**Figure S1** Read realignment via CIGAR modification using information from adjacent reads. (a) Elimination of Soft Clipping: A deletion with respect to the reference sequence is called in a fraction of reads at a given site, but induces some right-sided clipping (read 1, clipped sequence in green) or left-sided clipping (read 5) when reads cannot sufficiently frame the variant. Clipped reads may also occur when encountering high SNV density or compound variants. Testing the sequence of the read against the variant sequence predicted by other alignments to the same locus allows for extension of clipped alignments through the variant region, reducing the number of spurious clipping sites. (b) Variant regions near the ends of reads may also cause aligners to generate erroneous unclipped alignments, often preferring the introduction of multiple SNVs to the introduction of a gap (red tick marks, reads 1 and 5), as has been noted many times elsewhere. In both figure (a) and figure (b), analyzing each read for agreement with variant alignments at the same locus allows us to increase support for the predominant variant call(s) at the locus in question when consensus thresholds are implemented.