

# Retained reads

% reads

100  
75  
50  
25  
0

total reads

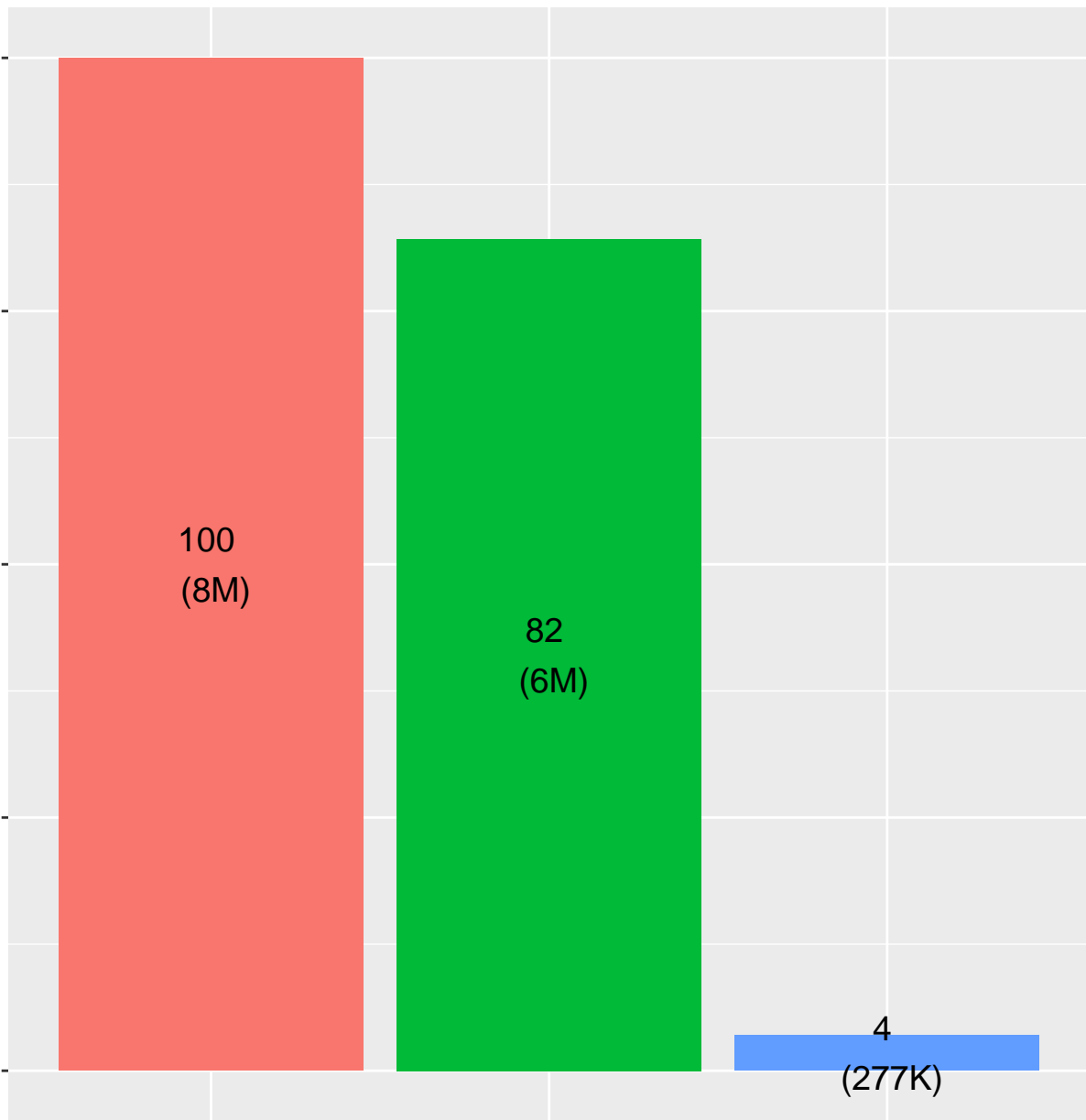
