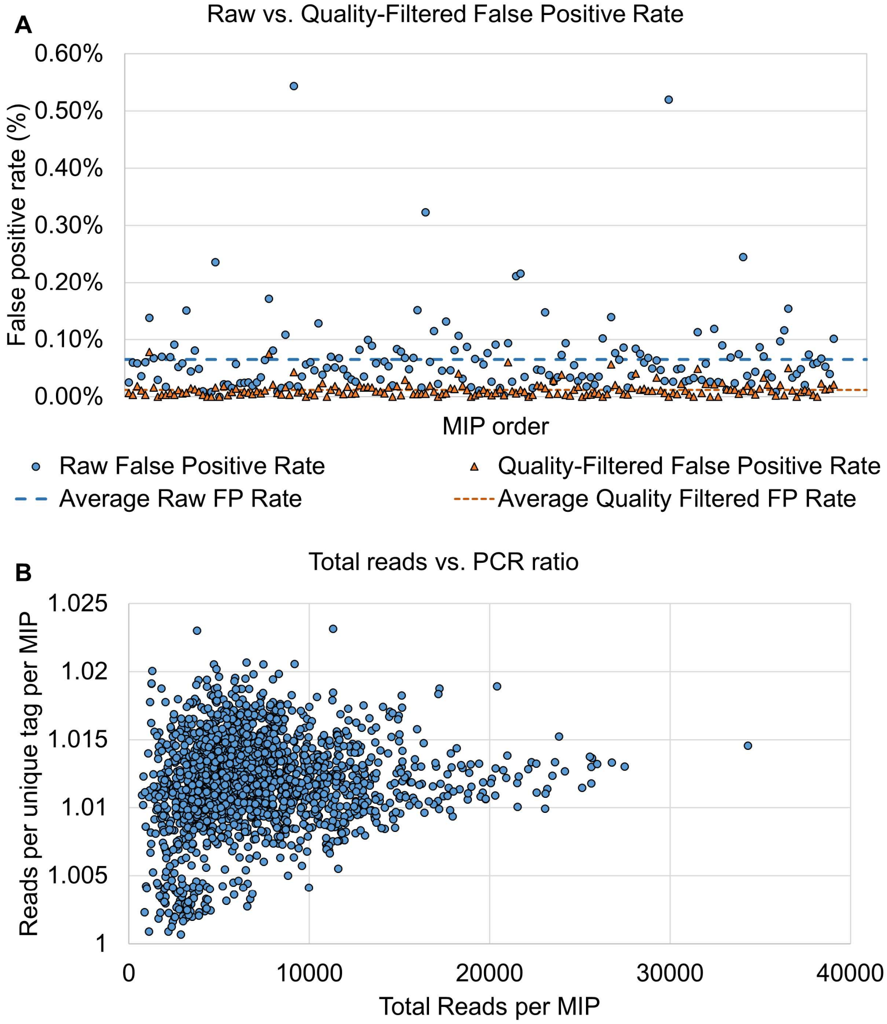

Figure S2. MIP accuracy and efficiency were tested on a range of samples. (A) The false positive rates of MIPs were investigated using a series of probes targeting 172 genomic loci. A mean raw false positive read rate of 0.0651% ± 0.0696% was observed with a maximum of 0.543%. By filtering reads at the SNV site for quality scores of Phred >= 30, the false positive rate was decreased to a mean of 0.0122% ± 0.0129% with a maximum value of 0.0785%. (B) MIP capture and library preparation produces a high concordance of sequence reads vs. UMIs. Using 24 sets of MIP capture reactions with the same 89 MIPs, the observed mean rate of UMI duplication via PCR is 1.011 ± 0.003. The ratio of reads per tag was not correlated to the total reads per MIP when analysing the same 24 sets by total read count on a per MIP per capture reaction basis.