

Table S1. Neuropeptide staining of 39C4-D1 alleles

	Allele
Reduced neuropeptide levels	<i>dimm</i> ^{KG02598} <i>Df(2L)Rev4</i> <i>Df(2L)DS8</i> <i>Df(2L)Rev8</i> <i>Df(2L)R6*</i> <i>Df(2L)R6</i>
Normal neuropeptide levels	<i>crc</i> ¹ <i>crc</i> ⁹²⁹ <i>crc</i> ^{R1*} <i>crc</i> ^{R2} <i>Df(2L)TW1</i> <i>Sco</i> <i>Rev(KG02598)S2a</i>

The phenotype of each allele was assessed either in homozygotes, in hemizygotes (in trans with a deficiency of 39C4-D1) or in both homozygotes and hemizygotes.

*Chromosomes outcrossed for at least seven generations.

Table S2. Complementation analysis of *dimm*^{KG02598}

<i>dimm</i> class	<i>crc</i> class	Allele	<i>n</i>	% Cy ⁺ expected
Severe hypomorph	+	<i>dimm</i> ^{KG02598}	124	0 [‡]
Severe hypomorph	+	<i>dimm</i> ^{KG02598§}	120	0 [‡]
Null	Null	<i>Df(2L)Rev4</i>	176	3 [‡]
N.D.	Null	<i>Df(2L)DS8</i>	135	0 [‡]
N.D.	Null	<i>Df(2L)DS5b</i>	148	0 [‡]
Hypomorph	Null	<i>Df(2L)Rev8</i>	219	11 [‡]
Hypomorph	Severe hypomorph	<i>Df(2L)R6¶</i>	120	0 [‡]
Hypomorph	Severe hypomorph	<i>Df(2L)R6</i>	269	2 [‡]
N.D.	Severe hypomorph	<i>crc</i> ⁴³⁵¹	145	54 [‡]
+	Severe hypomorph	<i>crc</i> ¹	263	70 [‡]
+	5' hypomorph*	<i>crc</i> ⁹²⁹	247	120 [†]
+	5' hypomorph*	<i>crc</i> ^{R1¶}	130	100
+	+	<i>Df(2L)TW1</i>	264	120
+	+	<i>Sco</i>	148	108
N.D.	N.D.	<i>Rev(KG02598)I</i>	141	132 [‡]
N.D.	N.D.	<i>Rev(KG02598)I3</i>	150	122

The female parents in each cross were *dimm*^{KG02598} (*dimm*^{KG02598} males were used for crosses with *crc*^{R1} and *Sco*). Two precise excisions of *KG02598*, *Rev(KG02598)I* and *Rev(KG02598)I3* (females), were crossed to *Df(2L)Rev4* (males). The percentages of expected Cy⁺ progeny were calculated from the number of Cy⁻ siblings.

*Specific disruption of only the 5' exons of *crc* (exons encoding *crc*-b transcript are intact) (Hewes et al., 2000).

[†] $P < 0.05$ (χ^2 test)

[‡] $P < 0.001$ (χ^2 test)

§Chromosomes outcrossed for eight generations

¶Chromosomes outcrossed for at least seven generations.

N.D., not done.