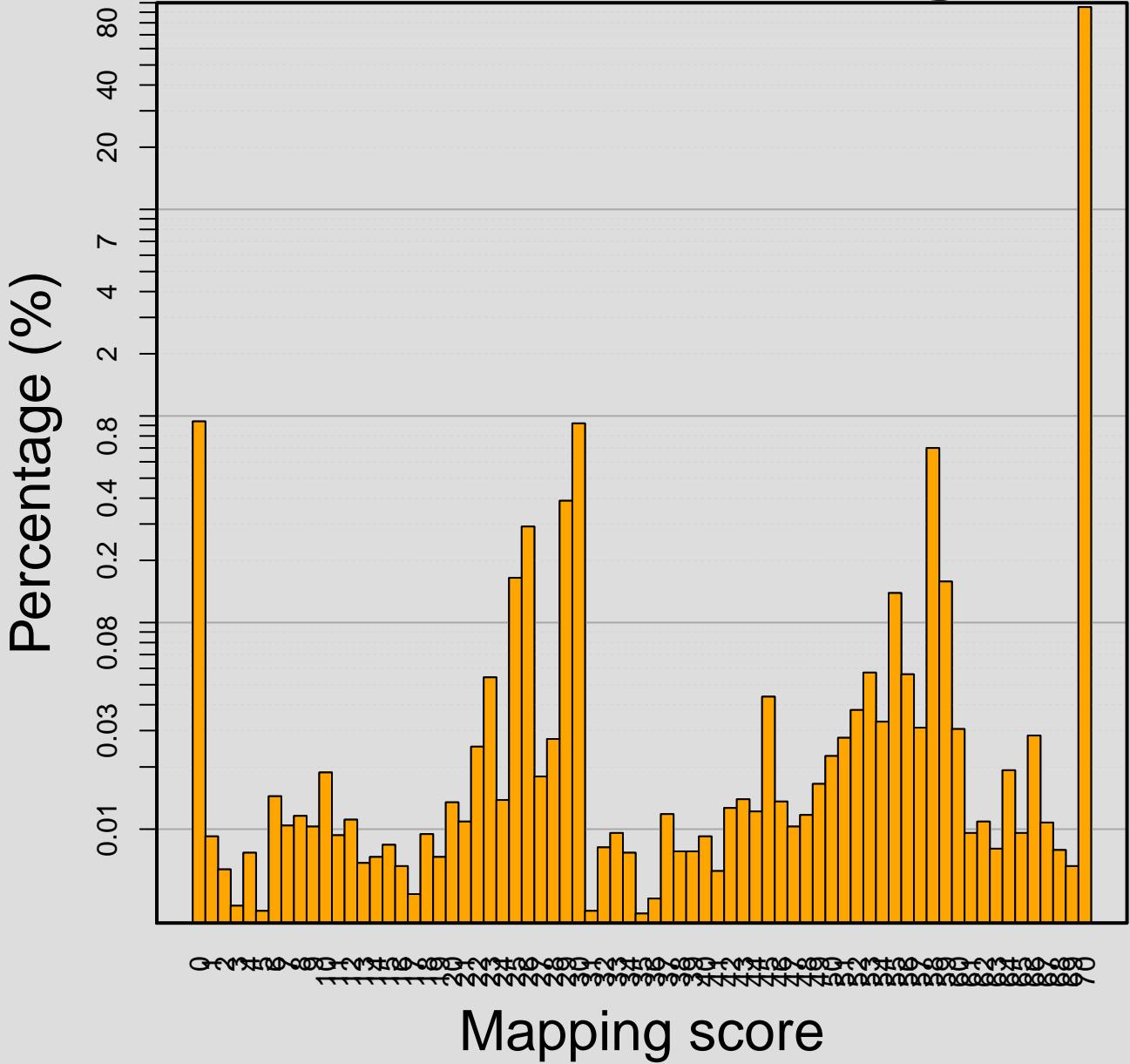
Score distribution



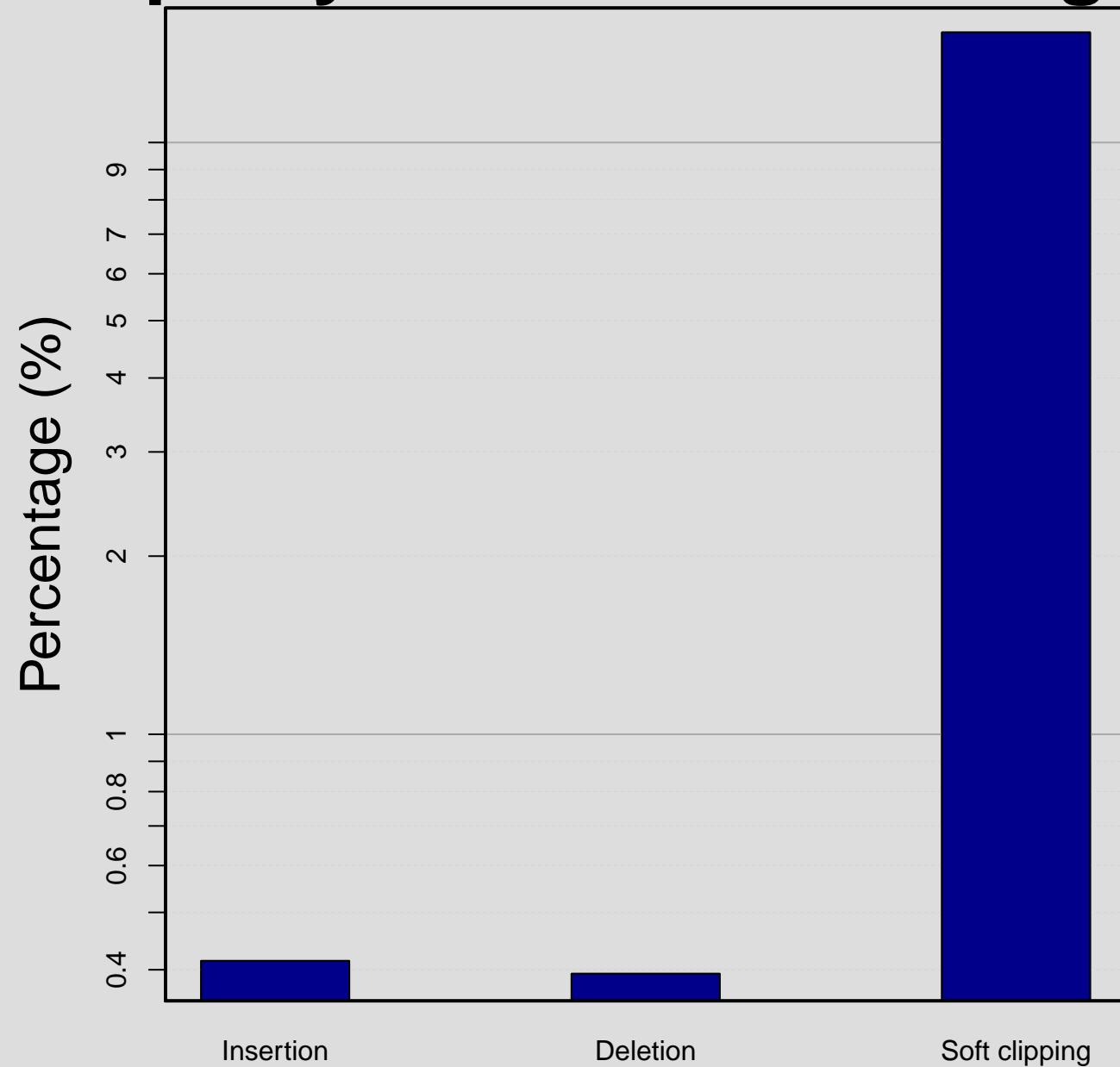
Position-specific quality



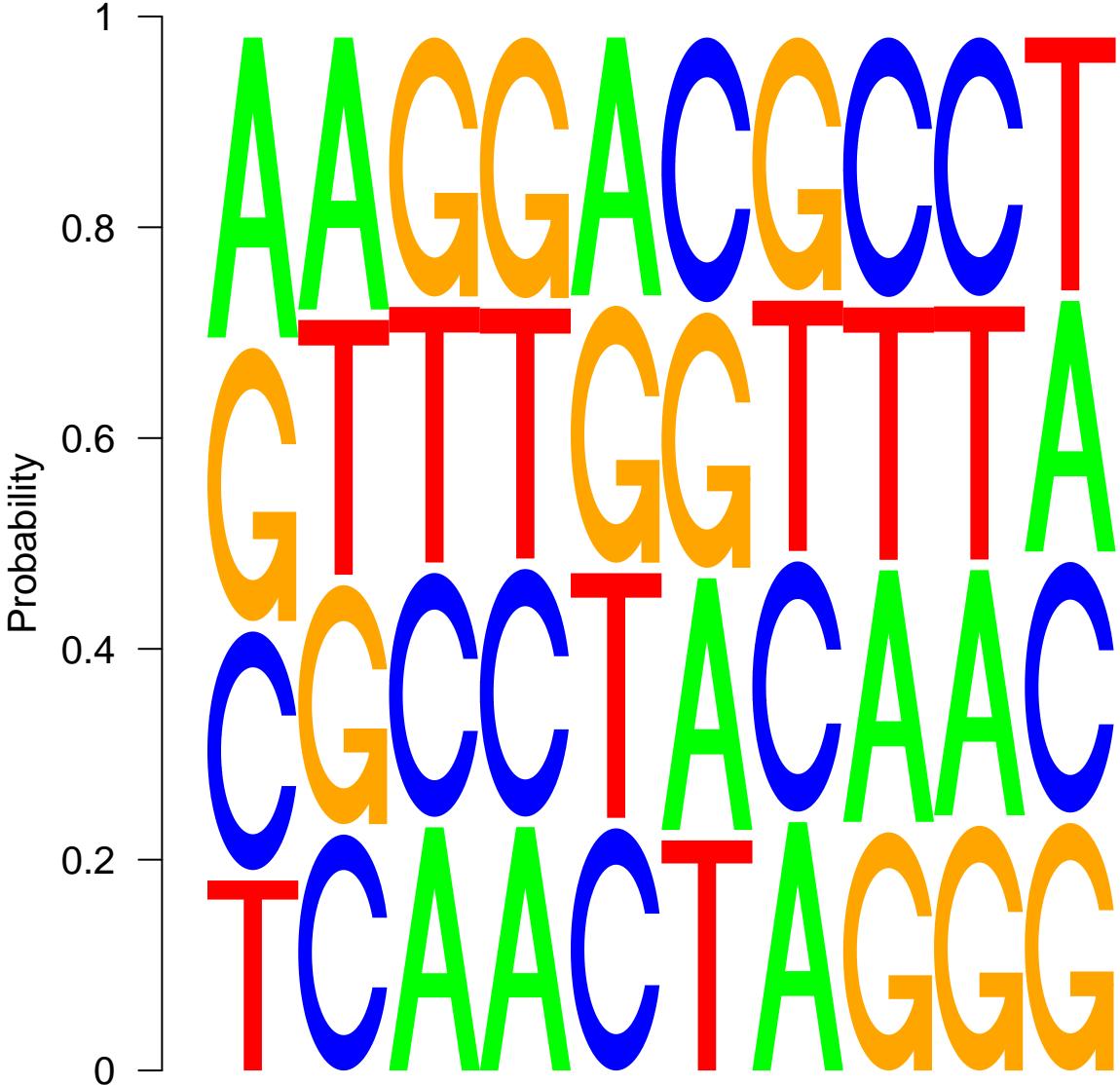
Distribution of mapping score



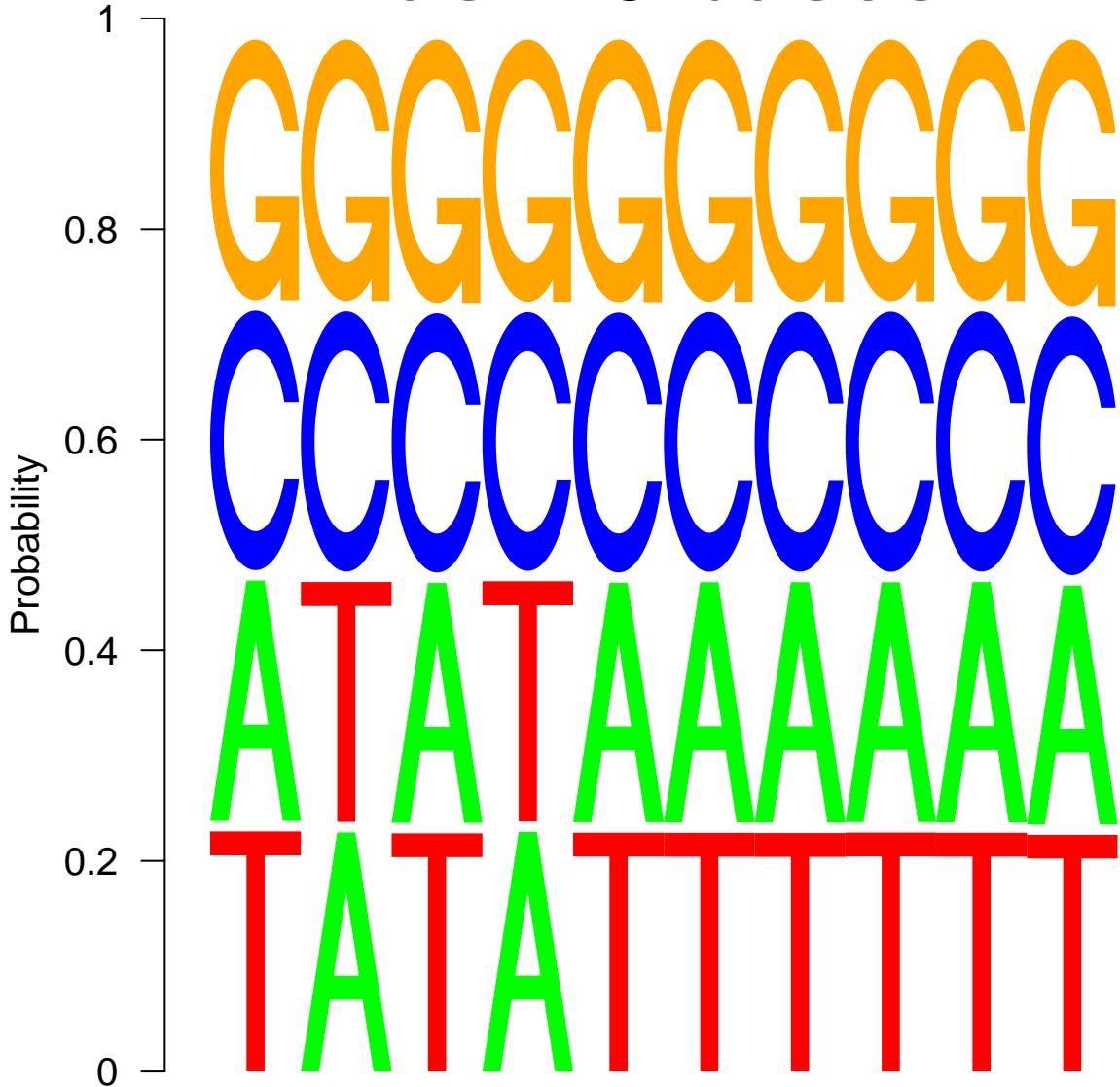
Frequency of mismatch catego



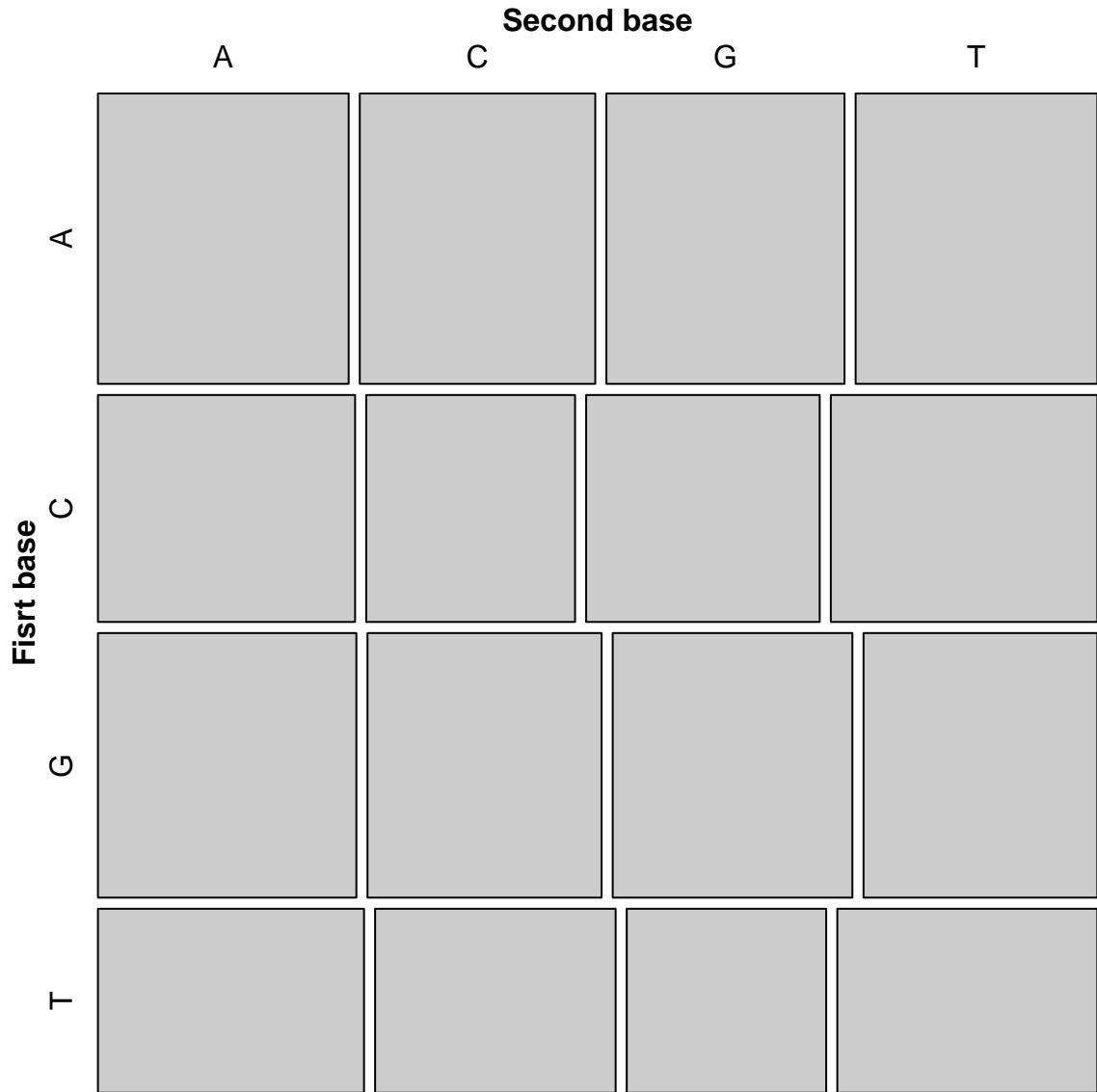
First 10 bases



