

TABLE S1***D. subobscura* O chromosome gene regions**

	<i>AcpH-1</i>	<i>rp49</i>	S25	P22	P154	P2	S1	P21	
Chromosomal location in <i>D. subobscura</i>	91C	91C	92B	93B	94A	94E	95A	95B	
Chromosomal location in <i>D. melanogaster</i>	99D1	99D3	97D1	96A20	87B11	89E4	100A6	100B1	
GenBank accession no.	AE003772	AE003772	AE003757	AE003749	AE003696	AE003715	AE003775	AE003776	
Gene name	<i>AcpH-1</i>	<i>RpL32</i>	—	<i>Ast</i>	—	—	<i>abd-A</i>	<i>BcDNA:GH03163</i>	<i>CanAI</i>
Genome Annotation	CG7899	CG7939	CG14247	CG13633	CG5333	CG5961	CG10325	CG1408	CG1455
Molecular function	acid phosphatase	ribosomal protein	chitin binding protein (putative)	neuropeptide hormone	programmed cell death (putative)	ciclin-F like (putative)	transcription factor	SH3/SH2 adaptor protein	protein phosphatase

Sequences from selected recombinant phages were compared with the *D. melanogaster* nucleotide database (Flybase) using the heuristic search algorithm BLASTN at Berkeley Drosophila Genome Project (BDGP). The 6 newly reported gene regions (S25, P22, P154, P2, S1 and P21) are named according to the phages from which they were obtained.

TABLE S2Nucleotide sites and polymorphism in the gene regions of the O chromosome of *D. subobscura*

	<i>Acph-1</i>	<i>rp49</i>	S25	P22	P154	P2	S1	P21	Total ^a
n	41	34	28	28	28	28	28	28	28
Sites	2170	1798	2156	1788	2226	2186	1220	2418	11994
Sites without gaps	2145	1470	2051	1703	2219	2017	1182	2370	11542
Sites in coding regions	1341	402	357	363	1845	213	141	1128	4047
Sites without gaps in coding regions	1341	402	339	363	1839	213	141	1128	4023
<i>S</i> (η)	163 (167)	89 (92)	126 (131)	110 (111)	104 (105)	121 (124)	50 (51)	89 (90)	600 (612)
% Singletons	36.2	42.7	51.6	43.6	43.3	57.0	50.0	46.1	48.8
Silent sites	1135.1	1164.2	1794.0	1434.9	807.6	1863.1	1073.8	1508.1	8481.5
Silent mutations	142	92	121	104	74	122	50	89	560
Nonsynonymous sites	1009.9	305.8	257.0	268.1	1411.4	153.9	108.2	862.0	3060.5
Nonsynonymous mutations	25	0	10	7	31	2	1	1	52

n, sample size or number of sequences; *S*, number of polymorphic sites; η , number of mutations. ^a Data only from the 6 newly reported gene regions.

TABLE S3

Neutrality tests

	<i>AcpH-1</i>		<i>rp49</i>		S25		P22		P154		P2		S1		P21		Concatenated data ^a	
	O _{ST}	O ₃₊₄	O _{ST}	O ₃₊₄	O _{ST}	O ₃₊₄	O _{ST}	O ₃₊₄	O _{ST}	O ₃₊₄	O _{ST}	O ₃₊₄	O _{ST}	O ₃₊₄	O _{ST}	O ₃₊₄	O _{ST}	O ₃₊₄
Tajima's <i>D</i>	-0.752	0.109	-1.326	-1.001	-1.266	-1.465	-1.155	-0.562	-0.484	-1.416	-0.833	-1.101	-0.699	-0.767	-0.057	-0.729	-0.808	-0.861
Fu and Li's <i>D</i> (without outgroup)	-0.875	0.000	-1.560	-1.168	-1.472	-1.852	-1.158	-0.445	-0.501	-1.757	-1.180	-1.718	-1.127	-1.054	-0.133	-1.048	-0.929	-1.142
Fu and Li's <i>F</i> (without outgroup)	-0.979	0.038	-1.725	-1.300	-1.626	-2.006	-1.329	-0.548	-0.570	-1.911	-1.246	-1.779	-1.159	-1.120	-0.129	-1.103	-1.029	-1.224
Fu and Li's <i>D</i> (<i>D. madeirensis</i>)	-1.208	0.201	-1.786	-1.542	-1.825	-2.176 *	-1.654	-0.637	-0.659	-2.123 *	-2.030 #	-2.166 *	-1.532	-0.965	-0.318	-1.371	-1.347	-1.386
Fu and Li's <i>F</i> (<i>D. madeirensis</i>)	-1.323	0.215	-1.987	-1.659	-2.017	-2.396 *	-1.834	-0.764	-0.740	-2.333 #	-2.055	-2.317 *	-1.556	-1.105	-0.290	-1.424	-1.448	-1.506

