



Figure S2. The $-\log_{10}(\text{p-values})$ for leading factors in simulated GWASs using the DGRP lines. Above are histograms of the $-\log_{10}(\text{p-value})$ for the QTL of largest effect, for random traits generated based on the DGRP SNPs, 100 randomly chosen QTL loci with exponentially distributed effect sizes, and the specified heritability value. We assume a GWAS is conducted using the DGRP founder lines with 20 replicate flies per line and using a standard ANOVA for computing p-values. Shown are histograms for random traits with A) $h^2 = 0.2$, B) $h^2 = 0.5$, and C) $h^2 = 0.8$ (100 random trait simulations each). (For smaller numbers of QTLs [not shown], the leading factor $-\log_{10}(\text{p-value})$'s are larger than those shown here). The results show that under the assumed genetic architecture used in this study the leading factor should be readily detectable by a GWAS unless heritability is low. In practical cases, where a leading effect is not detected in a GWAS for a trait with modest or high heritability, it may be because the leading effect is smaller and/or at lower frequency than the simulated values used here. Together with Supplementary Figure S1 these results highlight that for some traits the results of this simulation study may not be applicable.