

**Table S2 Details of QTL mapped for larva-to-adult viability on control food**

Name	LOD score	Chr	Peak cM (2-LOD CI) <sup>a</sup>	Peak Mb (2-LOD CI) <sup>a</sup>	Number of genes <sup>b</sup>
i (pA)	8.1	2R	82.8 (82.6–83.4)	13.44 (13.38–13.60)	50
ii (pA) <sup>c</sup>	8.9	2R	88.2 (88.0–89.9)	15.26 (15.19–15.86)	75
iii (pA)	9.2	3R	47.2 (47.2–47.3)	1.30 (1.21–1.47)	50
iv (pB) <sup>d</sup>	8.7	X	32.6 (31.8–33.2)	10.73 (10.52–10.89)	37
v (pB) <sup>d</sup>	7.5	X	39.4 (37.9–40.7)	12.44 (12.10–12.73)	41
vi (pB) <sup>d</sup>	8.4	2L-2R	53.8 (53.7–58.5)	2L:19.76 (2L:19.59–2R:4.44)	733

<sup>a</sup> 2-LOD CI indicates the 2-LOD support interval of the QTL.

<sup>b</sup> The number of protein-coding genes in the 2-LOD support interval.

<sup>c</sup> The location of this control viability QTL overlaps that of Q3 (Table 1), a QTL contributing to viability on nicotine food.

<sup>d</sup> Given the relatively small number of RILs phenotyped for population pB, coupled with the low level of within-line replication we recommend caution in interpreting QTL mapped in pB.