Supplemental Figures

Natural variation in fecundity is correlated with species-wide levels of divergence in *Caenorhabditis elegans*

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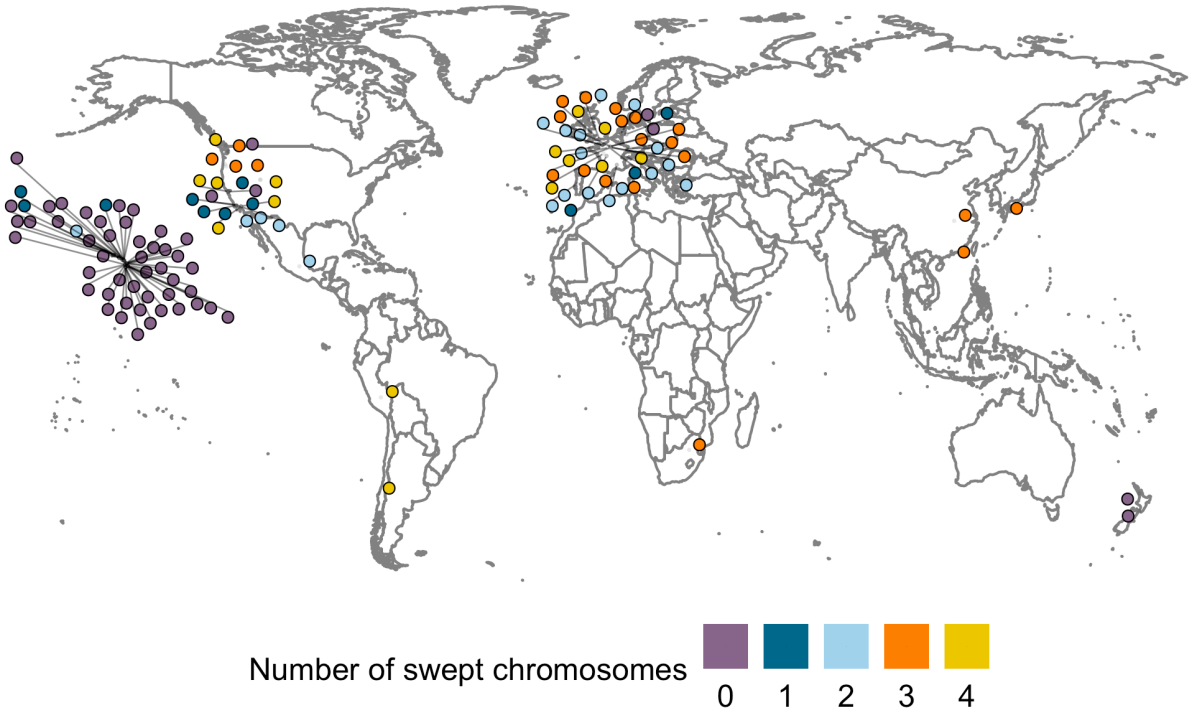

Figure S1 Global distribution of the 121 wild *C. elegans* strains used in this study. Each point corresponds to the isolation location and is colored by the number of swept chromosomes.

