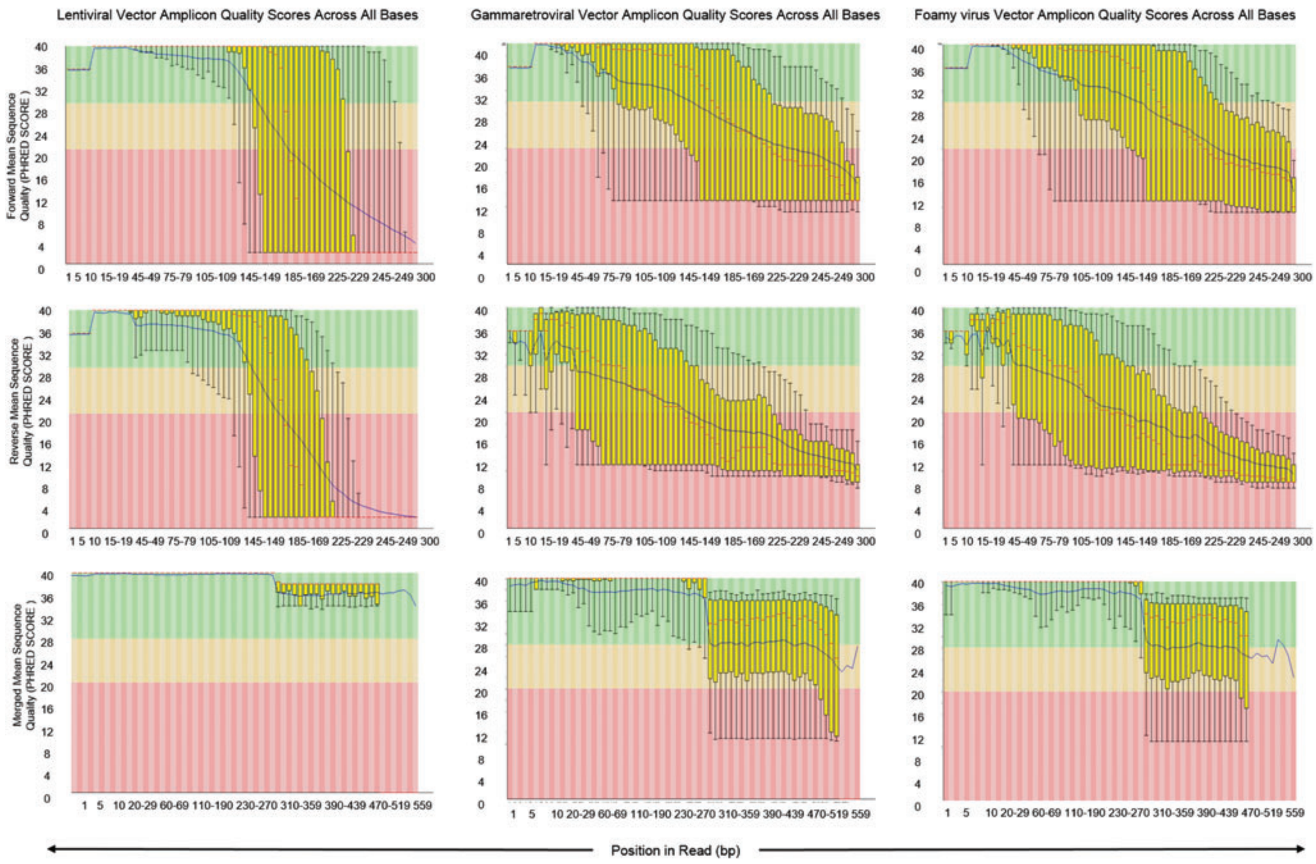

Supplementary Figure S2. FastQC analysis of forward/reverse sequence reads demonstrate improved quality and length of merged paired reads. PHRED scores measure the probability a base call is incorrect during sequencing with PHRED score of 10 indicating 1 in 10 error rate, 20 indicating 1 in 100, 30 indicating 1 in 1,000, and 40 indicating 1 in 10,000 error rate or 99.99% accuracy. Green color indicates good-quality PHRED scores 30–40, pink indicates moderate PHRED scores 20–30, and red indicates poor sequence quality with PHRED scores 20 and below. Representative sequence quality and lengths are displayed for all vector types. Single forward and reverse sequence reads have good PHRED quality for approximately 145 bp before sequence quality begins to fail. The total length of a single read is in the range of ∼300 bp. Merged paired sequences have higher PHRED scores across a much longer query sequences.