

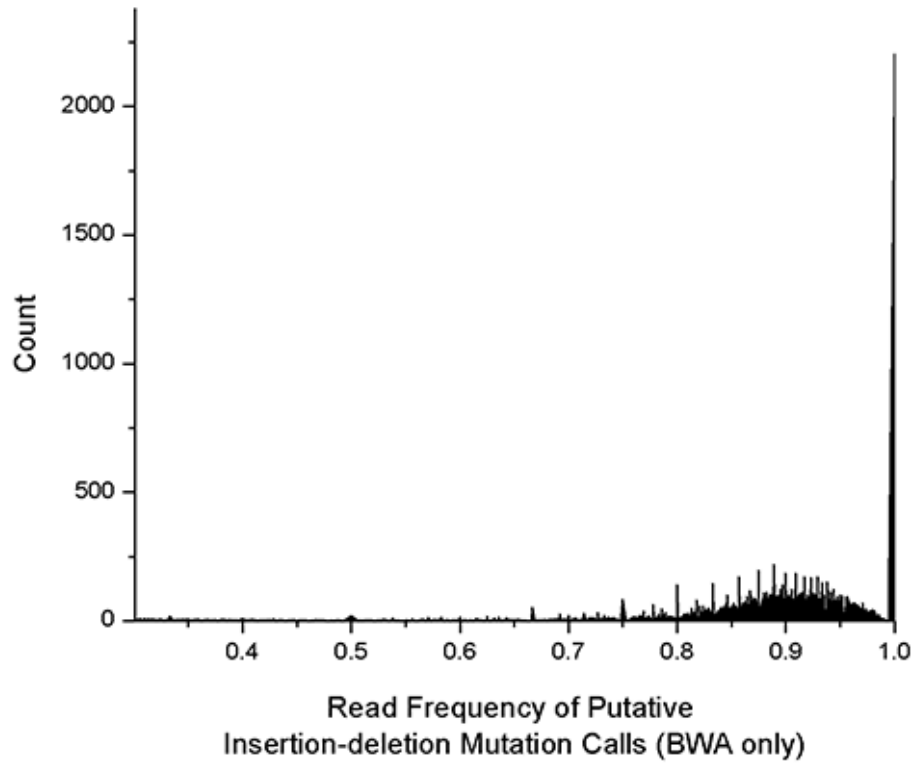
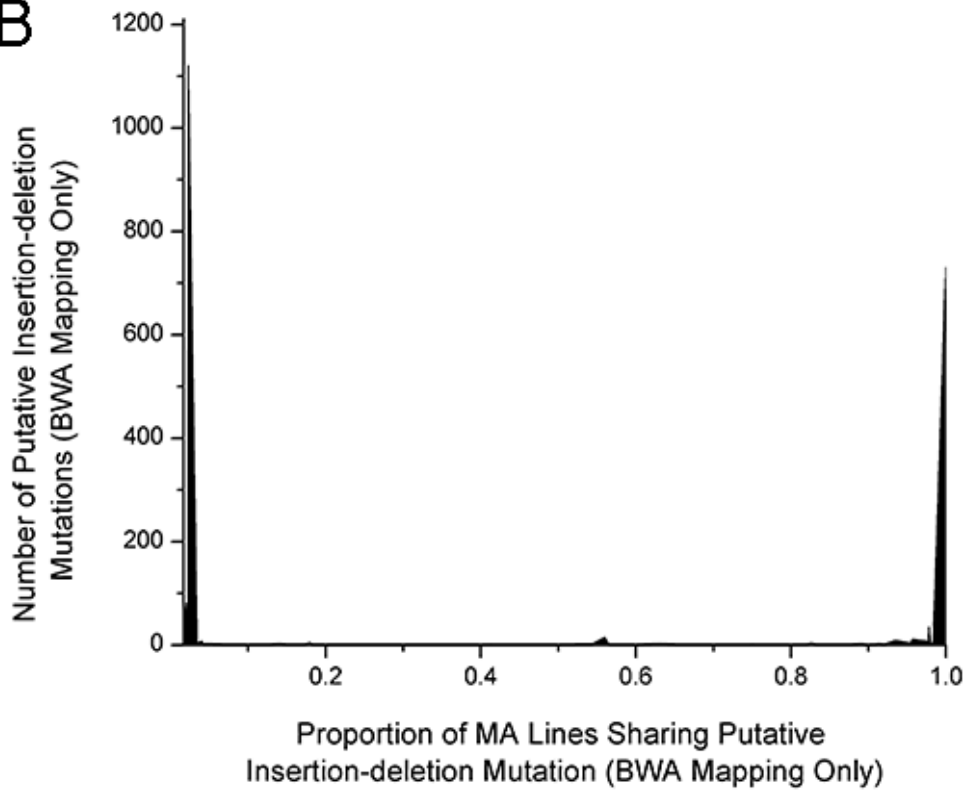
A**B**

Figure S3. **A)** Distribution of the read frequency for insertion-deletion mutation calls using BWA mapping. Read frequency is determined by the number of reads representing the putative insertion-deletion mutation call at a site, divided by the total number of reads spanning that site. The total number includes counts from *Agrobacterium tumefaciens*, *Bacillus subtilis*, *Escherichia coli*, *Mesoplasma florum*, *Staphylococcus epidermidis*, and *Vibrio cholerae* MA experiments prior to filtering (see Mutation Calling). **B)** Bimodal distribution displaying the proportion of MA lines sharing the same (size and motif) putative insertion-deletion mutation call using BWA mapping for same organisms.