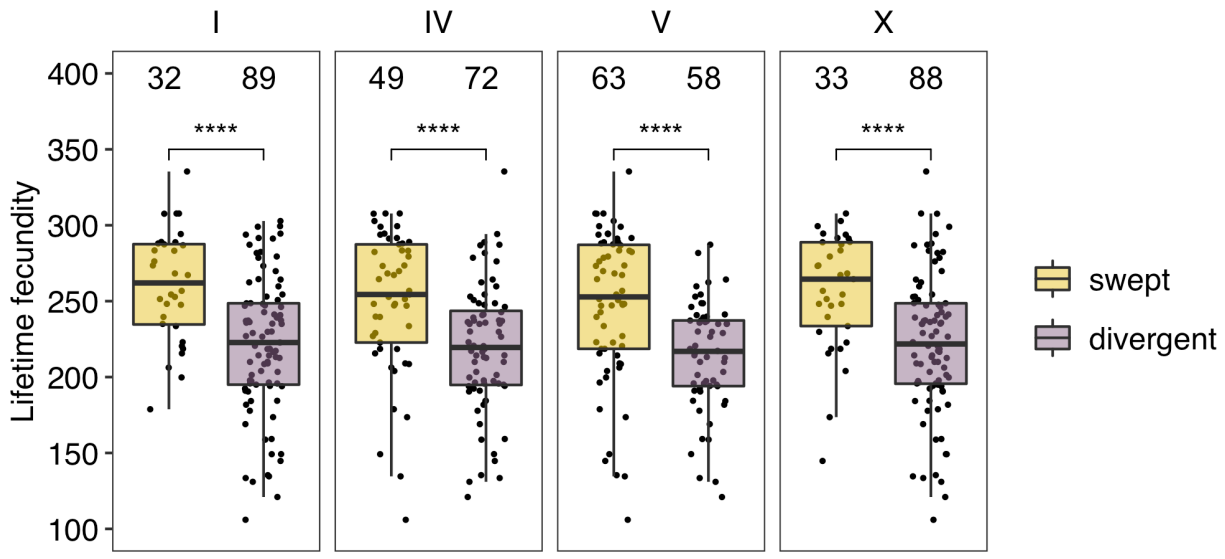

Figure S2 Comparisons of *C. elegans* lifetime fecundity between swept groups (gold) and divergent groups (purple) classified by single chromosome are shown as Tukey box plots. Only swept chromosomes (I, IV, V, and X) are shown. For each chromosome (panel), strains with swept chromosomes were assigned to swept groups; strains with divergent chromosomes were assigned to divergent groups. Statistical significance was calculated using the Wilcoxon test, with adjusted p-values 3.7E-5, 5.5E-5, 6.5E-6, and 6.6E-5 in the comparisons by chromosomes I, IV, V, and X, respectively. Significance of each comparison is shown above each comparison pair (****: adjusted p-value ≤ 0.0001). The number of strains in each group is indicated above significance.

