

**Supplementary Data S1.** Summary of QTL and loci previously implicated in the genetic control of posterior lobe development and adult morphology in *Drosophila melanogaster*.

McNeil et al. (2011) - PMID: 22384345. See Table 3.

Identified three QTL for a measure of posterior lobe shape (PC1):

QTL	Chr.	Cytology
Q1	2L	27E-29A
Q2	2L	66B-69B
Q3	3c	75F-86C

Takahara & Takahashi (2015) - PMID: 26182199. See Supplementary Tables 2, 3, and 4.

No sites were significant after formal correction for multiple tests, but a number of variants showed associations with measures of posterior lobe shape (PC1, PC2) and size at a nominal significance threshold of  $p < 10^{-5}$ .

PC1 (16 variants at  $p < 10^{-5}$ )

Variant ID <sup>a</sup>	p-value <sup>b</sup>	Position (Release 6) <sup>c</sup>	Gene <sup>d</sup>
2L_11917838_SNP	$8.7 \times 10^{-6}$	2L:11917838	<i>Pde1c</i> (FBgn0264815)
2L_16982042_SNP	$3.5 \times 10^{-6}$	2L:16982042	<i>beat-IIIb</i> (FBgn0053179), <i>CG44406</i> (FBgn0265579)
2L_17282029_SNP	$9.3 \times 10^{-6}$	2L:17282029	-
2L_582234_SNP	$4.7 \times 10^{-6}$	2L:582234	-
2R_16809817_INS	$7.0 \times 10^{-6}$	2R:20922312	<i>Rx</i> (FBgn0020617)
2R_17146075_SNP	$8.4 \times 10^{-6}$	2R:21258570	<i>Rgk3</i> (FBgn0085426)
2R_8919718_SNP	$2.9 \times 10^{-6}$	2R:13032213	-
3L_15296932_SNP	$4.8 \times 10^{-6}$	3L:15303832	-
3L_15297000_SNP	$5.2 \times 10^{-6}$	3L:15303900	-
3L_15297065_SNP	$6.6 \times 10^{-7}$	3L:15303965	-
3L_16826245_SNP	$1.3 \times 10^{-6}$	3L:16833145	-
3L_9276471_SNP	$1.1 \times 10^{-6}$	3L:9283371	<i>GluRIB</i> (FBgn0264000)
3R_15744495_SNP	$5.8 \times 10^{-6}$	3R:19918773	<i>CG4770</i> (FBgn0038751)
3R_19183951_SNP	$4.6 \times 10^{-6}$	3R:23358229	<i>Sec13</i> (FBgn0024509)
3R_19184076_SNP	$2.9 \times 10^{-7}$	3R:23358354	<i>Sec13</i> (FBgn0024509)
X_20429265_INS	$8.9 \times 10^{-6}$	X:20558238	<i>RunxB</i> (FBgn0259162)

PC2 (14 variants at  $p < 10^{-5}$ )

Variant ID <sup>a</sup>	p-value <sup>b</sup>	Position (Release 6) <sup>c</sup>	Gene <sup>d</sup>
2L_16460631_SNP	$1.0 \times 10^{-5}$	2L:16460631	-
2L_5540863_SNP	$1.8 \times 10^{-6}$	2L:5540863	<i>Hel25E</i> (FBgn0014189)
2R_18594569_SNP	$4.0 \times 10^{-6}$	2R:22707064	<i>Obp58d</i> (FBgn0034770)
2R_18659021_SNP	$9.9 \times 10^{-6}$	2R:22771516	<i>CG42260</i> (FBgn0259145)
2R_18914361_SNP	$2.9 \times 10^{-6}$	2R:23026838	<i>twi</i> (FBgn0003900), <i>CG42741</i> (FBgn0261705)
2R_7583208_SNP	$1.0 \times 10^{-5}$	2R:11695703	<i>CG13197</i> (FBgn0062449)
3L_7290732_SNP	$5.5 \times 10^{-7}$	3L:7297632	<i>unc-13-4A</i> (FBgn0035756)
3R_10150581_SNP	$3.8 \times 10^{-7}$	3R:14324859	<i>Afti</i> (FBgn0038223)
3R_11532259_SNP	$3.5 \times 10^{-6}$	3R:15706537	<i>CG5404</i> (FBgn0038354)
3R_11532260_SNP	$1.5 \times 10^{-6}$	3R:15706538	<i>CG5404</i> (FBgn0038354)
3R_11532266_MNP	$3.3 \times 10^{-6}$	3R:15706544	<i>CG5404</i> (FBgn0038354)
3R_11532271_SNP	$2.5 \times 10^{-6}$	3R:15706549	<i>CG5404</i> (FBgn0038354)
3R_2137747_SNP	$4.3 \times 10^{-6}$	3R:6312025	<i>Osi17</i> (FBgn0037427)
X_16331129_DEL	$6.2 \times 10^{-6}$	X:16437096	<i>hang</i> (FBgn0026575)

Size (15 variants at  $p < 10^{-5}$ )

