File Name: Supplementary Information
Description: Supplementary Figures and Supplementary Tables.

File Name: Supplementary Movie 1
Description: *Caenorhabditis* **dauer larva hitchhiking on a small beetle** Dauer larva of *C. latens* nictating on the back of a fast-walking beetle on the surface of a rotten apple.

File Name: Supplementary Movie 2
Description: **Nictating *Caenorhabditis* dauer larva** Dauer larva of *C. latens* nictating on the tip of a rotten apple.

File Name: Supplementary Data 1
Description: **Natural variation of nictation behavior** Nictation fractions of 12 divergent *C. elegans* wild isolates are included.

File Name: Supplementary Data 2
Description: **Nictation variation among RIAIL strains** Nictation fractions of 186 recombinant inbred advanced intercross lines (RIAILs) are included.

File Name: Supplementary Data 3
Description: **NIL-based fine mapping of *nict-1* QTL** Nictation fractions of near isogenic lines (NILs) are included.

File Name: Supplementary Data 4
Description: **Genomic variants in *nict-1* QTL** Genomic features and variants of NIL-narrowed 73 kb *nict-1* QTL are included.

File Name: Supplementary Data 5
Description: **Expression analysis for *nict-1* QTL** Expression levels of genes in the NIL-narrowed 73 kb *nict-1* QTL are included.

File Name: Supplementary Data 6
Description: **Candidate gene assay** Nictation fractions of strains with deletion mutations in genes in the NIL-narrowed 73 kb *nict-1* QTL are included.
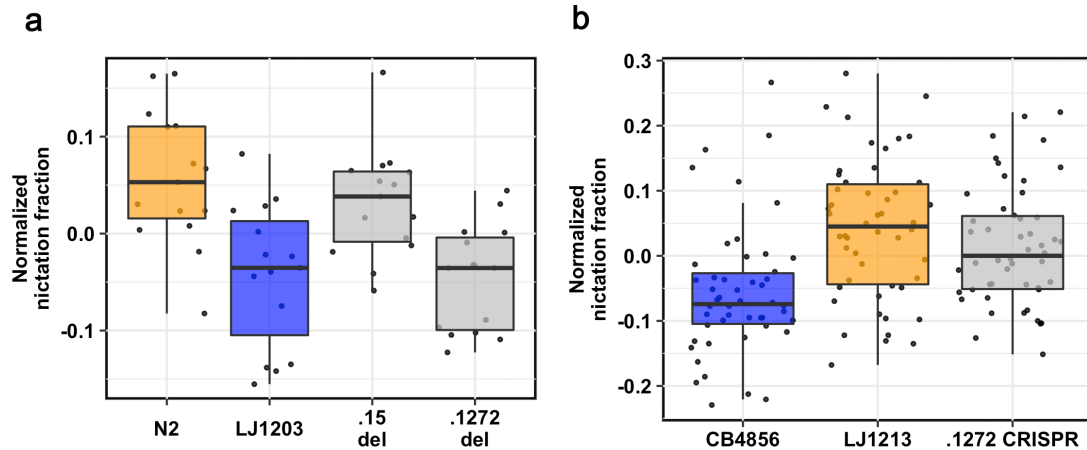
File Name: Supplementary Data 7
Description: **Brood size assay** Brood sizes of the parental and NIL strains are included.

File Name: Supplementary Data 8
Description: **Transmission competition assay** Isopod transmission competition assay allele frequencies are included.

