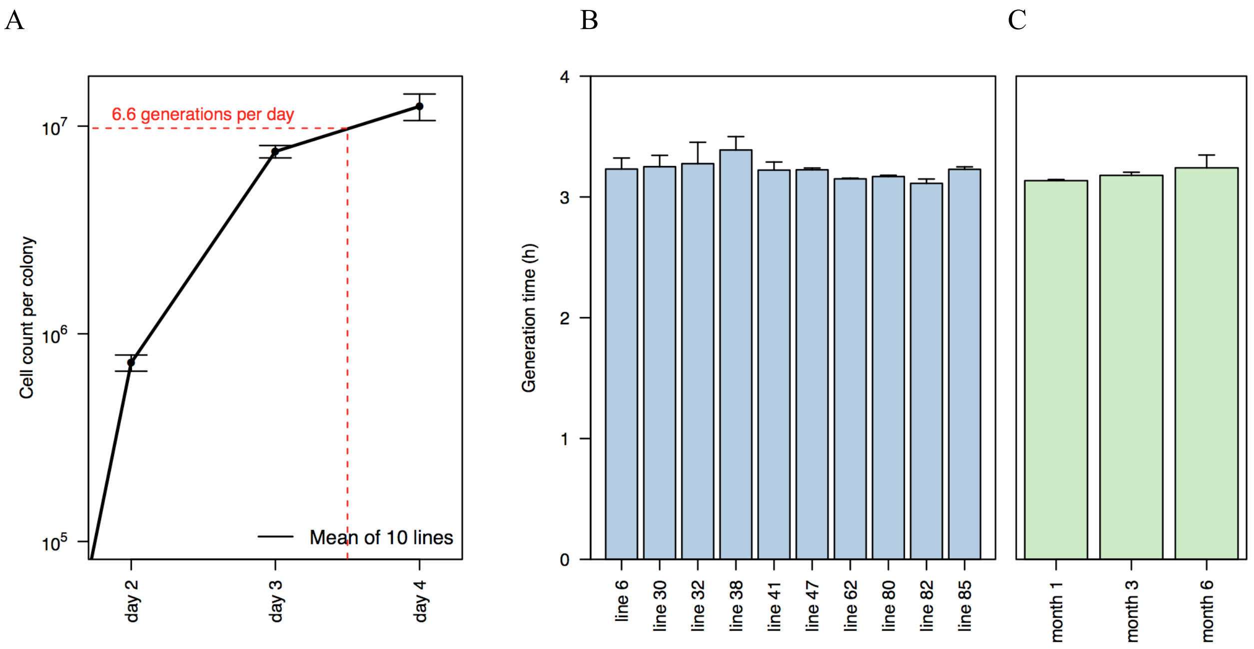

Fig. S1. Generation time estimates of MA lines on YES media plates at 32°C. A. Cell count estimates on day 2, 3 and 4 post-streaking from 10/96 random MA lines. On average, there was 23.2 ± 0.22 (SD) generations per 3.5 days cycle. **B**. Generation time estimate (from day 3 cell count) for 10 random MA lines. **C**. Average day 3 generation time for 10 lines after 1, 3 and 6 months of MA. Error bars are SE.