length filter

unique mapping

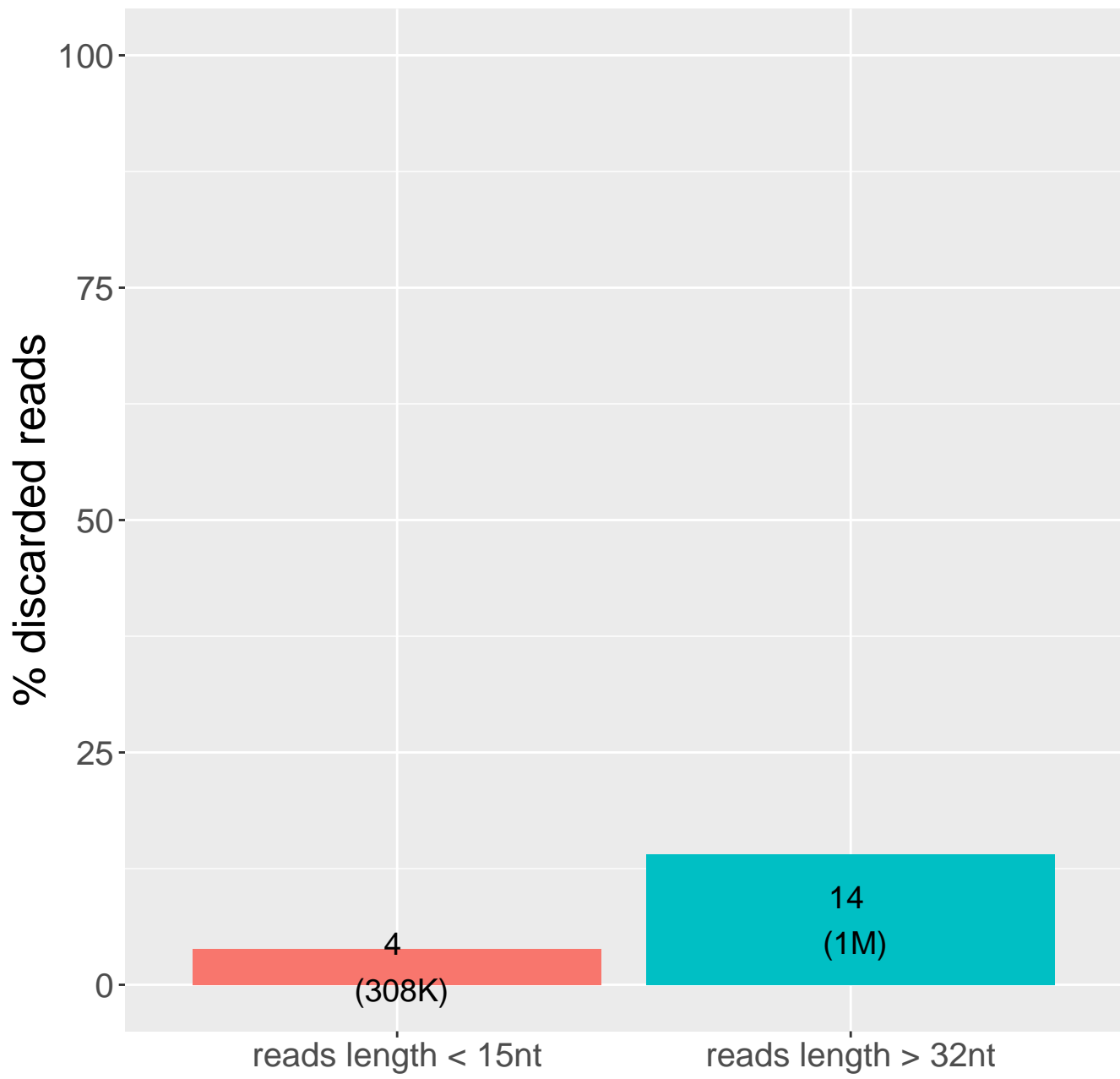
100  
(8M)

82  
(6M)

4  
(277K)