#, 0.05 < P < 0.10; *, P < 0.05 (two-tailed test).

^a Analysis performed in the concatenated sample including the information for the loci sequenced in the same 28 lines (see Materials and Methods).

Figure S1

Amplification Primers

P154 gene region

Name	Forward/Reverse	Sequence (5' → 3')
P154-55	F	ctgtctgcaaaggcttctatg
P154-1292	R	accagcacttggacaatcag

S1 gene region

Name	Forward/Reverse	Sequence (5' → 3')
S1-29	F	tcgagcagcgggtggacaagc
S1-6666	R	gcgatacaaaatgcgacatac

P22 gene region

Name	Forward/Reverse	Sequence (5' → 3')
P22-122	F	caaagttgaagggctgcggac
P22-2136	R	tttcgcctattatctcgtgg

P21 gene region

Name	Forward/Reverse	Sequence (5' → 3')
P21-475	F	taccgcttaccatgtccgagg
P21-71	R	acatggaagctgcgaattgag

S25 gene region

Name	Forward/Reverse	Sequence (5' → 3')
S25-68	F	acggccacgaatgcaacatgc
S25-371	R	ctgcattgactctgggcaaac

P2 gene region

Name	Forward/Reverse	Sequence (5' → 3')
P2-799	F	ataccagtcgatgagcgtacc
P2-p2amp	R	cctcaaaactcgtatccaacc

Amplification Conditions:

All regions have been amplified with similar conditions, except region P2.

Amplification conditions have been optimized in a GeneAmp® PCR System 2400

For P154, S1, P22, P21 and S25 gene regions:

# cycles	Temp (°C)	Time	Temp (°C)	Time	Temp (°C)	Time
1	95	1'	50	10''	68	2' 30''
32	94	10''	50	10''	68	2' 30''
1	94	10''	50	10''	68	5'

For P2 gene regions:

# cycles	Temp (°C)	Time	Temp (°C)	Time	Temp (°C)	Time
1	95	1'	45	10''	68	2' 30''
32	94	10''	45	10''	68	2' 30''
1	94	10''	45	10''	68	5'

Figure S2. Polymorphic sites at the six new gene regions in *D. subobscura* and *D. madeirensis* (Supplementary Material).

