



Figure S3 Estimation of effective population size. N_e is estimated for each replicate and each chromosome arm, using 4 different models. The lowest estimate (purple) uses all SNPs, but is downwardly biased because it does not account for SNPs that are under positive selection during lab adaptation. Trimming 20% of the SNPs that diverge the most in allele frequency (green, corresponding to the upper limit of the estimated fraction in LD with sites under selection) increases the estimate on average from N_e -50 to N_e -75. Further adjustment for sampling error in frequency estimation from the sequence data increases the estimate of N_e up to a further 25%. Trimming 50% of the SNPs results in N_e -150, but is almost certainly an over-estimate since it reduces the variance estimate. Note that the estimates on 3R are lower, likely reflecting the increased selection on that chromosome arm possibly due to the presence of a common inversion - IN(3R)Payne, while those for the X are elevated and need to be down-weighted to account for the smaller number of X chromosomes in the population. We conclude that the effective population size is between 75 and 100 in all replicates, consistent with the experimental design in which 12 bottles with up to 15 flies of each sex were selected each generation.