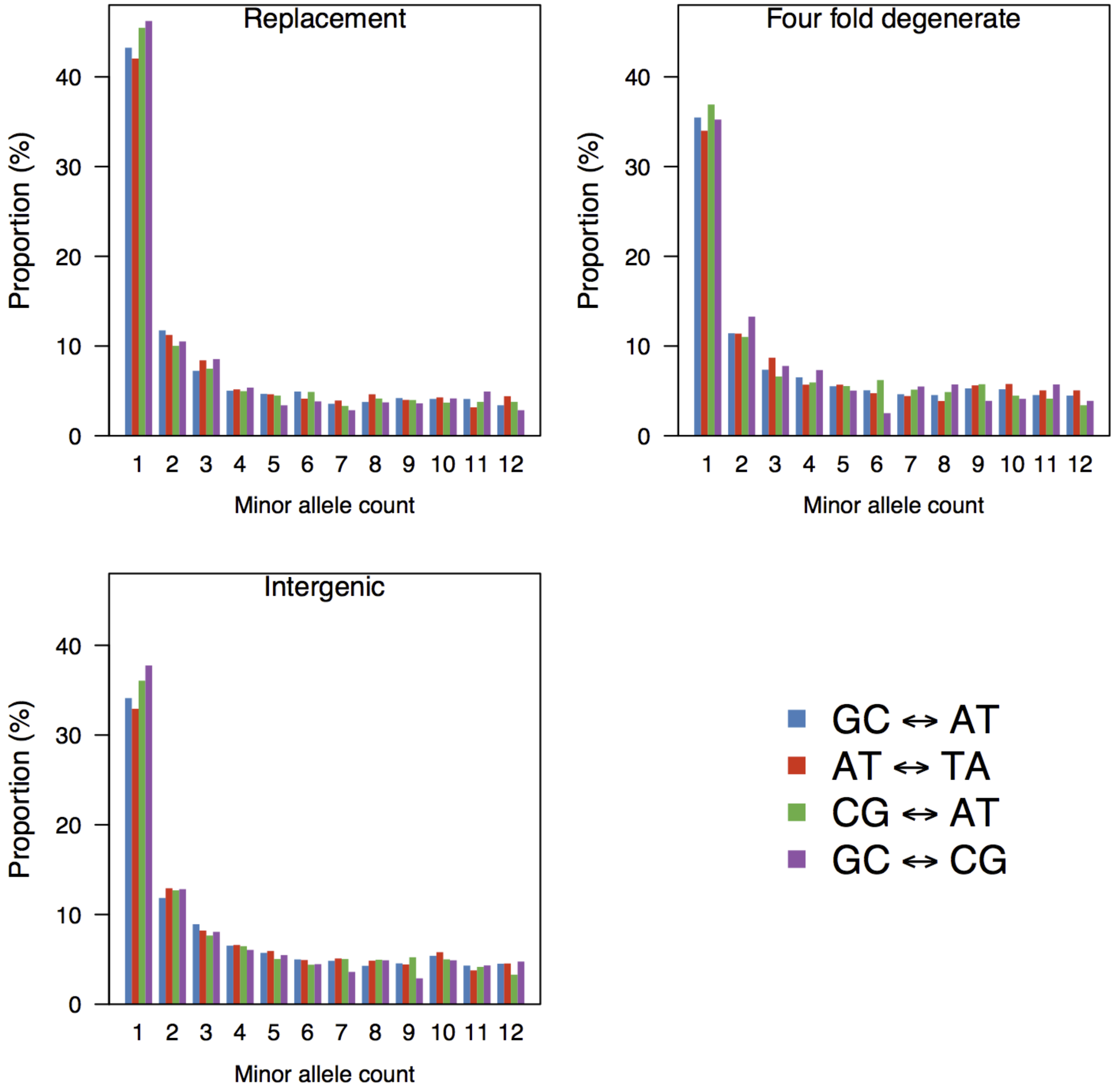

Fig. S2. The minor allele count (out of 25 lines) for SNPs in each substitution class at replacement, four fold and intergenic sites.

