Supplemental Table S1.

Gene	Loc	M/F	Sites	Syn	Non	n	Ds	Ps	Dn	Pn	P	TDs	TDn
Male-Biased													
CG11379	1E3	3.04	603	155	448	12	17	7	5	4	0.4130	-1.07	-1.39
CG2574	11A9	7.34	846	166	542	9	16	14	15	7	0.2783	0.95	0.64
CG1314	19E4	8.95	1056	238	817	10	33	12	80	4	0.0004	-1.30	-0.82
CG9156	13B9	6.65	906	212	694	9	37	15	1	0	1.0000	0.01	na
CG12681	4D3	12.14	1104	244	860	11	47	5	120	3	0.0490	0.98	0.60
CG12395	14A6	7.11	765	159	603	12	18	4	20	0	0.1100	1.27	na
CG2577	11A9	8.26	1035	241	791	11	32	26	4	0	0.1320	-0.98	na
CG1950	11A2	6.68	1023	228	792	10	33	20	64	15	0.0175	0.12	-0.80
CG1503	19F1	6.16	1007	224	697	12	20	12	24	6	0.1260	0.03	-1.43
CG6789	4F1	7.40	972	227	742	12	33	20	47	17	0.2000	0.62	0.07
CG11697	10C7	4.81	669	155	511	12	28	1	17	5	0.0730	-1.13	-0.32
CG5662	13B3	4.06	861	198	663	12	15	23	20	8	0.0133	-0.01	0.23
CG6999	8C8	3.49	665	126	471	12	26	3	81	6	0.5600	-1.18	-1.11
CG5334	12F4	3.93	450	99	351	11	21	5	63	3	0.0340	0.25	-1.61
CG18341	5C2	4.66	1081	233	688	11	26	22	18	2	0.0026	-0.08	-1.42
CG10920	7C1	4.91	1197	297	894	12	43	24	56	11	0.0099	-0.06	-0.27
CG7860	13D3	3.11	996	258	738	12	19	22	10	5	0.1741	-0.64	-0.99
Female-biased													
CG14434	6D7	0.24	564	136	425	12	7	4	6	2	0.6000	1.07	-0.24
CG15717	11E1	0.28	919	185	571	12	12	7	16	8	0.8107	-0.90	0.12
CG9125	15A9	0.31	1218	257	868	12	34	11	62	5	0.0125	-0.70	0.52
CG3024	4C11	0.35	1098	236	784	10	35	5	51	6	0.7637	-0.68	-0.58
CG8326	16B9	0.34	1068	228	768	12	18	13	9	5	0.6922	-0.20	0.14
CG3704	1D2	0.33	1267	264	879	8	29	11	14	1	0.0690	-0.29	-1.09
CG12117	7E11	0.38	786	193	590	11	20	12	5	2	1.0000	0.43	0.85
CG3004	8F1	0.37	998	218	721	10	23	18	7	0	0.0360	-0.43	na
CG4593	6E4	0.37	630	137	490	12	12	19	3	0	0.0760	0.48	na
CG8675	15F4	0.42	705	146	556	12	13	5	2	1	0.8500	-1.29	-1.16
CG2222	9B14	0.40	759	152	484	10	10	11	2	4	0.5310	-0.31	-1.79
CG9915	14B9	0.43	1261	233	832	12	17	8	4	1	0.5800	0.02	-1.15
CG1749	10B15	0.42	1307	290	922	10	26	5	4	9	0.0007	-0.94	-0.62
Unbiased													
CG14629	1E1	1.09	756	180	576	8	16	2	6	3	0.1700	-1.31	0.33
CG1751	10B15	1.03	727	139	458	12	10	1	1	2	0.0450	-1.14	-1.45
CG15247	9A3	1.01	1130	261	801	10	11	22	3	13	0.2780	0.44	-0.44
CG9919	14B13	1.02	1070	223	728	11	29	17	2	2	0.6110	-0.38	-1.43
CG2555	11B1	1.00	854	159	432	10	9	15	4	4	0.5400	-0.75	0.50
CG1397	10A8	0.97	702	108	345	12	7	2	8	4	0.5700	-0.39	0.47
CG9571	19B1	0.95	765	170	592	12	14	10	8	10	0.3700	-0.14	-1.29
CG14797	2B7	1.05	787	165	498	12	9	8	7	4	0.5800	0.25	-0.25
CG3603	3C3	0.98	818	195	552	8	28	18	1	1	0.7600	-0.12	-1.07
CG14772	2A2	0.99	640	126	369	12	10	2	3	5	0.0330	-1.46	-1.12
CG11126	10A4	1.01	713	140	451	9	10	12	8	11	0.8300	-0.36	-0.70
CG15313	9A5	0.99	614	141	417	12	14	10	6	11	0.1440	-0.39	-1.55
CG9723	14F5	0.95	1251	299	883	11	36	18	61	5	0.0003	-0.46	-1.01
CG9164	13C1	1.02	1245	210	678	9	14	28	1	8	0.1530	-0.38	-1.80
CG15336	7D16	1.08	480	111	366	12	10	17	10	13	0.6400	-1.47	-0.68

Table S1 column descriptions:
1. Gene = CG number (D. melanogaster genome release 4)
2. Loc = Cytological location
3. M/F = Average male/female expression ratio
4. Sites = Total number of sites sequenced, including introns
5. Syn = Number of synonymous sites
6. Non = Number of nonsynonymous sites
7. n = Sample size (number of D. melanogaster alleles sequenced)
8. Ds = number of synonymous fixed differences between species
9. Ps = number of synonymous polymorphisms within D. melanogaster
10. Dn = number of nonsynonymous fixed differences between species
11. Pn = number of nonsynonymous polymorphisms within D. melanogaster
12. P = P-value from MK test. Red numbers indicate significant tests in the direction of positive selection. Blue numbers indicate significant tests in the direction of weak purifying selection.
13. TDs = Tajima's D for synonymous sites
14. TDn = Tajima's D for nonsynonymous sites