File Name: Peer Review File

**Supplementary Figure 1. The nictation difference is not regulated by protein-coding genes in *nict-1* QTL.** Tukey box plots of normalized nictation percent of are shown with data points plotted behind. The horizontal line in the box is the median, and the box denotes the 25th to 75th quantiles of the data. The vertical line represents the 1.5 inter-quartile range. (**a**) N2 (orange), LJ1203 (*nict-1* CB4856>N2, blue), FX1161 *Y105C5A.15(tm1161)* and FX6979 *Y105C5A.1272(tm6979)* were scored in 15 biological replicates. (**b**) CB4856(blue), LJ1213 (*nict-1* N2>CB4856, orange) and LJ1216 (*nict-1* N2>CB4856); *Y105C5A.1272*(*snu33*) were scored in 50 biological replicates.
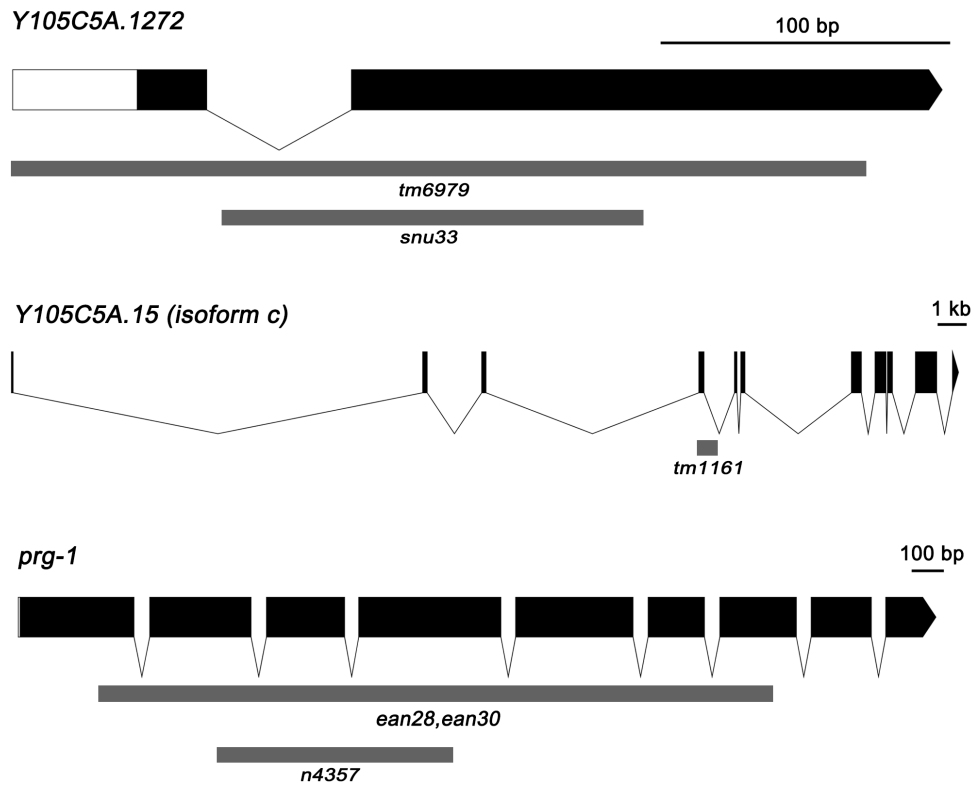
**Supplementary Figure 2. Deletion mutations in candidate genes and the *prg-1* gene.** The locations and sizes of the deletions are marked by gray rectangles.
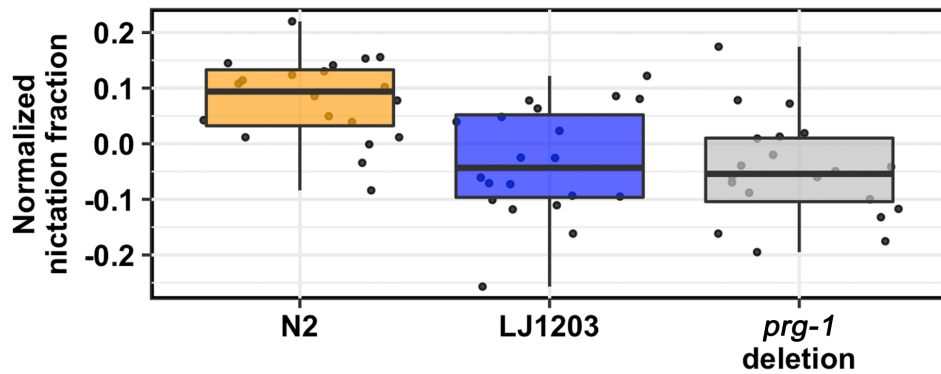
**Supplementary Figure 3. An independent *prg-1* mutation allele causes a decrease in nictation frequency.** Tukey box plots of normalized nictation percent of N2 (orange), LJ1203 (*nict-1* CB4856>N2, blue), and ECA286 *prg-1(n4357)* are shown with data points plotted behind. The horizontal line in the box is the median, and the box denotes the 25th to 75th quantiles of the data. The vertical line represents the 1.5 inter-quartile range. All strains were scored in 20 biological replicates.
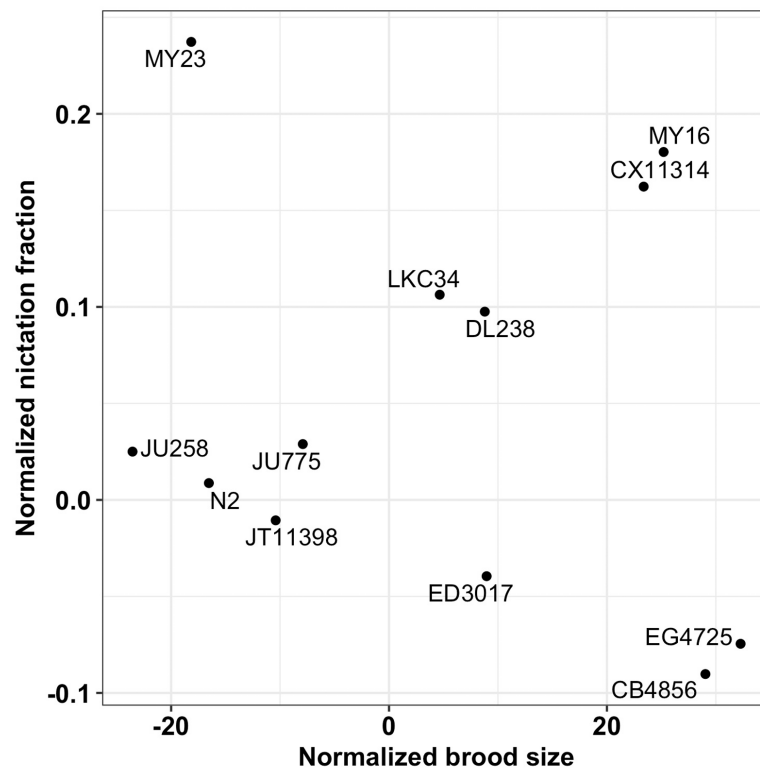
**Supplementary Figure 4. The correlation between nictation and offspring production of wild isolates were analyzed.** A scatter plot of normalized nictation fractions and normalized brood sizes of 12 *C. elegans* wild isolates are shown.

