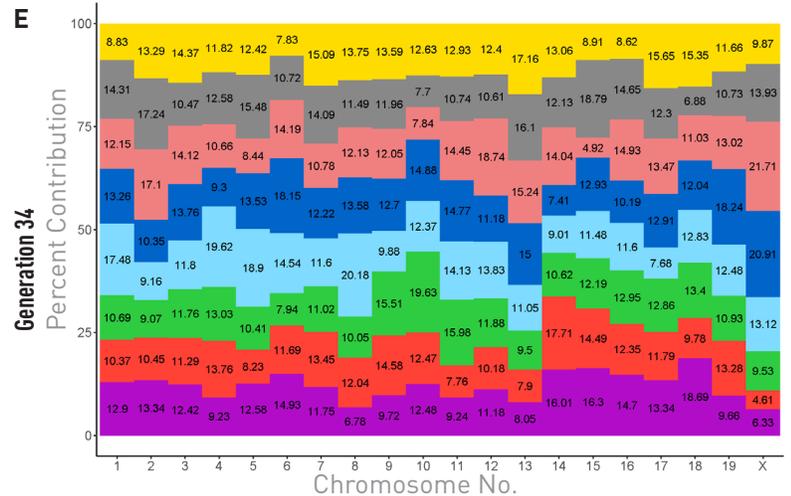
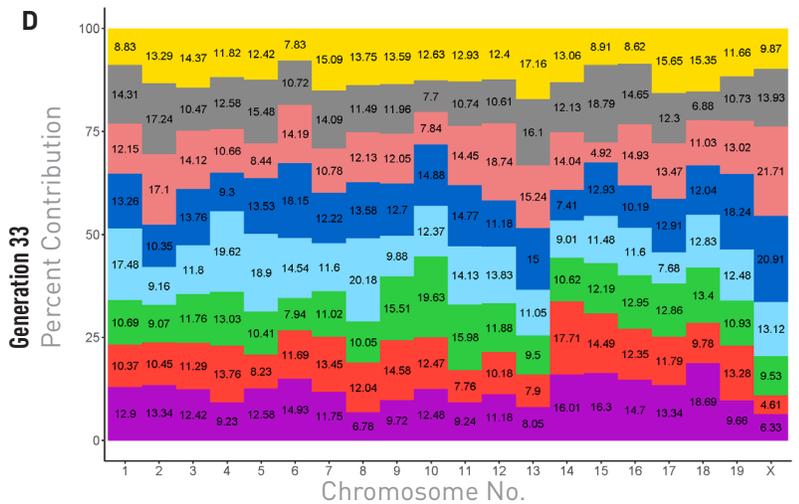
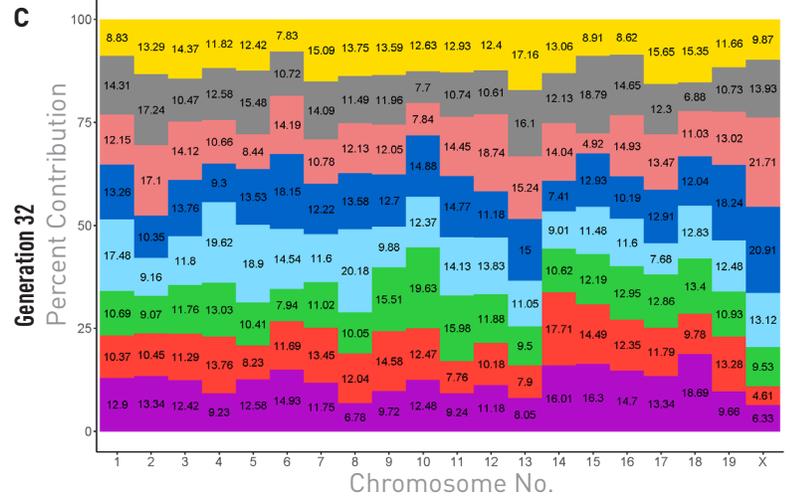
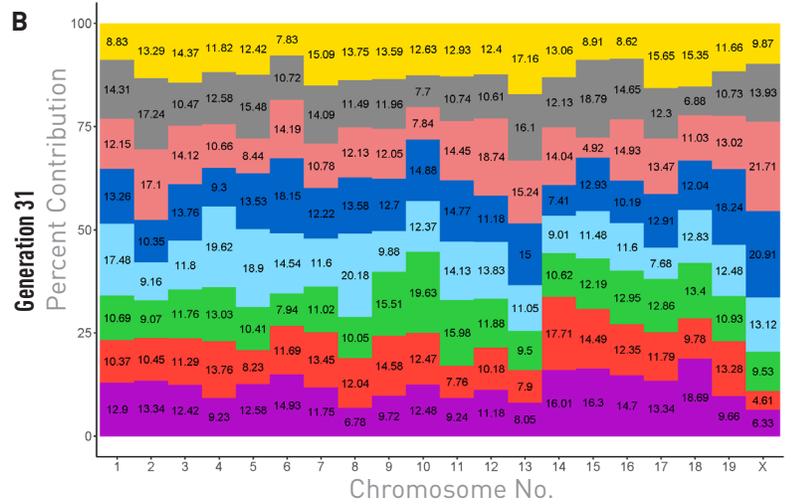
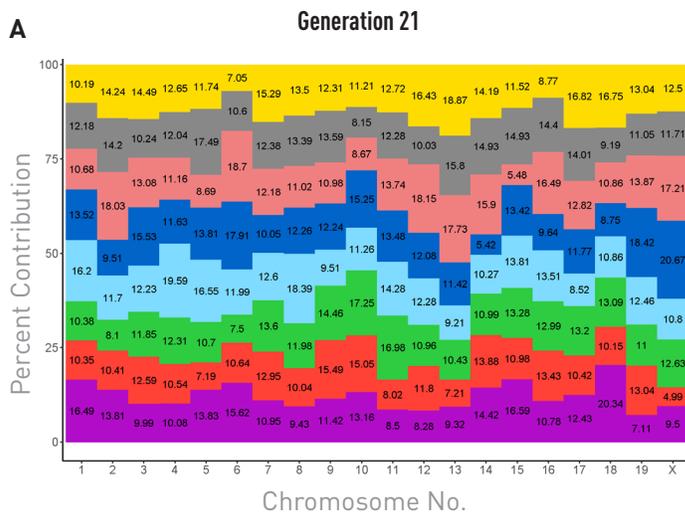
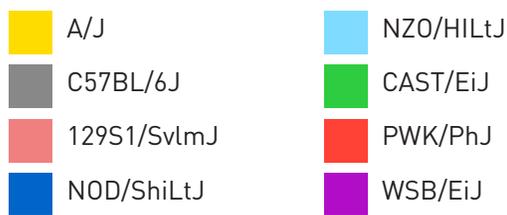


