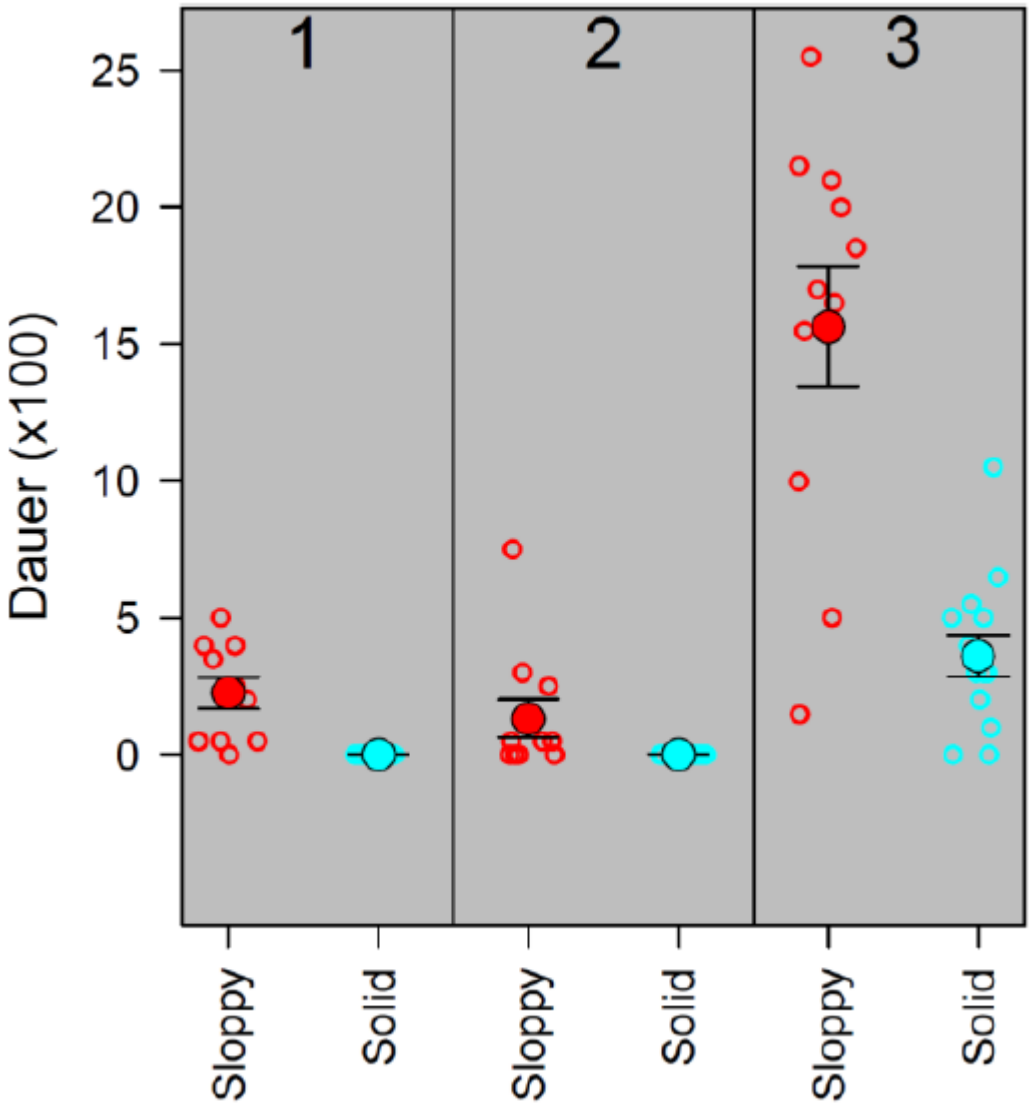
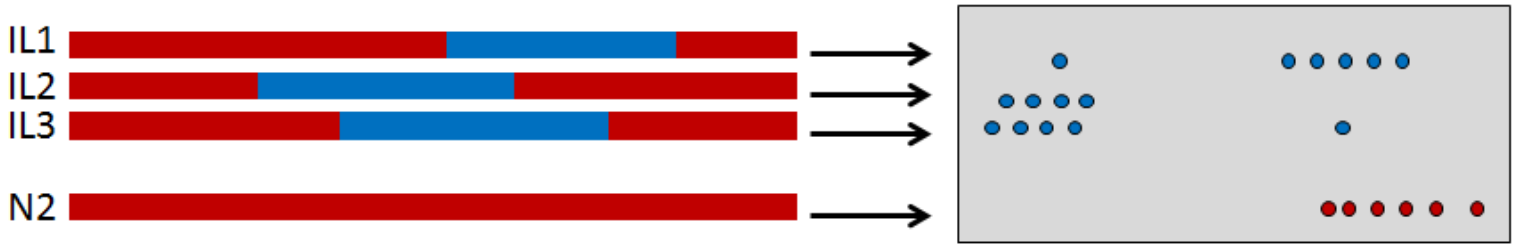
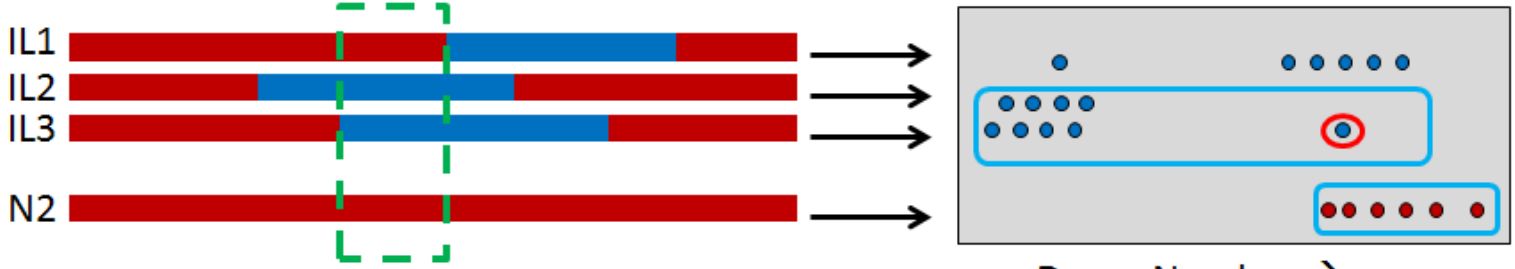