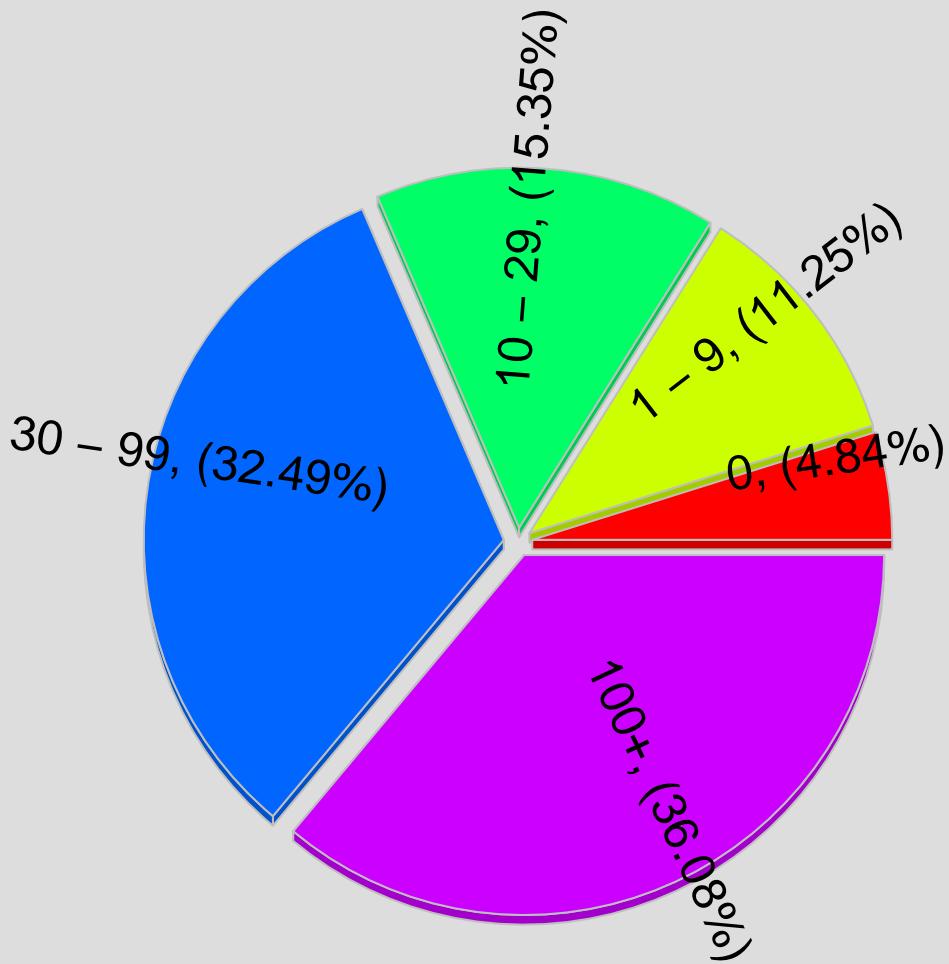
Last 10 bases



Frequency of two–base combinations



On-target depth



Accumulative distribution

Accumulative Percentage (%)

100

80

60

40

20

0

0

200

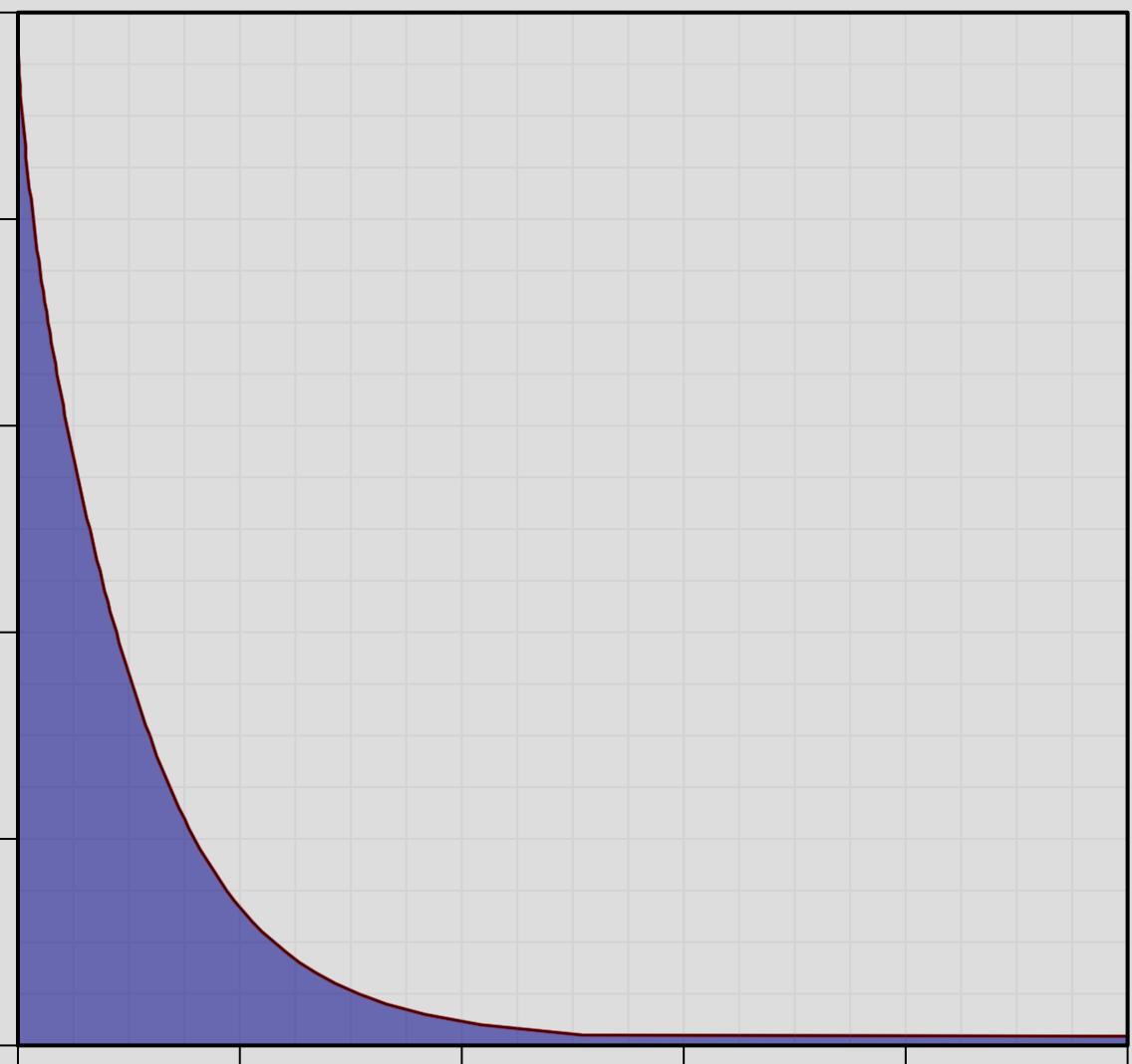
400

600

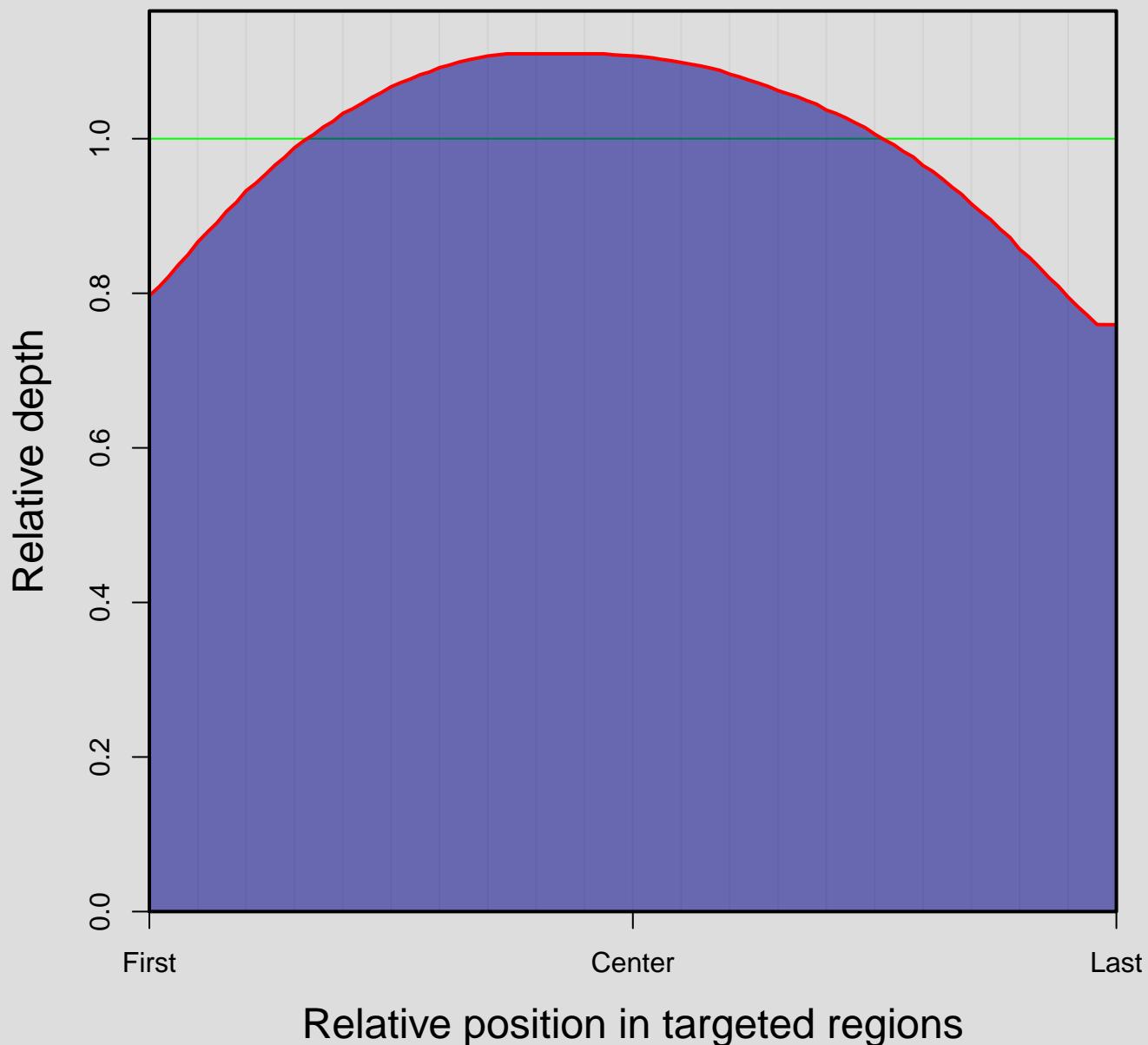
800

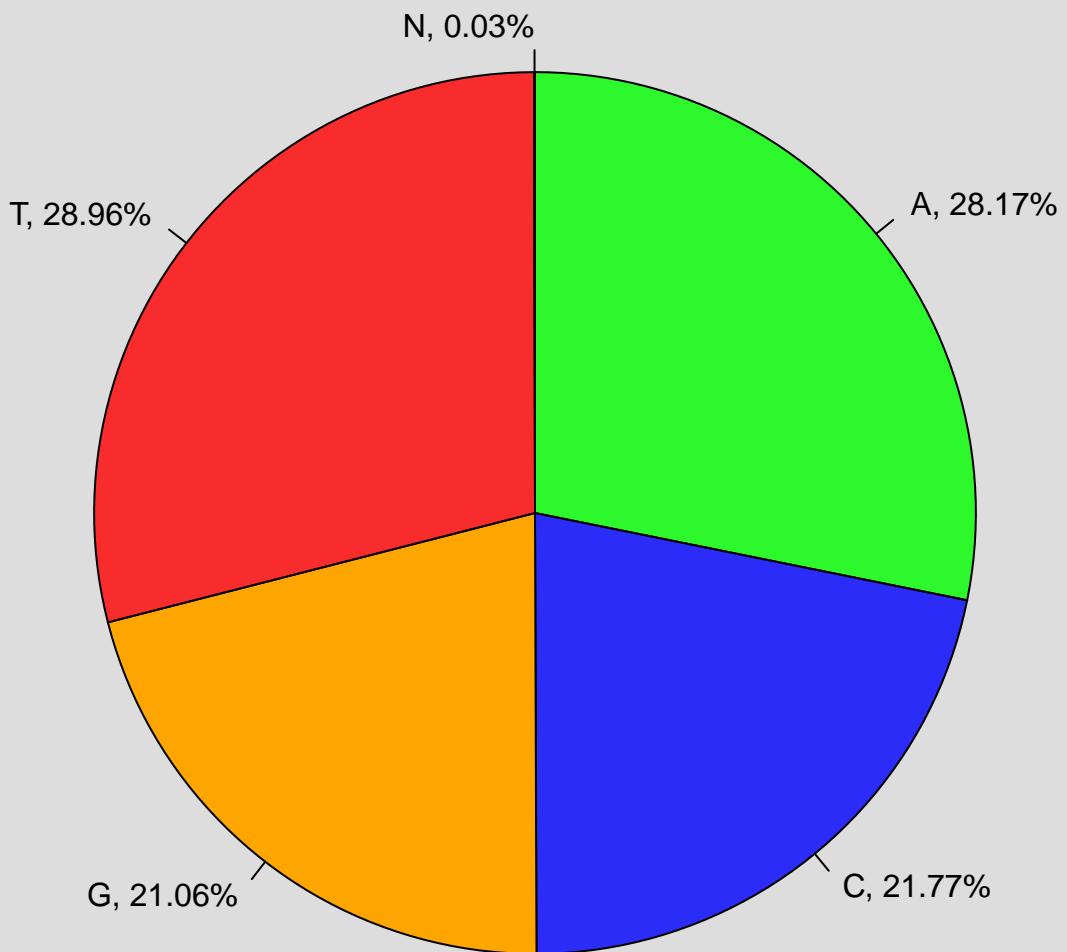
1000

Depth (X)