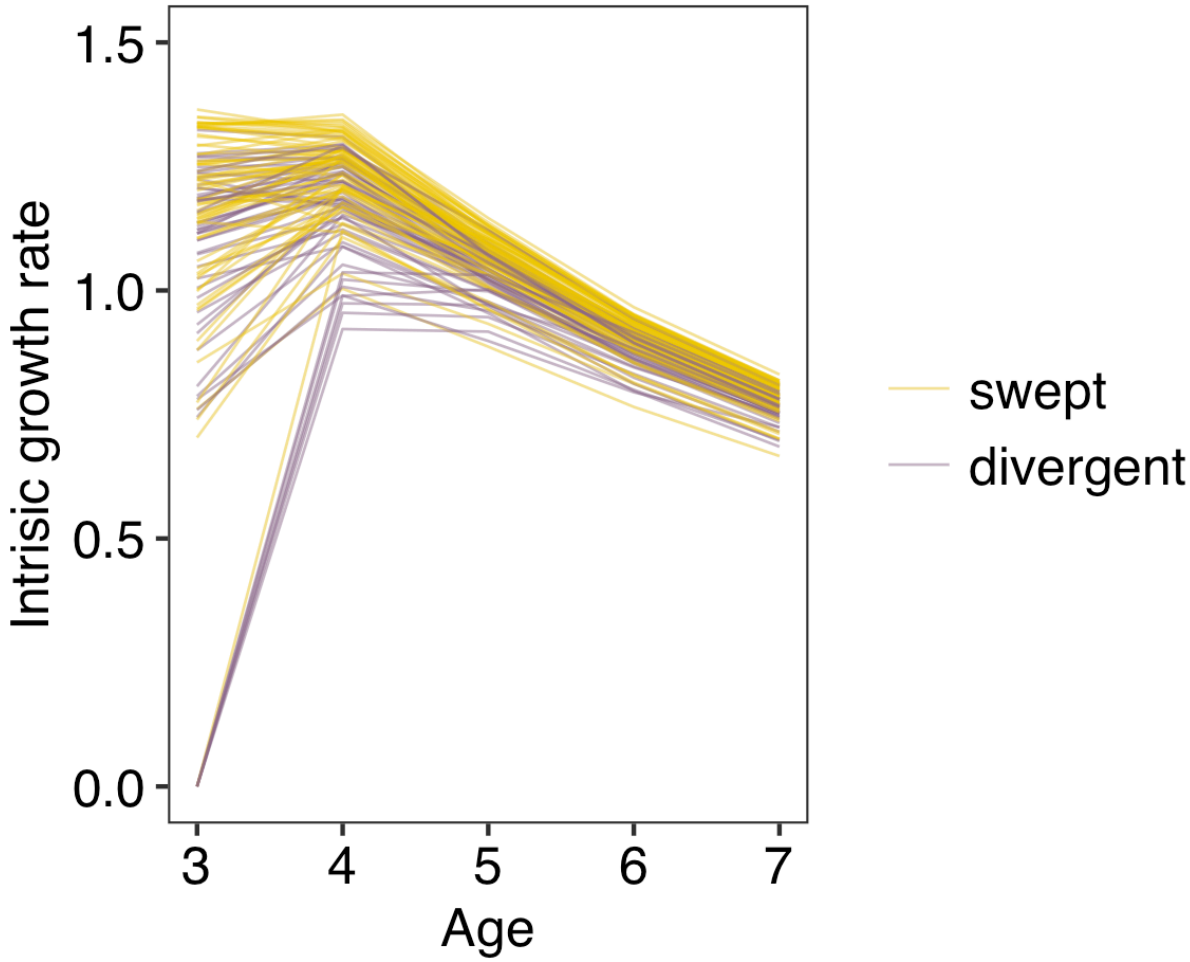

Figure S3 Intrinsic growth rate by age (2 + day of adulthood) of the 121 wild *C. elegans* strains used in this study. Each line corresponds to a strain and is colored gold for swept strains and purple for divergent strains. The maximum intrinsic growth rate is at age 4 (second day of adulthood) for most strains.

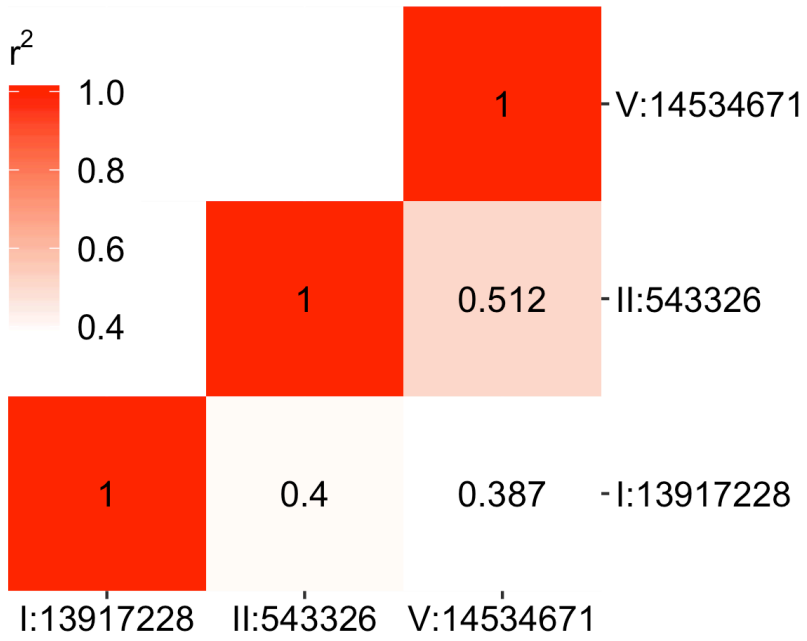

Figure S4 Linkage disequilibrium values of QTL peak markers associated with *C. elegans* lifetime fecundity are shown. Correlations (r^2) between each marker pair are indicated in the tiles and are represented by the tile color.

