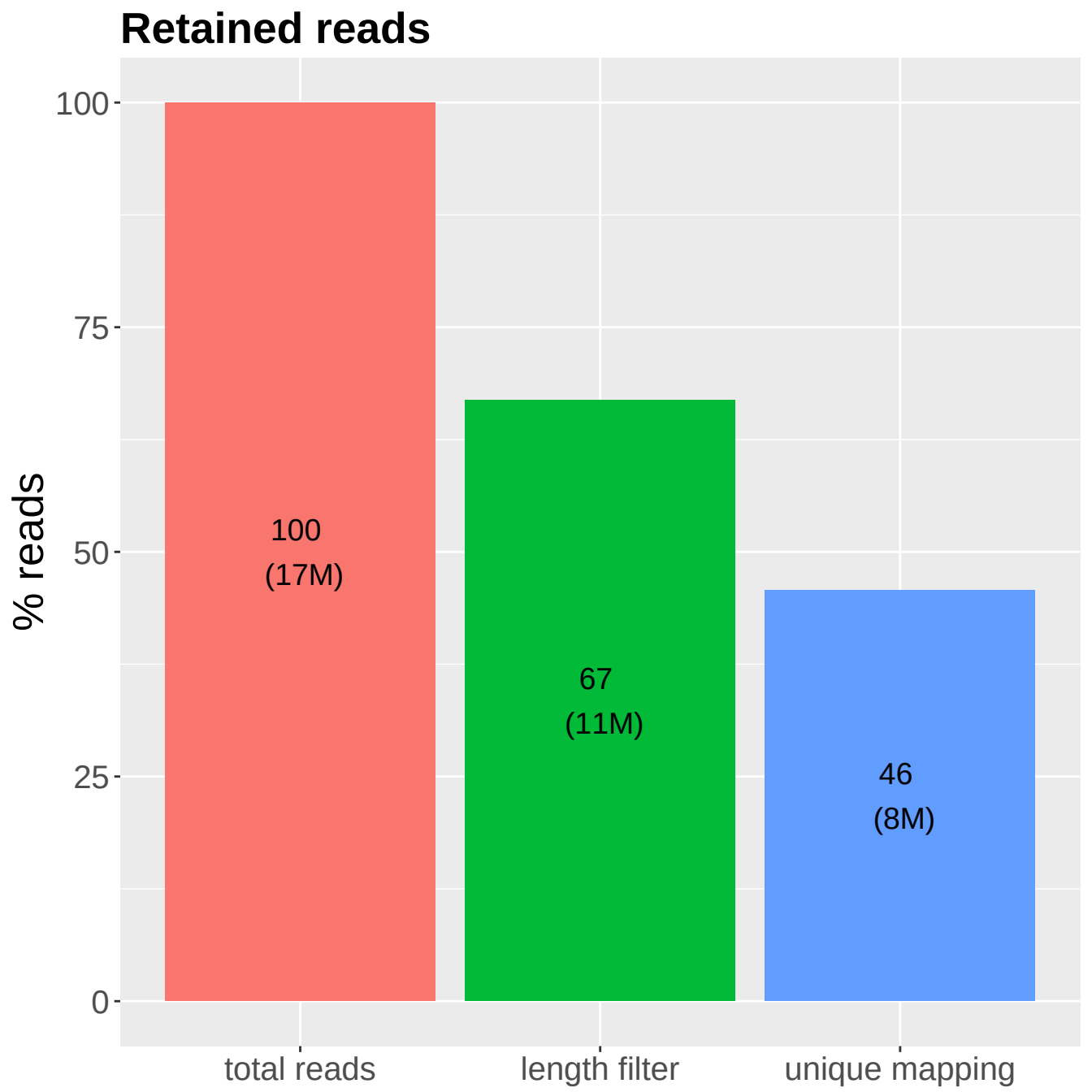
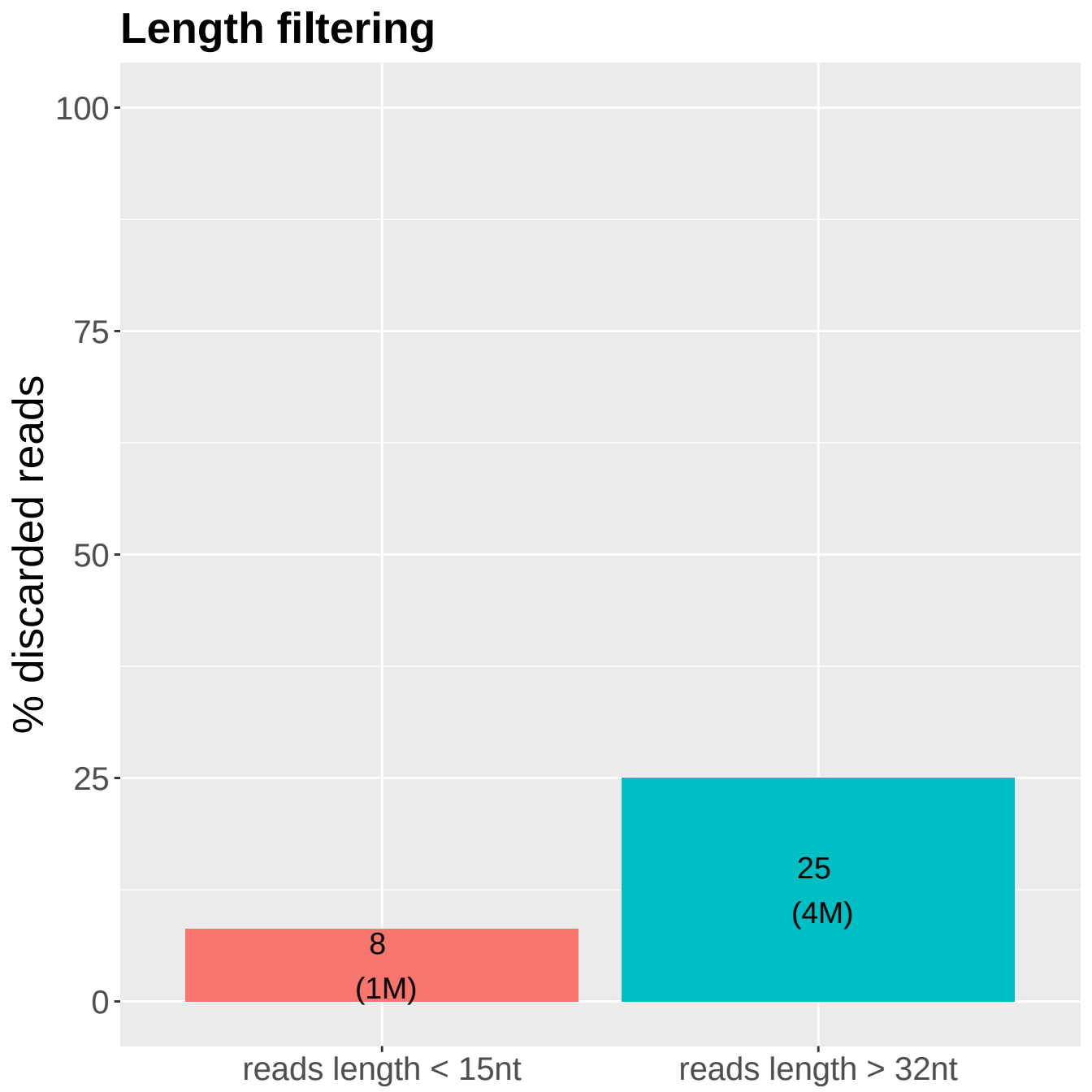
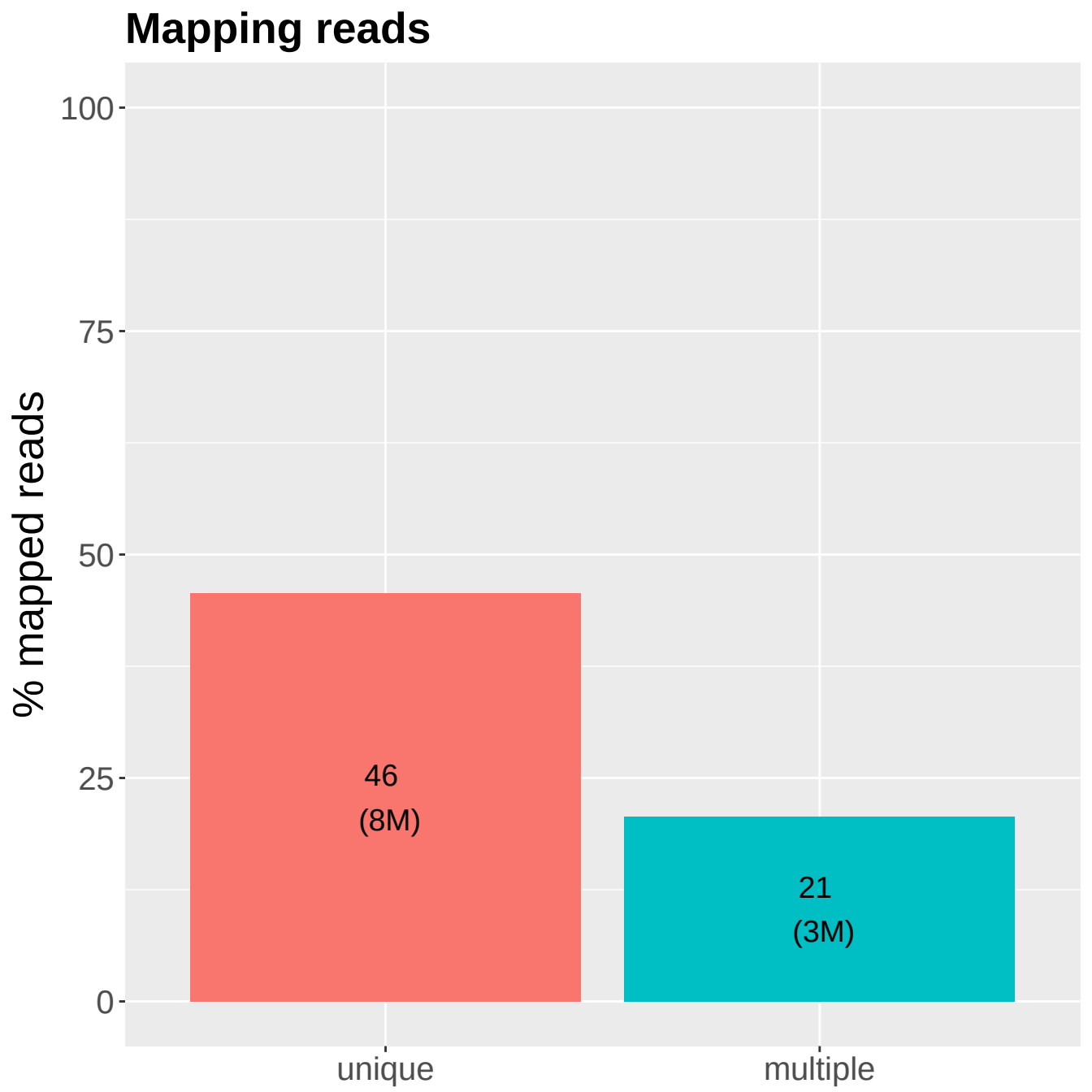
