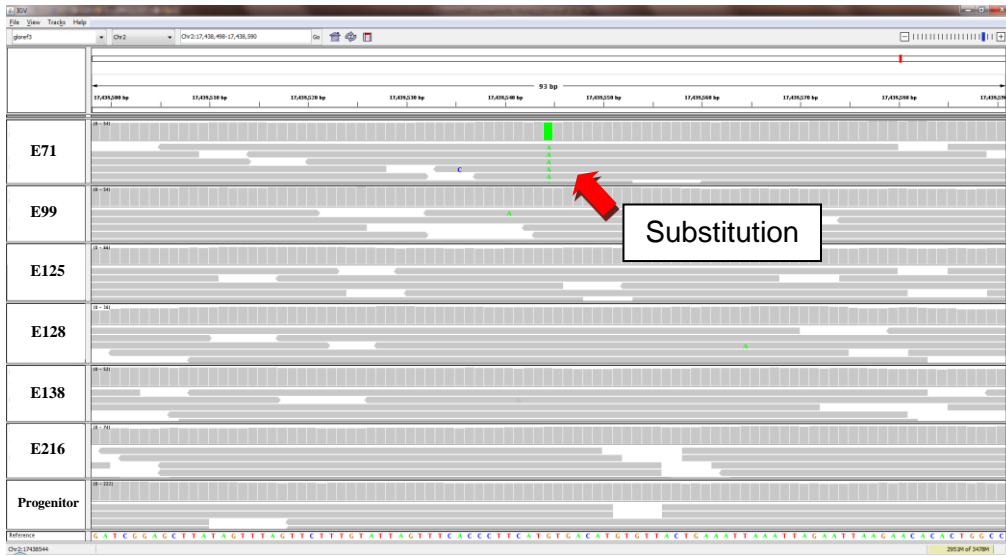
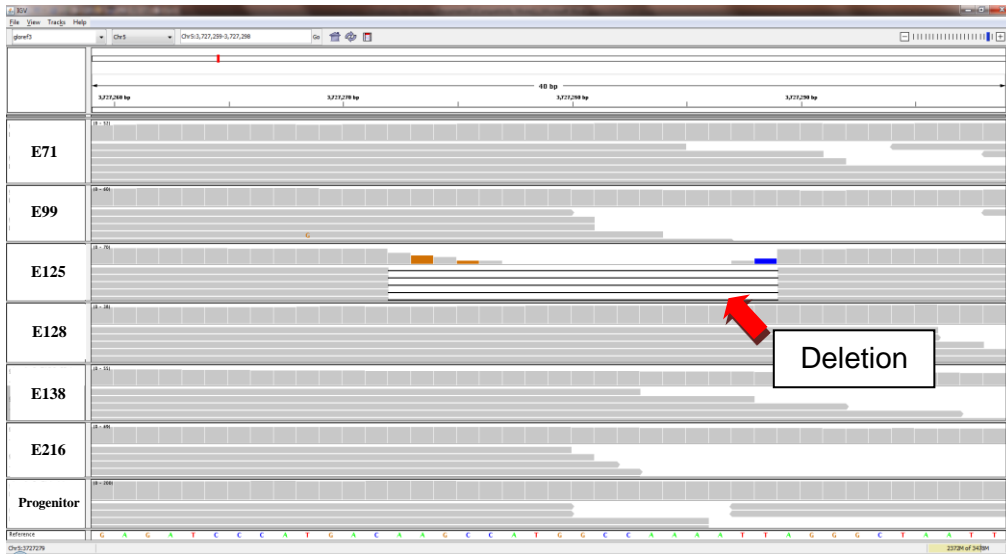


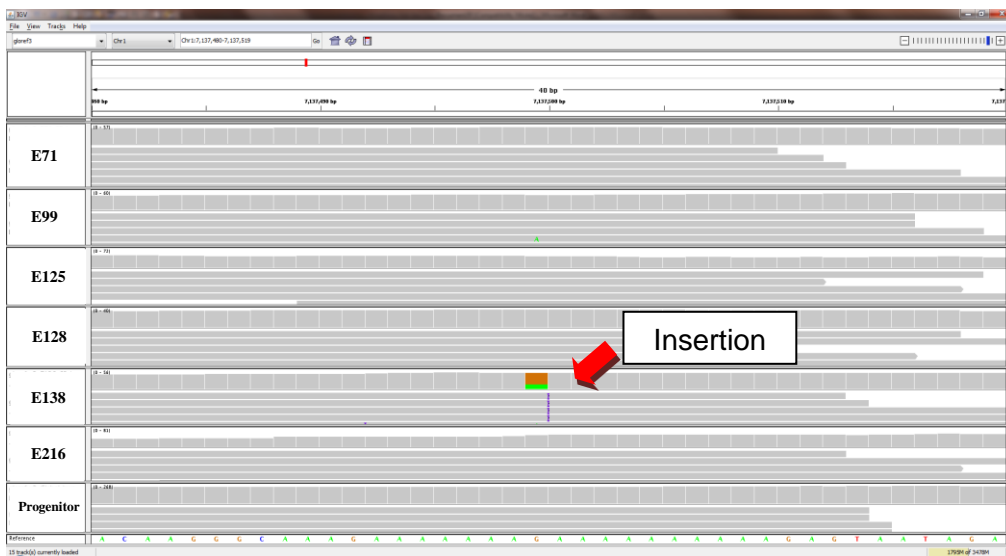
A



B



C



Supplemental Figure 4. Integrated Genome Viewer (IGV) screenshots of Illumina sequencing data of six FN M₃ irradiated mutants shown along with the progenitor sequencing reads. All sequencing data was aligned to the progenitor reference genome. (A) a single base substitution (SBS; C:G to A: T) that is detected only in the E71 line (Chr2:17,438,544), (B) a 17 bp deletion detected only in the E125 line (Chr5:3,727,272) and (C) a 1 bp insertion (adenine) detected only in the E138 line (Chr1:7,137,500). Bases that match the reference genome are grey and base substitutions are shown in other colors.