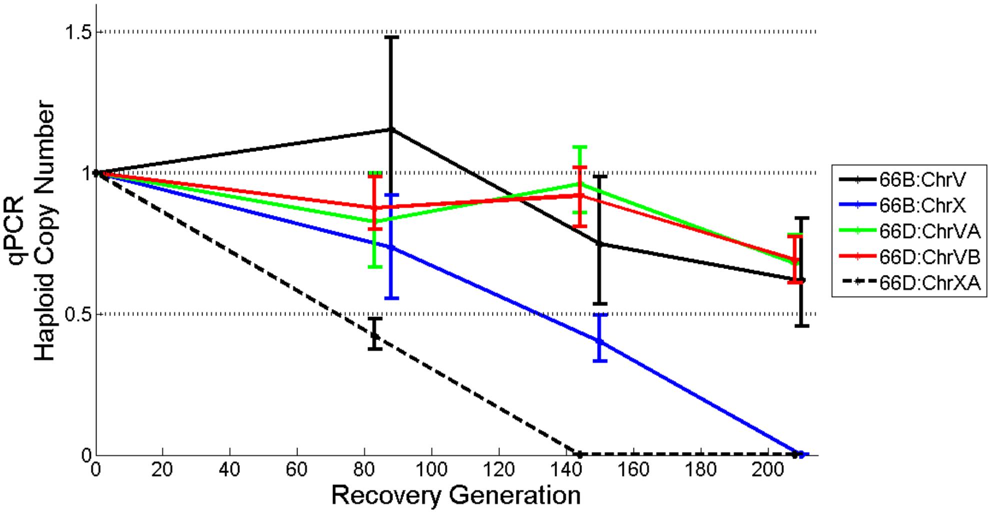
Additional File 10: Suppl Figure S8



Supplemental Figure S8. Copy-number decreases for five unique deletion events in two adaptive recovery populations (66B, and 66D) that lack overlap in their deletion spans. The average copy-number per haploid genome was calculated from qPCR results and is indicated on the vertical axis. The generation from which the copy-number was estimated is indicated on the horizontal axis. The deletions have reached fixation when the average copy-number has reached 0.