

In-gene IS insertion positions (*D. radiodurans*)

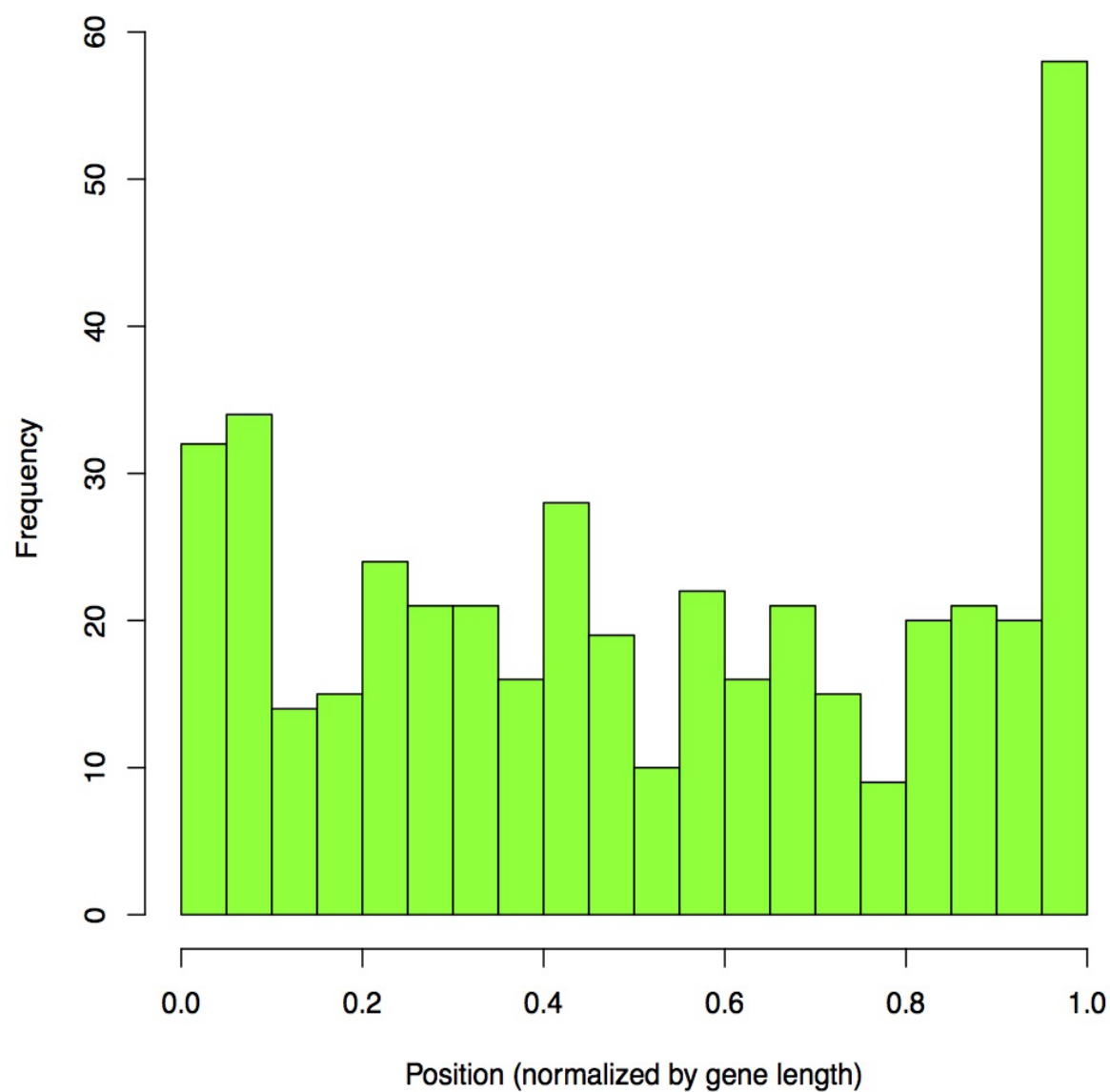


Figure S2. In-gene IS insertion positions from wild-type lines. For each in-gene insertion recovered in wild-type lines, relative distance from 5' end of gene is calculated by dividing the length of the gene. Histogram of relative positions for all in-gene insertions are shown with bin size of 0.05.