Table S1. *Primers, probes and $MgCl_2$ concentrations used to assay gene expression by qRT-PCR*

Protein	EC	Gene (CG)	F primer (5′–3′) R primer (5′–3′)	Probe (5′Fam – 3′MGB)	$MgCl_2$ (mmol l^{-1})*
Acetyl-CoA synthetase	6.2.1.1	*AcCoAS* (9390)	CGGAAACCGGTGGTCATG CCGCACTCATCCAGCAAAG	CGGGATCTGCTTCATT	3.75
		CG6432	TCCGCACGCTTTACTTTCAA GATATAGCCACGTTCGTCCTTGT	AGTTTCCGGGTTACTATGA	3.50
		CG8732	GCCTGGGTGATAAGTCCTTTGA CGGGAACCTCATATTTTTGCA	TGCGCGGAAATGTAAA	3.50
Acetaldehyde dehydrogenase	1.2.1.3	*Aldh* (3752)	GTCCAGCCCACGGTGTTC GGCGGCCAATCCGTACT	TTGCAAGGGAGGAGAT	3.50
Alcohol dehydrogenase	1.1.1.1	*Adh* (3481)	GACCAACAAGAACGTGATTTTCG GGGTTCTCAATGCGGTCGA	CTGAAGAACCTGGTGATC	3.25
CDP-ethanolamine diglyceride transferase	2.7.8.1	*Cdpet* (6016)	CCGCCAAGGTCACCAATAA CGTGAACCACAGTAGCCAGATCT	TGATCGCTCACATGAC	3.50
Fatty acid desaturase	1.14.19.1	*desat1* (5887)	CGCCTTCGGTTACCTCCAT CCTAGGCCAGAAATGACGTATAGAA	CGTGCATCTTAGCTTATT	3.50
Phosphoethanolamine cytidylyltransferase	2.7.7.14	*Pect* (5547)	AGCGCGTGCTCAGTGTTTT GCGTCCATGACAGACAACATC	CCTGCAAGTTTGTCAAT	3.50
Phosphatidate phosphatase	3.1.3.4	*wunen* (8804)	TGGCAGGATCGCTTATTGG GCTTCGTGTTGGGCTTTTGA	TCGTGGCCAACTAT	3.75
Phospholipase D	3.1.4.4	*Pld* (12110)	CGCATGAATGGCAAGAAGTATC CCGACTGGAACCTTCGCTTT	AGAACACTTAGGCCTCC	3.50
Ribosomal protein L32	NA	*RpL32* (7939)	AGGCCCAAGATCGTGAAGAA GACGCACTCTGTTGTCGATACC	AGCTGTCGCACAAAT	3.50
Sphinganine-1-phosphate lyase	4.1.2.27	*Sply* (8946)	CCTGAATGCGCTGCAGTTT CGACTCCGGGCTGTGTGT	CCATCTGGTATCCACC	3.50
Sterol regulatory element binding protein	NA	*Srebp/HLH106* (8522)	GAGAAGTTCCAGACCGATTTGAA GCGACAAACTGCCTCGTACA	TACCGAACGCCCAATC	3.50

*Final concentration of $MgCl_2$ in a 50 ml reaction containing 200 μmol l^{-1} dATP, dCTP and dGTP, 400 μmol l^{-1} dUTP, 900 nmol l^{-1} each primer, 250 nmol l^{-1} probe and 0.025 i.u./μl AmpliTaq Gold; PCR, 10 min hold at 95°C followed by at least 30 cycles of 15 s at 95°C and 60 s at 60°C.

Table S2. *Adh genotypes for the F/S amino acid and ∇1 indel polymorphisms*

	Innisfail									
Line	2	31	55	65A	72B	75A	77B	78A	80B	90
F/S*	H‡	S	S	S	S	H	H	H	S	H
∇1f/∇1s†	H	∇1s	∇1s	∇1s	∇1s	H	H	H	∇1s	H
	Tasmania									
Line	28	31	55	67	79	81	125	148	151	187
F/S	F	F	H	F	H	H	F	H	F	H
∇1f/∇1s	∇1f	∇1f	H	∇1f	H	H	∇1f	H	∇1f	H

*Forward primer, agctccctggcggtaagttgat; Reverse primer, acgagggctgggtgggatgag; PCR concentrations, 1.5 mmol l^{-1} $MgCl_2$, 0.2 mmol l^{-1} dNTPs, 0.3 μmol l^{-1} each primer, 0.02 i.u./μl *Taq*; PCR, 30 cycles of 50 s at 94°C, 50 s at 65°C and 30 s at 72°C; restriction digest, 1 μg of PCR product with 2.5 i.u. of *Hpy*CH4IV at 37°C for 1.5 h.

†Common reverse primer, agggctccgttagttgttggtttc, in combination with the control forward primer, gccaagtgcggaaataaaatgacag, and either the ∇1f forward primer, caagcatcaggcatataatata, or the ∇1s forward primer, 5′-caagcatcaggcatagttgggc; ∇1f PCR concentrations, 2.5 mmol l^{-1} $MgCl_2$, 0.2 mmol l^{-1} dNTPs, 0.3 μmol l^{-1} control forward primer, 0.3 μmol l^{-1} ∇1f forward primer, 0.6 μmol l^{-1} reverse primer and 0.025 i.u./μl *Taq*; ∇1f PCR, 30 cycles of 50 s at 94°C, 50 s at 58°C and 50 s at 72°C; ∇1s PCR concentrations, 4.5 mmol l^{-1} $MgCl_2$, 0.2 mmol l^{-1} dNTPs, 0.3 μmol l^{-1} control forward primer, 0.3 μmol l^{-1} ∇ 1s forward primer, 0.6 μmol l^{-1} reverse primer and 0.015 i.u./μl *Taq*; ∇1s PCR, 30 cycles of 50 s at 94°C, 50 s at 68°C and 50 s at 72°C.

‡H, both alleles were present in a sample of 20 flies.