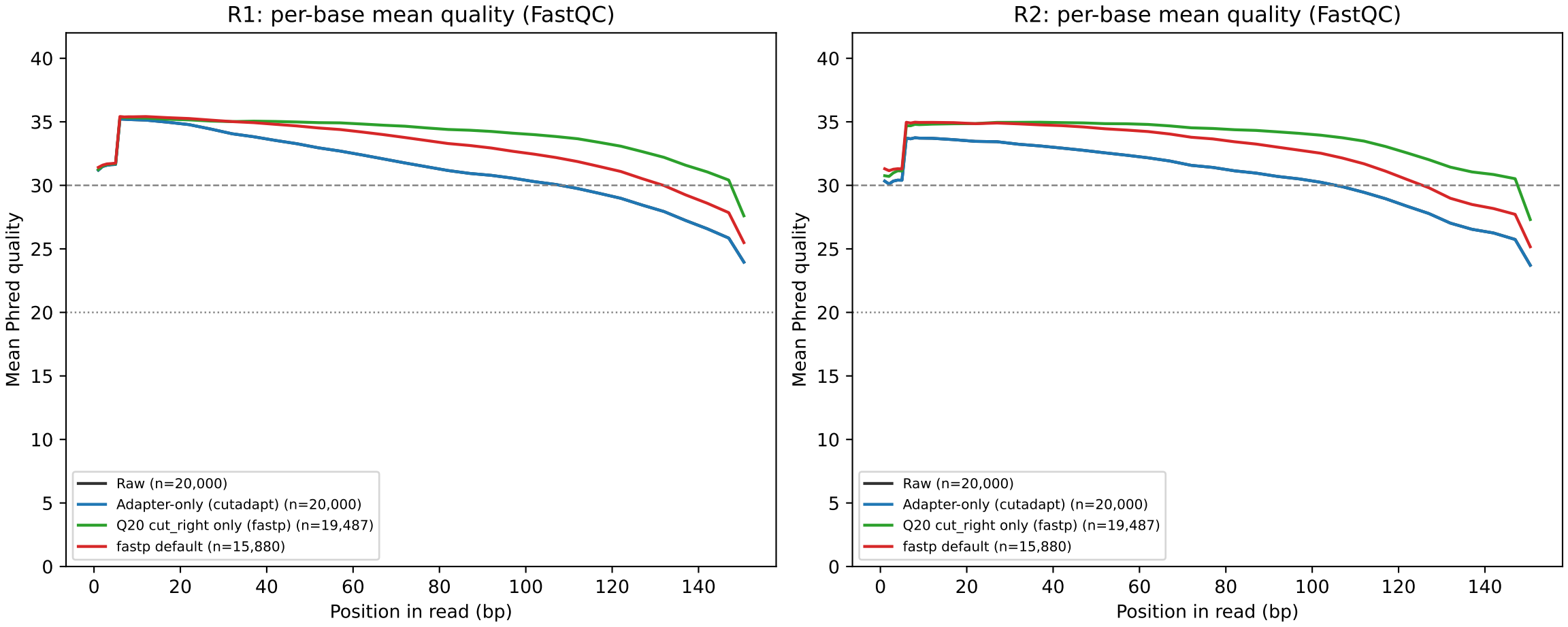
R1: per-base mean quality (FastQC)
R2: per-base mean quality (FastQC)
Mean Phred quality
Position in read (bp)
0
5
10
15
20
25
30
35
40
0
20
40
60
80
100
120
140
Raw (n=20,000)
Adapter-only (cutadapt) (n=20,000)
Q20 cut_right only (fastp) (n=19,487)
fastp default (n=15,880)