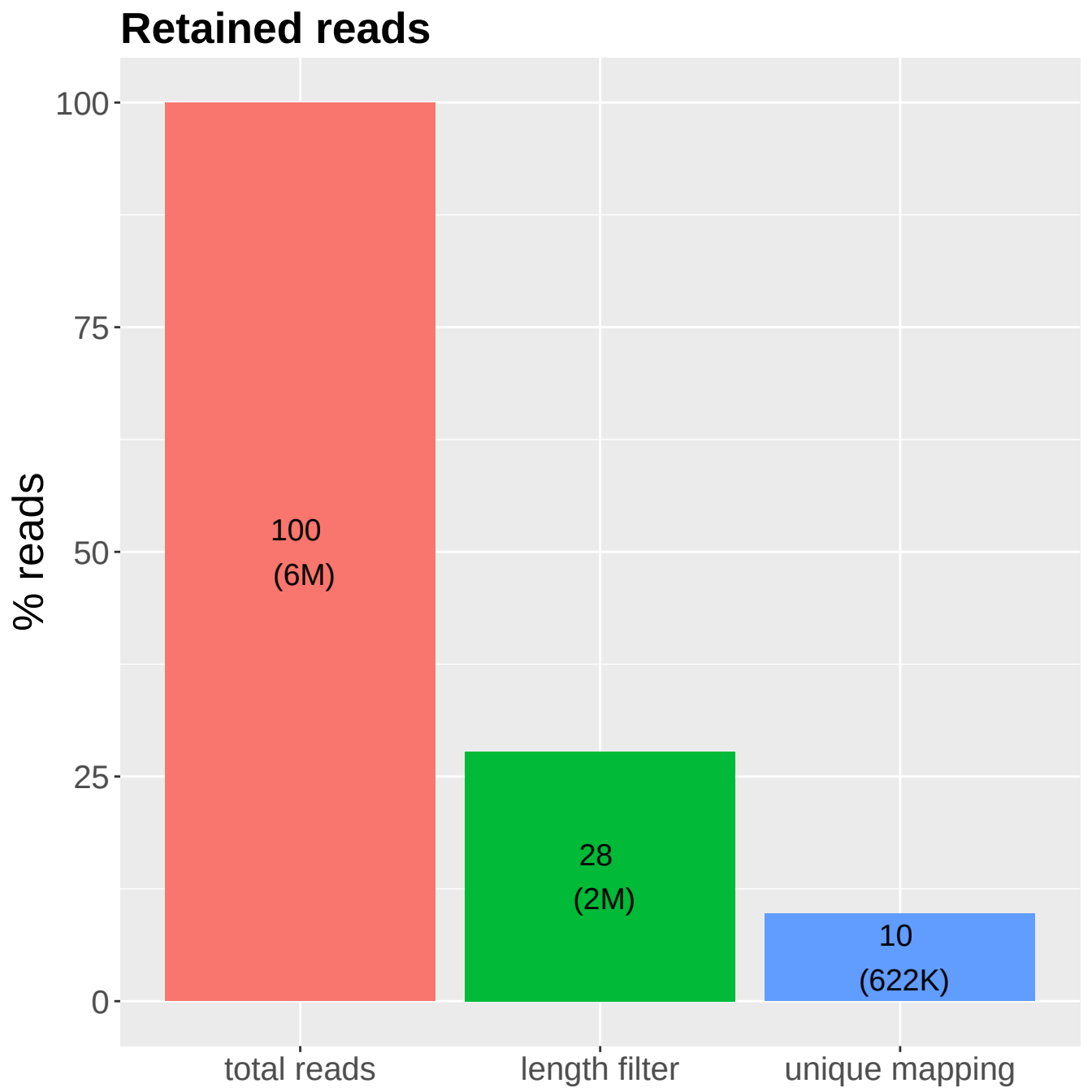
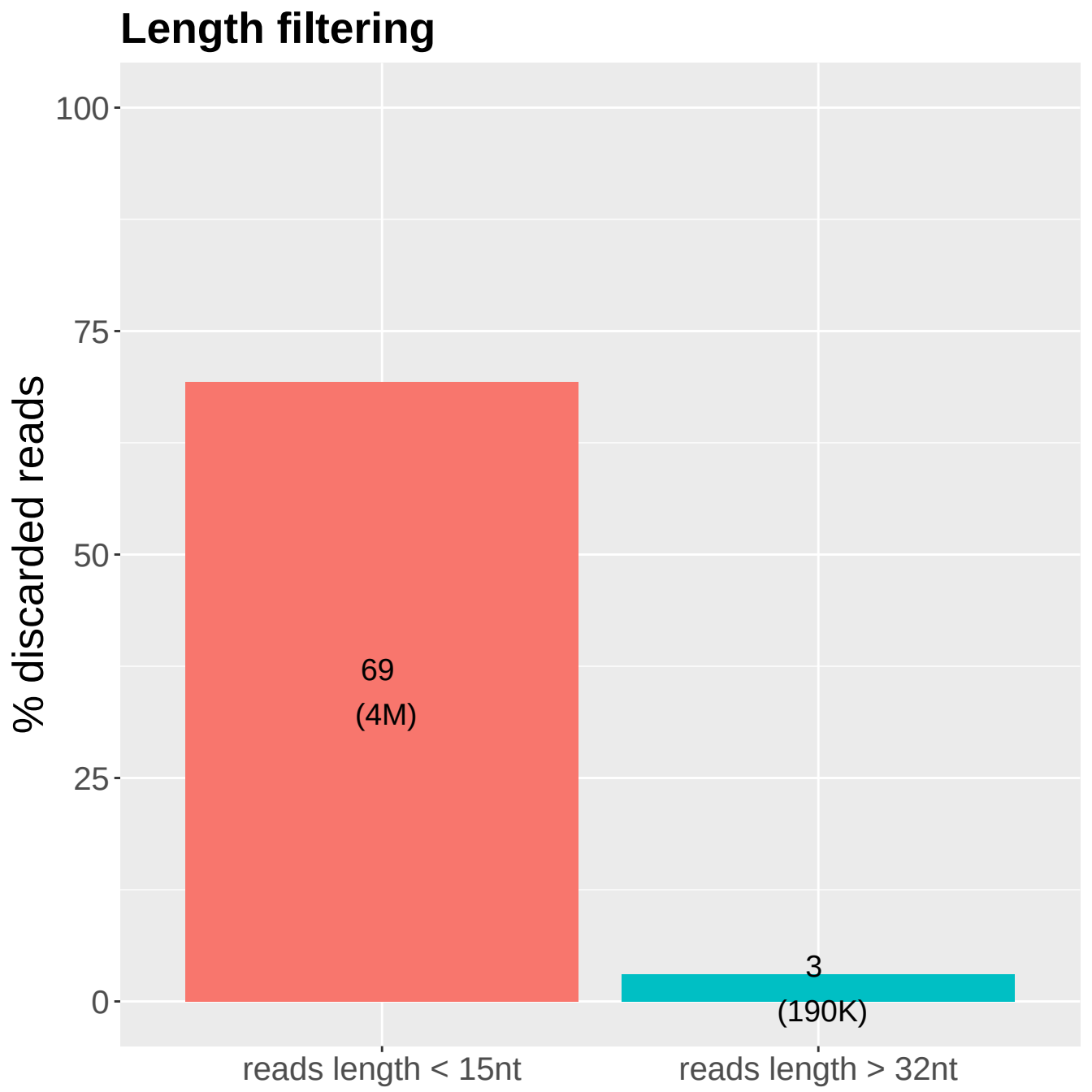
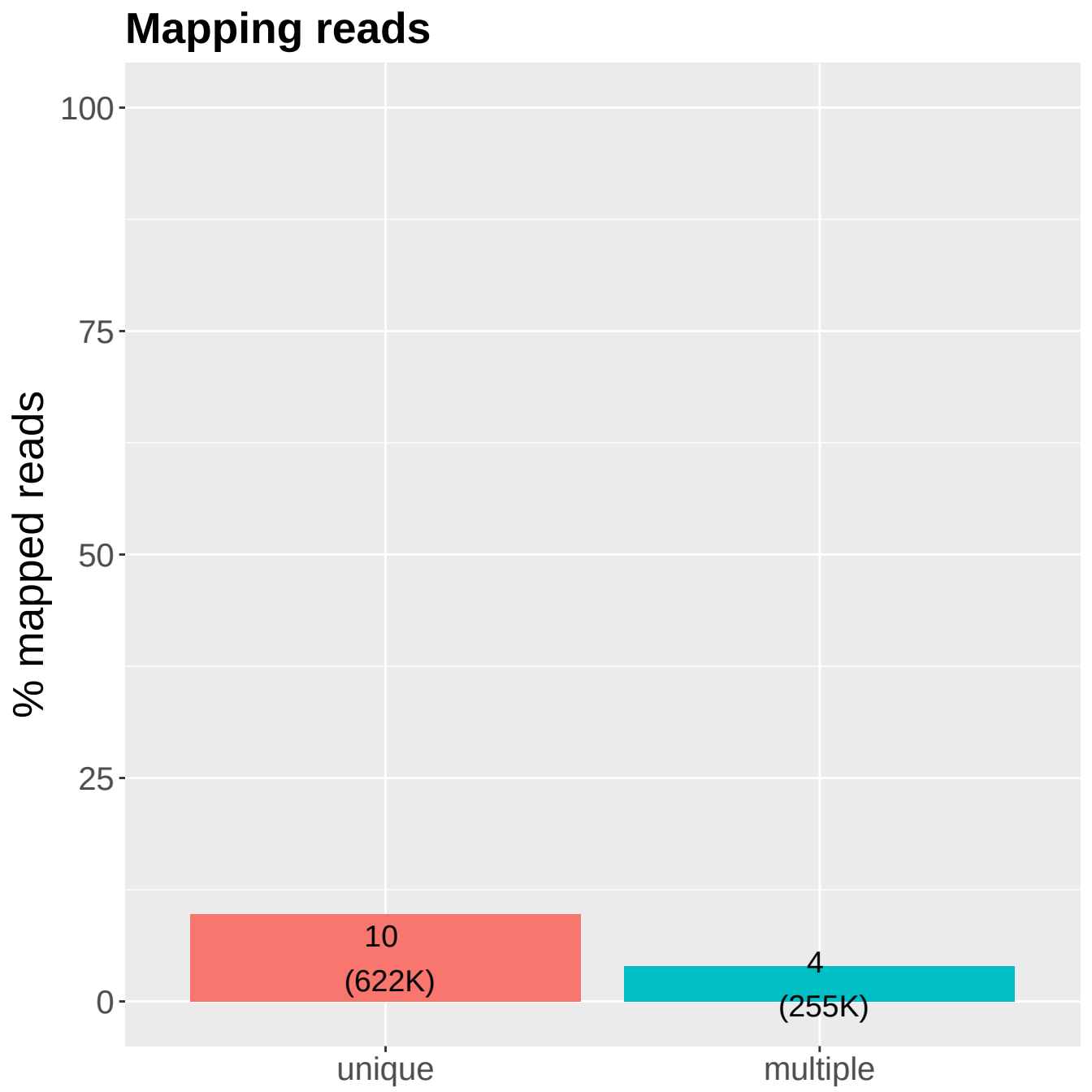
