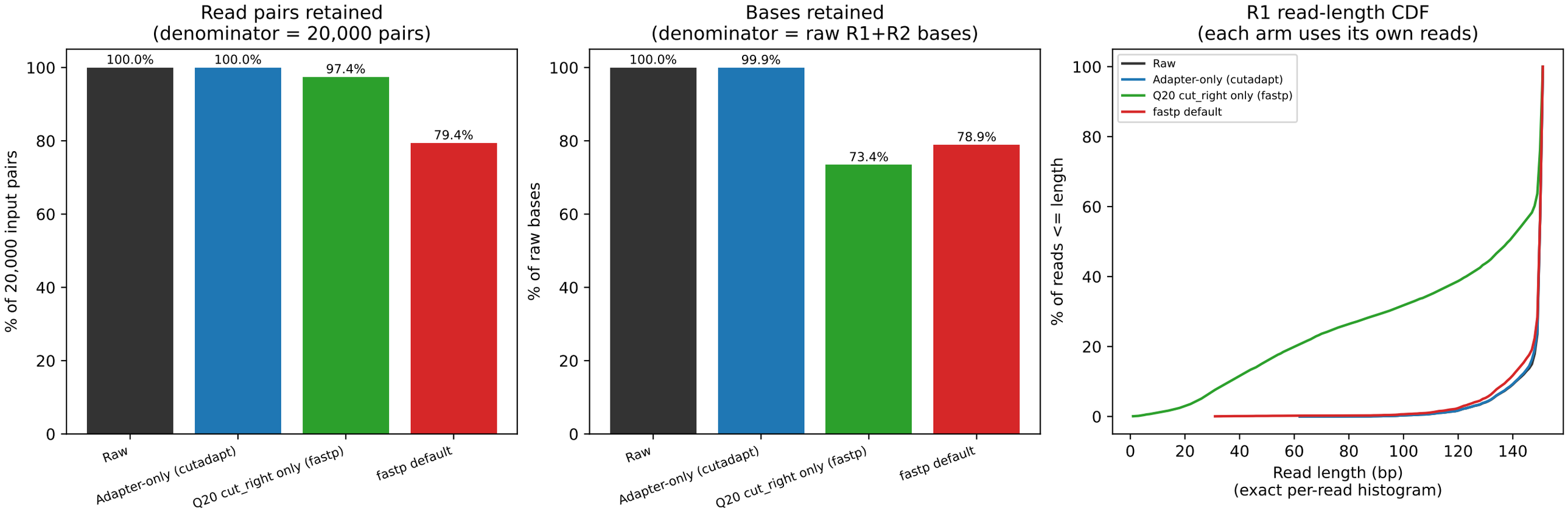
Read pairs retained
(denominator = 20,000 pairs)
% of 20,000 input pairs
100.0%
100.0%
97.4%
79.4%
Raw
Adapter-only (cutadapt)
Q20 cut_right only (fastp)
fastp default
Bases retained
(denominator = raw R1+R2 bases)
% of raw bases
100.0%
99.9%
73.4%
78.9%
R1 read-length CDF
(each arm uses its own reads)
% of reads <= length
Read length (bp)
(exact per-read histogram)