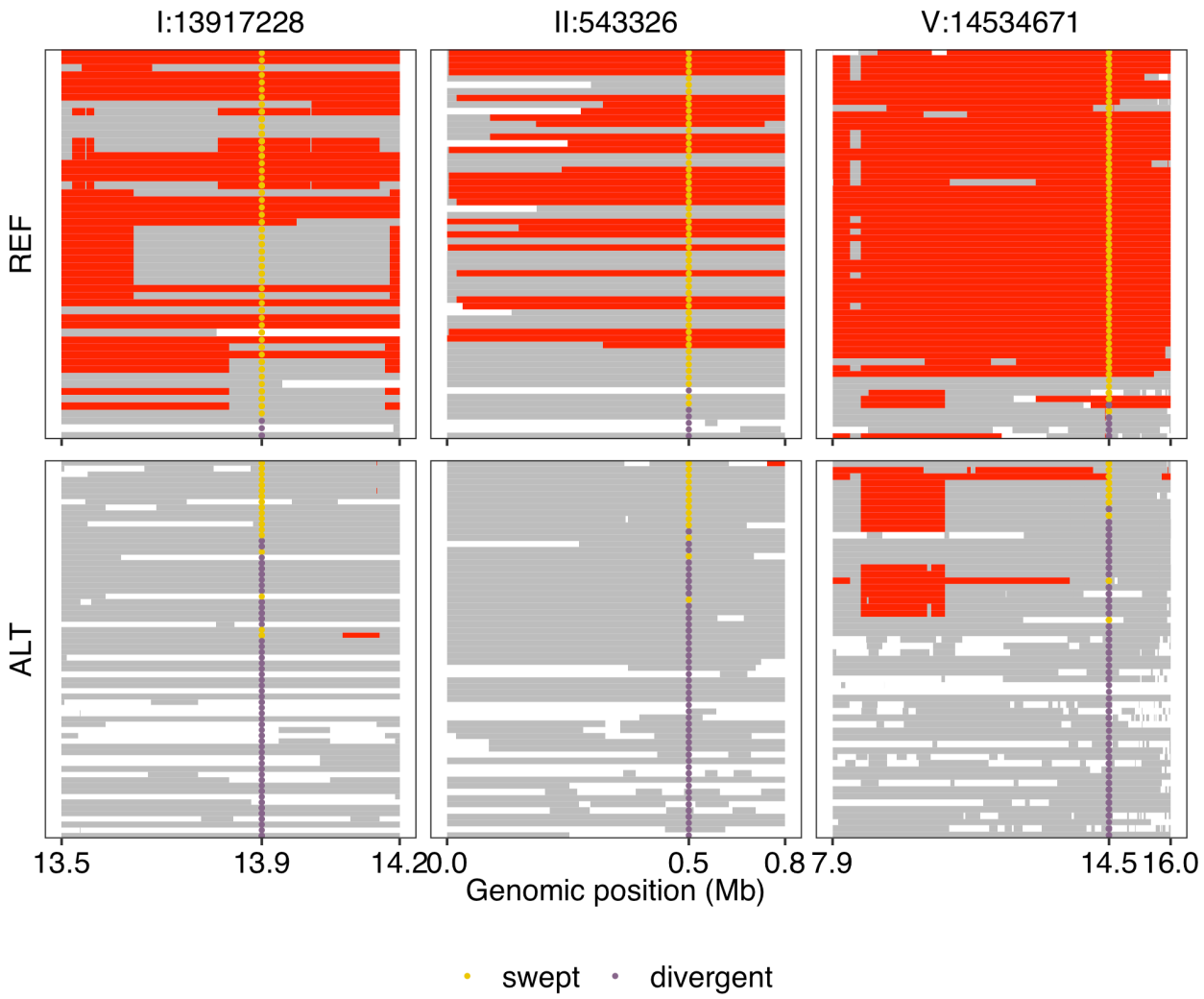

Figure S5 Sharing of haplotypes within QTL associated with lifetime fecundity variation among 121 *C. elegans* strains is shown. Genomic regions of most common, rare, and undetermined haplotypes are colored red, gray, and white, respectively. For each QTL (represented by peak markers on the top), strains were divided into REF (N2 reference alleles) panels or ALT (alternative alleles) panels by their genotypes at the peak markers as in Figure 3B. The genomic positions of each QTL are plotted on the x-axis. In the two panels of each QTL, each row on the y-axis represents one of the 121 strains and is ordered by their relative positions in Figure 1B. Swept strains and divergent strains are indicated as gold dots and purple dots, respectively, at the peak markers.

