A powerful new quantitative genetics platform combining *Caenorhabditis elegans* high-throughput fitness assays with a large collection of recombinant strains


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Figure S1A Length (TOF) and optical density (EXT) for bubbles (red) and nematodes (black) are plotted. Bubbles have lengths and optical densities similar to nematodes. A simple line excluding the majority of bubble data can not be used to effectively separate bubbles from nematodes. The data obtained from a pure bubble data set and a pure nematode data set were used to train a support vector machine (SVM) to differentiate bubbles from nematodes. The red fluorescence measurements can be used to effectively separate these two mixed data classes.
Figure S1B A receiver operating characteristic (ROC) curve for the performance of the SVM is plotted as false positive rate (FPR or type I error, sensitivity) by true positive rate (TPR or specificity). The inset shows the same data but for a smaller range to emphasize the accuracy of the prediction model.
A bar chart of the mean embryonic lethalities among offspring of crosses using the N2, QX1430, and Hawaii (CB4856) strains is shown. When N2-provided PEEL-1 is present without N2-provided ZEEL-1, increased embryonic lethality is observed. QX1430-provided PEEL-1 without N2- or QX1430-provided ZEEL-1 still has low levels of embryonic lethality higher than background, suggesting that the transposon insertion does not completely eliminate peel-1 function.

Figure S2
Figure S3A The frequency of the N2 allele for each SNP in the collection of 359 N2xCB4856 RIAILs is plotted by the genomic position. Each chromosome is in a separate box. The dotted red line denotes a 50% allele frequency. The tick marks on the x-axis denote every five Mb.
Figure S3B The genotypes of each of the 359 N2xCB4856 RIAILs are plotted as orange (N2) or blue (Hawaii).
Figure S4 Intra-assay correlation (rho=0.47) and inter-assay correlation (rho=0.51) are much better using the high-throughput fecundity assays than using standard plate-based fecundity assays (rho=0.08).
Figure S5A Correlations among the brood (n) and 24 size traits for control traits are shown. Size summary statistic traits are grouped from smallest to largest. Normalized optical density (norm.EXT) is shown last. Fecundity is not correlated well with any other summary statistic. Small size traits are more correlated with each other than they are with large size traits, and the reciprocal is true. Normalized optical density is weakly correlated with the equivalent optical density trait.
Figure S5B Correlations among the brood (n) and 24 size traits in paraquat conditions are shown. Size summary statistic traits are grouped from smallest to largest. Normalized optical density (norm.EXT) is shown last. Fecundity is not correlated well with any other summary statistic. Small size traits are more correlated with each other than they are with large size traits, and the reciprocal is true. Normalized optical density is weakly correlated with the equivalent optical density trait.
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**Figure S6** The locations of every QTL confidence interval for all significant mappings are shown. The tick marks on the x-axis denote every five Mb. Each chromosome is in its own box labeled on top.
Figure S7 The locations of every identified QTL are shown binned every 100 kb across the genome. On top, QTL identified in control conditions are shown. Enrichment of QTL is observed in the center of chromosome IV, the left of chromosome V, and the right of the X chromosome. On bottom, QTL identified from the residuals after regressing control conditions from paraquat conditions are shown. QTL specific to paraquat growth conditions are observed on chromosomes IV and V.
**Figure S8** A histogram of the percentages of phentoypic variance explained by each QTL is plotted. The dotted line denotes 4% variance explained or where 80% statistical power exists to detect QTL using this RIAIL strain collection.
Files S1-S4

Available for download at http://www.g3journal.org/lookup/suppl/doi:10.1534/g3.115.017178/-/DC1

File S1  This file contains the genotype data for each of the new N2xCB4856 RIL strains. Values of 1 are N2, and values of 2 are CB4856.

File S2  This file contains the processed phenotype data after pruning outlier data. These phenotype data were used for linkage mapping.

File S3  This file contains summary data for every significant QTL detected.

File S4  This file contains plots of all QTL detected.