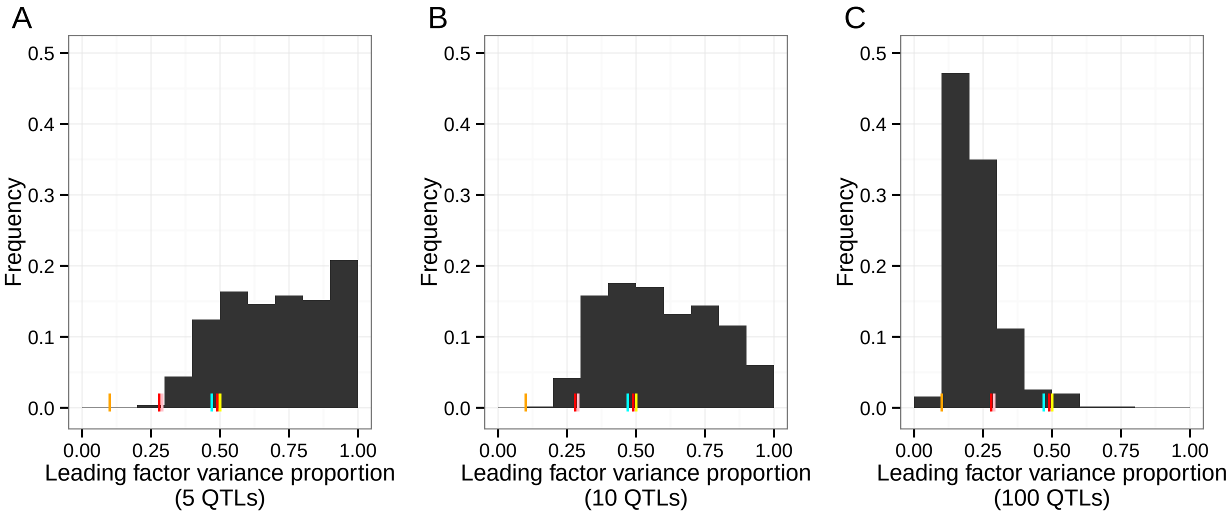

Figure S1. Proportion of variance explained by leading factor. Above are histograms of the proportion of variance explained by the QTL of largest effect, for random traits generated based on the DGRP SNPs and exponentially distributed effect sizes. Shown are histograms for random traits with A) 5 QTLs, B) 10 QTLs, and C) 100 QTLs (500 random trait simulations each). For comparison, we have included colored segments to indicate the proportion of variance explained by the leading factor of several quantitative traits as reported by selected empirical studies. [*Adh* activity, 2 experimental lines (.49, .28, red) (King *et al.*, 2012); susceptibility to viral infection, Drosophila C virus (.47, cyan), Sigma virus (.29, pink) (Magwire *et al.*, 2012); larval nicotine resistance (.50, yellow) (Marriage *et al.*, 2014); bristle number (.1, orange) (Mackay and Lyman, 2005)]. Note that the calculation of variance proportion assumes that QTLs segregate independently in the population (no linkage disequilibrium), which is generally not true for natural populations nor for the simulated populations.