

Supporting Information

Table S1. Vector correlations of selected dictionary knockdown effects and SNPs related to core Notch, (Ser, Kuz, Mam), hippo (Ds, Sd, Ser), decapentaplegic (Sd, Mam, Ttv) and wingless (Sd, Ttv) pathway genes. We did not attempt to test for similarity among Dictionary or SNP vectors.

			Vector correlations					
			Dictionary		SNP			
		SNP location	sd	Ser	Act5C	kuz	mam	ttv
Dictionary	Ds		0.647	0.609	0.715	0.615	0.632	0.896**
Dictionary	Sd			0.688	0.792**	0.798**	0.717*	0.592
Dictionary	Ser				0.768*	0.661	0.743*	0.487
SNP	Act5	X:5902461				0.699	0.665	0.666
SNP	Kuz	2L:13600842					0.804	0.539
SNP	Mam	2R:13995678						0.546
SNP	Ttv	2R:14523066						

*SNP-wise P<0.05; ** SNP-wise P<0.01.

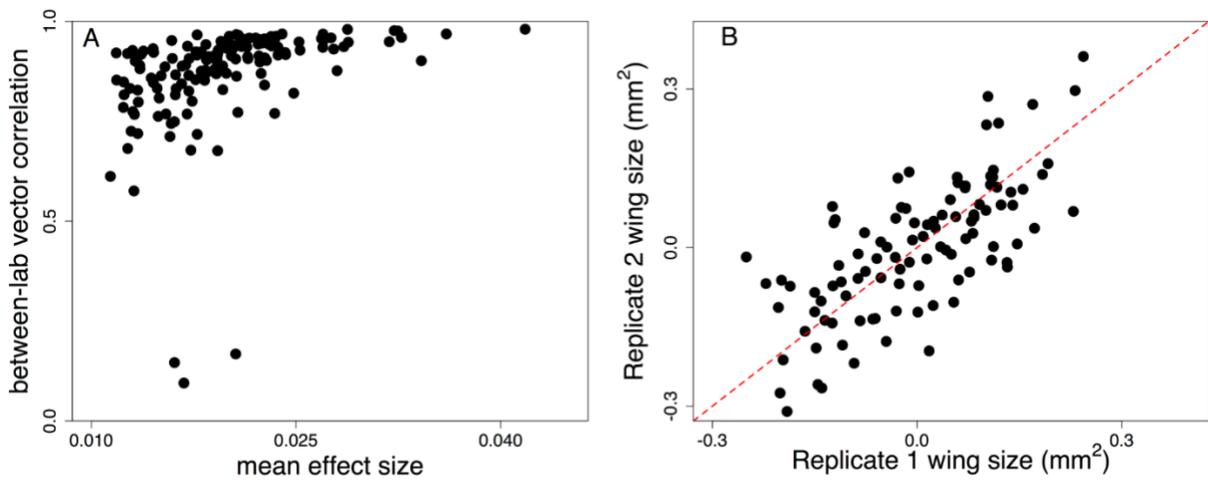


Figure S1. Inter and intra-lab repeatability: A) Vector correlations of deviations of line means from the grand mean. The vast majority of estimates are highly correlated. Estimates with large angles are those with small effect sizes. B) Estimates of wing size in experimental replicates in the Dworkin lab (centered on zero).

