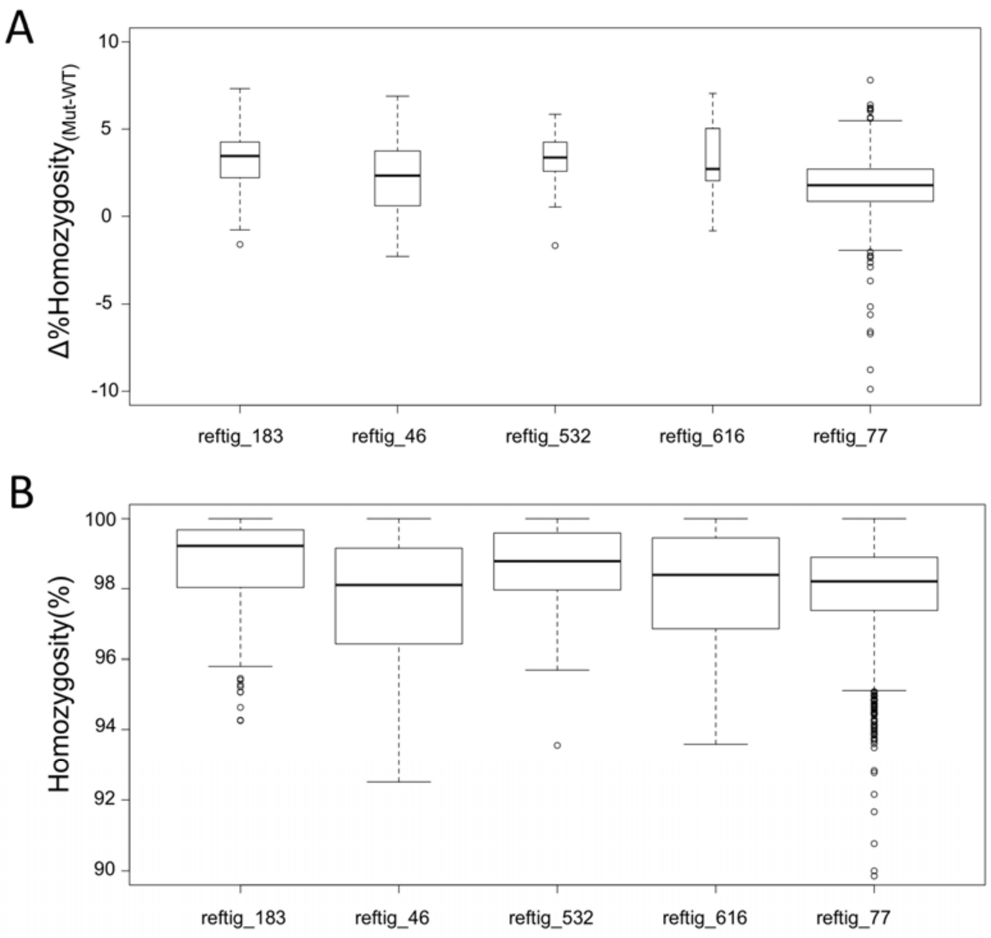

Figure S4 Homozygosity mapping analysis for *bugeye.* **A)** Box-whisker plot of Δhomozygosity values for each candidate high value reftig from Figure 2B. Δhomozygosity values were calculated for 1 Kb windows across each reftig. Width of boxplots depicts amount of data points for each reftig. Solid lines indicate median values, and whiskers indicate extreme values of reftig. Reftig 183 had the highest median Δhomozygosity value (3.46%). **B)** Box-whisker plot of homozygosity values for the candidate reftigs (mutant sample only). Plots were done as above for panel A.