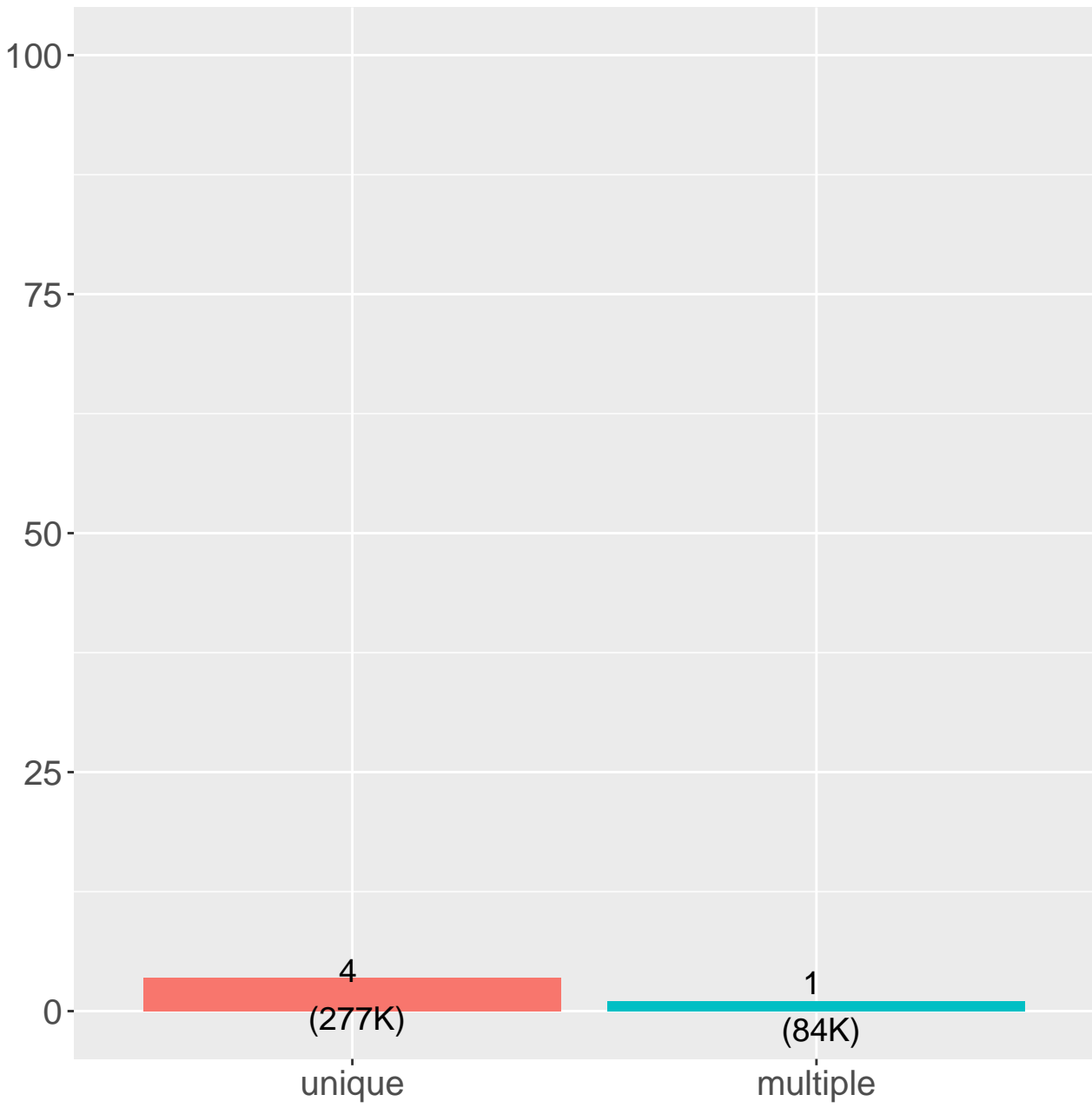


# Length filtering



# Mapping reads

% mapped reads



# Read distribution

% reads

100

75

50

25

0

miRNA

piRNA

snoRNA

snRNA

rRNA

34  
(93K)

45  
(124K)

13  
(36K)

2  
(5K)

4  
(11K)