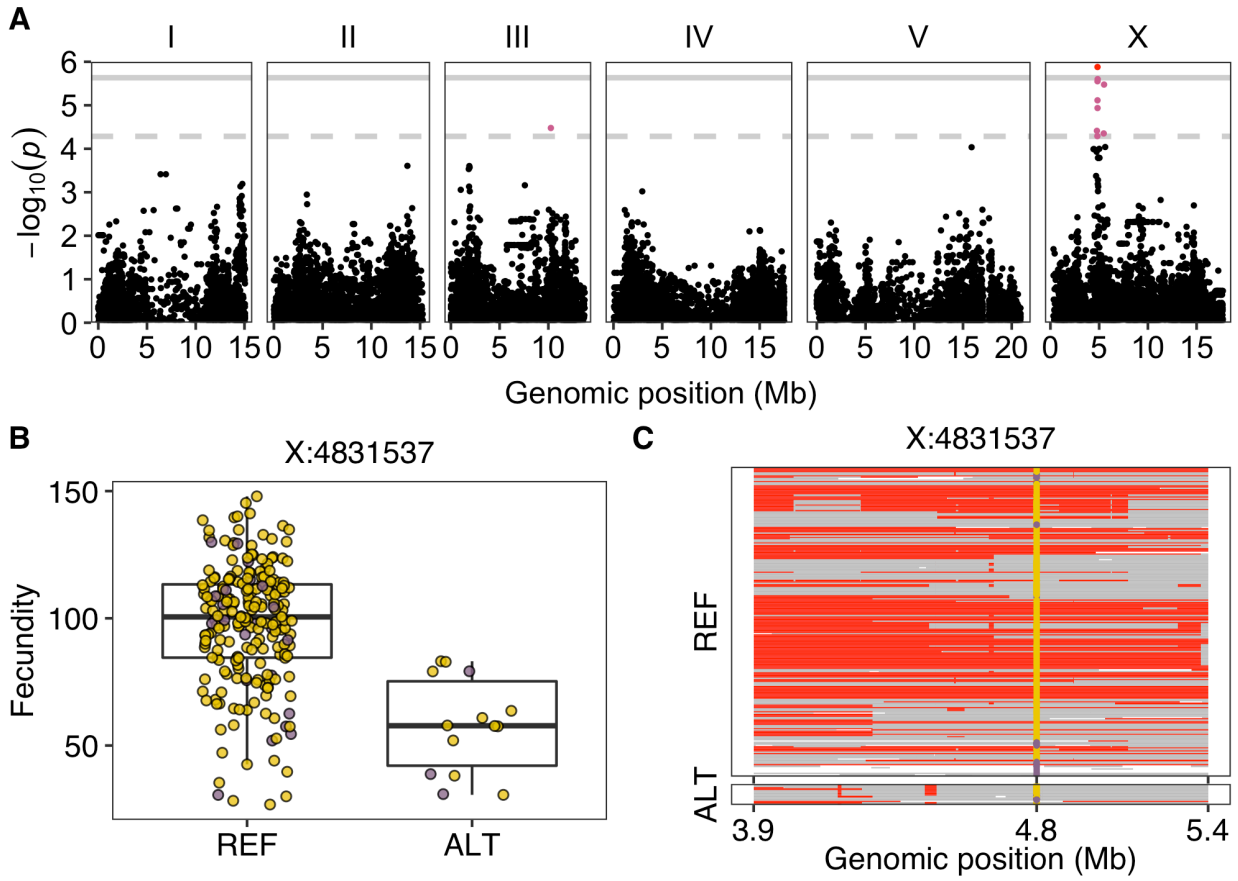

Figure S6 One QTL was identified in GWA mapping of *C. elegans* fecundity variation in 236 strains. (A) Manhattan plot indicating GWA mapping results. Each point represents an SNV that is plotted with its genomic position (x-axis) against its -$\log_{10}$(p) value (y-axis) in mapping. SNVs that pass the genome-wide EIGEN threshold (the dotted gray horizontal line) and the genome-wide Bonferroni threshold (the solid gray horizontal line) are colored pink and red, respectively. (B) Tukey box plot showing fecundity (norm.n) between strains with different genotypes at the peak marker position in the QTL. Each point corresponds to a *C. elegans* strain and is colored gold for swept strains and purple for divergent strains. On the x-axis, REF represents strains with the N2 reference allele and ALT represents strains with the alternative allele. (C) Sharing of haplotypes within the QTL is shown. Genomic regions of most common, rare, and undetermined haplotypes are colored red, gray, and white, respectively. Strains were divided into REF (N2 reference alleles) panels or ALT (alternative alleles) panels by their genotypes at the peak markers as in (B). The genomic positions of the QTL are plotted on the x-axis. In the two panels of the QTL, each row

on the y-axis represents one of the 236 strains, ordered by their relative positions in Figure 1B. Swept strains and divergent strains are indicated as gold dots and purple dots, respectively, at the peak markers.

