



Figure S3 Sequence view at the region with the top candidate SNP. Sequence reads from the mutant pool and the non-mutant pool were viewed along the reference sequences with IGV software (<http://www.broadinstitute.org/igv/>). Non-reference alleles are indicated by green. All eight reads in the mutant pool has a non-reference base 'A' while all four reads in the non-mutant pool has the reference base of 'T'.