# 2021 J:DO Genetic Diversity Report

**Figure 1. The Jackson Laboratory's breeding practices are effectively maintaining genetic diversity in the Diversity Outbred population.**

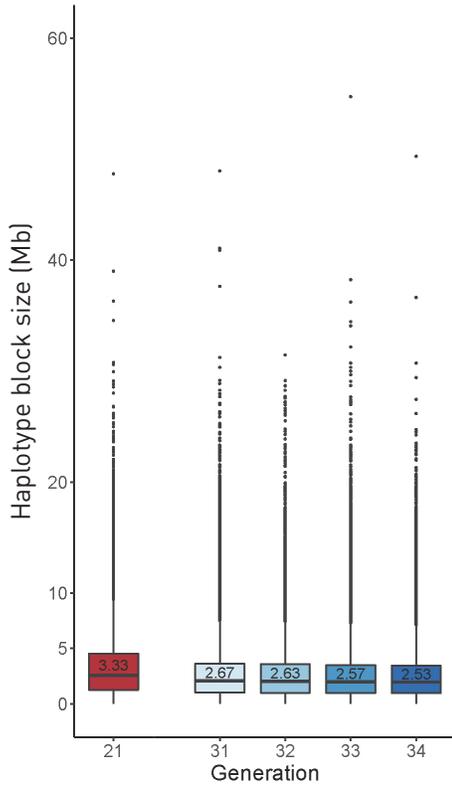
Stacked bar plots represent percent founder strain contribution per chromosome for J:DO generations (B) G31, (C) G32, (D) G33 and (E) G34. Founder contributions in these generations are generally consistent with distributions observed in (A) G21, the assumed benchmark for the population, and not significantly different from the expected 12.5% contribution of each founder within the population ( $\chi^2$ ,  $p > 0.99$ ). Additionally, we were able to confirm that the WSB/EiJ locus under meiotic drive on Chromosome 2 (Chesler *et al.* (2016) G3) remains absent in more recent generations (data not shown). See Figure 2 for  $n$  evaluated in each generation. J:DO GigaMUGA data were donated by Center for Systems Neurogenetics of Addiction (NIH P50 DA039841) and analyzed by JAX Computational Sciences using a Hidden Markov Model to estimate the probability of 36 diplotype states at each marker for each mouse. All analyses were conducted in R and with R/qt12 package 14.