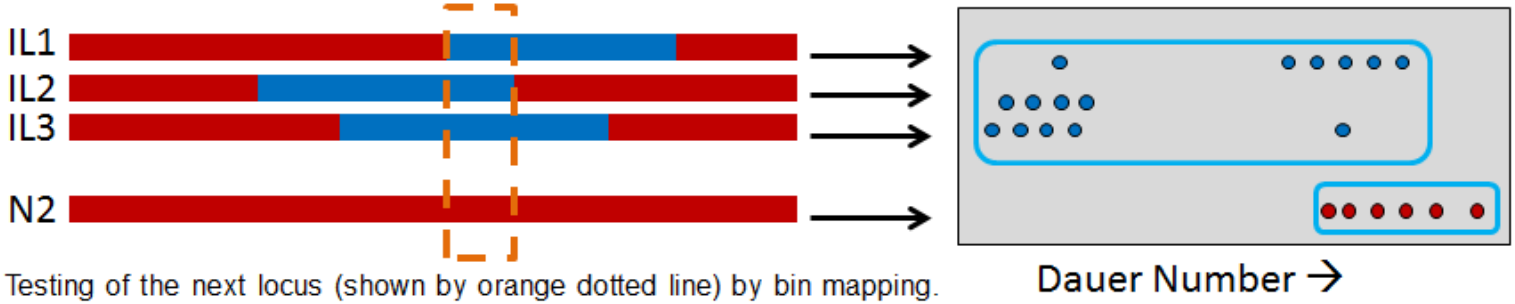
Supplemental Figure 1: Dauer (Solid) vs sloppy-agar. Dauer larvae formation in growing populations of N2 on Sloppy (red) vs. Solid (blue) agar. The number of dauer larvae is shown on the Y-axis, agar type on the x-axis. Three independent experiments indicated by 1, 2 and 3. Individual plates are shown as coloured circles. Means are shown by filled circles. Error bars show standard errors. In all three replicas sloppy agar has significantly more dauer larvae than solid agar ($p < 0.05$).



A: Measurements per genotype, ILs and N2. The horizontal bars show the genotypes, red for N2 and blue for CB. The individual values per line are shown in the grey box on the right.