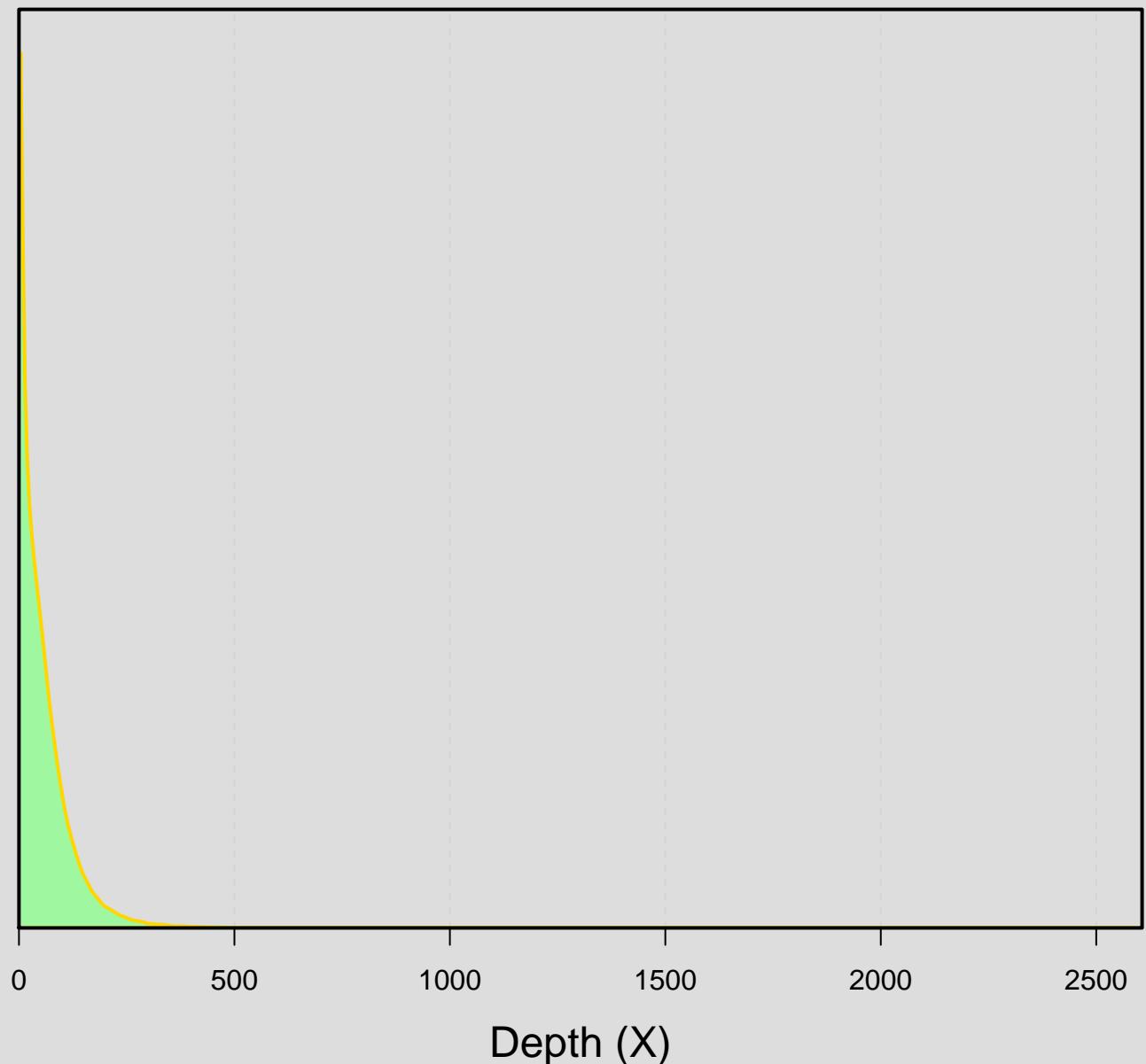


Center vs. ends

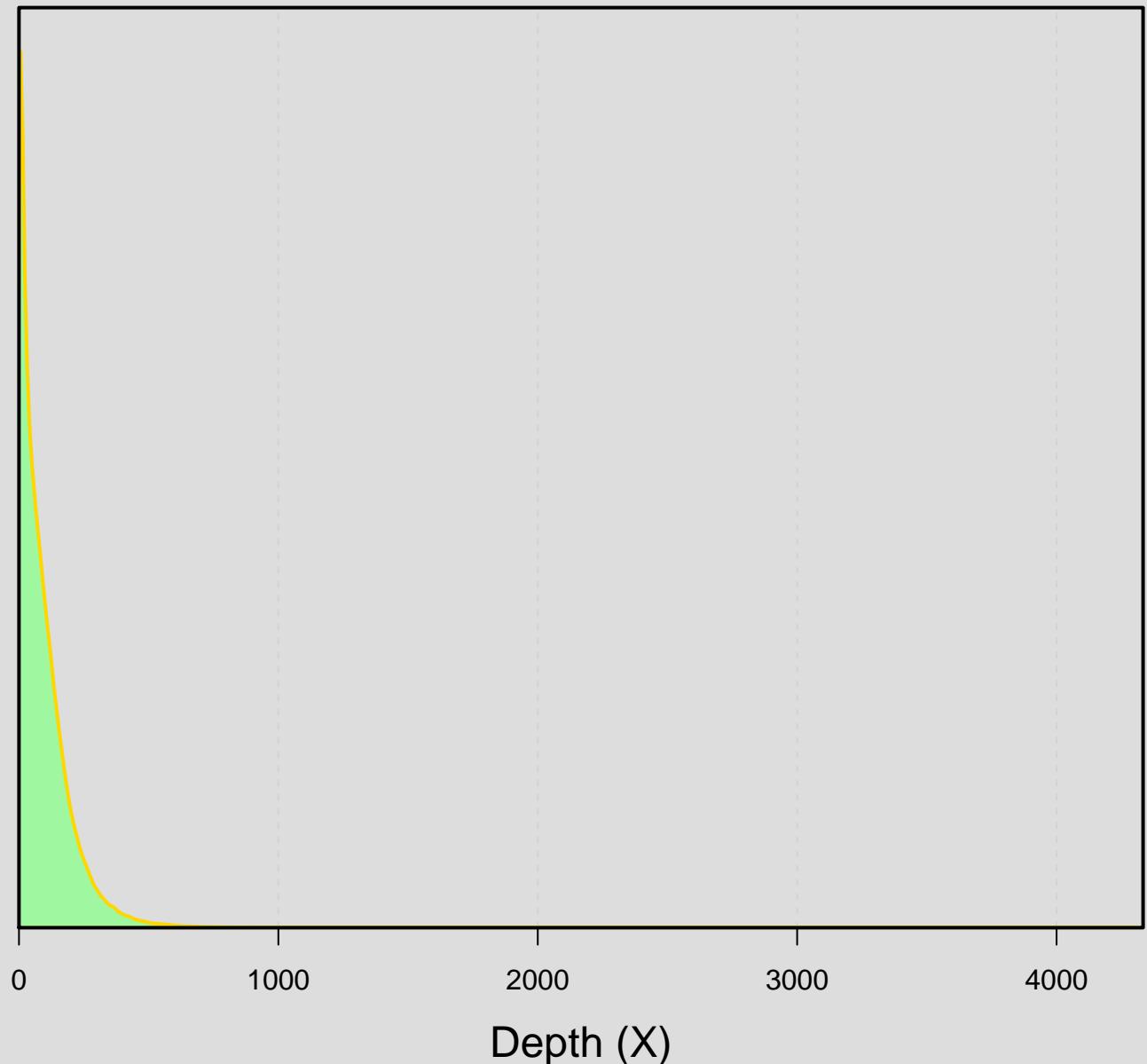




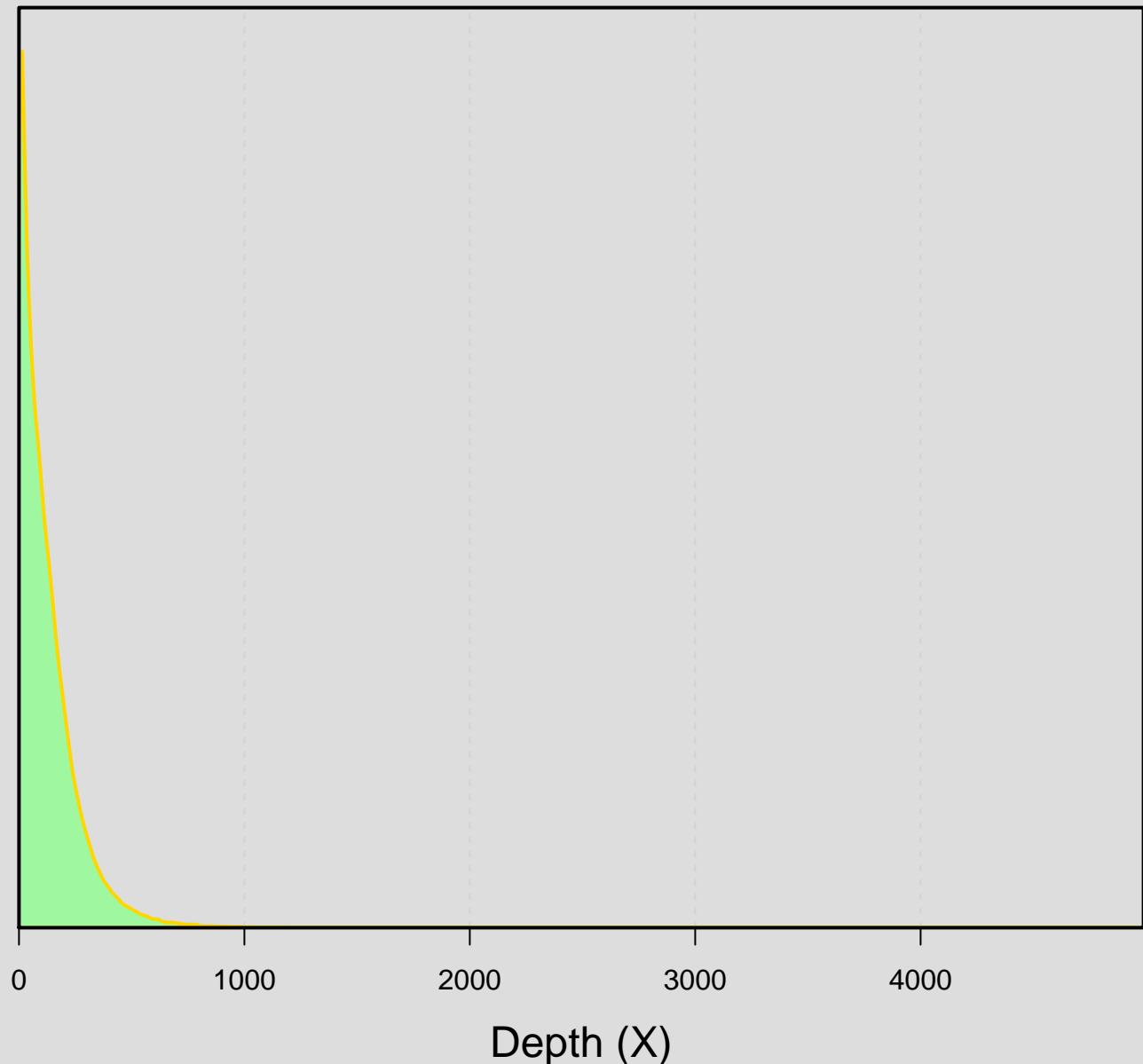
Minimum depth



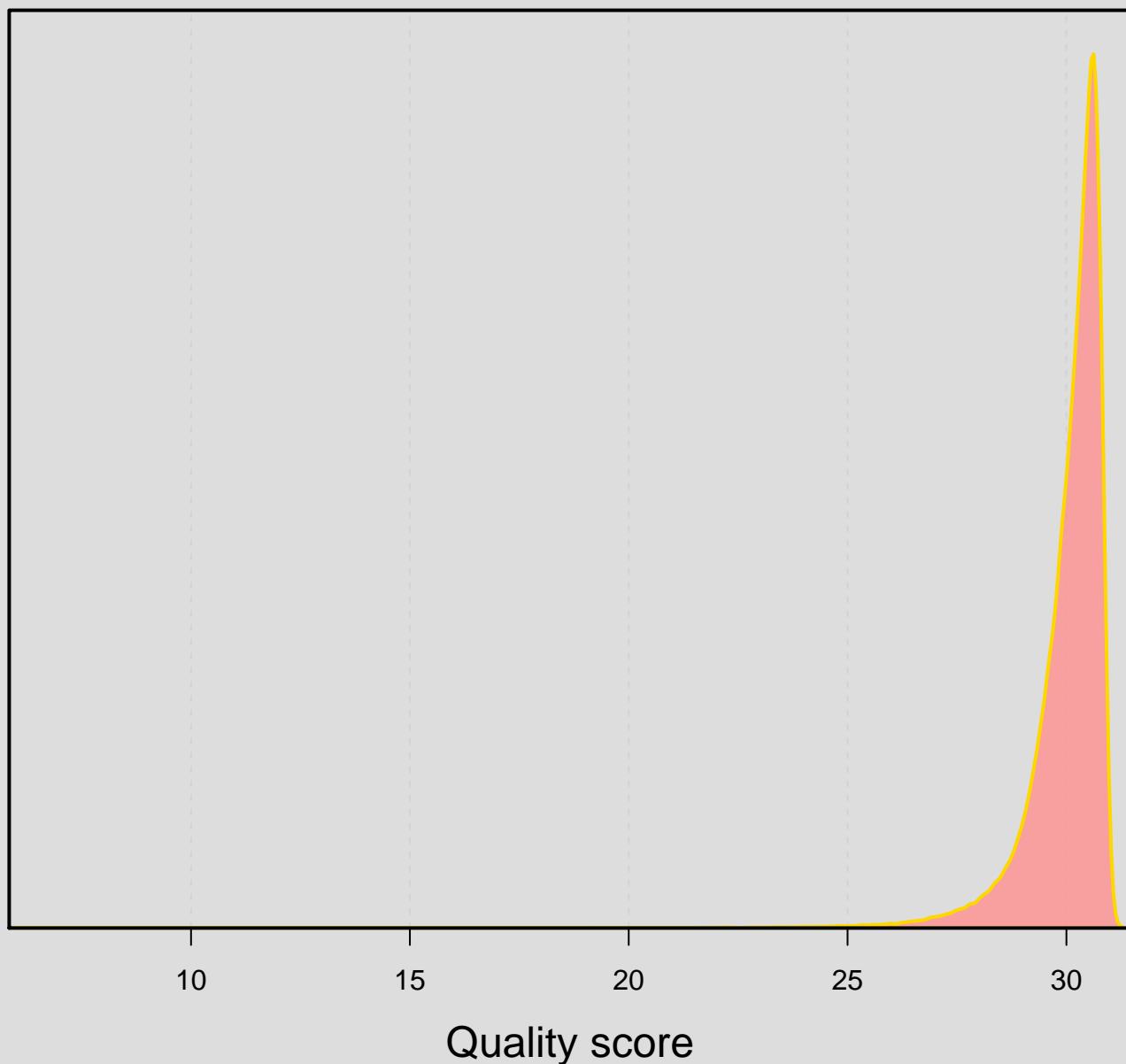
Average depth



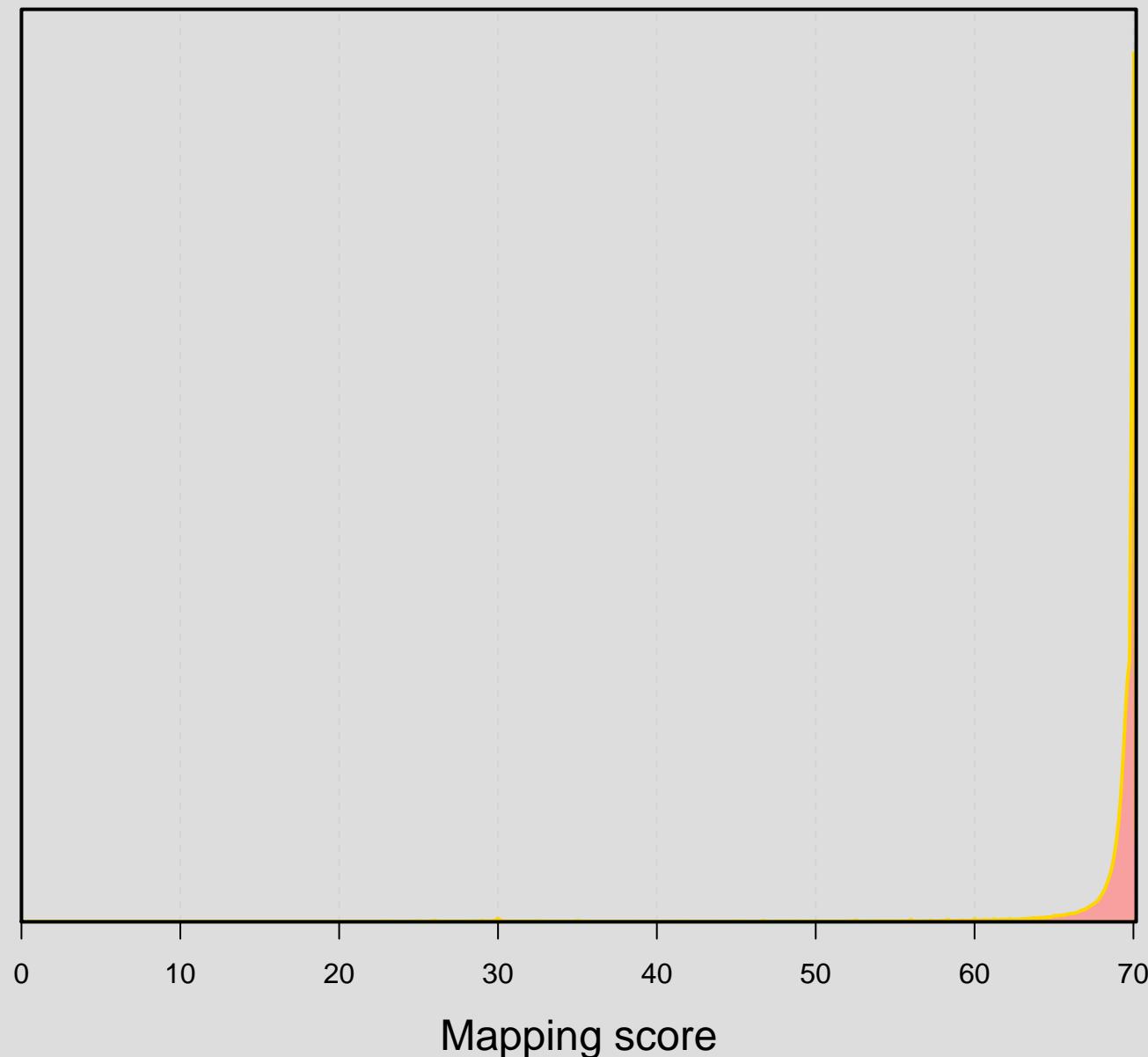
Maximum depth



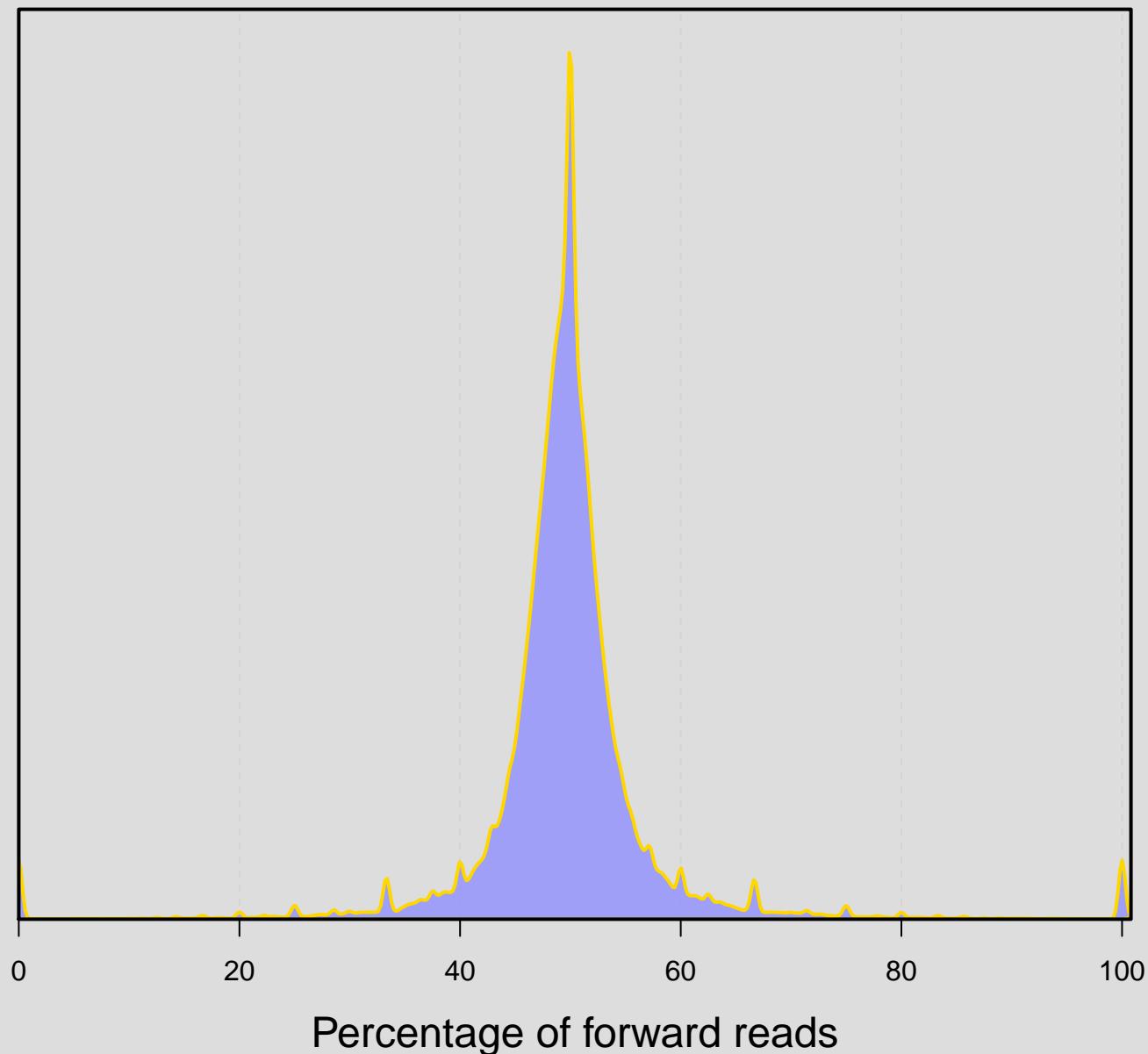
