Table S22 Candidate convergent nonsynonymous SNPs

Position	N1	N2	Fst	Codon		AA	mel and outgroup ref sequence state
hkl							
AUS 19,045,921	20	29	0.34	aac/gac	N/D	D= mel,sim, sech, yak, ere; Q = ana	
AUS 19,045,936	20	30	0.21	aaa/gaa	K/E	many changes from E to K and reverse	
NA 19,045,921	not segregating						
NA 19,045,936	not segregating						
NA 19,046,788	28	34	0.35	aca/cca	T/P	P = mel,sim, sech, yak, ere, ana; other species not T	
NA 19,046,828	29	27	0.48	aac/agc	N/S	S=mel,sim,sech,ana,pse,pers,vir,moj,grim; T = ere, L=will	
AUS 19,046,788	not segregating						
AUS 19,046,828	not segregating						
otk							
AUS 7,890,468	29	22	0.38	gtg/ctg	V/L	L = all species	
AUS 7, 890,646	18	26	0.33	gat/gag	D/E	D = mel; E = other species	
AUS 7,901,503	36	43	0.26	ttg/tcg		L/S	L = all species
NA 7,890,468		not segregating					
NA 7, 890,646	not segregating						
NA 7,901,503		not segregating					
NA 7,892,834				0.71	tct/gct		S/A
NA 7,892,839				0.70	agc/aac	S/N	
AUS 7,892,834	not segregating						
AUS 7,892,839	not segregating						

Position	N1	N2	Fst	Codon		AA	mel and outgroup ref sequence state
ana1							
AUS 20,359,353	31	37	0.36	gag/gcg	E/A	E=mel;A=sim,sech,yak,ere	
AUS 20,359,385	33	36	0.45	cga/gga	R/G	R=mel,sim,yak,ere,ana	
NA 20,359,353	15	49	0.007				
NA 20,359,385	not segregating						

NA 20,360,921	36	52	0.33	atg/ctg	M/L	L=all flies except virilis; virilis=M			
NA 20,361,171	36	39	0.38	cag/ctg	Q/L	Q= mel, si, sech,yak, pse, pers. will, moj; R=ere;H=ana;L=vir, gri			
AUS 20,360,921	43	28	0.007						
AUS 20,361,171	35	27	0.06						
Chm									
AUS 7,413,693	23	29	0.52	cag/gag	Q/E	Q= all species			
NA 7,413,693		not segregating							
NA 7,412,813		30	56	0.24	gat/tat		D/Y	Y=mel;D=si, sech, yak, ere, ana, wil, vir, moj, gri;E=pse,pers	
NA 7,413,132		23	36	0.22	cca/cga	P/R	R=all species; no data for willistoni		
AUS 7,412,813	not segregating								
AUS 7,413,132	not segregating								
Trp									
AUS 25,740,476	20	24	0.35	ggc/agc	G/S	S=mel;G=sim,sech,yak,ere,ana,;A=pse;T=will, other no data			
AUS 25,741,376	36	27	0.22	tca/cca	S/P	P=mel,si,sech,ya,ere,ana,pse,pers,will;T=vir,gri;others ND			
NA 25,740,476	38	52	0.02						
NA 25,741,376	36	56	0.06						
NA 25,741,665	27	28	0.34	ttc/tcc		F/S	S=mel,sim,sech,yak,ere;A=ana,pse.pers.will.moj.gri		
NA 25,743,316	32	40	0.24	cac/aac	H/N	N=ana; H=all other species			
AUS 25,741,665	not segregating								
AUS 25,743,316	27	18	0.10						

CANDIDATE NORTH AMERICAN SPECIFIC DIFFERENTIATED NONSYNONYMOUS SNPS

Gene	Position	N1	N2	Fst	codon		residue	references sequence states	
Lsp2 (3L)	12,122,543	37	36	0.41	atg/gtg	M/V		V=mel,sim,sech,yak,ere,ana,pse,pers,grim;	
	Not segregating in AUS								L=wil,vi,moj
Oatp33Ea (2L)	12,442,835	31	65	0.50	tgt/ggt		C/G		L=all species
In AUS		29	37	0.08					