

**Supplementary Table 3      Largest Magnitude of Genotype Effects by Trait**

Trait	Site	Location	P-value	Estimate	S.D.U.	Allele 1	Allele 2
B1	36749	Intron 2 (3')	0.025	0.01454	1.06	80 T	5 A
B2	41262	Exon 6	0.047	0.00883	1.02	137 C	10 T
B3	31626	Intron 2 (5')	0.043	0.00689	1.08	10 A	77 C
C1	31626	Intron 2	0.004	0.01720	1.36	77 C	10 A
C2	30565	Exon 2	0.031	0.00746	1.21	4 A	93 C
C3	31333	Intron 2 (5')	0.088	0.00398	0.91	105 A	6 T
D1	6063	Exon 1	0.002	0.01411	0.75	22 T	181 C
D2	31333	Intron 2 (5')	0.019	0.01409	1.27	105 A	6 T
D3	31164	Intron 2 (5')	0.036	0.01186	1.26	7 A	96 G
W1	31626	Intron 2 (5')	0.023	0.01515	1.02	77 C	10 A
W2	31333	Intron 2 (5')	0.027	0.01528	1.18	6 T	105 A
W3	31210	Intron 2 (5')	0.050	0.01007	1.12	84 A	14 T
W4	37282	Intron 2 (3')	0.069	0.00777	0.96	169 A	14 G
W5	35955	Intron 2 (3')	0.039	0.00593	0.82	82 G	5 A
W6	31210	Intron 2 (5')	0.030	0.00741	0.92	14 T	84 A
W7	5917	5' to Ex 1	0.007	0.00322	1.22	17 A	123 C
W8	31619	Intron 2 (3')	0.058	0.00378	1.11	7 T	79 G
W9	30727	Exon 2	0.004	0.00290	0.95	12 A	129 G
TA	42241	3' UTR	0.044	0.93711	0.31	76 C	34 G

P-value for the Genotype term after fitting the full model with Sex and Population  
Estimate and S.D.U: Estimate in relative warp units and as a fraction of the sex-averaged  
standard deviation of the trait line means.

Alleles 1 and 2 arbitrarily defined to give a positive difference in warp LSMs

TA is total area of the wing, a representative size measure.