Average sequencing quality

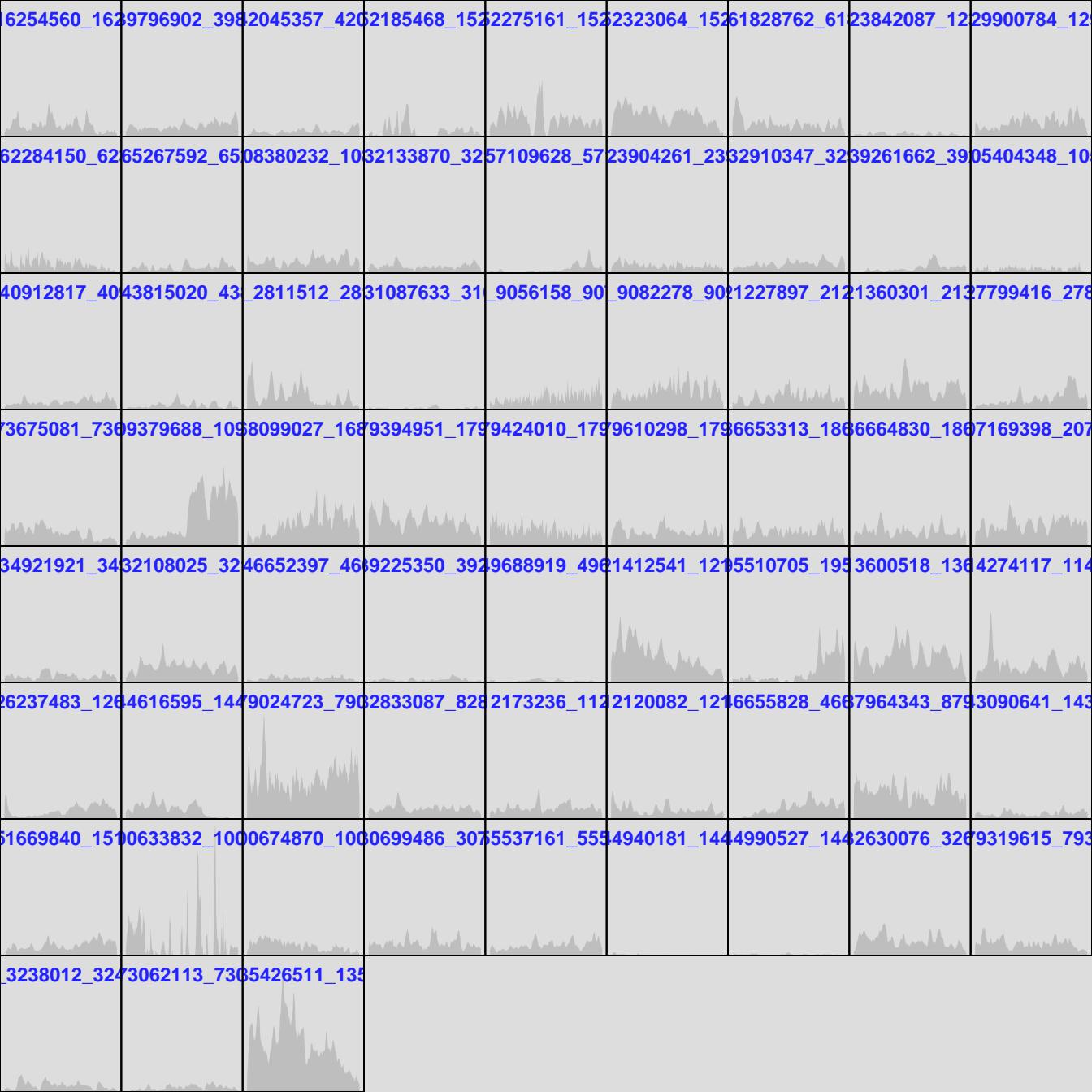


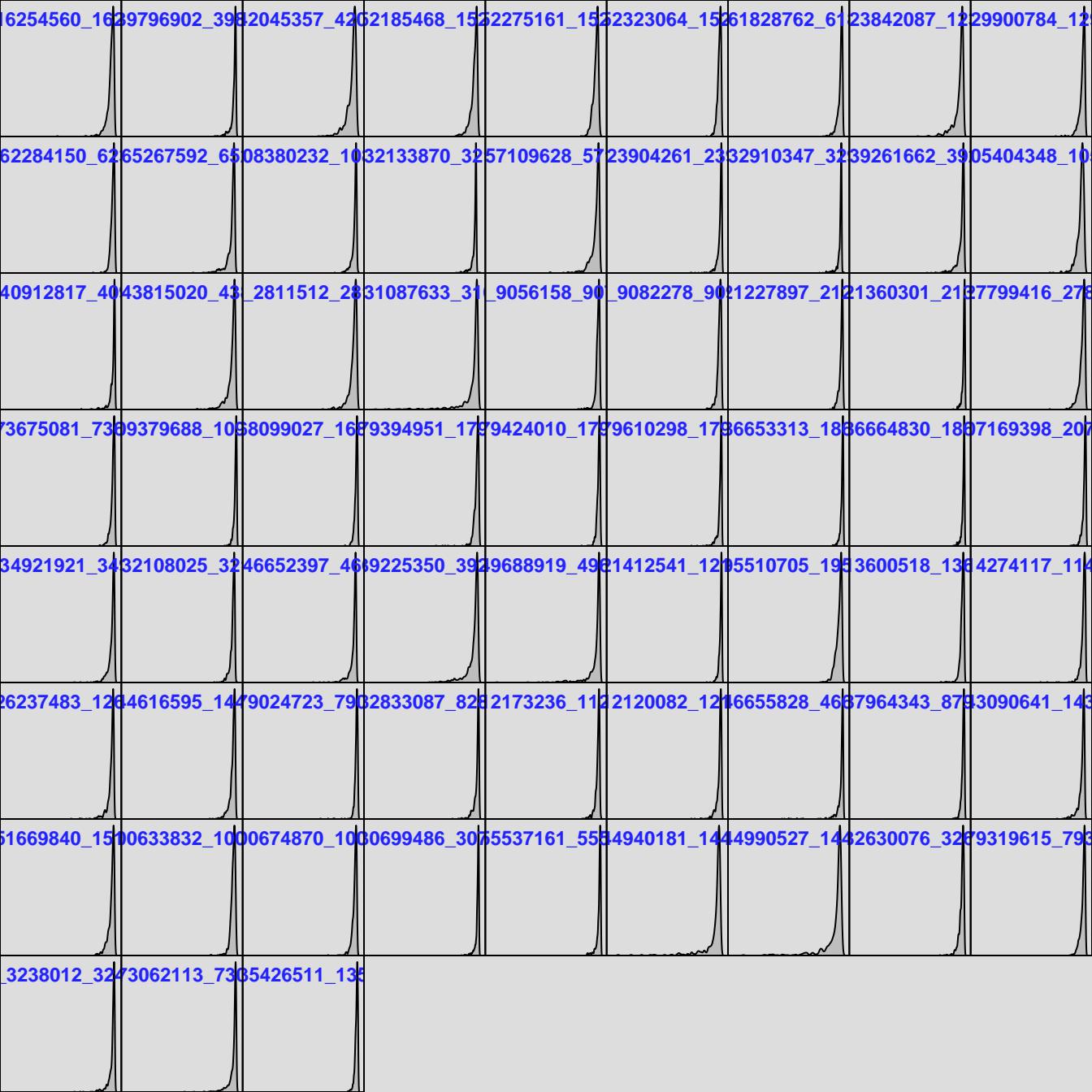
Average mapping quality

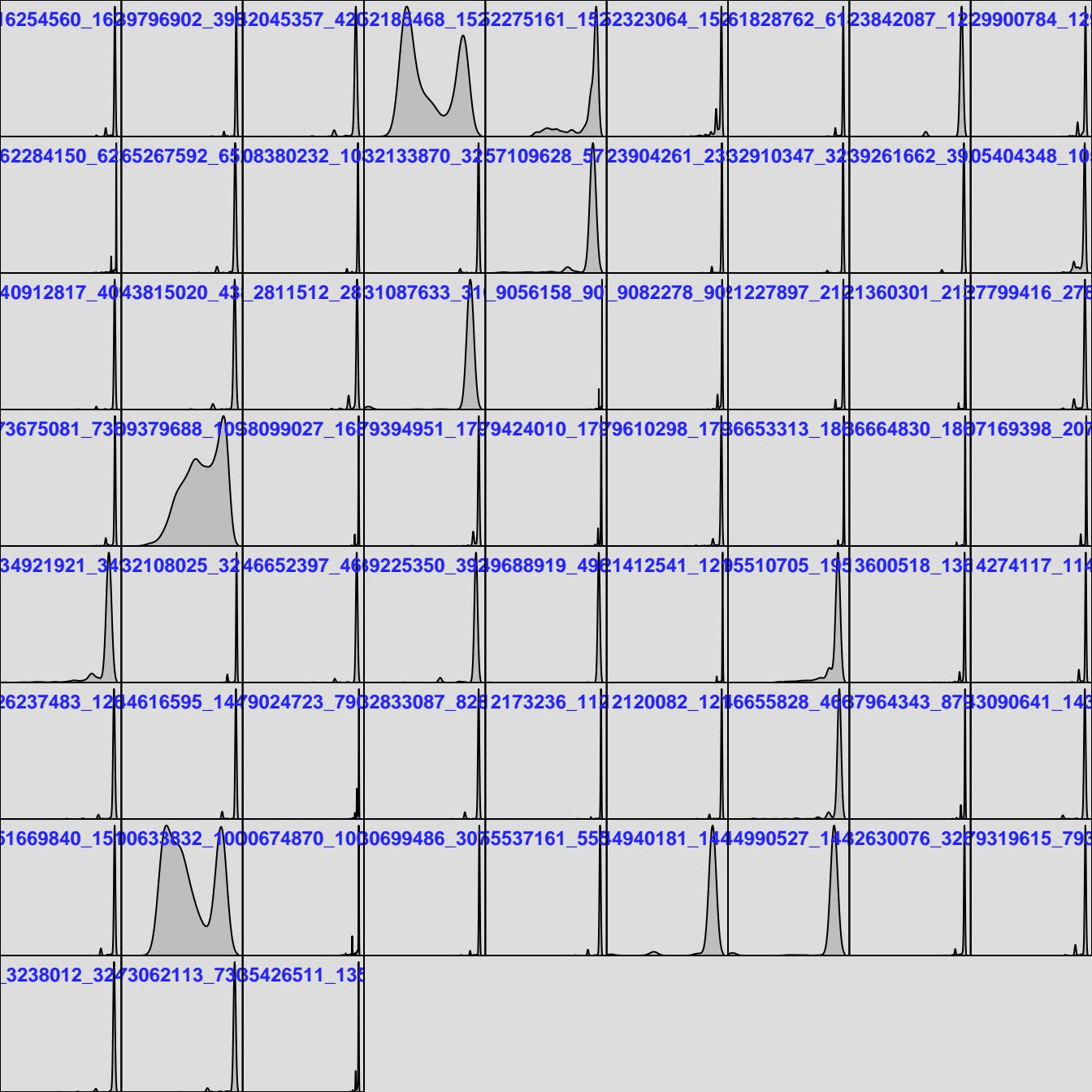


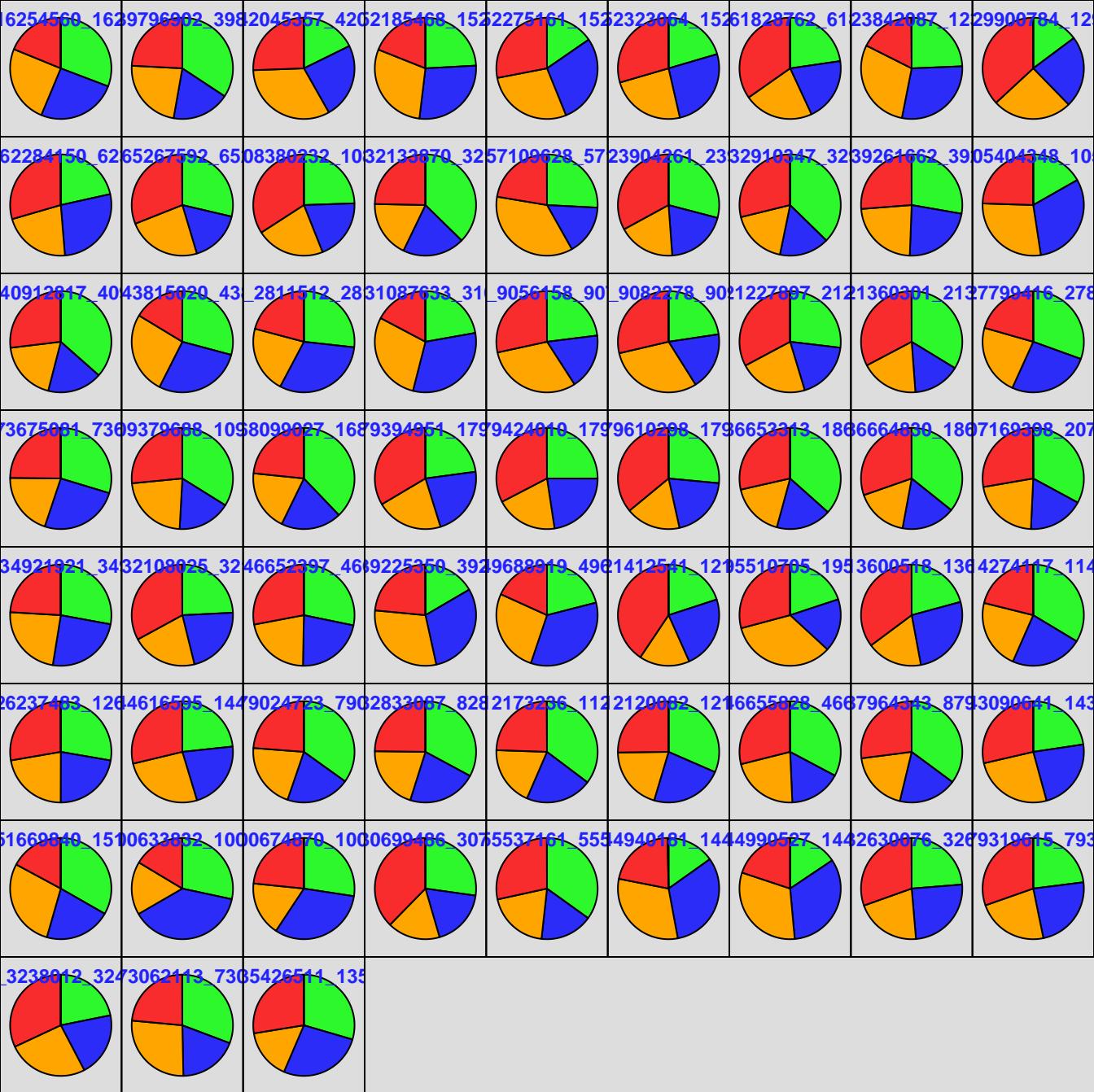
Forward read frequency

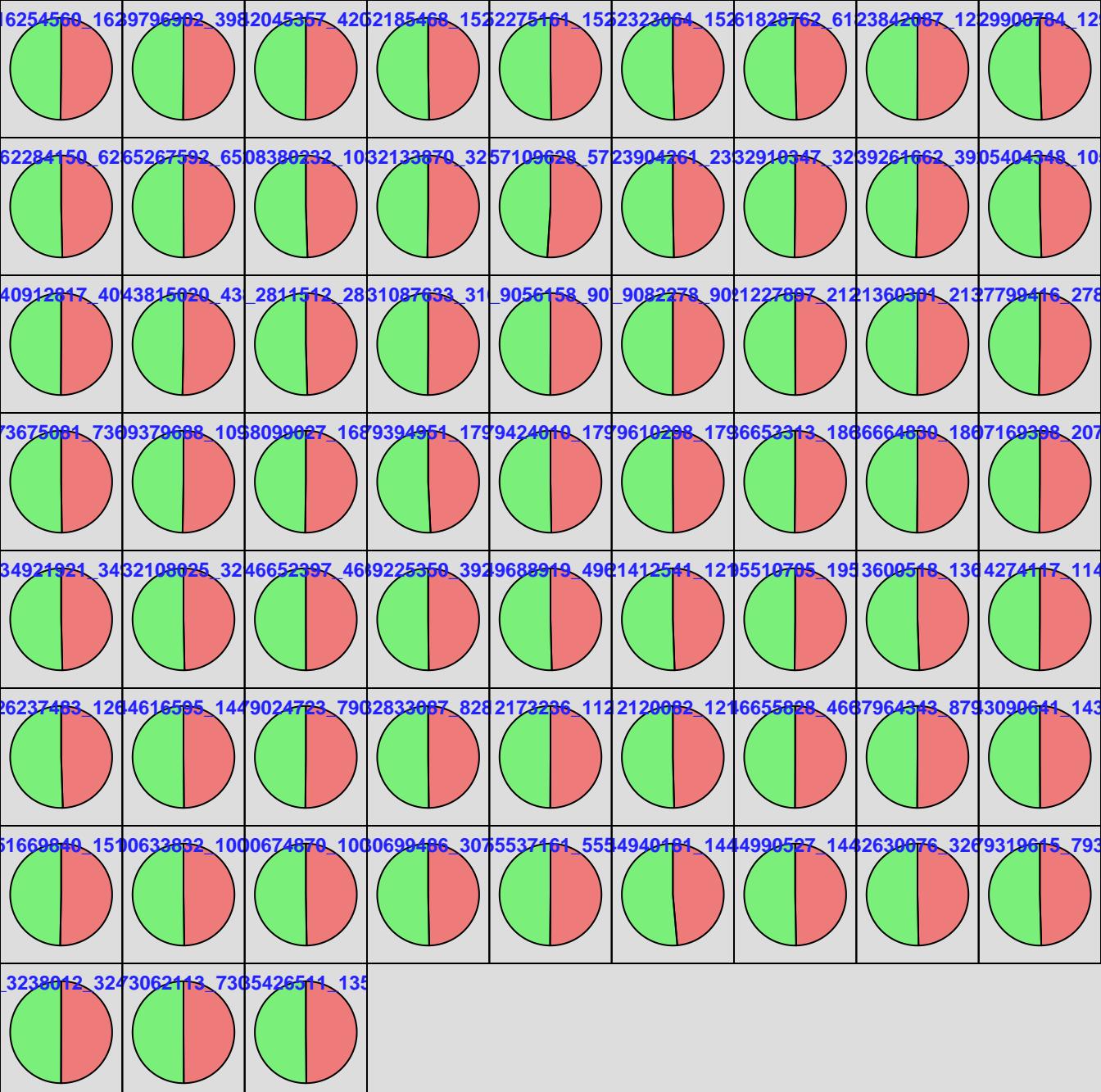