Variant ID <sup>a</sup>	p-value <sup>b</sup>	Position (Release 6) <sup>c</sup>	Gene <sup>d</sup>
2L_1823396_SNP	$4.2 \times 10^{-6}$	2L:1823396	-
2L_7045893_SNP	$8.5 \times 10^{-6}$	2L:7045893	<i>milt</i> (FBgn0262872)
2R_13646097_DEL	$4.8 \times 10^{-6}$	2R:17758592	<i>HLH54F</i> (FBgn0022740)
2R_13815024_SNP	$9.1 \times 10^{-6}$	2R:17927519	-
2R_13815048_SNP	$2.8 \times 10^{-6}$	2R:17927543	-
3L_11031740_INS	$5.3 \times 10^{-6}$	3L:11038640	<i>CG43693</i> (FBgn0263776)
3L_11031783_SNP	$8.4 \times 10^{-6}$	3L:11038683	<i>CG43693</i> (FBgn0263776)
3L_11037323_DEL	$4.9 \times 10^{-6}$	3L:11044223	<i>CG43693</i> (FBgn0263776)
3L_11037405_SNP	$2.3 \times 10^{-6}$	3L:11044305	<i>CG43693</i> (FBgn0263776)
3L_12148634_SNP	$2.5 \times 10^{-6}$	3L:12155534	<i>Nrx-IV</i> (FBgn0013997)
3L_12175730_SNP	$2.4 \times 10^{-7}$	3L:12182630	<i>CAH2</i> (FBgn0027843)
3L_13764854_SNP	$8.7 \times 10^{-6}$	3L:13771754	<i>bru-3</i> (FBgn0264001)
3L_13764855_SNP	$8.3 \times 10^{-6}$	3L:13771755	<i>bru-3</i> (FBgn0264001)
3L_20214515_INS	$8.0 \times 10^{-6}$	3L:20221415	-
3R_14913820_SNP	$3.3 \times 10^{-6}$	3R:19088098	<i>cdi</i> (FBgn0004876)

<sup>a</sup> Variant ID from DGRP analysis software (dgrp2.gnets.ncsu.edu/). The first component is the chromosome on which the variant resides, the second is the position in Release 5 of the *D. melanogaster* reference genome, and the third is the type of variant (SNP, INS, DEL).

<sup>b</sup> The p-value of the association test.

<sup>c</sup> The position of the variant on Release 6 of the reference genome (converted from Release 5 positions via flybase.org/static\_pages/downloads/COORD.html).

<sup>d</sup> The name (and FlyBase ID) of any gene in which the variant resides. A "-" implies the variant does not reside in a gene.

Chatterjee et al. (2011) - PMID: 21343364.

Found 23 genes with male- or female-biased gene expression in the genital disc across three developmental timepoints. (Two of these genes - *CG4267* and *CG31686* - have since been merged into the single gene *CG4267*.)

<i>Chr.</i>	<i>Gene Name</i>	<i>FlyBase ID</i>
X	<i>CG4766</i>	FBgn0027546
X	<i>Nep1</i>	FBgn0029843
X	<i>lz</i>	FBgn0002576
X	<i>FucTC</i>	FBgn0044872
2	<i>al</i>	FBgn0000061
2	<i>CG4267</i>	FBgn0264979
2	<i>CG31686</i>	FBgn0264979
2	<i>msl-2</i>	FBgn0005616
2	<i>salr</i>	FBgn0000287
2	<i>ap</i>	FBgn0267978
2	<i>Wnt2</i>	FBgn0004360
2	<i>Poxn</i>	FBgn0003130
3	<i>bab1</i>	FBgn0004870
3	<i>toe</i>	FBgn0036285
3	<i>eyg</i>	FBgn0000625
3	<i>caup</i>	FBgn0015919
3	<i>AP-2</i>	FBgn0261953
3	<i>dsx</i>	FBgn0000504
3	<i>Ctr1B</i>	FBgn0062412
3	<i>abd-A</i>	FBgn0000014
3	<i>bnl</i>	FBgn0014135
3	<i>Dr</i>	FBgn0000492

Glassford et al. (2015) - PMID: 26343453.

Highlighted a number of genes expressed in the developing genital disc, and those having effects on the posterior lobe following RNAi.

<i>Chr.</i>	<i>Gene Name</i>	<i>FlyBase ID</i>
X	<i>dome</i>	FBgn0043903
X	<i>hop</i>	FBgn0004864
X	<i>upd1</i>	FBgn0004956
2L	<i>eya</i>	FBgn0000320
2L	<i>salm</i>	FBgn0261648
2R	<i>en</i>	FBgn0000577
2R	<i>Poxn</i>	FBgn0003130
3L	<i>RhoGEF64C</i>	FBgn0035574
3R	<i>Abd-B</i>	FBgn0000015
3R	<i>Cad86C</i>	FBgn0261053
3R	<i>crb</i>	FBgn0259685
3R	<i>ems</i>	FBgn0000576
3R	<i>Stat92E</i>	FBgn0016917

Tanaka et al. (2015) - PMID: 25783699. See Figure 4.

Identified several genes that influence posterior lobe morphology in *D. melanogaster* via RNAi. These candidates were selected based on their presence within regions of *D. mauritiana* that when introgressed into a *D. simulans* background affect genital morphology.

<i>Chr.</i>	<i>Gene Name</i>	<i>FlyBase ID</i>
3	<i>CG6673</i>	FBgn0035906
3	<i>CG11652</i>	FBgn0036194
3	<i>CG14130</i>	FBgn0036210
3	<i>CG14835</i>	FBgn0035782
3	<i>CG14838</i>	FBgn0035799
3	<i>CG32055</i>	FBgn0052055
3	<i>CG32081</i>	FBgn0052081
3	<i>CG32082</i>	FBgn0052082
3	<i>dally</i>	FBgn0263930
3	<i>iPLA2-VIA</i>	FBgn0036053
3	<i>Mcm7</i>	FBgn0020633
3	<i>Mob2</i>	FBgn0259481
3	<i>msl-3</i>	FBgn0002775
3	<i>Prm</i>	FBgn0003149
3	<i>Rac1</i>	FBgn0010333
3	<i>Surf1</i>	FBgn0029117
3	<i>wls</i>	FBgn0036141