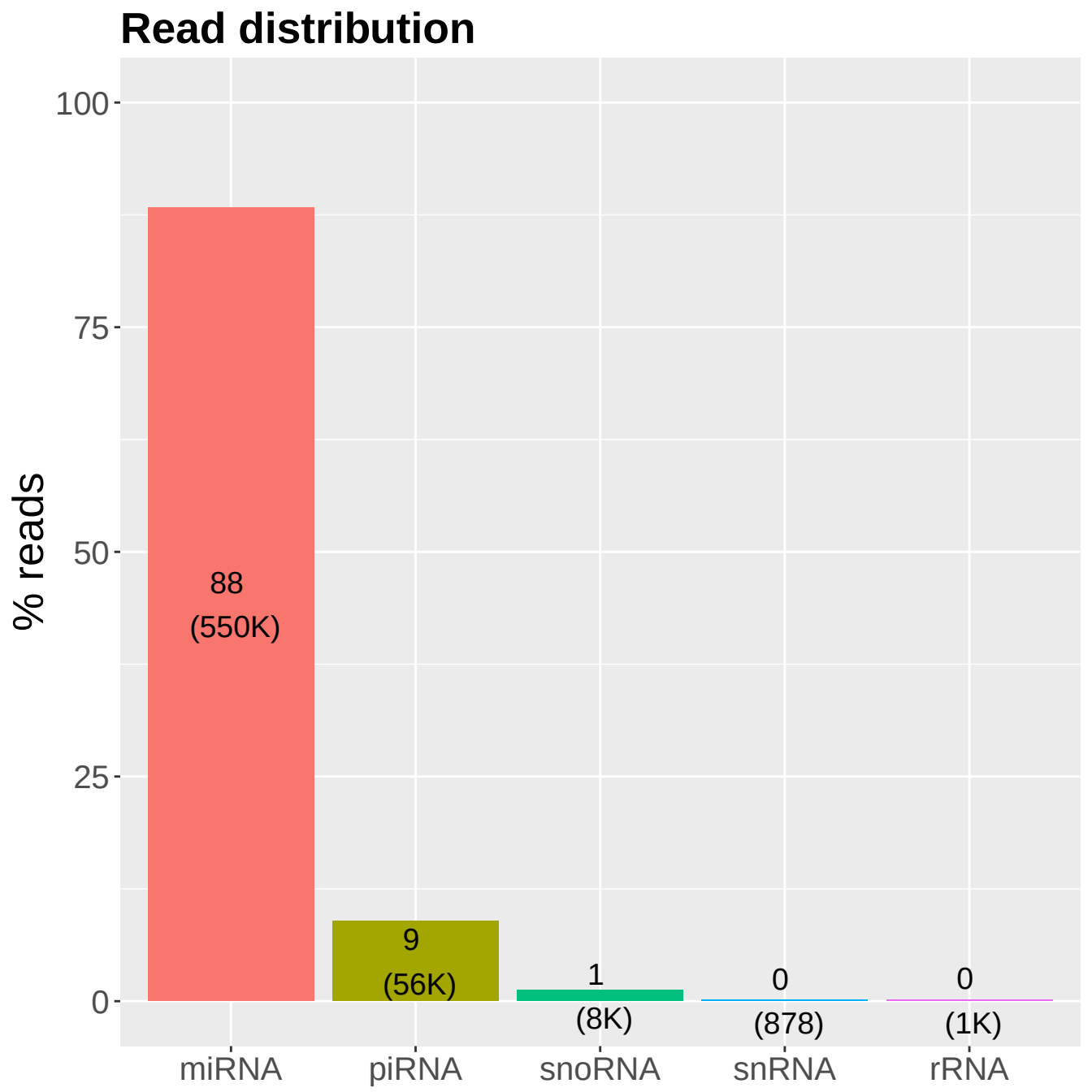

Retained reads
100
75
50
25
0
% reads
100
(6M)
28
(2M)
10
(622K)
total reads
length filter
unique mapping


Length filtering
100
75
50
25
0
% discarded reads
69
(4M)
3
(190K)
reads length < 15nt
reads length > 32nt


Mapping reads
% mapped reads
100
75
50
25
0
10
(622K)
4
(255K)
unique
multiple


Read distribution
100
75
50
25
0
% reads
88
(550K)
9
(56K)
1
(8K)
0
(878)
0
(1K)
miRNA
piRNA
snoRNA
snRNA
rRNA