S25 gene region

S25-01 (Ost) CAGGTGCGAGGGCCCCCAAGTGACGCCCATGGAAGATAAAGACAGTCTCGCTGTGAAGTACCGCCCTCGCGGCTCCCCACTACGAAAACATATAATCAAT
 S25-02 (Ost) G C A C . AT A C A CG
 S25-03 (Ost) A . . . G G CG C . G CG
 S25-04 (Ost) A . . . G A C . AT C T A GT CG . G -
 S25-05 (Ost) - G AT C A A CG
 S25-06 (Ost) G CG A A GC C . T T CG
 S25-07 (Ost) G . C A CG G
 S25-08 (Ost) G A CG C . AT C T GCG . . C
 S25-09 (Ost) . . . TG CG C A CG -
 S25-10 (Ost) A . . . G A C . AT A C A CGTG
 S25-11 (Ost) G C A . C CG
 S25-12 (Ost) G TA C T CG
 S25-13 (Ost) - . C
 S25-14 (Ost) . C . AT A C CG
 S25-21 (O₃₊₄) A . . . GAG . . CC . . AA C T . . GA . . C . . A . C T C . . TT . T . . . AA CG . . . T
 S25-22 (O₃₊₄) AT . . GAG . . CCA . A C T . . A . . CG . G - . A C T . . CTA CG T . T
 S25-23 (O₃₊₄) AT . . GAG . . CC . . AA A T . . A . . CG . G T C T . . AA CG -
 S25-24 (O₃₊₄) A . . . G . G . . CC . . A T . . A . . CG . G T G . C T . . A C . CG - . G
 S25-25 (O₃₊₄) A . . . G . G . . CC . . A . T . G . . C . . . T . . A . . CG G T C T . . A CG . . . T
 S25-26 (O₃₊₄) A . . . G . G . . CC . . A . . G . . C . . . T . . GA . . C . . A G T C T . . A CG . . . T
 S25-27 (O₃₊₄) AT . . G . G . . CC . . A C T . . A . . CGT T C T . . AA CG . . . T
 S25-28 (O₃₊₄) G A CG C . AT C T GCG . . C
 S25-29 (O₃₊₄) AT . . G . G . . CC . . A . T . . C . . AT . . A . . CG . G T C T . . A T . . CG . . T
 S25-30 (O₃₊₄) A . T . G . G . . CC . . A C T . . AATCG T . A C T . . C . A . T CG G . . G
 S25-31 (O₃₊₄) A . . . G . G . . CC . . A C AT . . A . . CG . G . G T . . T C AT . . A CG - . G
 S25-32 (O₃₊₄) A . . . G . G . . CC . . A C AT . . A . . CG . G G . . T . . T C T . . AA CG - . G
 S25-33 (O₃₊₄) AT . . G . GA . CC . . A A T . . A . . CG A T CG T . . C . A . A CG - . G . G
 S25-36 (O₃₊₄) A . . . G . G . . CC . . A C AT . . A . . CG . G T C T . . A T . . CG - . G
 S25-MAD . . T . . G . . . CCA . . A GTAT G TA . . . A . . . C T C . . C . . CG C . . A

S25 gene region (cont.)

S25-01 (Ost) CGCGATTGACTTGCTCGCATAACAGTATG-CAACATGGCGGCAGATTGCATTA
S25-02 (Ost) T.....T.....T.....A...G.....A.....G.....
S25-03 (Ost) T.....T.....T.....A...G.....A.....G.....
S25-04 (Ost) T.....T...C.....G.A...G.CG...A.....G...C..
S25-05 (Ost) T.....T..A.-.....G.....AT.....G.....
S25-06 (Ost) T.....T..A.-.....A...G.....AT.....G.....
S25-07 (Ost) T...A..T.....TG...A...G...G..A.....G.C.....
S25-08 (Ost) T...A..T..A.-..T.....A...-.....A.....
S25-09 (Ost) T.....T.....T.....A...G.....G.....
S25-10 (Ost) T.....T...-..A...G.A...G.....T.G.....
S25-11 (Ost) T.....T.....A...G.....G.....
S25-12 (Ost) T.....T...-.....G.....G.....
S25-13 (Ost) T.....T.....T.....A...G.....G.....
S25-14 (Ost) T.....T.....A...G.....A.....G.....
S25-21 (O₃₊₄) T...G...T...-T...T.G.A...GT...A...C..G.A...C
S25-22 (O₃₊₄) T...G...T...-...T.G.A...GT...A...C..G.....
S25-23 (O₃₊₄) T.T.G...T...-...ATCG.A...GT...T.A.A...C..G.....
S25-24 (O₃₊₄) T...G..A.T...-A...TTG.A...GT...A...C..G.....
S25-25 (O₃₊₄) T...G...GT...--...T.G..A...GT...A...C..GAA...C
S25-26 (O₃₊₄) T...G...T...-T...T.G.A...GT...A...C..G.....
S25-27 (O₃₊₄) T...G...GT.A.-...T.G.A...GT...AG...C..G.....C
S25-28 (O₃₊₄) T...A..T..A.-..T.....A...-.....A.....
S25-29 (O₃₊₄) T...G...T...-T...T.G.A...GT...A...C..G.A.....
S25-30 (O₃₊₄) T.....GT.A.-...T.G.A...GT...CA...C.GG.AT...C
S25-31 (O₃₊₄) T...G...TC...-...ATCGGA.T.GT...A.A..C.GG.AT...
S25-32 (O₃₊₄) T...-...T...--...T.G.A...GT...A...C..C.GG.....
S25-33 (O₃₊₄) T...G...T...-...T.G----.GT...A...C..GAA...C
S25-36 (O₃₊₄) TA..G...T...--...T.G..A...GT...A.AG...C..G.....C
S25-MAD T...A.G...T...T.....T.G.A..GAAT.....A.....G...T.C.