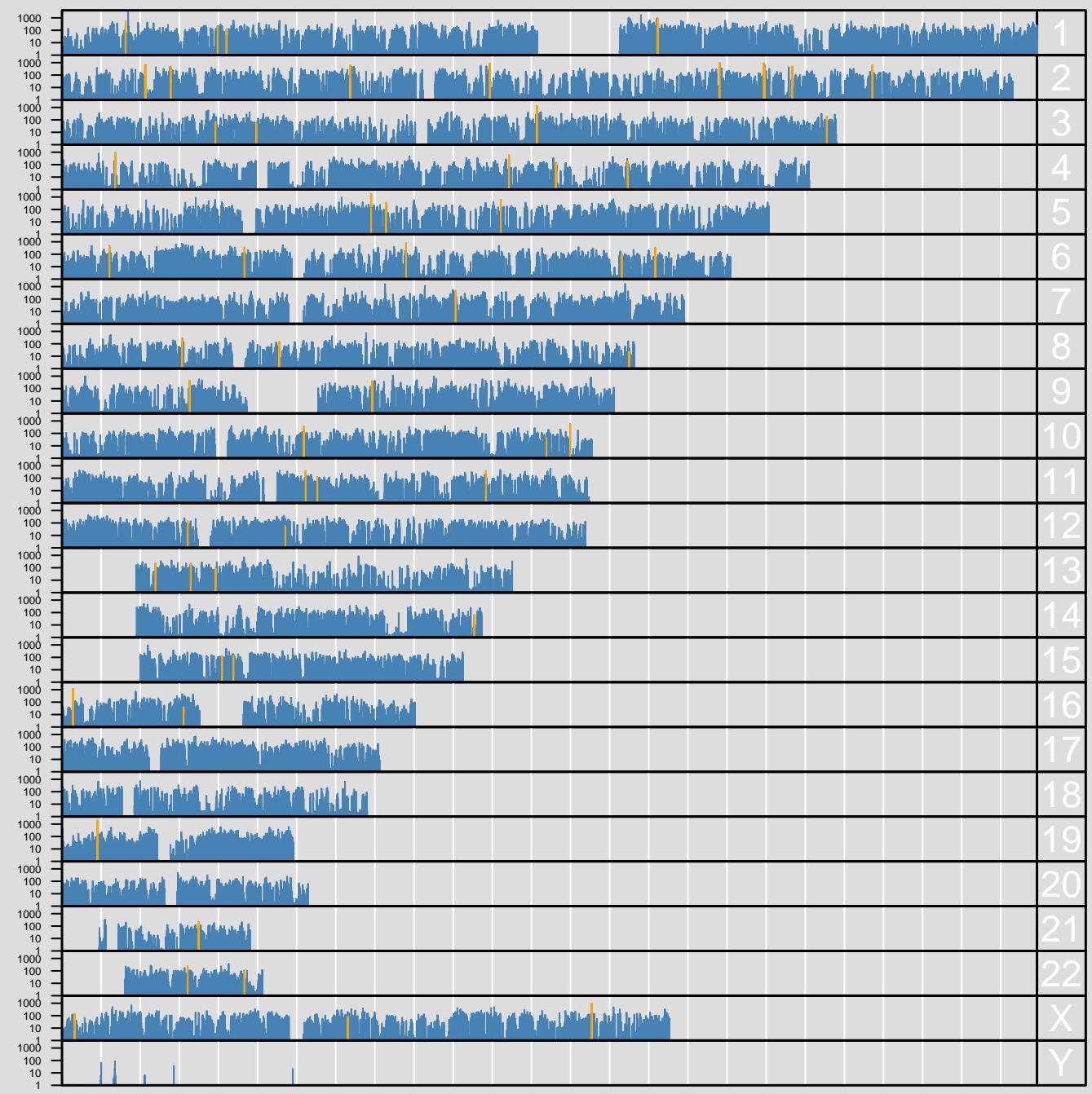




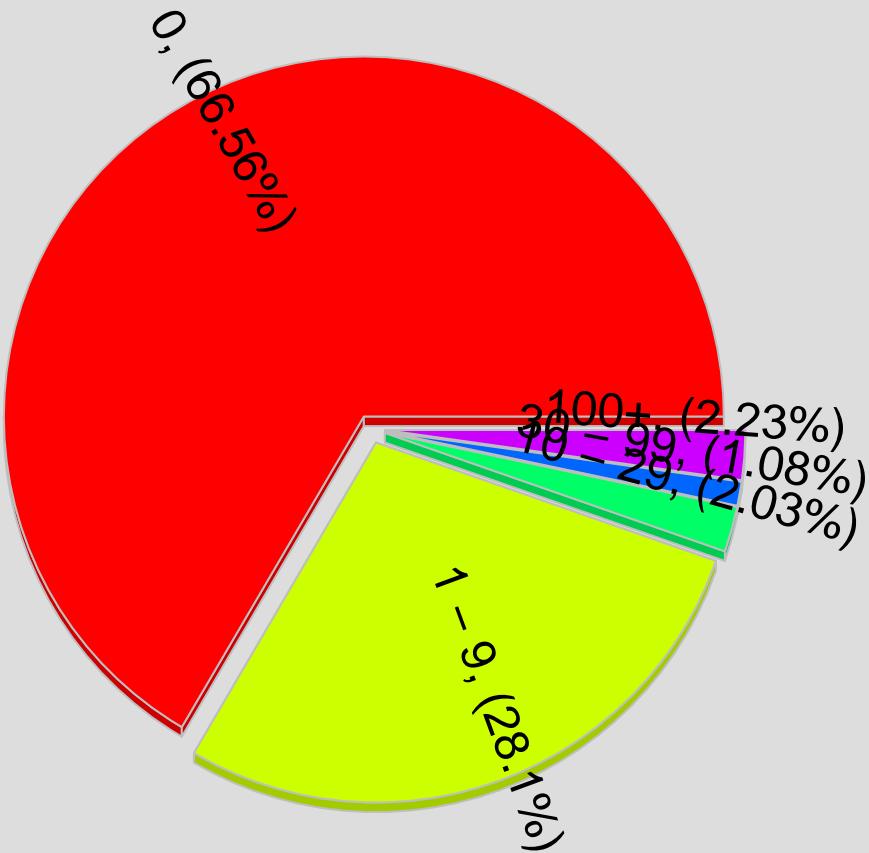




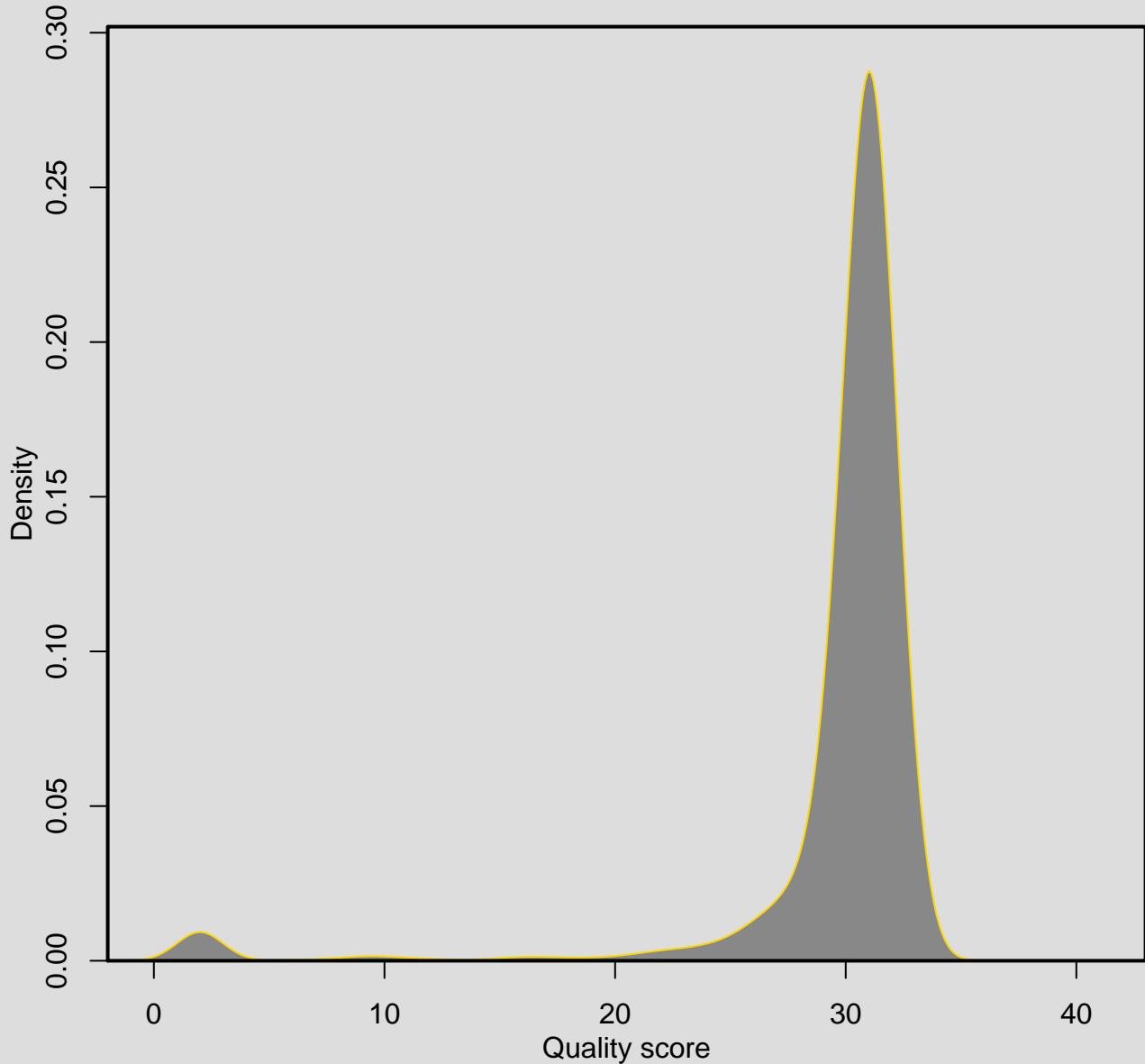




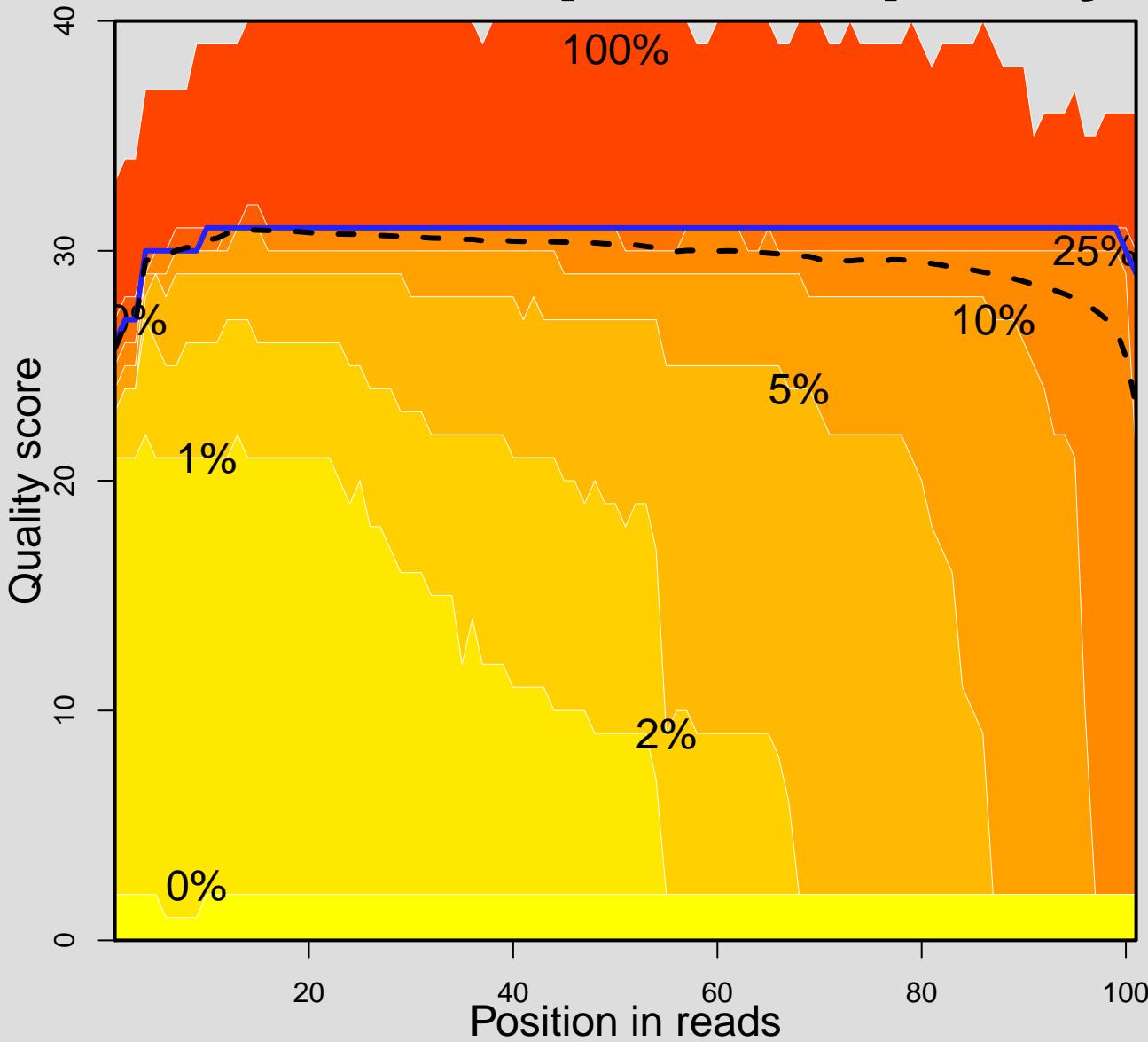
Whole genome depth



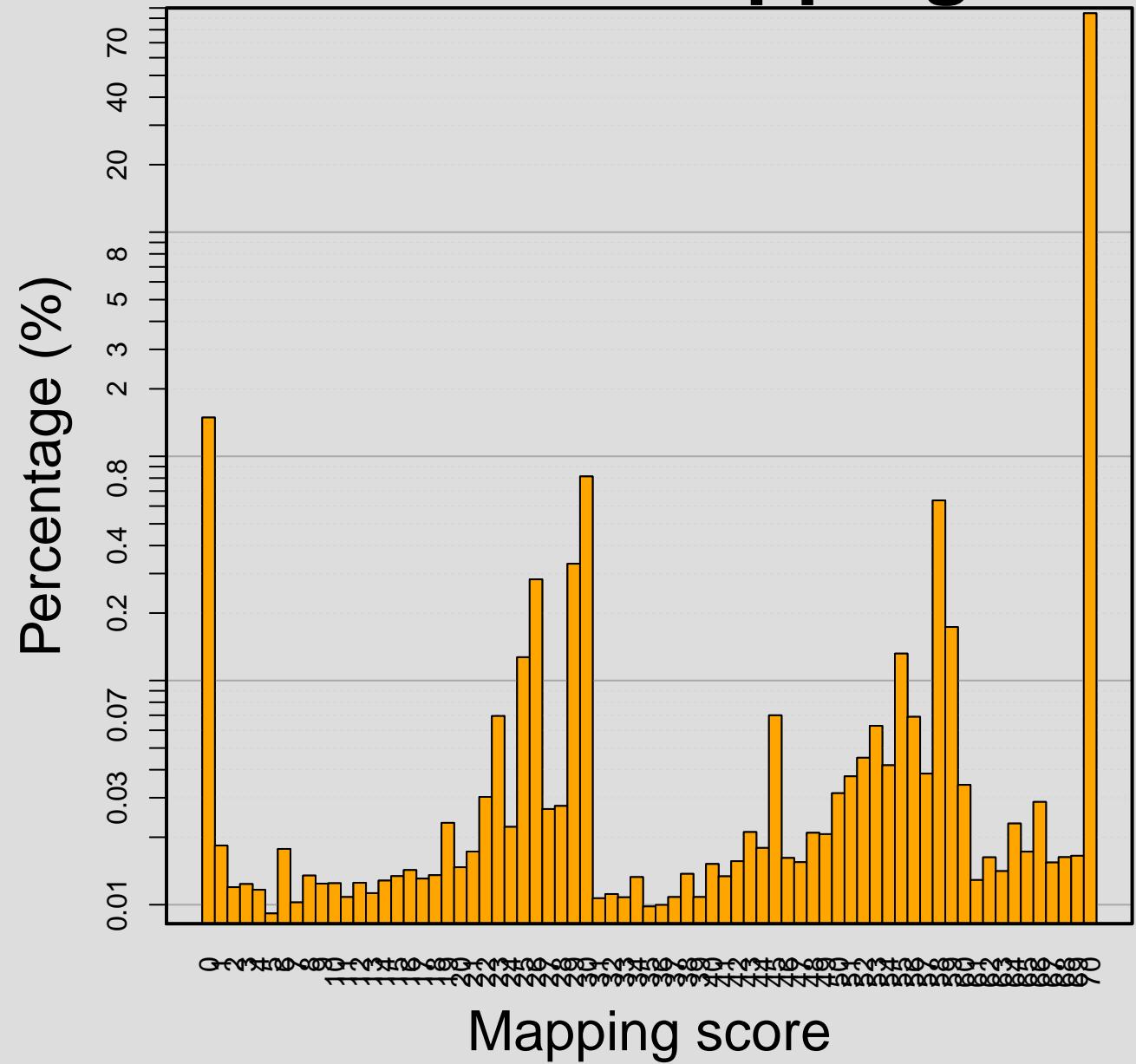
Score distribution



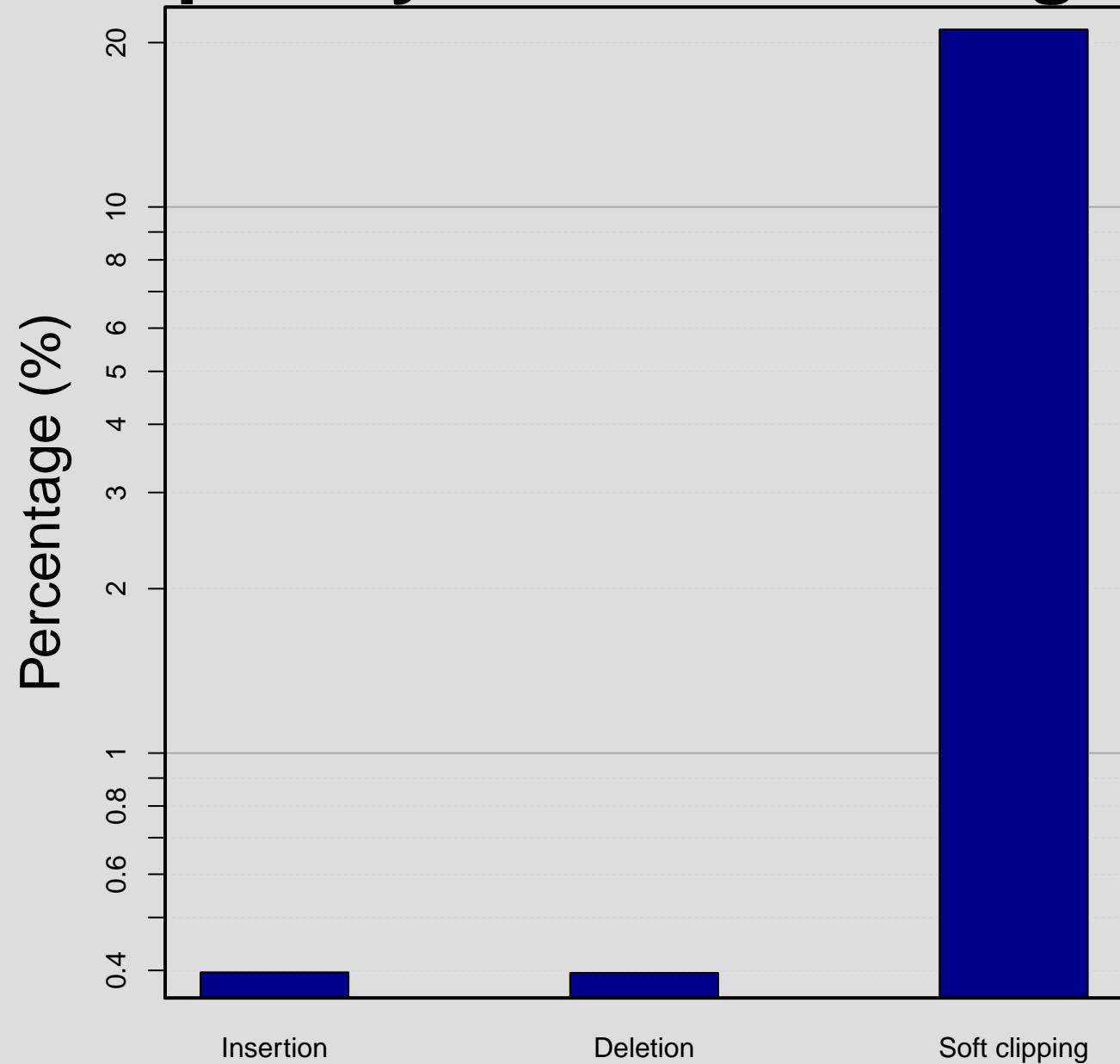
