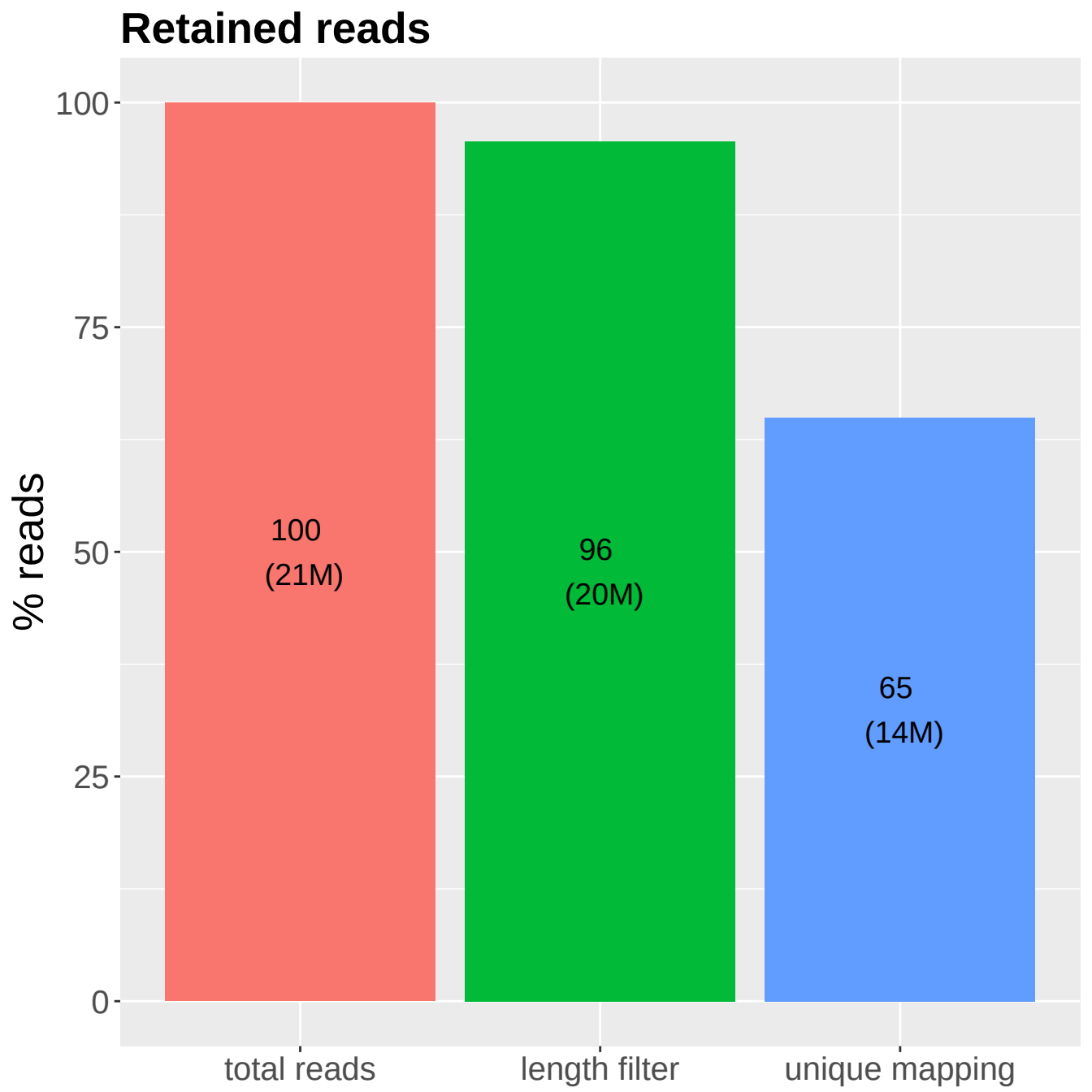
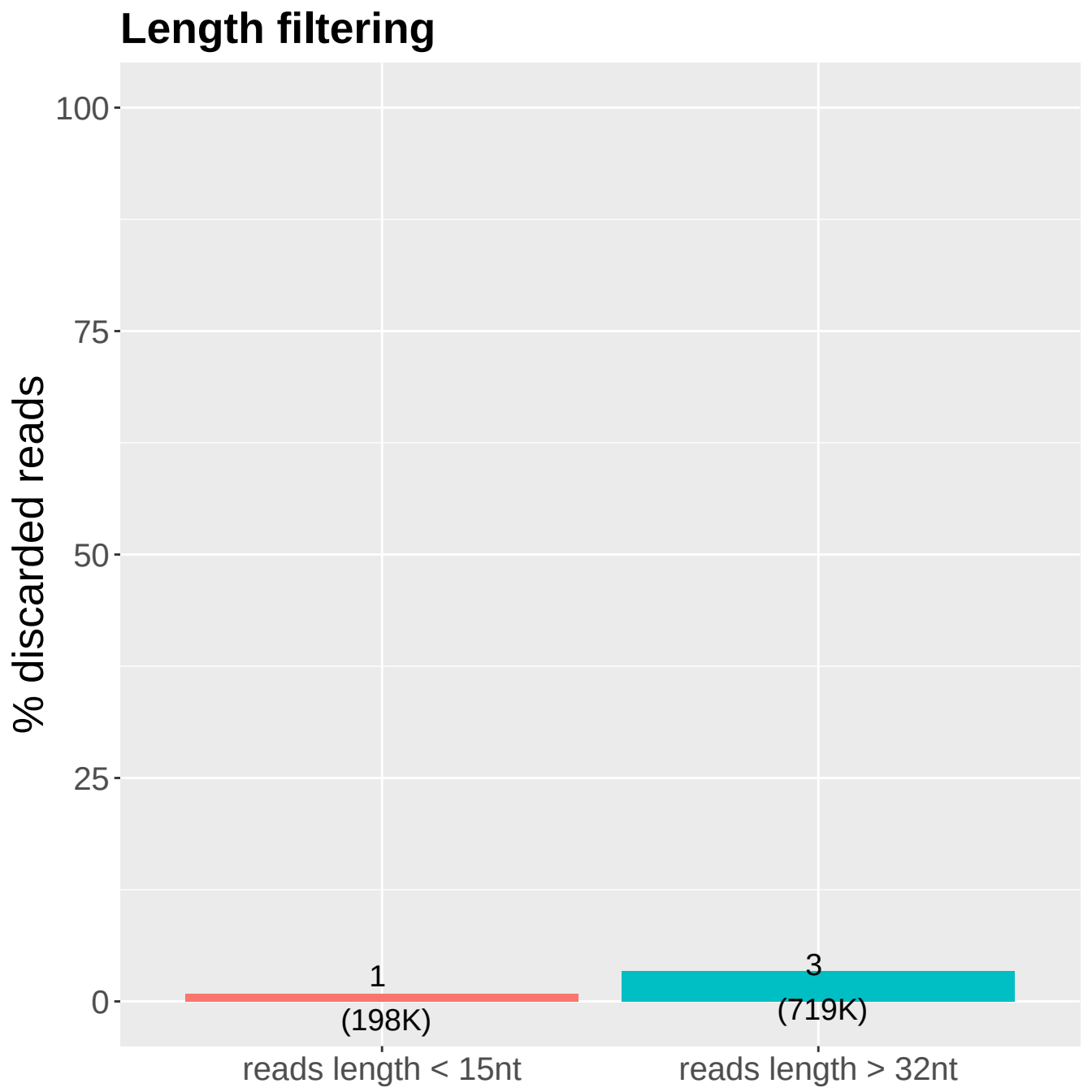
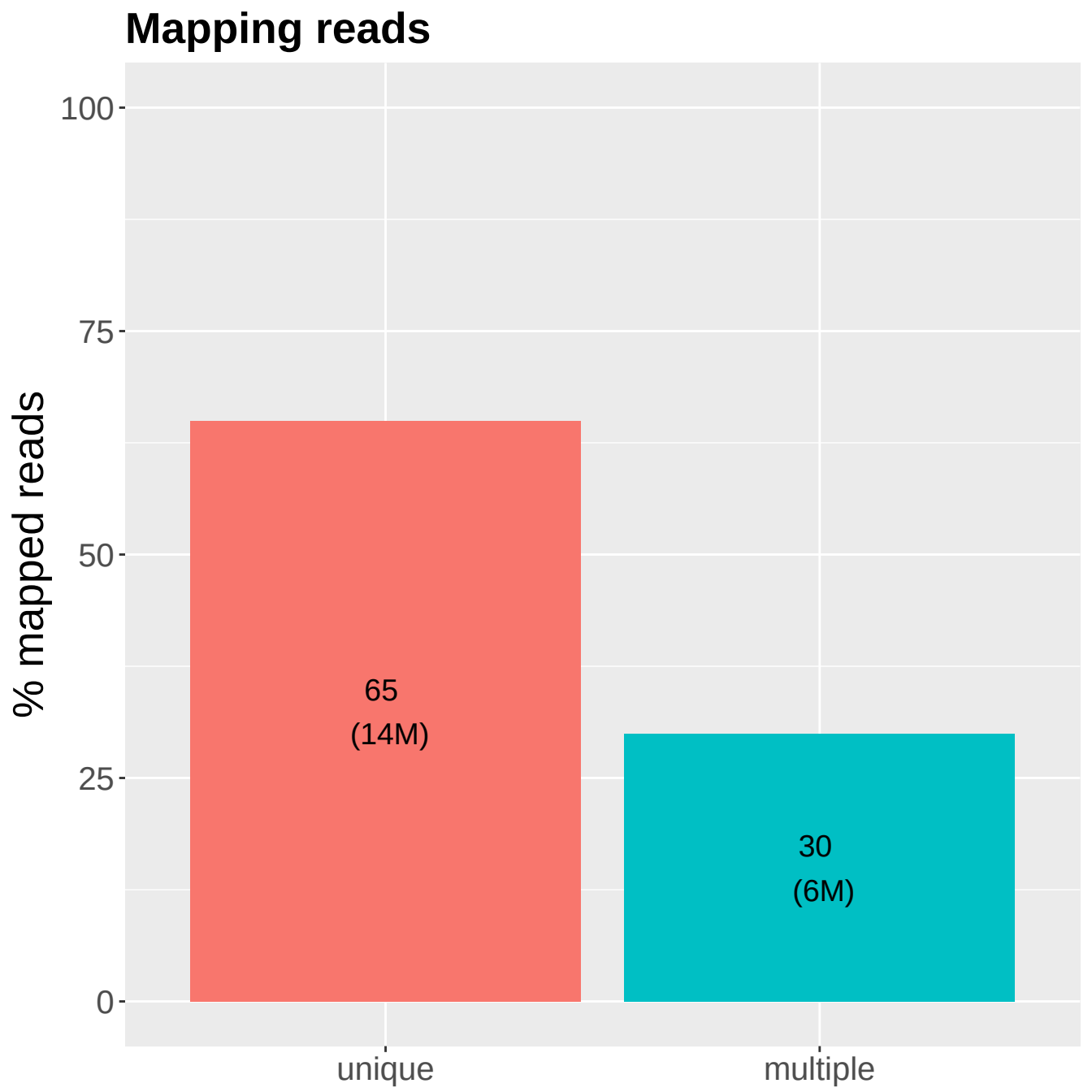
