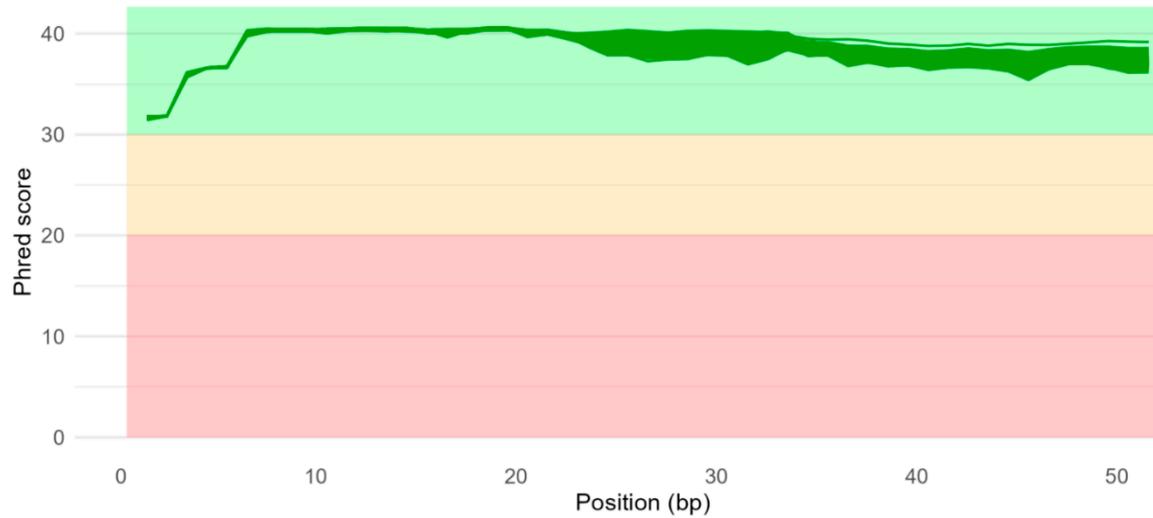


A FastQC: Mean quality scores



B FastQC: Per sequence quality scores

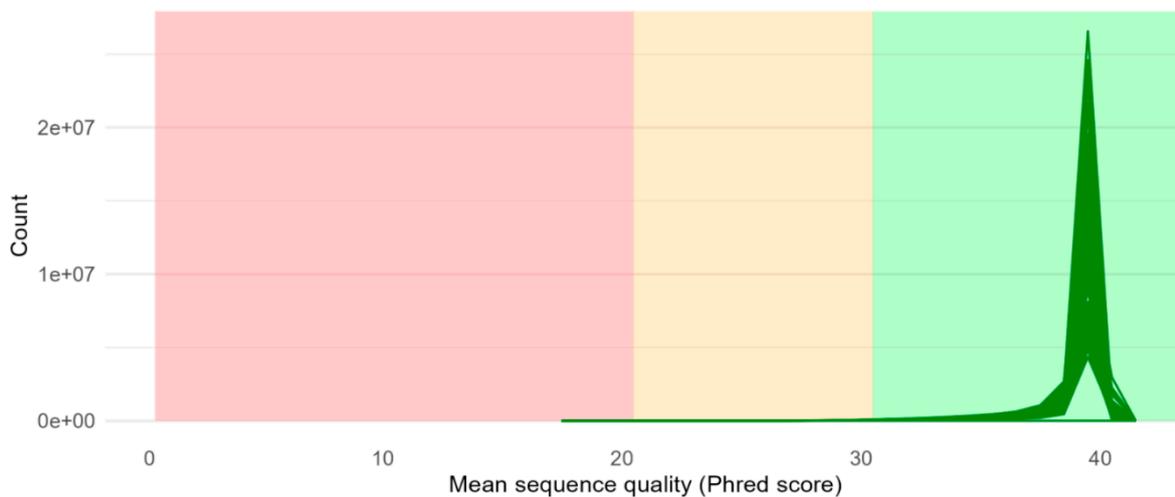


Figure S1. miRNA quality assessment using FastQC. Mean quality (phred) score per base (A) and sequence quality score distribution (B) for vascular IMA miRNA samples from CAD patients ($n=191$). Background colour indicates different quality thresholds – red:0–20 unacceptable, low sequence quality; yellow :20–30 acceptable, but not ideal; green: >30 excellent sequence quality.