Position-specific quality



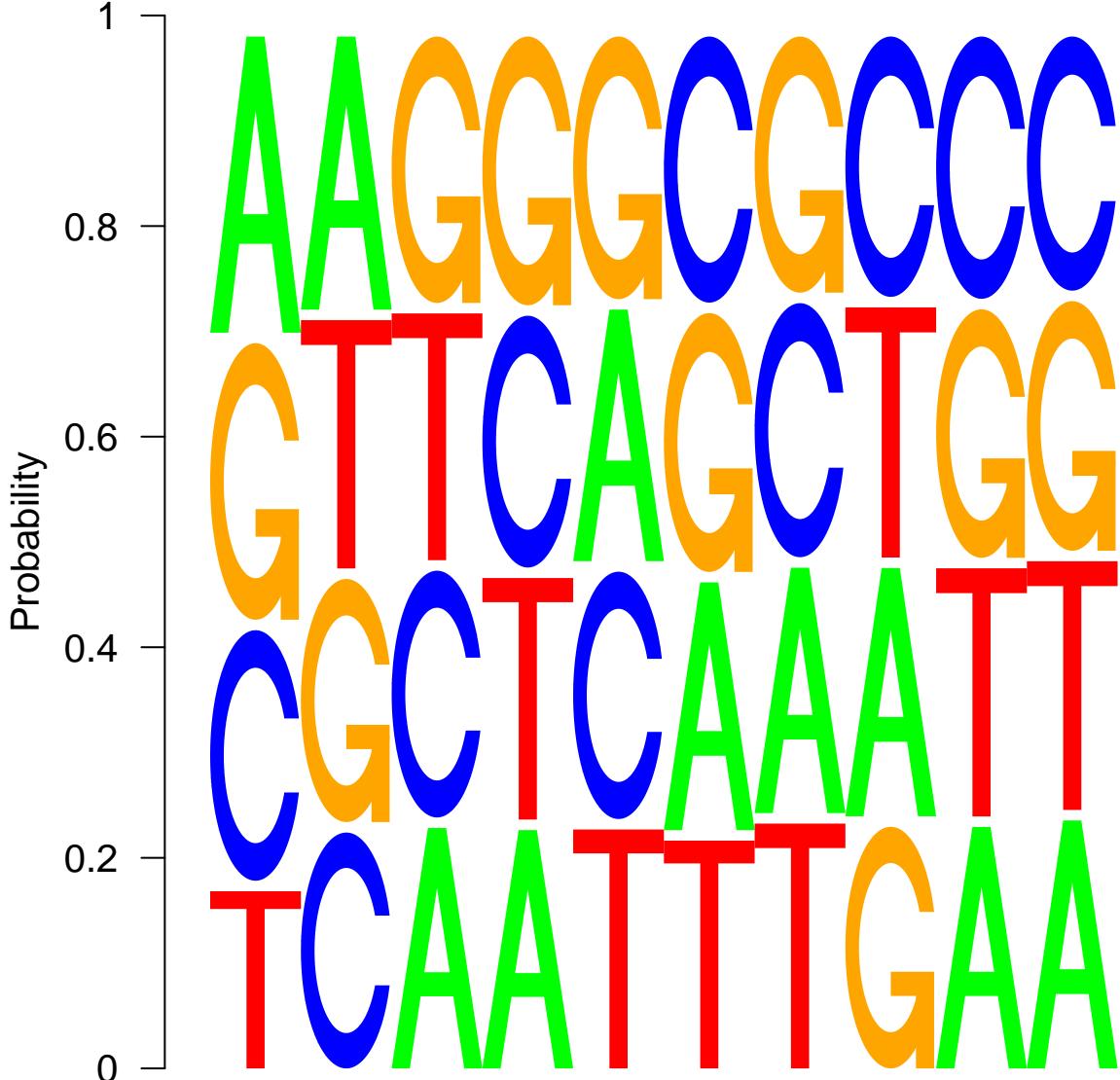
Distribution of mapping score



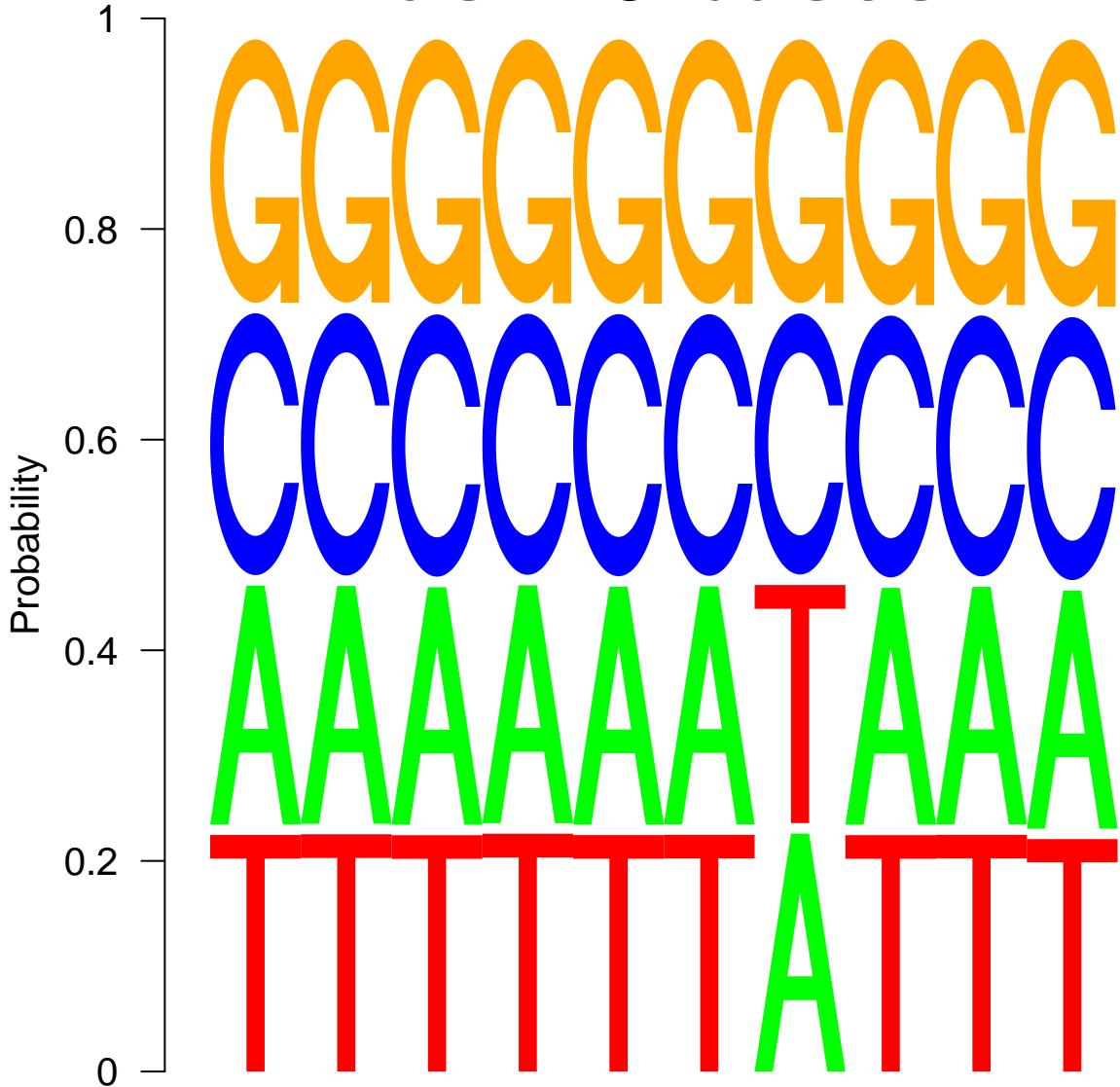
Frequency of CIGAR string type



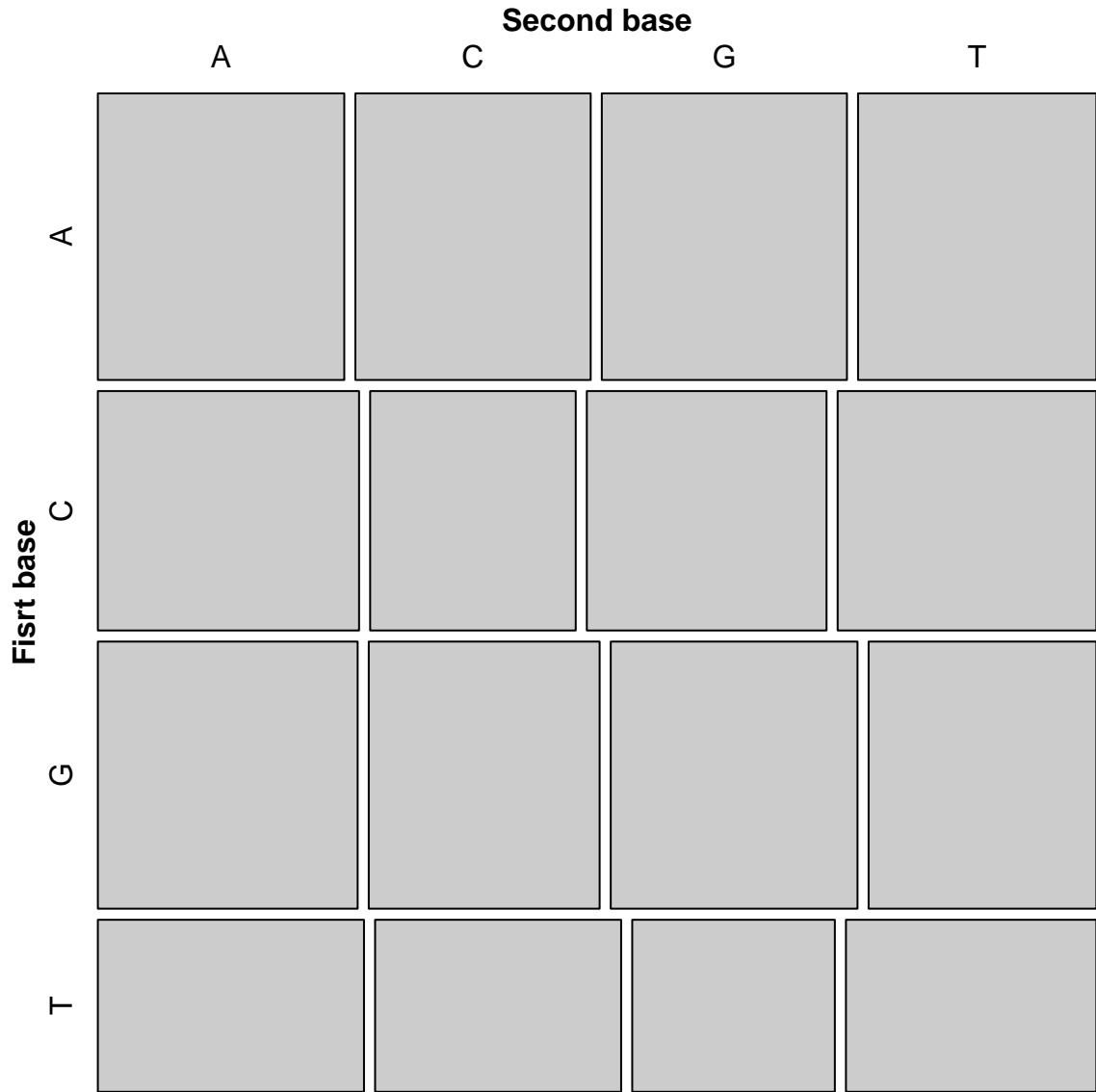
First 10 bases



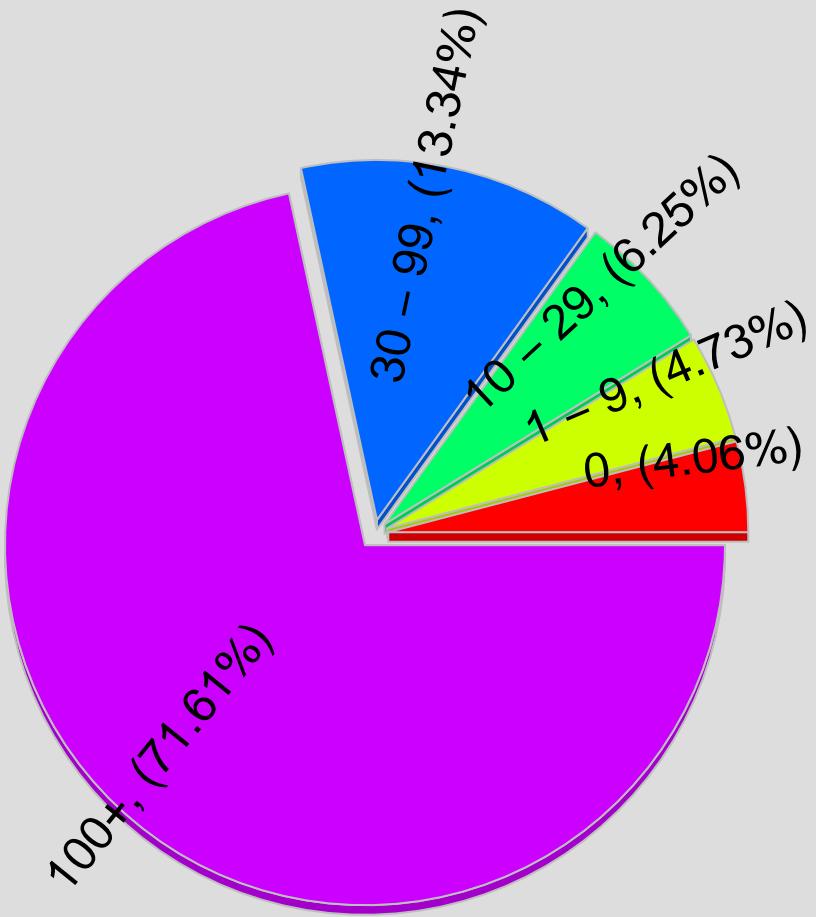
Last 10 bases