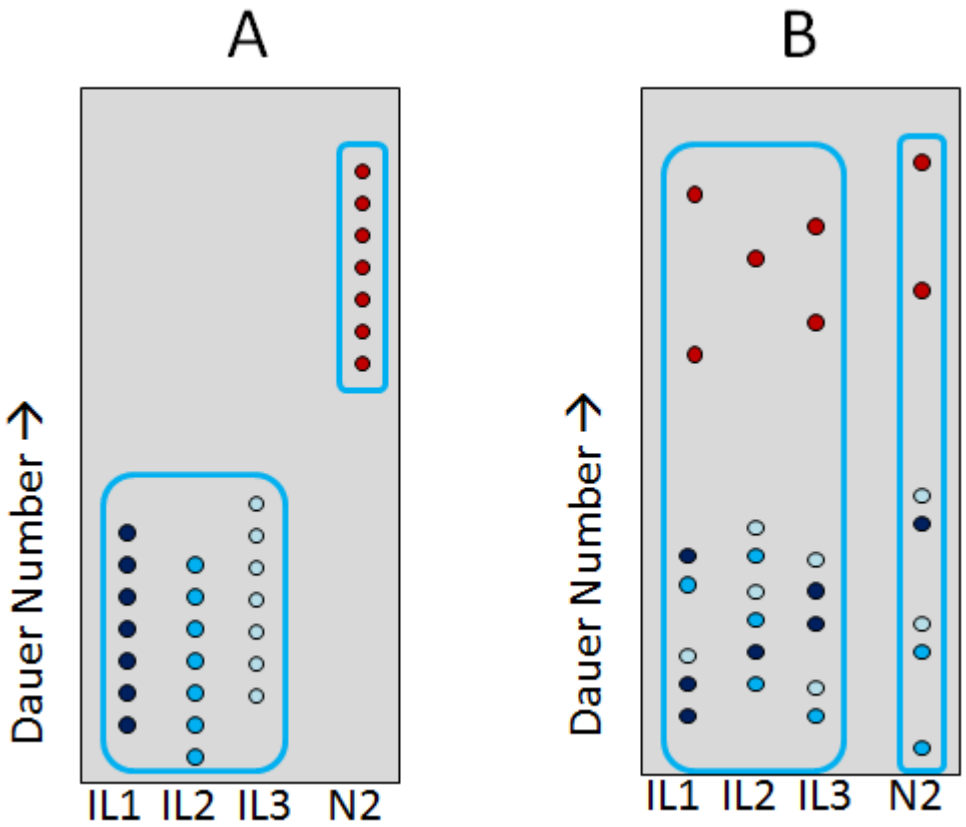


B: Testing of a locus by bin mapping. Locus under study is marked by the green dotted line. ILs 2 and 3 have the CB4856 genotype at this locus and are tested against N2. The two groups which are tested for a significant difference are indicated by the light blue box. The single measurement considered as an outlier is indicated with the red circle.

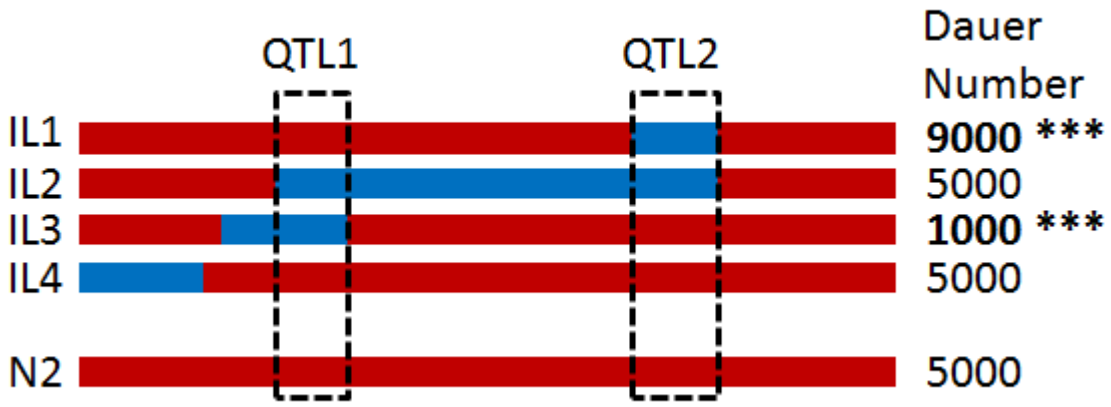


C: Testing of the next locus (shown by orange dotted line) by bin mapping. See panel B for legend and explanation of the colours.

Supplemental Figure 2: Representation of bin mapping strategy, showing how ILs were grouped per marker per chromosome, and tested against the N2 controls from the same block



Supplemental Figure 3: Permutation example for bin mapping. The permutation of trait values was used to determine the critical significance level. The question considered was: what is the chance of a significant difference between the two groups when the original values are randomly distributed. Blue boxes in both panels show the two groups under study. Panel A: Original measurements. Panel B: an example of one permutation. For analyses, the chromosome-wide significance threshold was determined by 1000 permutations per test.



Supplemental Figure 4: An extension of the single IL mapping approach to test the phenotypic effect of QTL1 and QTL2 using ILs1, 2 and 3 and N2. Effect of QTL1: -4000. Effect of QTL2: +4000. This approach can be more powerful than bin mapping when one (or more) of the ILs contain two (or more QTLs) and can be compared with ILs harbouring only one QTL.