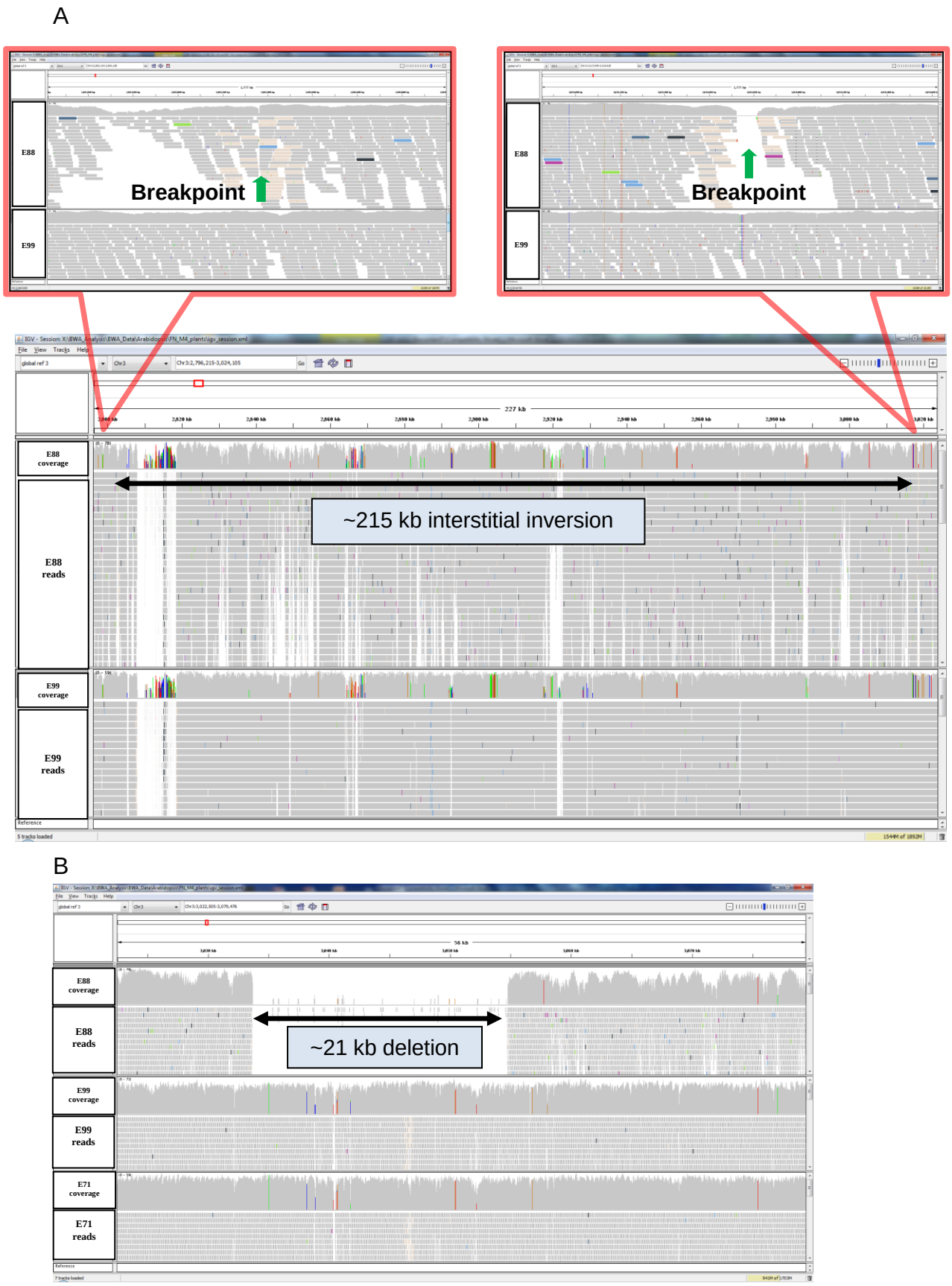

Supplemental Figure 3. IGV screenshots of Illumina sequencing datasets of FN-induced mutations observed in an M_3 irradiation mutant E88. All sequencing data was

aligned to the progenitor reference genome. (A) a ~215 kb interstitial inversion detected only in the E88 line (Chr3:2,803,361 – 3,018,820) with zoomed in regions showing the breakpoint sites (green arrows) versus E99, and (B) a ~21 kb deletion that is detected only in the E88 line versus E99 and E71 (Chr3:3,033,732 – 3,054,790). As a consequence of the inversion in E88 (see Fig. 3A), paired-end Illumina reads flanking the DNA breakpoints aligned 215 kb apart on the progenitor reference instead of the expected Illumina library size of ~300 bp and these reads are shown in light brown instead of the normally aligned gray reads (observable in the two zoomed-in views). Bases that match the reference genome are gray and base substitutions are shown in other colors.