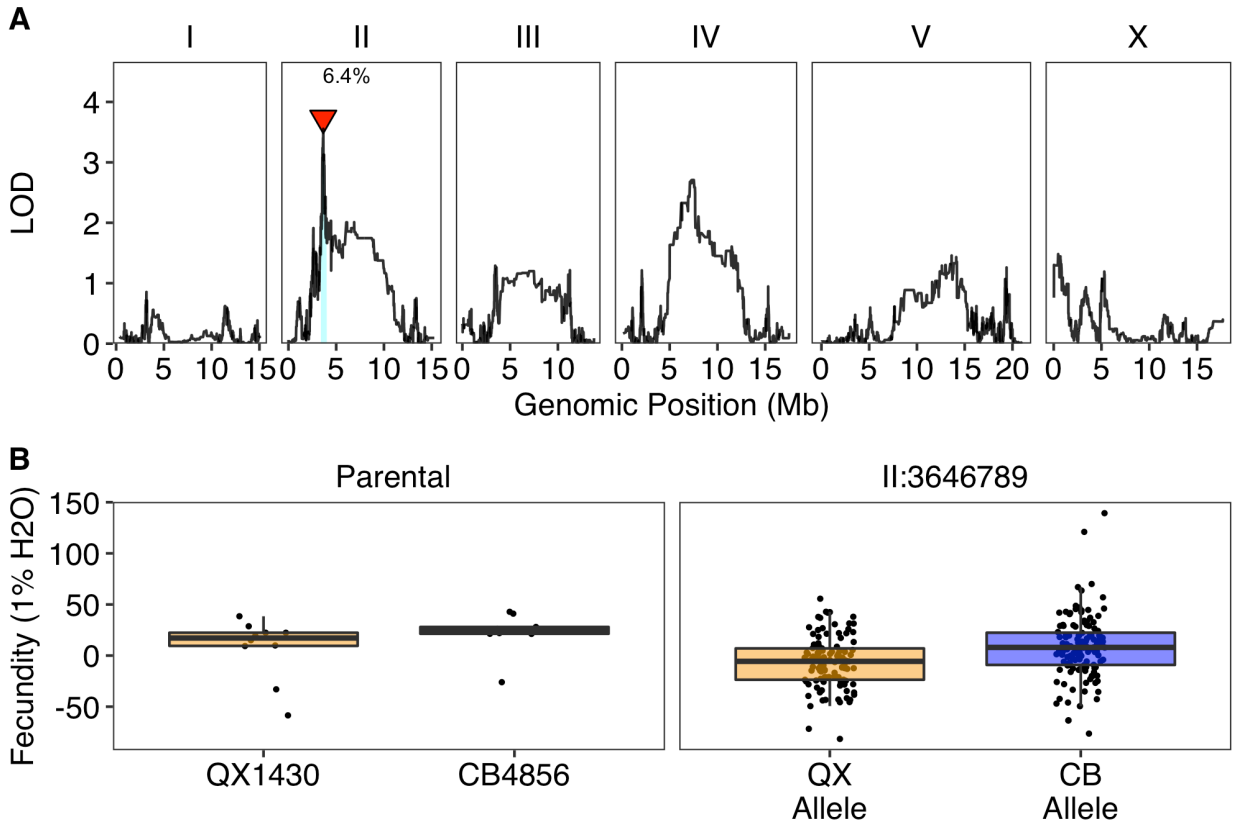

Figure S7 A QTL was identified using linkage mapping of *C. elegans* fecundity (norm.n) in 1% water conditions. (A) Linkage mapping results of *C. elegans* fecundity (norm.n) with RIAILs were shown with genomic position in Mb (x-axis) plotted against the logarithm of the odds (LOD) score (y-axis). The peak marker of the QTL on the left arm of chromosome II is indicated by a red triangle, next to which the percentage of the total phenotypic variance that can be explained by the QTL is shown. The 95% confidence interval of the QTL is shown by a blue rectangle. (B) Fecundity (norm.n) is shown between the parents (QX1430 and CB4856) and between RIAILs split by genotype at the peak marker of the QTL. Each dot in the parental panel represents one of the replicates. Each dot in the QTL panel corresponds to a unique recombinant strain. Strains with the QX1430 allele are colored orange, and strains with the CB4856 allele are colored blue.