Frequency of two–base combinations



On-target depth



Accumulative distribution

Accumulative Percentage (%)

100

80

60

40

20

0

0

200

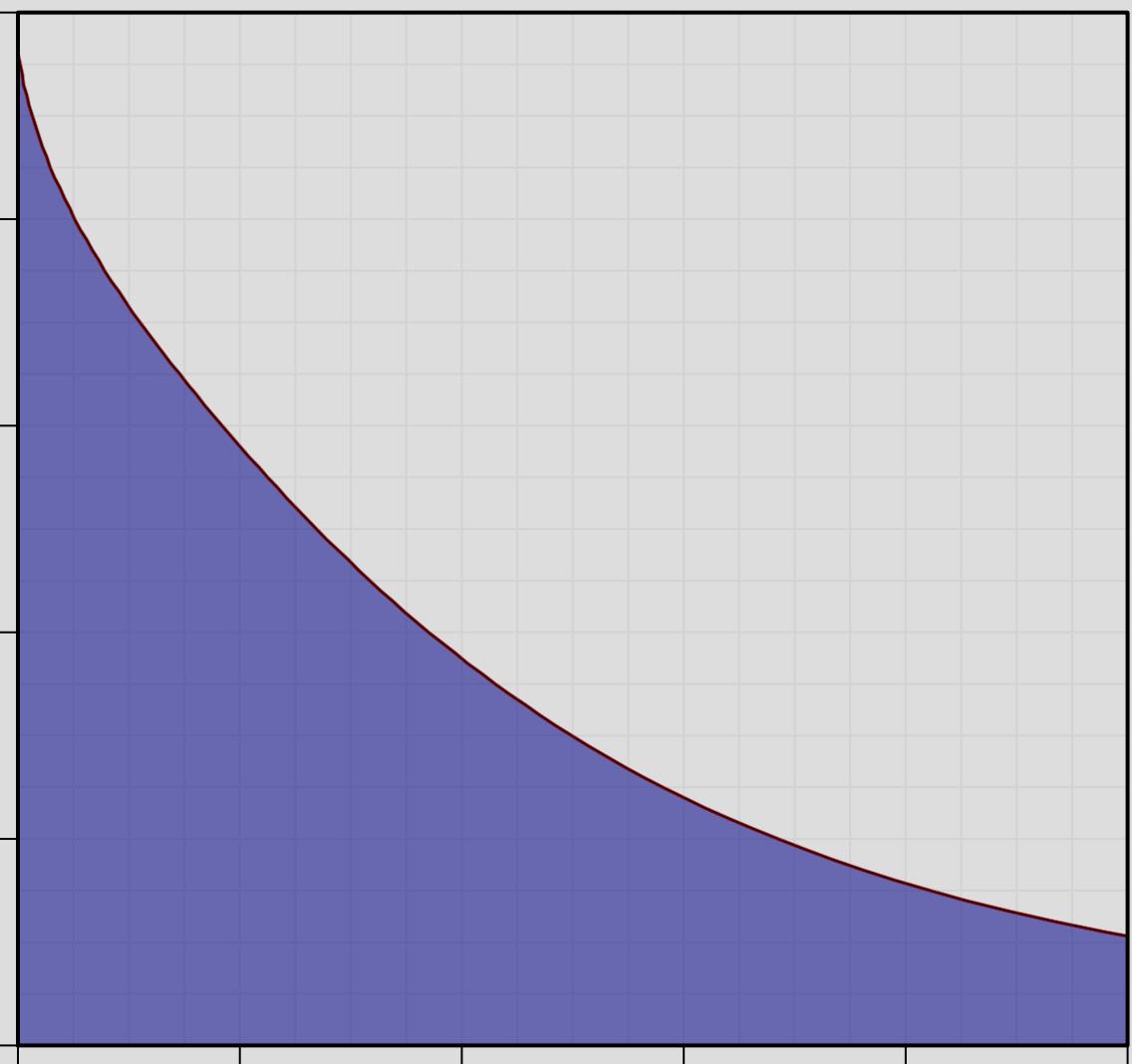
400

600

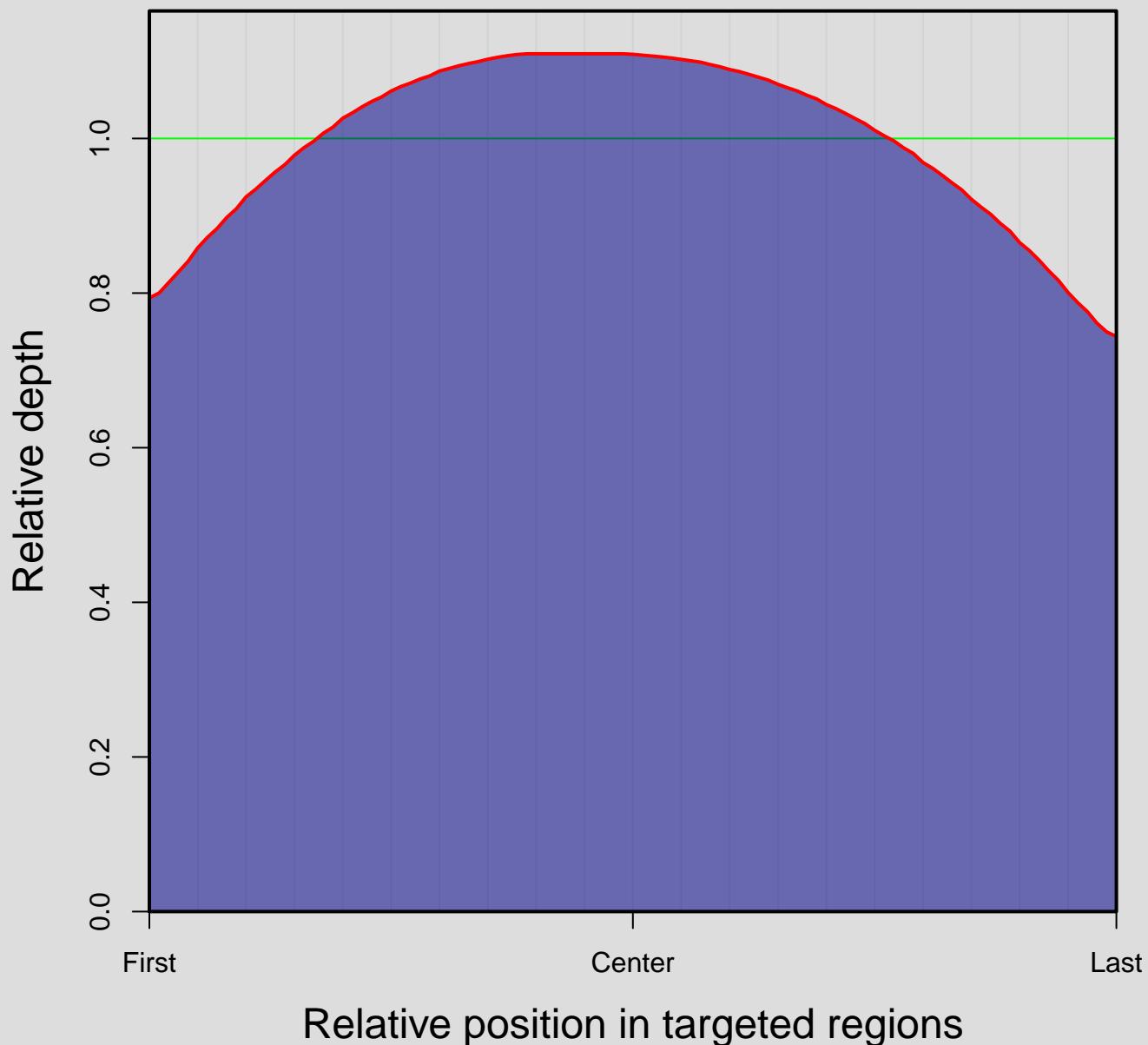
800

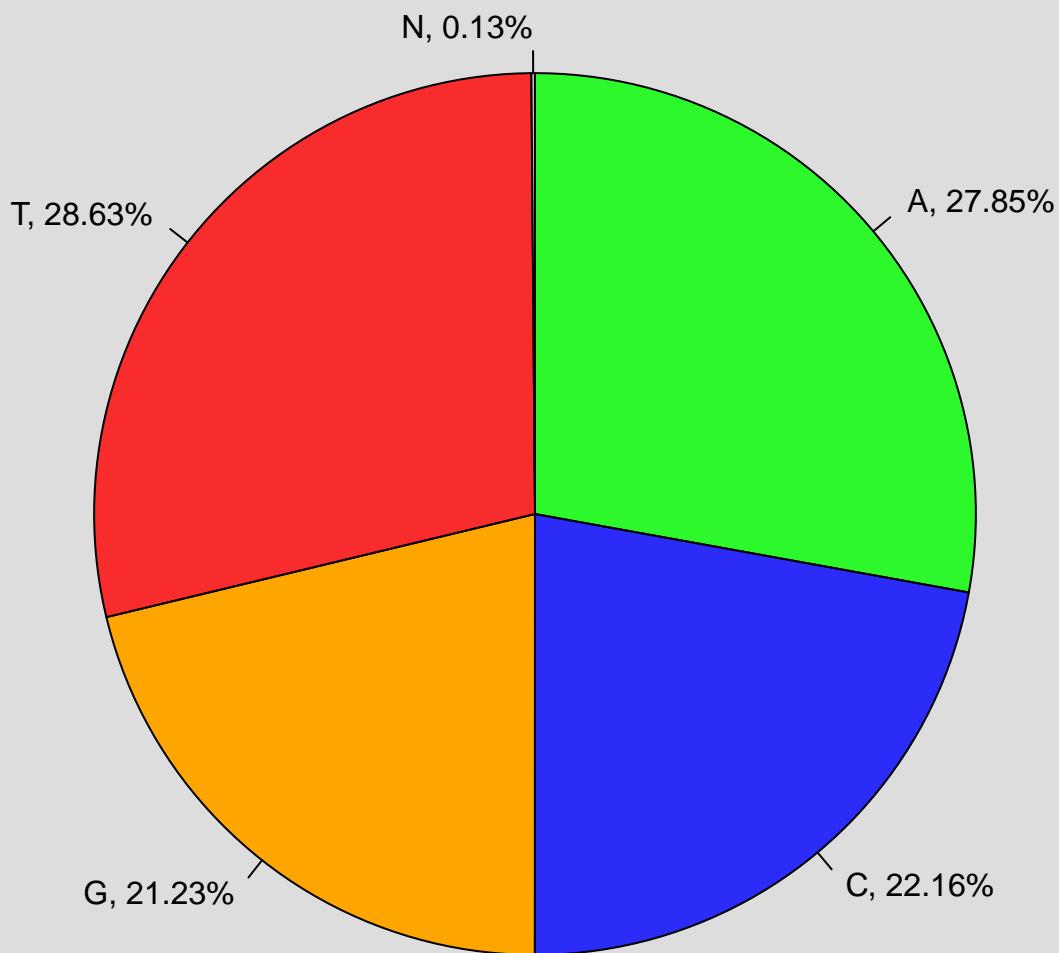
1000

Depth (X)

