

# Retained reads

% reads

100

75

50

25

0

100  
(21M)

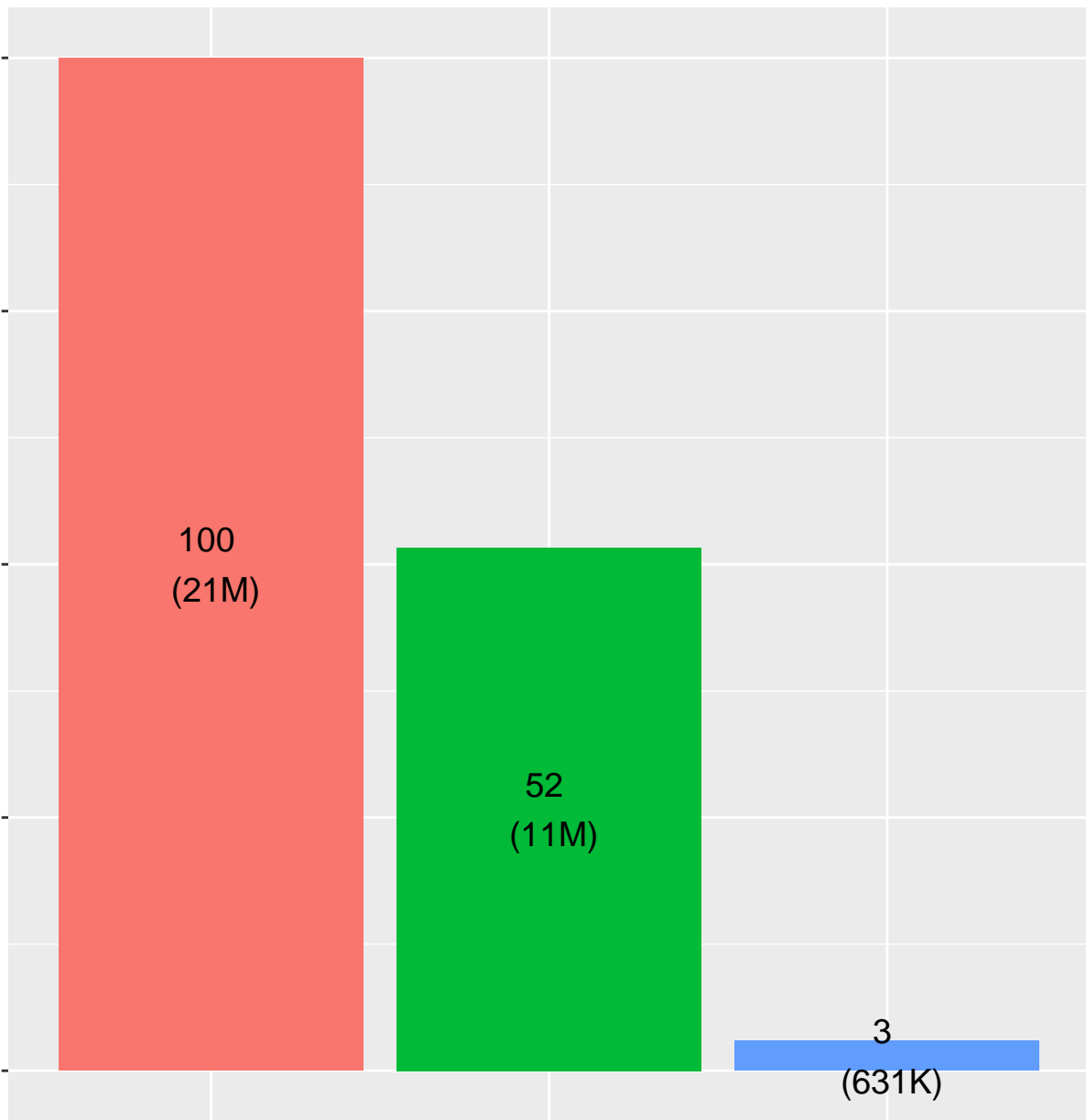
52  
(11M)

3  
(631K)