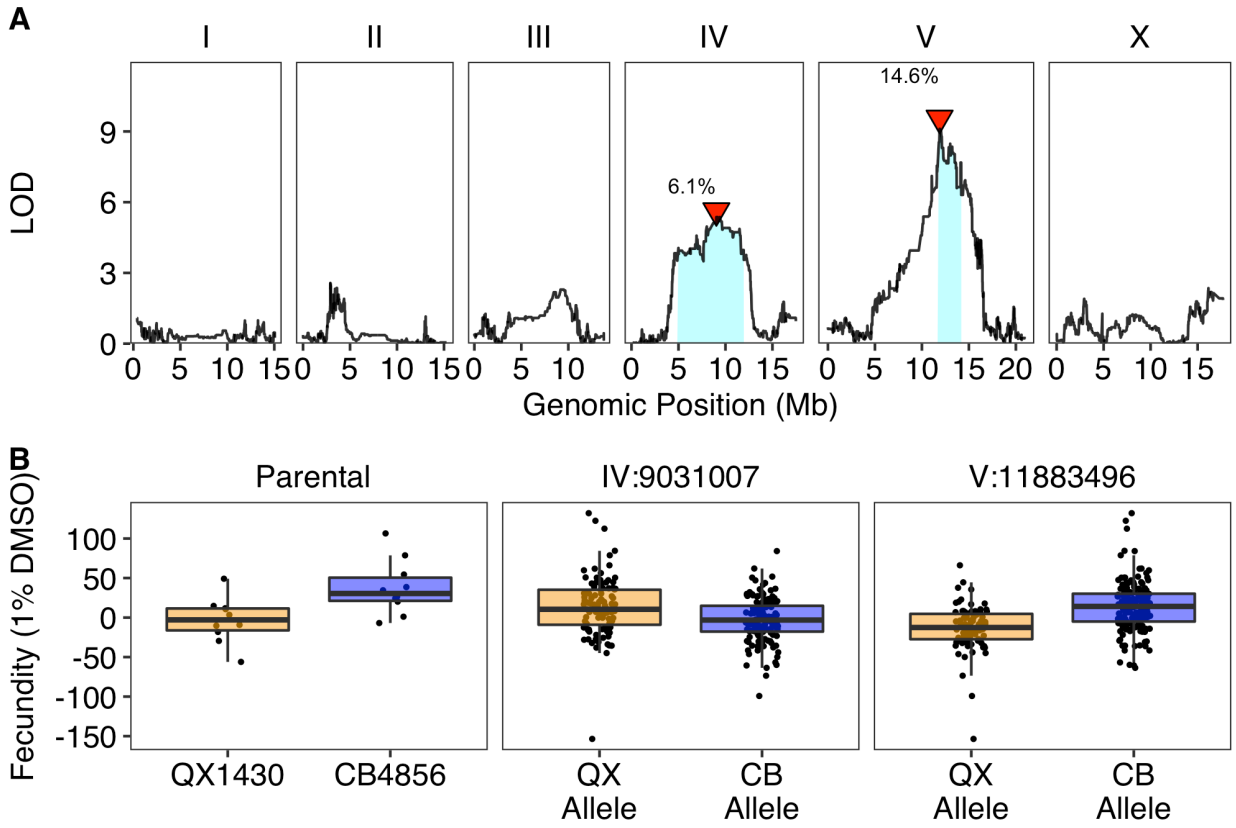

Figure S8 Two QTL were identified using linkage mapping of *C. elegans* fecundity (norm.n) in 1% DMSO conditions. (A) Linkage mapping results of *C. elegans* fecundity (norm.n) with RIAILs were shown with genomic position in Mb (x-axis) plotted against the logarithm of the odds (LOD) score (y-axis). The peak markers of QTL are indicated by red triangles, next to which the percentages of the total phenotypic variance that can be explained by the QTL are shown. The 95% confidence interval of each QTL is shown by a blue rectangle. (B) Fecundity (norm.n) is shown between the parents (QX1430 and CB4856), and between RIAILs split by genotype at the peak marker for each QTL. Each dot in the parental panel represents one of the replicates. Each dot in each of the QTL panels corresponds to a unique recombinant strain. Strains with the QX1430 allele are colored orange and strains with the CB4856 allele are colored blue.

