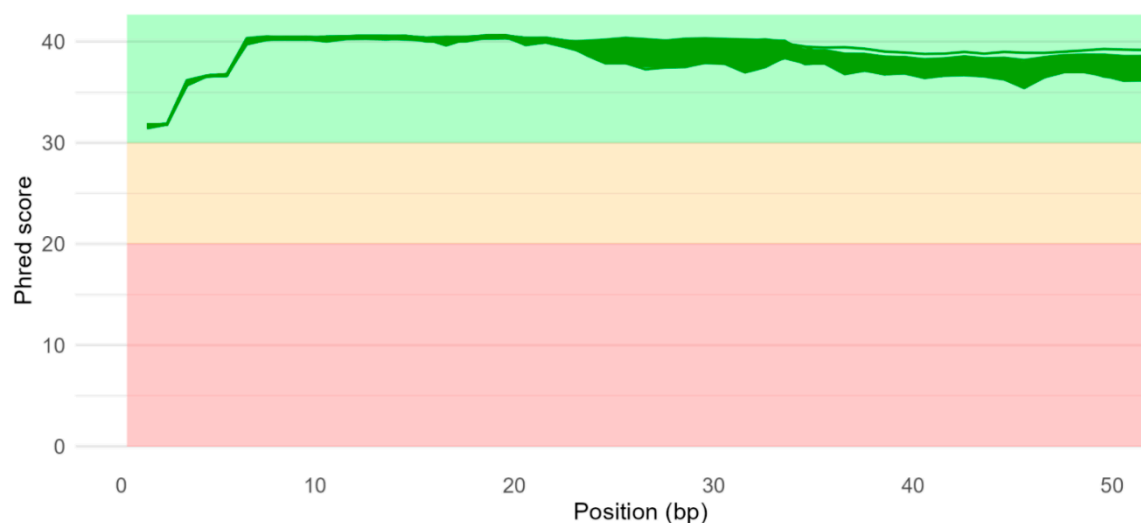
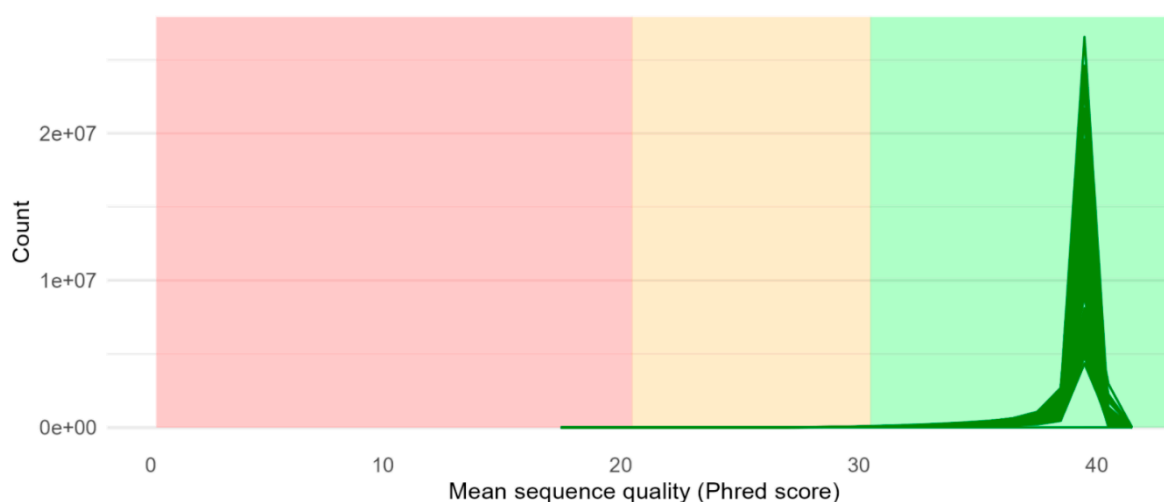
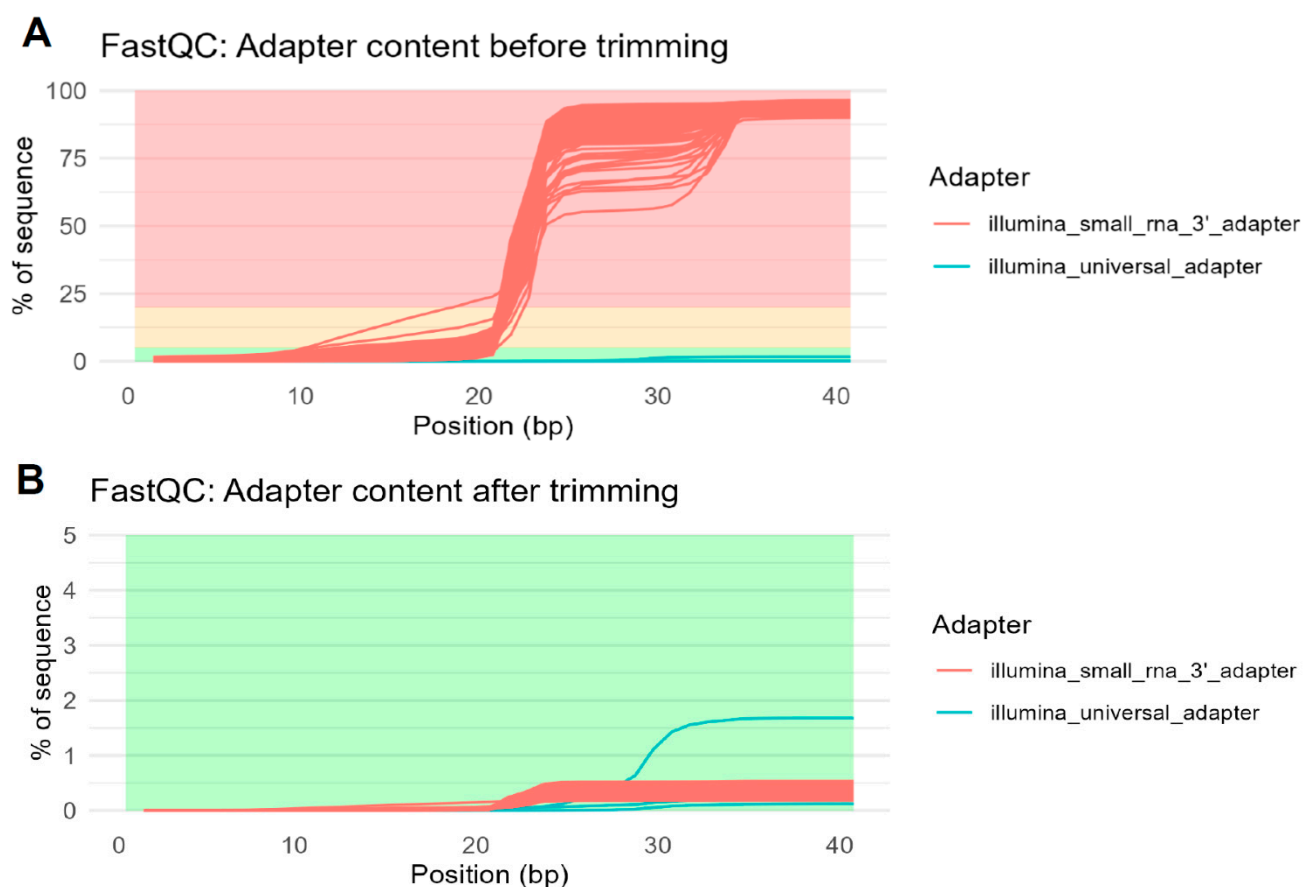


**A** FastQC: Mean quality scores**B** FastQC: Per sequence quality scores

**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**).