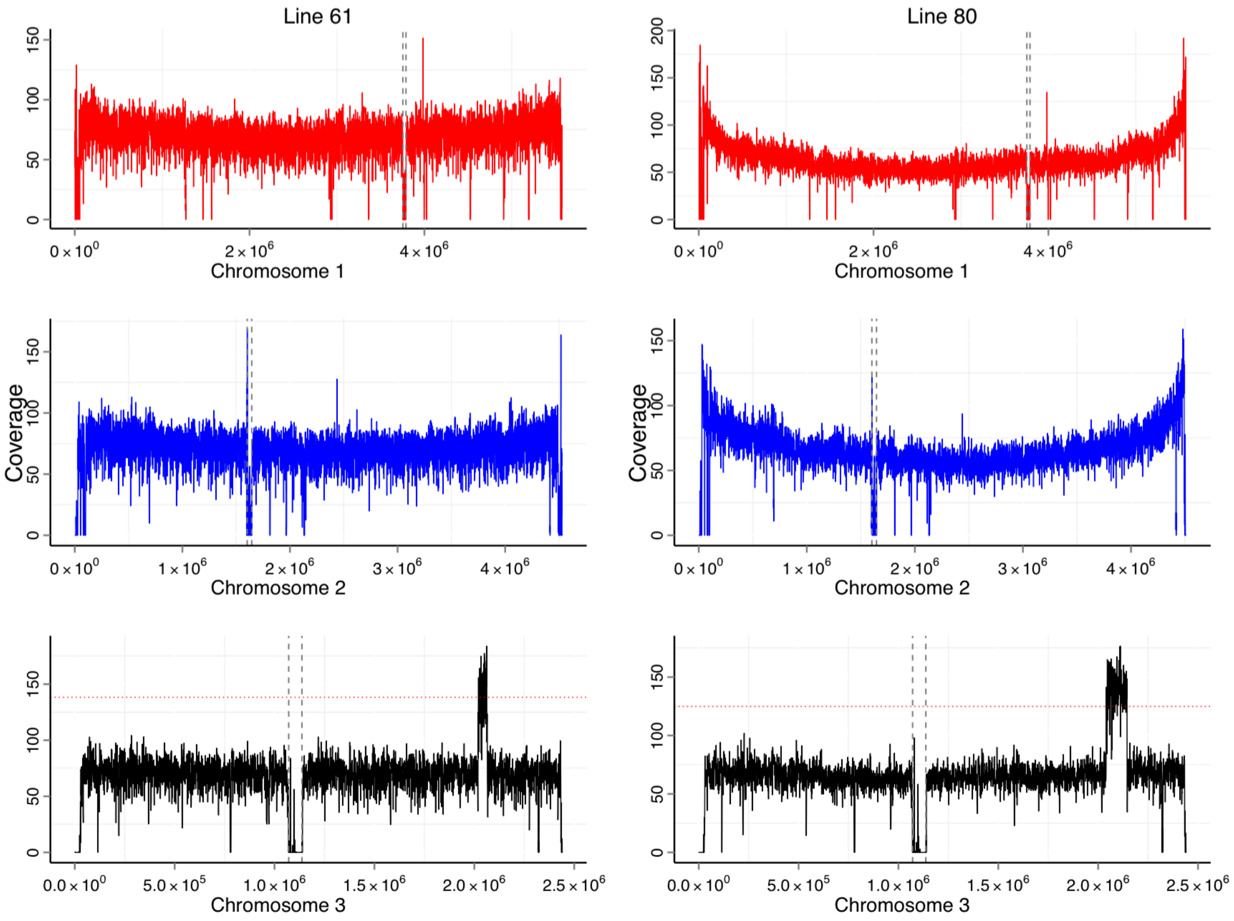

Fig. S3. Average read coverage in 1kb windows across MA line 61 and 80. Two duplications are clearly visible on chromosome 3 as regions of elevated coverage (dotted red lines represent 2 times the chromosomal median coverage). The start and end of both duplications occur within large repeat elements. Many other short regions of high or low coverage were observed but were common to most or all lines. Centromeric regions are indicated by grey dotted lines.

Tables S1-S4

Available for download as Excel files at www.genetics.org/lookup/suppl/doi:10.1534/genetics.115.177329/-/DC1

Table S1. Mutation stat per MA line (excluding flocculation genes)

Table S2. Details and functional context of all mutations

Table S3. Recalculation of polymorphism levels in the natural population

Table S4. Details and functional context of all indels (including repetitive context)