



Figure S1 Developmental expression of cuticle genes, mutant alleles of which were tested for genetic interactions with *col-182*. Expression trajectories (A), split by the presence of any detected genetic interaction (*col-182* interactors at right, with a small positional jitter added along the x-axis as a visual aid), and expression covariance (B) across embryonic and larval stages and young adult (YA) hermaphrodites and males. Mean values of replicate experiments per stage are shown from Boeck *et al.* (2016).

Probe	ID	Gene	Pos.	Chr.	QTL	LOD
A_12_P107311	R05F9.5	<i>gst-9</i>	4,893,372	2	134.26	8.78
A_12_P120030	B0464.1	<i>dars-1</i>	9,489,112	3	133.00	4.83
A_12_P116084	Y40B10A.2	<i>comt-3</i>	2,061,050	5	133.00	8.62
A_12_P111642	C45H4.17	<i>cyp-33C2</i>	2,186,492	5	134.26	5.34
A_12_P104828	C02A12.1	<i>gst-33</i>	3,467,564	5	133.00	8.50
A_12_P115936	F08F3.7	<i>cyp-14A5</i>	5,421,110	5	133.78	8.56
A_12_P108481	T04H1.9	<i>tbb-6</i>	12,263,208	5	134.26	6.42
A_12_P111217	C05C9.3		11,143,372	6	133.00	4.95
A_12_P105133	C35C5.6	<i>trpp-9</i>	11,569,206	6	133.78	8.13

■ **Table S1** Genes with expression linked to *col-182* in N2/CB4856 RIAILs (Rockman *et al.* 2010). Probe: Agilent microarray probe, ID: WormBase systematic identifier, Gene: common name (if any), Pos./Chr.: physical position of the transcript, QTL: genetic position of the quantitative trait locus in the RIAILs in cM (within 1 cM of *col-182*), LOD: logarithm of the odds of association between gene expression and the QTL peak.

LITERATURE CITED

- Boeck, M. E., C. Huynh, L. Gevirtzman, O. A. Thompson, G. Wang, *et al.*, 2016 The time-resolved transcriptome of *C. elegans*. *Genome Research* **26**: 1441–1450.
- Rockman, M. V., S. S. Skrovanek, and L. Kruglyak, 2010 Selection at linked sites shapes heritable phenotypic variation in *C. elegans*. *Science* (New York, N.Y.) **330**: 372–376.