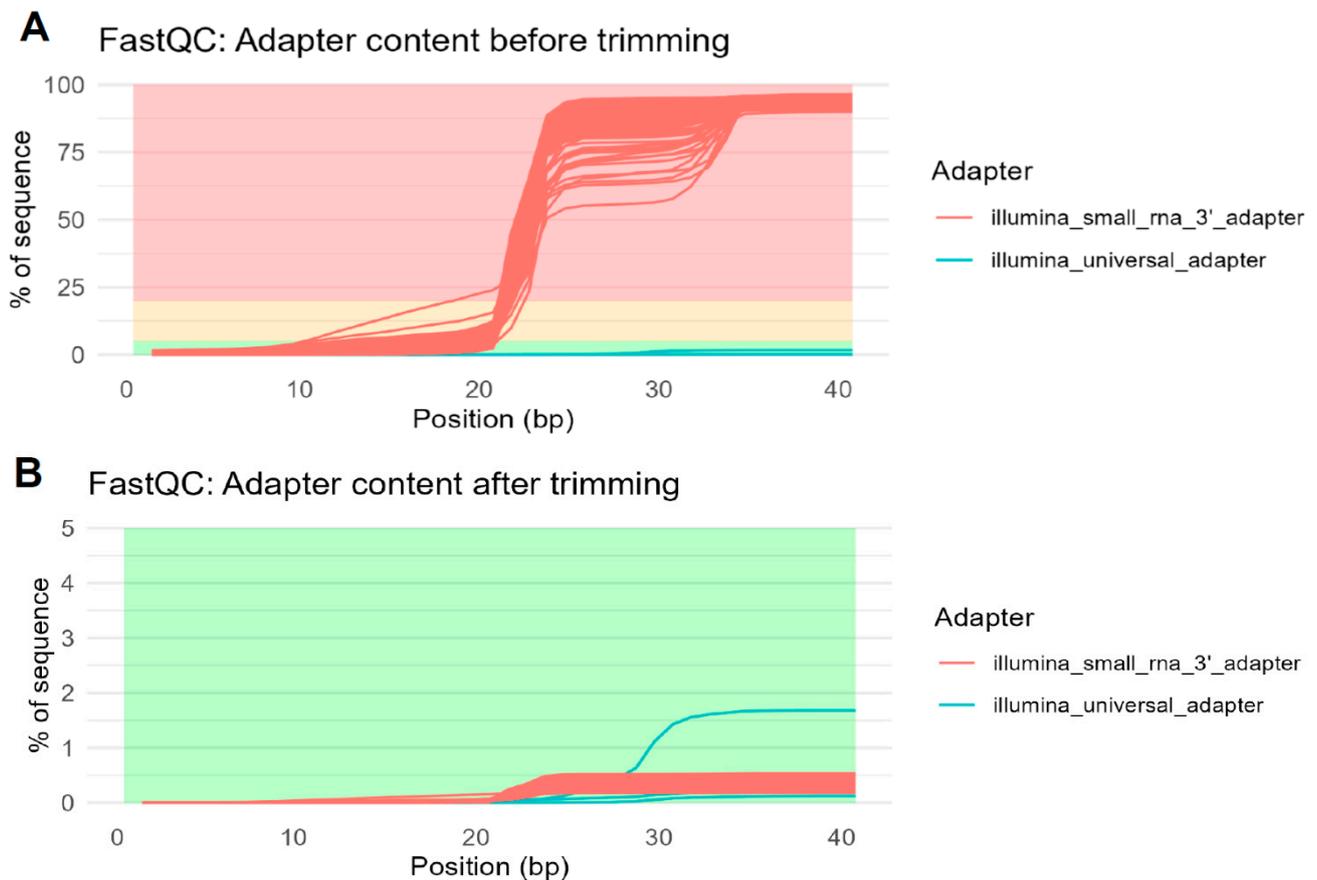


Figure S2. miRNA adapter content before and after trimming. Adapter content of vascular IMA miRNA sequences from CAD patients (n=191) before and after trimming. Background colour indicates accepted thresholds – green: 0 – 5% - excellent, minimal adapter content; yellow: 5 – 20% acceptable, but not ideal; red: 20 – 100% unacceptable high adapter content. As expected with miRNA data, unprocessed sequences show high adapter content after ~20 bp (A) which is the approximate length of target sRNAs. After performing adapter trimming with fastp, providing Illumina TruSeq Small RNA adapter sequence, adapter content dropped below 2% (B).