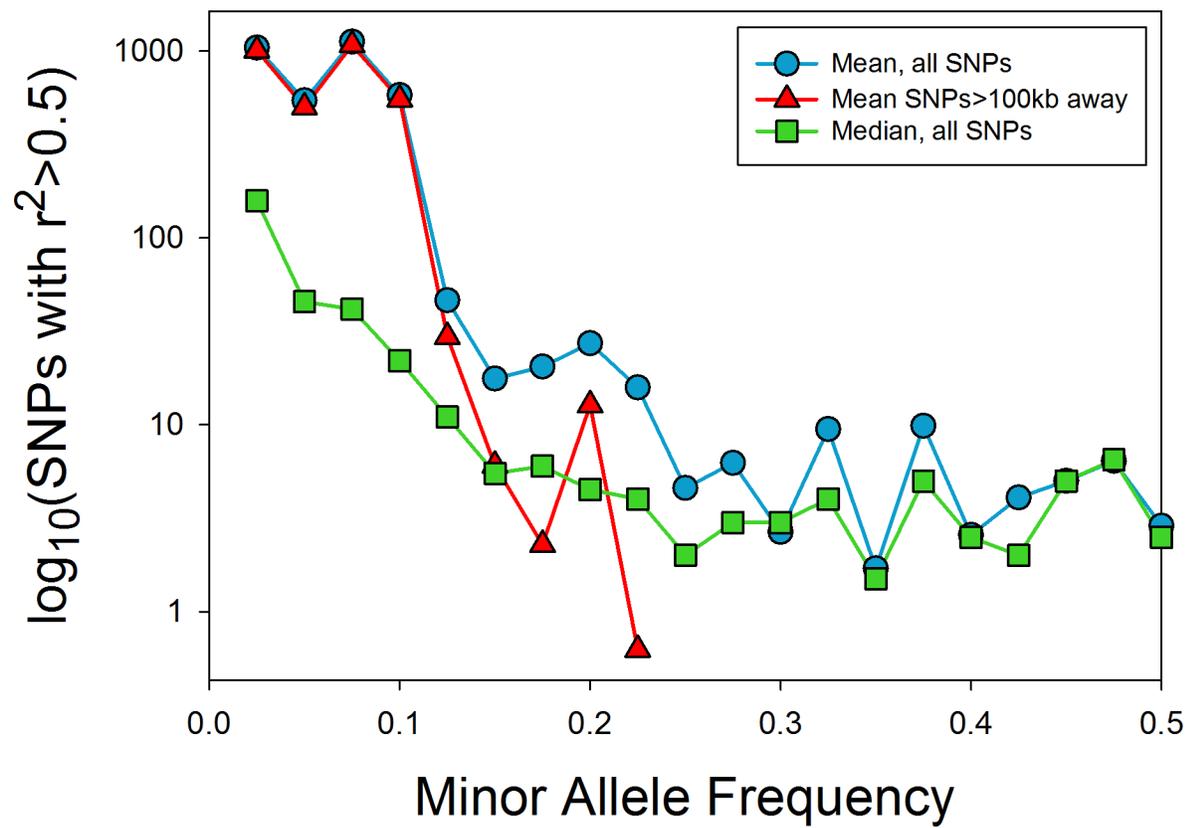


Figure S2. Mean and median number SNPs correlated at $r^2 > 0.5$ with significant SNPs, as a function of distance between sites and MAF.

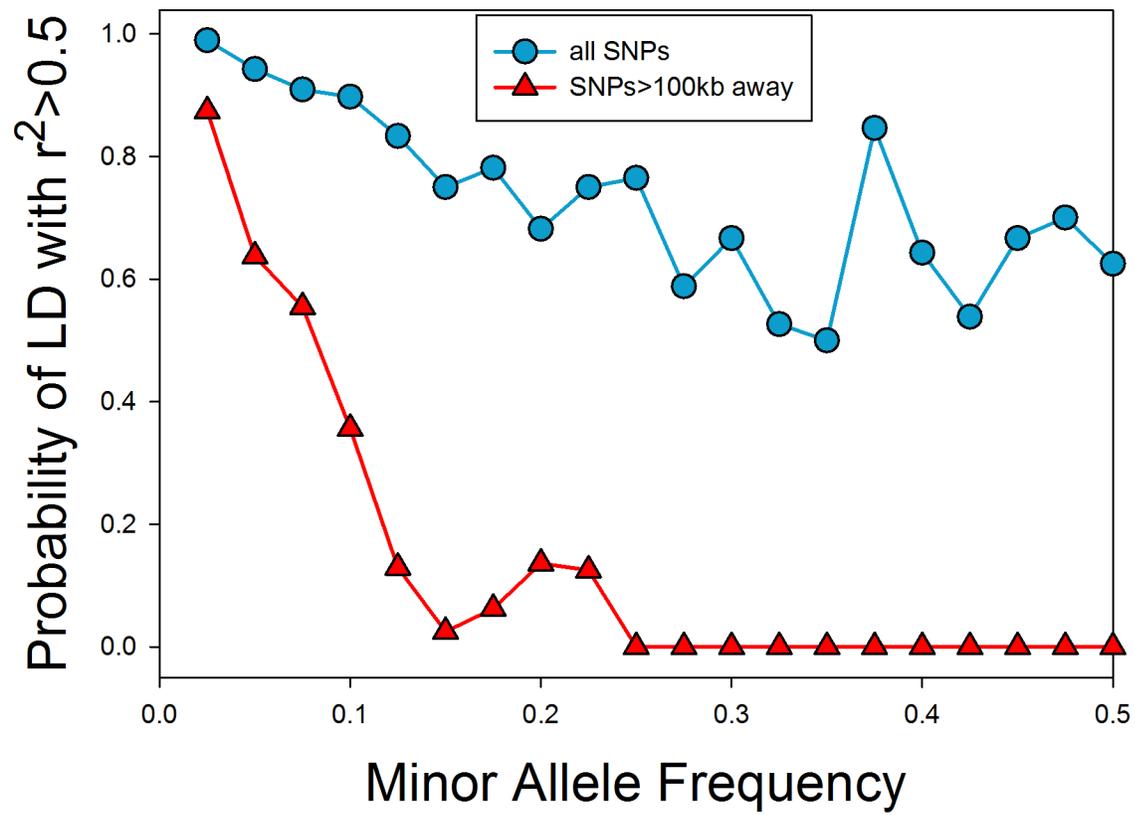


Figure S3. Probability that a SNP is correlated at $r^2 > 0.5$ with at least one other site in the genome as a function of MAF.