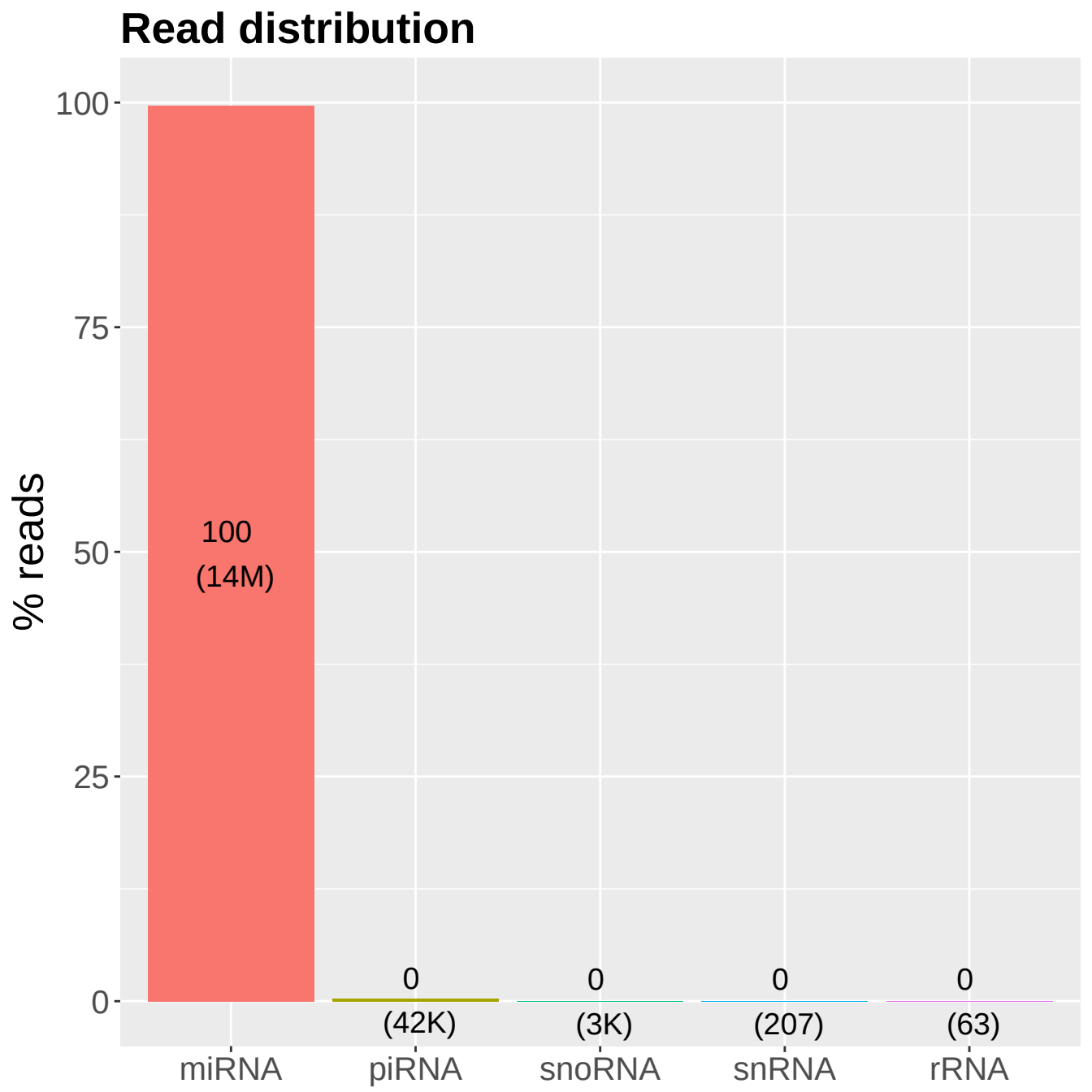

Retained reads
100
75
50
25
0
% reads
100
(21M)
96
(20M)
65
(14M)
total reads
length filter
unique mapping


Length filtering
100
75
50
25
0
% discarded reads
1
(198K)
3
(719K)
reads length < 15nt
reads length > 32nt


Mapping reads
% mapped reads
100
75
50
25
0
65
(14M)
30
(6M)
unique
multiple


Read distribution
100
75
50
25
0
% reads
100
(14M)
0
(42K)
0
(3K)
0
(207)
0
(63)
miRNA
piRNA
snoRNA
snRNA
rRNA