

Supplementary Table S4. Positions of QTL mapped for all 7 traits.

Trait	QTL ^a	LOD	Chr	Interval (cM) ^b	Interval (Mb) ^b
lobeArea	Q1 ³	5.2	3L	141-158	17.4-21.7
lobeHeight	Q1 ¹	2.7	X	1-45	3.5-9.3
lobeHeight	Q2 ²	4.6	2L	25-45	3.3-5.3
lobeHeight	Q3 ³	4.4	3L	142-166	3L:17.8-3R:8.3 ^c
lobeWidth	Q1 ²	5.8	2L	12-51	13.8-16.4
lobeWidth	Q2	3.8	2L	135-149	2.0-5.6
HWratio	Q1 ¹	2.7	X	1-90	3.5-12.5
HWratio	Q2 ²	10.6	2L	36-46	4.0-5.4
PC1	Q1	2.9	X	106-165	13.6-19.4
PC1	Q2 ²	9.8	2L	36-50	4.1-5.6
PC1	Q3	8.6	3L	85-119	10.4-13.7
PC1	Q4	4.6	3R	262-277	21.7-23.7
PC2	Q1	4.3	3L	34-72	4.5-9.5
PC2	Q2 ³	6.0	3L	146-155	18.7-21.2
PC3	Q1	4.2	2L	64-85	7.0-9.5

^a The superscript numbers indicate those QTL intervals that physically overlap. For instance, both QTL labeled "1" overlap with each other. QTL without a superscript label are uniquely found for a single trait.

^b QTL intervals are defined by 2-LOD drops from the peaks. Genetic distance is given on the expanded map (map distances on the typical *D. melanogaster* genetic map will be approximately 3 times shorter.) Physical distance is provided relative to Release 6 of the genome.

^c This QTL interval overlaps the chromosome 3 centromere, so the proximal and distal ends of the interval are on different chromosome arms.