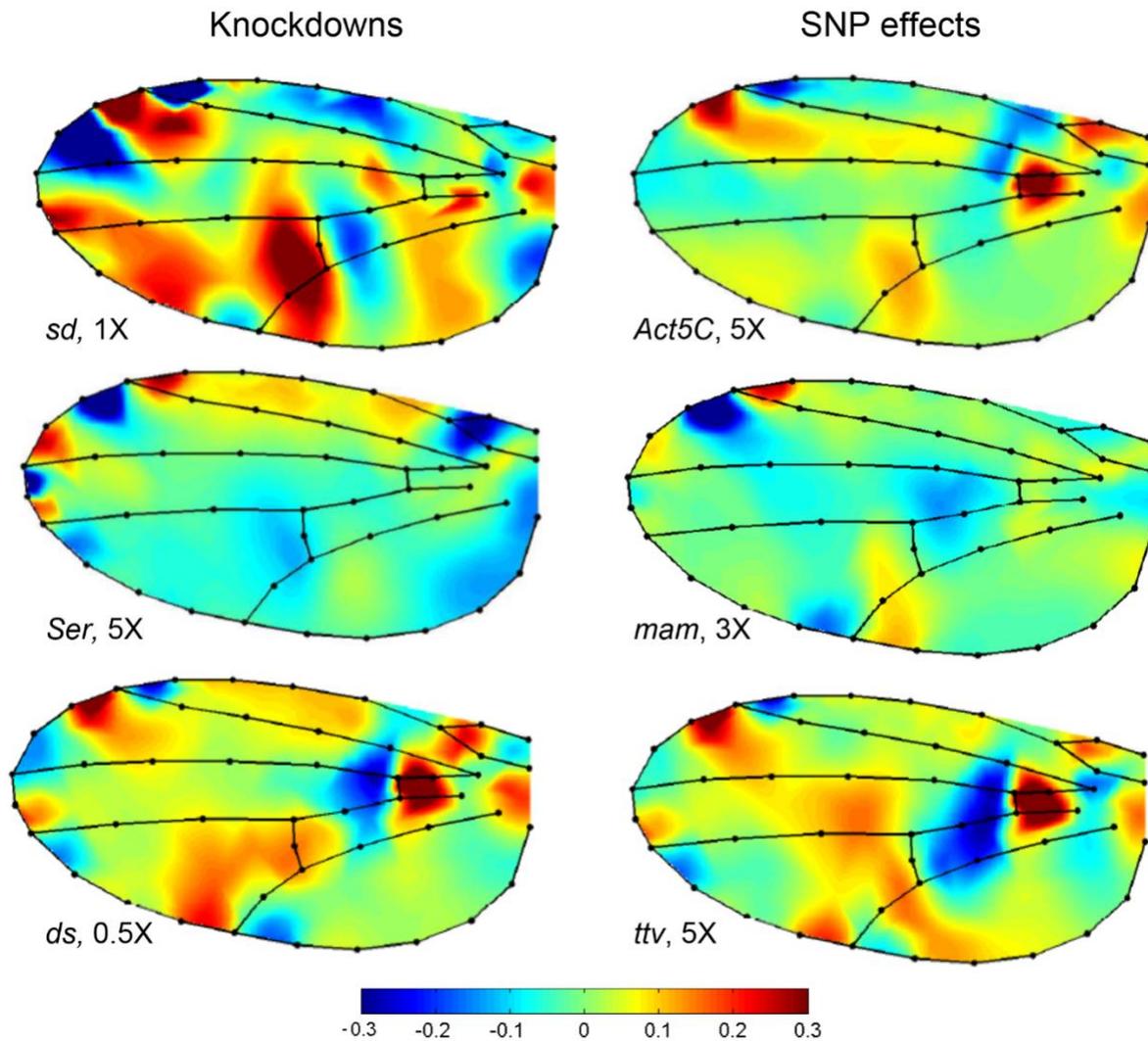


Figure S4. Similar wing-shape deformations for gene knockdowns (left) and SNP effects (right) at functionally related genes. Pictured SNP effects are *Act5C*: X:5,902,461 in intron; *mam*: 2R:13,995,678 in intron; *ttv*: 2R:14,523,066, 3201 bp upstream of coding region.

Supplementary Files have been uploaded to Figshare.

File S1. Supplementary Materials and Methods.

File S2. Means and S.D. of PC scores by lab and sex of fly, eigenvectors of the combined data set, and the estimated among-line genetic variance-covariance matrix in a 40-dimensional and phenotypic (97-dimensional) spaces.

File S3. Significant SNPs from the MANOVA and LASSO analyses.

File S4. Enriched biological process gene ontology categories. Table consists of the modified output from the WebGestalt analysis of the 479 genes implicated by the LASSO-significant SNPs.

File S5. Genes studied in RNAi knockdown experiments, the quantiles of maximum correlations out of 580 random comparisons, and the angles between effect vectors and the first 5 PCS of the combined data set.

File S6. Vectors correlations >0.5 between dictionary knockdown vectors and LASSO SNP vectors.