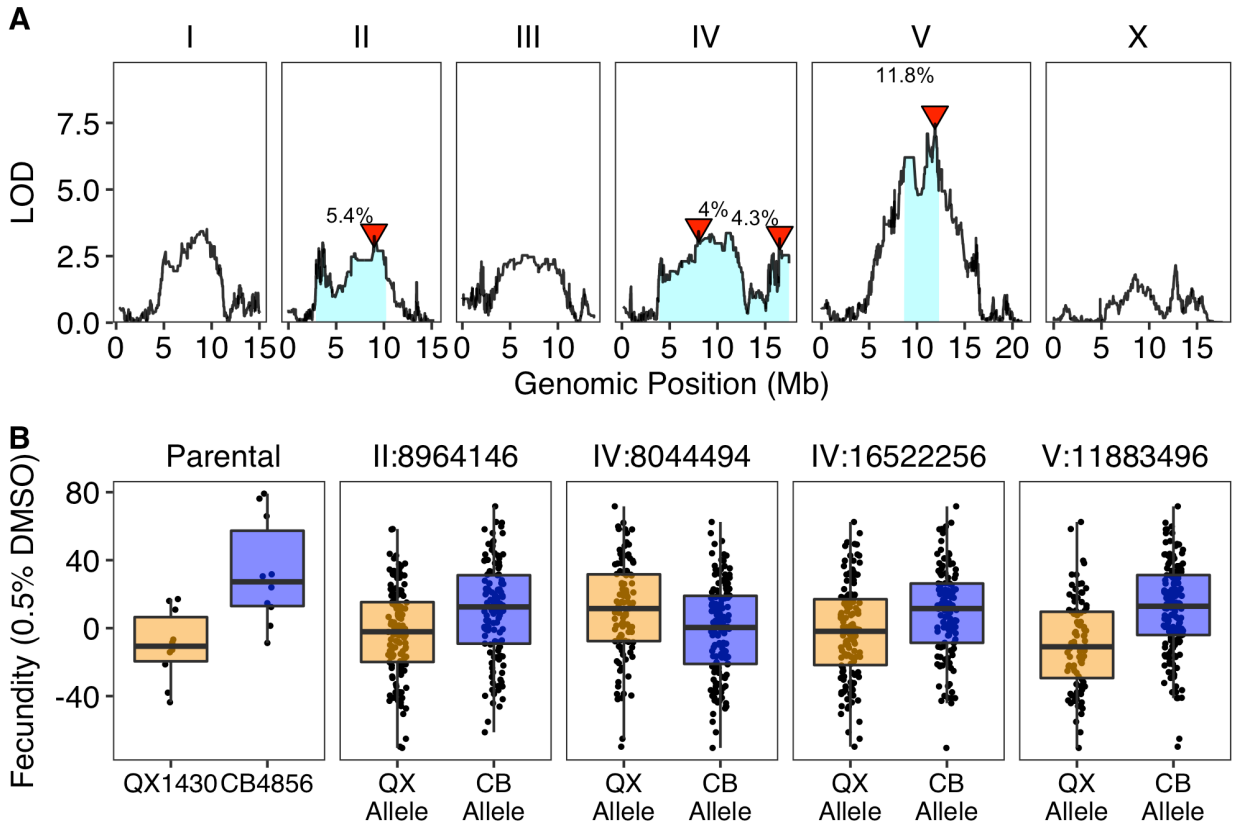

Figure S9 Four QTL were identified using linkage mapping of *C. elegans* fecundity (norm.n) in 0.5% DMSO conditions. (A) Linkage mapping results of *C. elegans* fecundity (norm.n) with RIAILs were shown with genomic position in Mb (x-axis) plotted against the logarithm of the odds (LOD) score (y-axis). The peak markers of QTL are indicated by red triangles, next to which the percentages of the total phenotypic variance that can be explained by the QTL are shown. The 95% confidence interval of each QTL is shown by a blue rectangle. (B) Fecundity (norm.n) is shown between the parents (QX1430 and CB4856), and between RIAILs split by genotype at the peak marker for each QTL. Each dot in the parental panel represents one of the replicates. Each dot in each of the QTL panels corresponds to a unique recombinant strain. Strains with the QX1430 allele are colored orange, and strains with the CB4856 allele are colored blue.