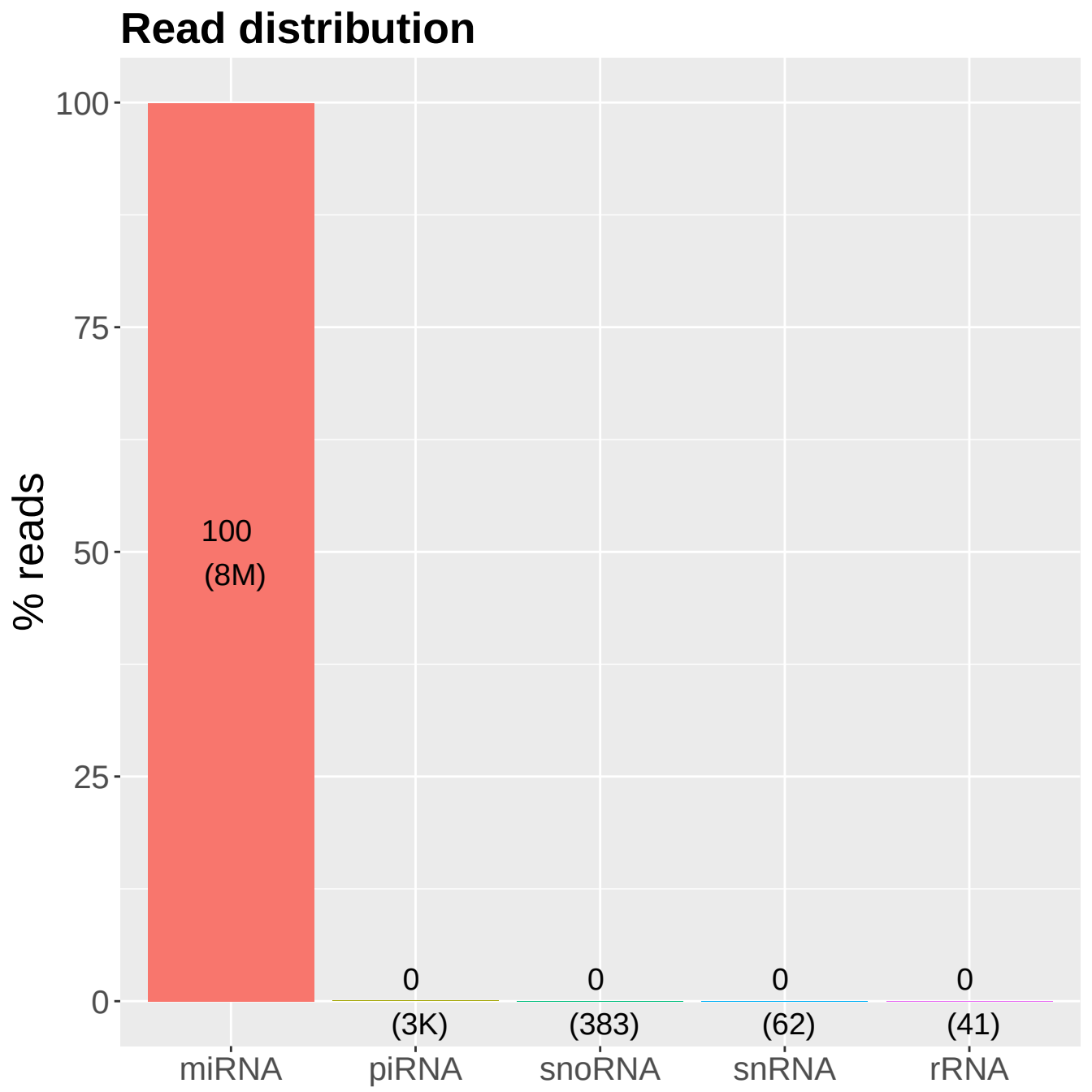

Retained reads
% reads
100
75
50
25
0
100
(17M)
67
(11M)
46
(8M)
total reads
length filter
unique mapping


Length filtering
% discarded reads
100
75
50
25
0
8
(1M)
25
(4M)
reads length < 15nt
reads length > 32nt


Mapping reads
% mapped reads
100
75
50
25
0
46
(8M)
21
(3M)
unique
multiple


Read distribution
100
75
50
25
0
% reads
100
(8M)
0
(3K)
0
(383)
0
(62)
0
(41)
miRNA
piRNA
snoRNA
snRNA
rRNA