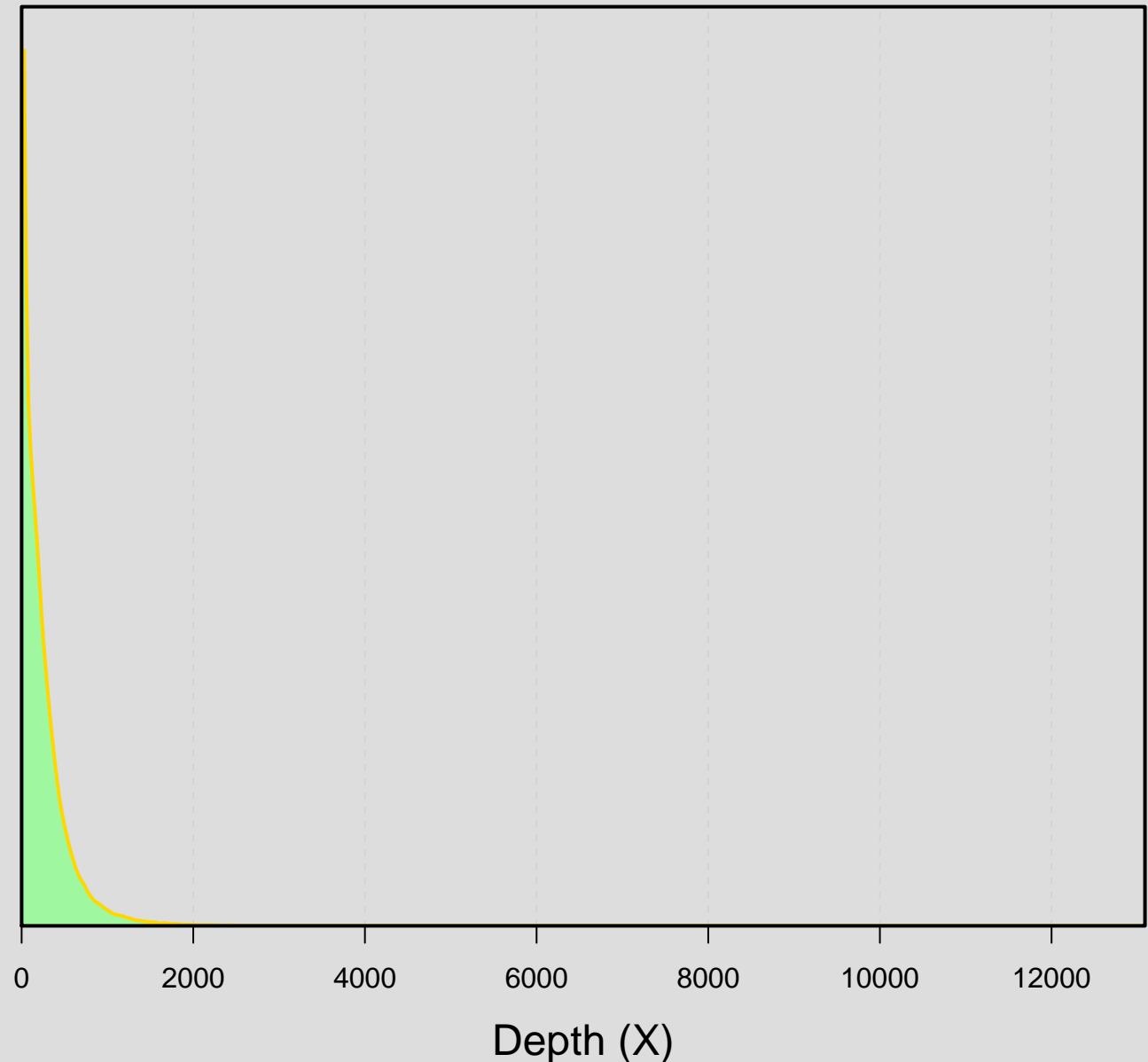


Center vs. ends

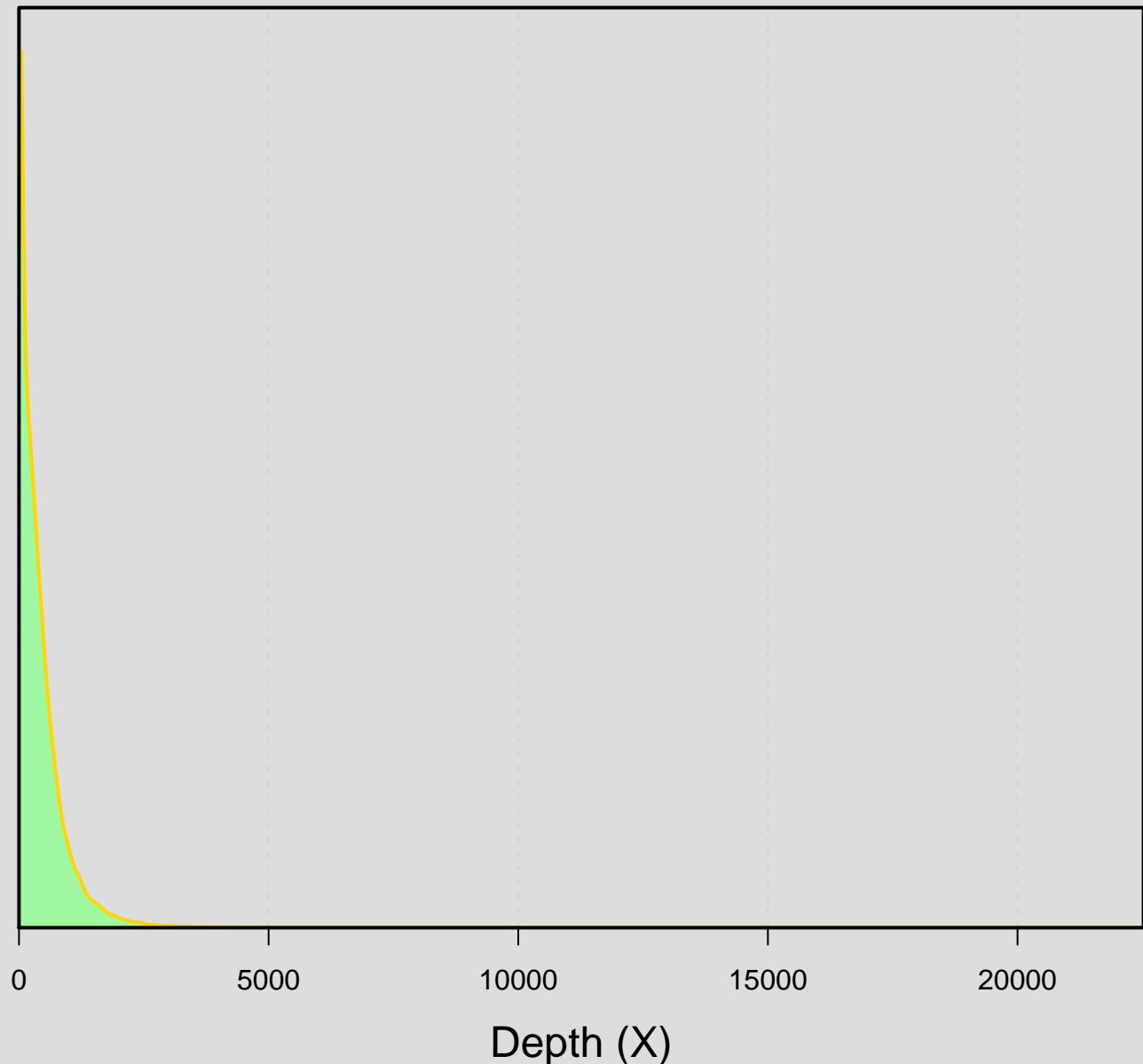




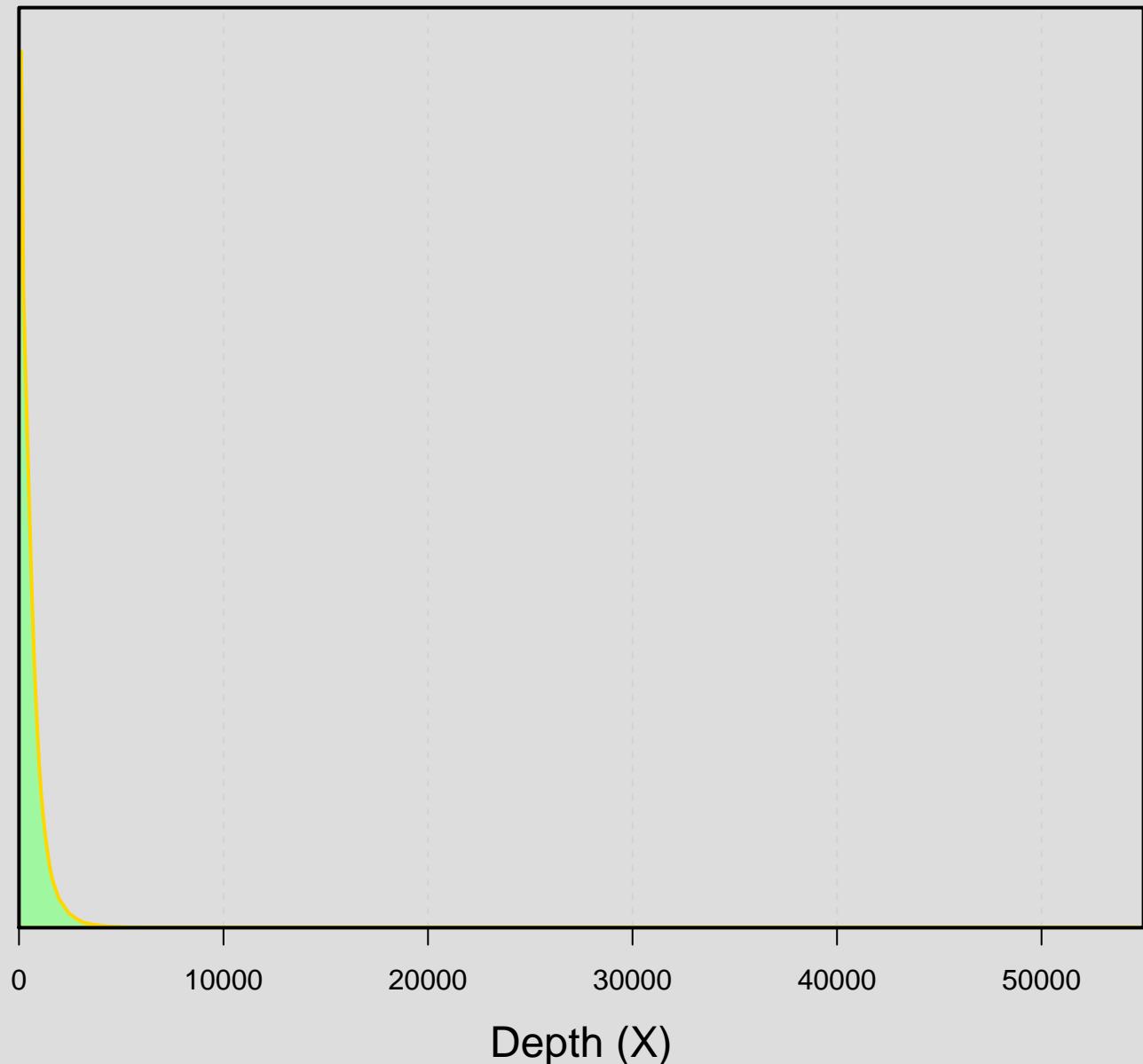
Minimum depth



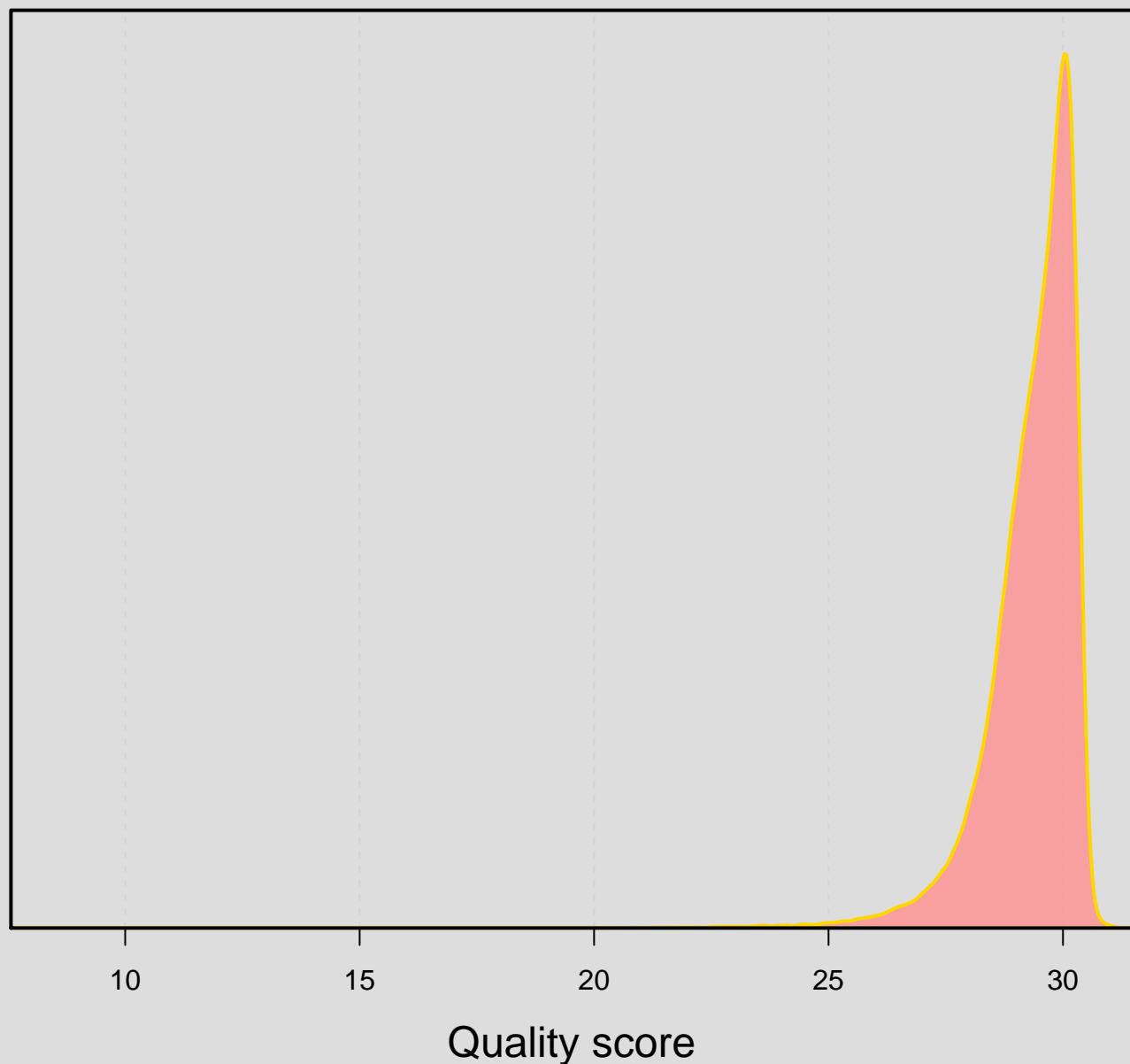
Average depth



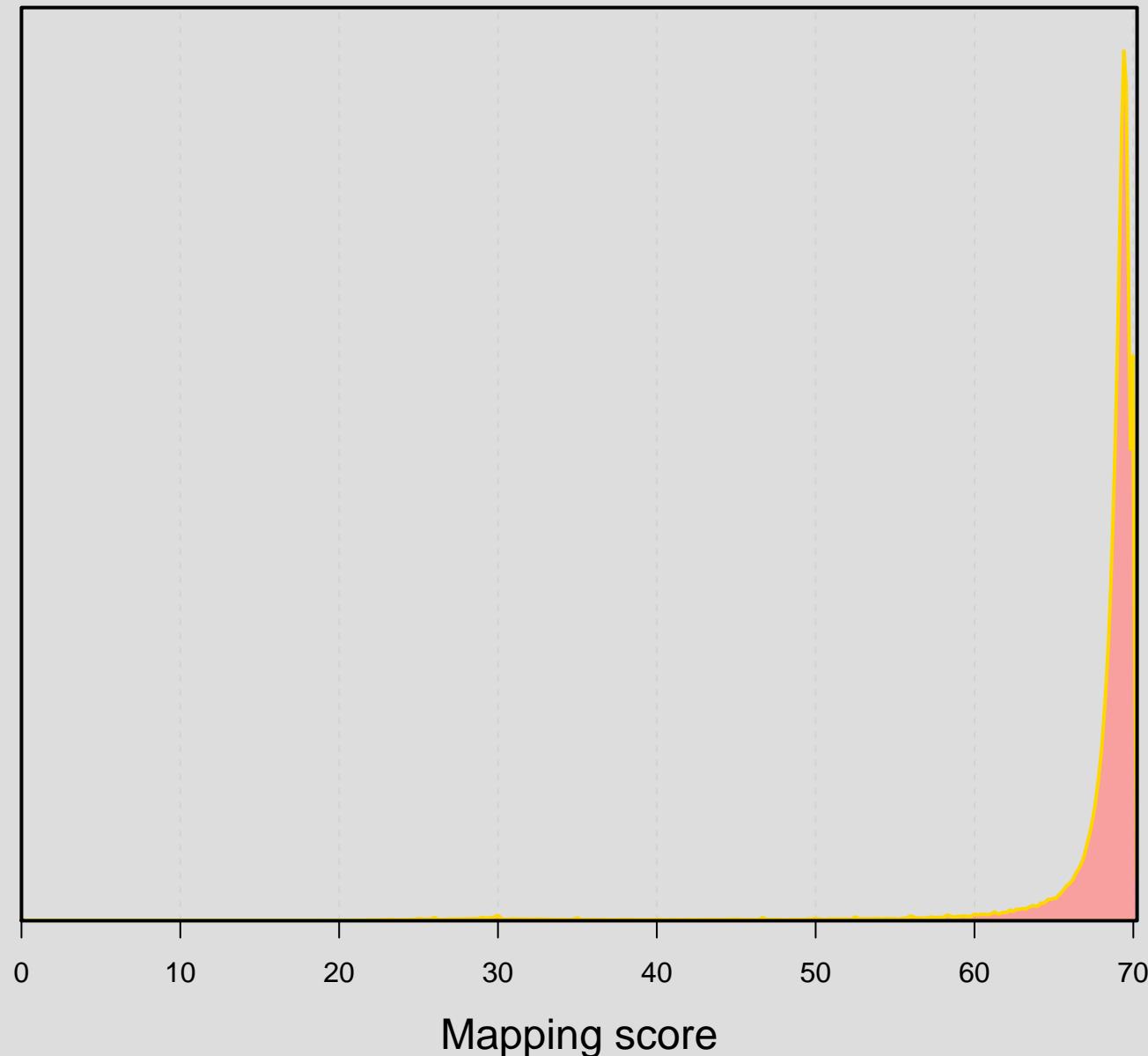
Maximum depth



Average sequencing quality



Average mapping quality



Forward read frequency