**Figure 2. Sex chromosome nondisjunction rates are low.** Sex chromosome calls were determined by SNP probe microarray hybridization intensities on the X and Y chromosome. No XXY males were detected.

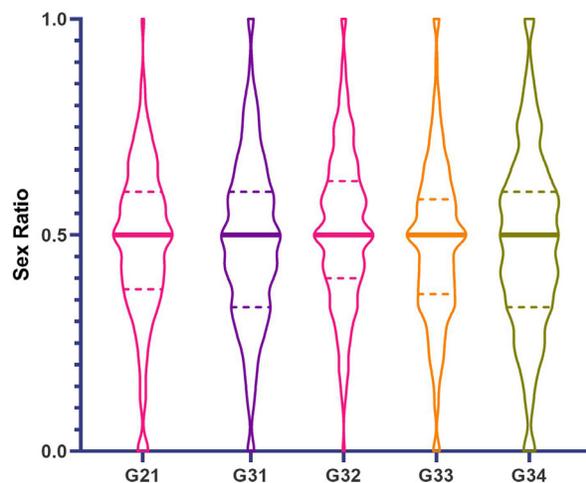
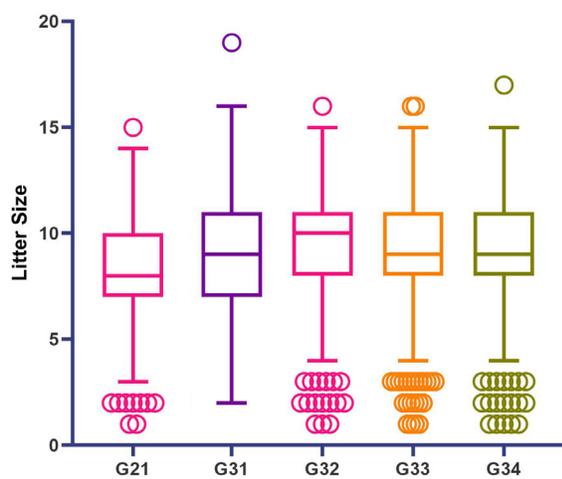
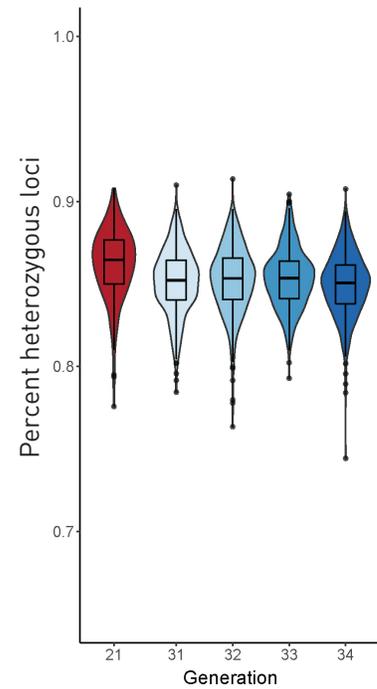
Overall, N = 2719 Female, N = 1418 <sup>†</sup> Male, N = 1294 <sup>†</sup> XO, N=7 <sup>†</sup>				
Generation				
21	148 (100%)	71 (48%)	74 (50%)	3 (2%)
31	418 (100%)	210 (50%)	206 (49%)	2 (0.5%)
32	317 (100%)	163 (51%)	153 (48%)	1 (0.3%)
33	450 (100%)	227 (50%)	223 (50%)	0 (0%)
34	306 (100%)	199 (65%)	107 (35%)	0 (0%)

<sup>†</sup>Statistics presented: n(%)



**Figure 3. Haplotype block size decreases with each generation, increasing genetic mapping resolution.** Box plots represent median haplotype block size and interquartile range as calculated by estimated founder identify breakpoints.

**Figure 4. Individual and overall population heterozygosity remain high.** Each data point represents and individual mouse's genomic heterozygosity value. Box plots represent median and interquartile range. Approximately 12.5% of loci should be homozygous in any individual J:DO mouse. While there has been a decrease in heterozygosity since G21 (Students T-test,  $p < 0.01$ ), the magnitude of the difference is small.



**Figure 4. Breeding statistics per generation.** The number and sex of pups per litter is recorded. (A) There has been a significant increase in litter size since G21 (Students T-test,  $p < 0.01$ ). (B) Sex ratio is calculated as the number of females divided by the total number of pups. While some litters can have a skewed sex ratio, there is no significant difference in litter sex ratios since G21 (Students T-test,  $p > 0.91$ )