Genotyping data from the Illumina GoldenGate assay for the 183 SNPs in the \textit{unc-4 – rol-1} region for each set of 96 DNA samples assayed.

**Confirm genotype assignment for all SNPs for each DNA sample.** Generate plots of the SNP’s allele fluorescence intensities overlaid with the assigned genotype designation for each DNA sample for that SNP. For each SNP specific plot, assess genotyping quality by:

A. Identifying and removing SNPs that failed to show three distinct clusters, one each for each of the genotype classes expected.

B. Using the appropriate control samples as guides, checking the concordance of the clustering pattern in each SNP plot with the genotype class assigned to the DNA samples for a particular SNP.

Subset of successfully genotyped SNPs

Check for and remove any DNA samples that failed to genotype across multiple SNPs in this subset of successful SNPs.

**Identify the location of the crossover in each DNA sample.** By comparing the genotype of adjacent SNPs for each DNA sample, a switch from one genotype class to another informed the location of the crossover. Care was taken to identify two crossovers (in the hermaphrodite-specific dataset) per sample and gene conversion tracks if present.

Tabulate all the crossovers in the \textit{unc-4 – rol-1} region. Flag any crossovers that cannot be unambiguously assigned to a particular SNP interval.

Group all the crossover data together to result in the final data set consisting of 122 SNPs genotyped for each of the DNA samples.

**Figure S1** Genotype analysis pipeline.