| Strain | Left breakpoint marker | Right breakpoint marker |
|---|---|---|
| LJ1205 | 15,363,068 (haw64325)<br>15,399,910 (haw64411) | 15,721,883(haw64913)<br>15,731,721(CE4-211) |
| LJ1206 | 15,363,068 (haw64325)<br>15,399,910 (haw64411) | 15,570,359 (haw64768)<br>15632637 (CE4-210) |
| LJ1207 | 15,731,721 (CE4-211)<br>15,769,804 (haw64984) | 15,874,012 (haw65181)<br>15,907,604 (haw65266) |
| LJ1209 | 15,363,068 (haw64325)<br>15,399,910 (haw64411) | 15,731,721 (CE4-211)<br>15,769,804 (haw64984) |
| LJ1210 | 15,363,068 (haw64325)<br>15,399,910 (haw64411) | 15,787,240 (haw65037)<br>15,812,722 (haw65069) |
| LJ1211 | 15,714,544 (cewivar00695185)<br>15,718,040 (cewivar00695189) | 15,874,012 (haw65181)<br>15,907,604 (haw65266) |
| LJ1212 | 15,363,068 (haw64325)<br>15,399,910 (haw64411) | 15,645,536 (haw64838)<br>15,646,308 (haw64840) |
| LJ1213 | 15,644,563 (cewivar00215554)<br>15,645,536 (haw64838) | 15,787,240 (haw65037)<br>15,812,722 (haw65069) |
| LJ1215 | 15,589,708 (haw64785)<br>15,641,444 (haw64835) | 15,731,721 (CE4-211)<br>15,769,804 (haw64984) |

**Supplementary Table 1.** Breakpoint markers for the generation of near isogenic lines (NILs)

| Position | Forward primer | Reverse primer |
|---|---|---|
| 15,363,068 | CCGTACCTCGGAAGTTGAAA | AAGAGCCATAACACATGAGCTG |
| 15,399,910 | ATGGTGGTTTTCAAGAGTTTTCA | GCTGGAATCAATTAAGAAATTACAAA |
| 15,570,359 | TGACCGAAAATGAAAAATTCG | TCCCTTACTCACCCTGTCACTT |
| 15,570,612 | TGACCGAAAATGAAAAATTCG | TCCCTTACTCACCCTGTCACTT |
| 15,589,708 | TGCGGTAAAGTCGAATTTTTA | AAAAGCAATGCTGATGATGC |
| 15,632,637 | ATCGGATGTTTCAGCTTGTGG | ATACGGAGGATTTTGCATGTCC |
| 15,641,444 | AGGCGAATGACTCATGCTTT | AGCCAAAATGCCCACTACAC |
| 15,644,563 | CATTGGCTGGTCCCACTC | AAATGTTGGCCTTGTTGAAAA |
| 15,645,536 | TTTTCAACAAGGCCAACATTT | AATGATCCGCAACTTTTTCG |
| 15,646,308 | TGGTATTGTAGAAAATAAAAGTTCCA | AAAGGGTGAGTACGCAATGG |
| 15,696,457 | TCGAAAATTCTAAAACCGAACT | AAAACGGAAGGACATGTTGTG |
| 15,714,544 | GCCCCATCGAAACAGTAGAA | CGTGGGAAAACACACACTGA |
| 15,718,040 | CAACCAATATCACGCTGTCG | CGCCACGCAGTTTCTTATTT |
| 15,721,883 | TTCATGATGTTCATTTATTTTTGGA | TTTCTGTCACAGCCAAGTTCA |
| 15,731,721 | ACCATTCTTTCAGATTGTTCCT | CAATACTGATGAAAACTGTTTGA |
| 15,769,804 | TCACCACTGGTTTTCACTTCA | AAAAAGTGTGAATTCGTTTTGGA |
| 15,787,240 | TTTCAAATGTGCTTTGCTAATGA | AAATTTTGAAACAGGAACAAAAA |
| 15,812,722 | AAAATCAGAATTTGAACTGTTTTGG | CATCGAAAATTTACAGTTTCACATTA |
| 15,874,012 | GCTCCGCTGAGCACTAAAGA | TGAAGGATGCGATACTCTCTCTC |
| 15,907,604 | AGCATTCTCACGCGCAG | TTTTGCTGTTTCGAATCAAACA |
| 16,003,539 | ATCTTTGAAGCAGCGGACAT | TTGAAAGTTTACAAGTCAAGCACA |

**Supplementary Table 2.** Primer sequences for the markers used to genotype the NILs