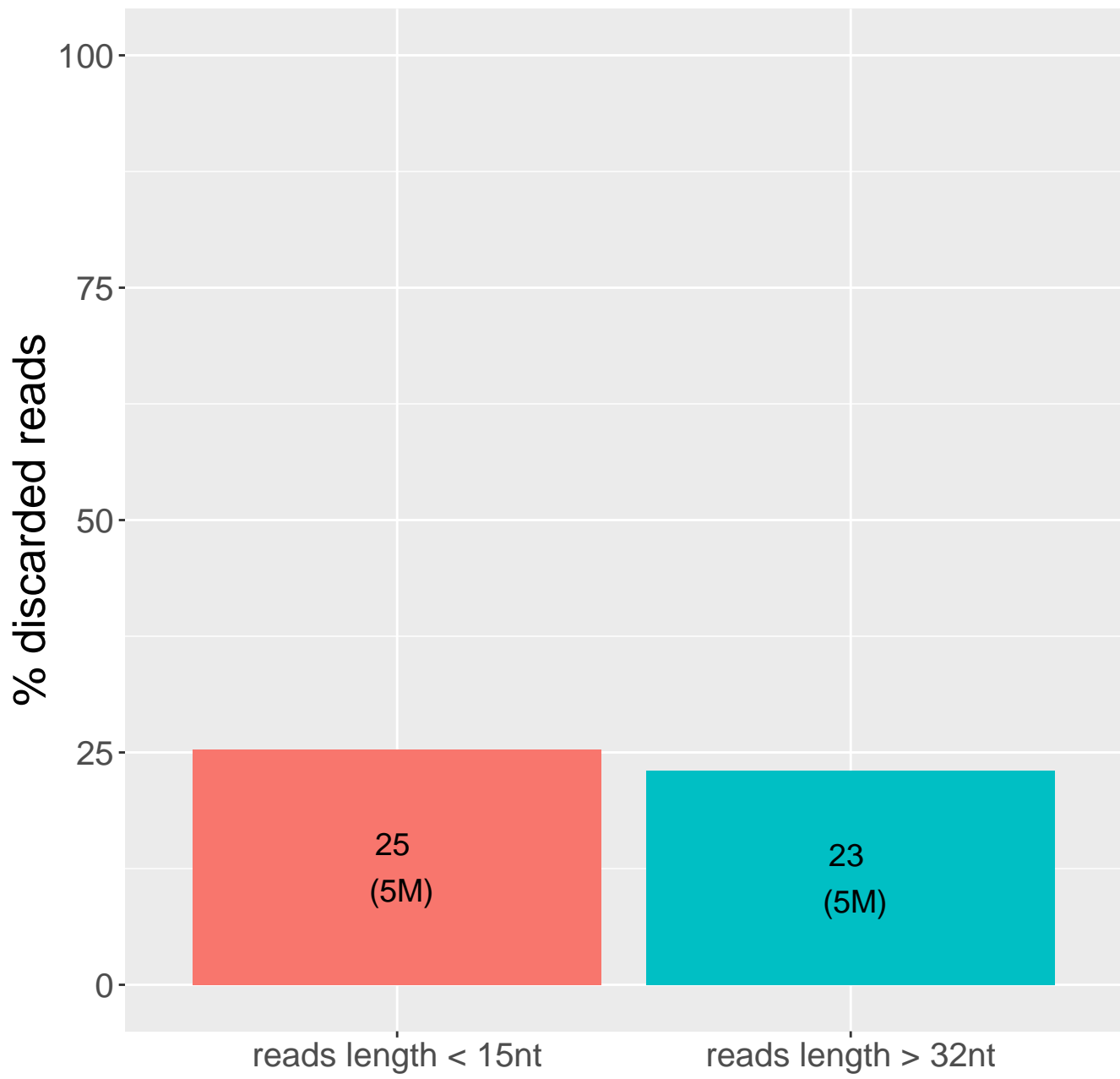
total reads

length filter

unique mapping

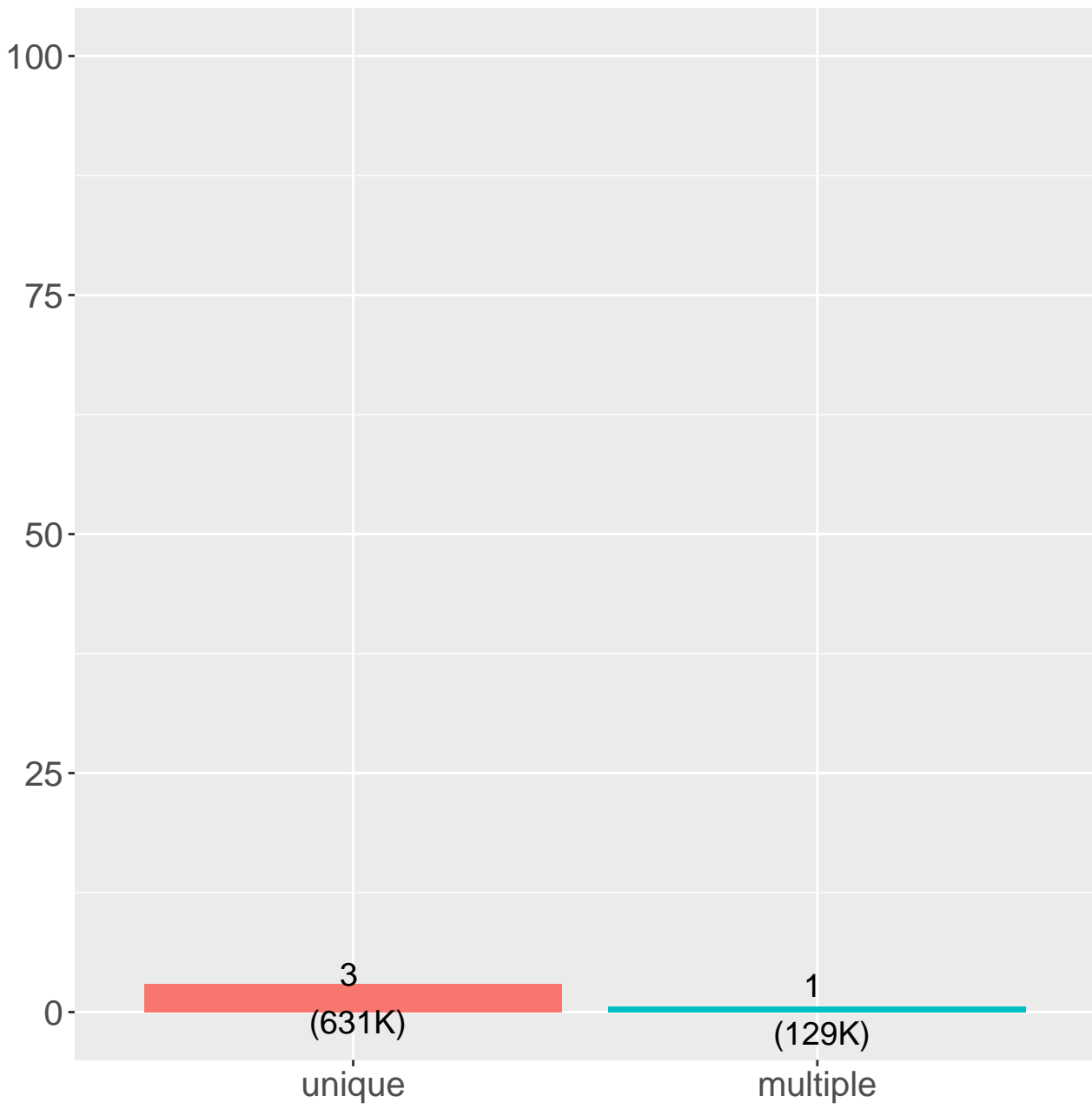


# Length filtering



# Mapping reads

% mapped reads



# Read distribution

% reads

100

75

50

25

0

miRNA

piRNA

snoRNA

snRNA

rRNA

45  
(286K)

35  
(223K)

2  
(12K)

1  
(5K)

3  
(20K)