P22 gene region

P22-01 (Ost) TGTTTAGAGGTCAATTCCAAACTATACGTGTGGCGGTTTCGGTTGGCCAGGAGAAGGCATATCAAGTTTATAGTTCCTCCACTCGGGTTTTTGCAATATTGAAC
 P22-02 (Ost) .A.....CA..A.....T.....C.....T.....
 P22-03 (Ost)CA.....A.....T.....
 P22-04 (Ost)CA..A.....G.....T.....
 P22-05 (Ost) .A.....CA..A.....T.....G.....C.....
 P22-06 (Ost)CA..A.....G.....TT..A.....G.....
 P22-07 (Ost)CA..A.....T.....T.....G.....
 P22-08 (Ost)CA..A.....A..T.....T.....T.....
 P22-09 (Ost)CA..A.....T.....TT.....T.....G.....
 P22-10 (Ost)CA.....CA..A.....T.....T.....G.....
 P22-11 (Ost)C.....CA..A.....G.....T.....G.....
 P22-12 (Ost)CA..A.....A..T.....T.....G.....T.....G.....
 P22-13 (Ost)CA.....A.....T.....C.....
 P22-14 (Ost)CA..A.....T.....TT.....T.....
 P22-21 (O₃₊₄) A..C.....C..CAT..AC.....C..T.....T..G..A..TT.....CCC.....T..T..A.....T..T.....
 P22-22 (O₃₊₄) A.....C..CAT..AC.....C..T.....T..G..A..TT.....CCC.....T..T..A.....T..T.....
 P22-23 (O₃₊₄) A.....CA..AC..A.....C..T.....T..AG..A..TT..A.....CA..TA.....AC..T.....A.....
 P22-24 (O₃₊₄) A.....CA..AC..A..T..C..T.....T..AG..A..TT.....CA..TA.....AC..T.....A.....
 P22-25 (O₃₊₄)GA..C..A..G.....CA..AC.....C..T.....T.....C..A..C..A..AC..T.....A.....G.....
 P22-26 (O₃₊₄) A..C..T.....CA..AC.....C..T.....T.....TT.....CCC.....AC..T.....G.....
 P22-27 (O₃₊₄) A.....CA..AC..A.....C..T.....T.....TT.....C..A.....ACTT.....A.....G.....
 P22-28 (O₃₊₄) A.....C.....A..G..CA..ACT.....C..T.....T.....TT.....CCC.....A..CG..G..AC..T.....A.....G.....
 P22-29 (O₃₊₄) A.....CA..AC..C.....C..T.....T.....CCC.....A..A..AC..T.....A.....-.....A.....
 P22-30 (O₃₊₄) A.....C.....CA..AC.....C..T.....AT.....CCC.....G..AC..T..G.....
 P22-31 (O₃₊₄) A.....A.....CA..AC..C.....C..T..G..T.....TT.....C..A.....AC..T.....A..T.....G..G.....
 P22-32 (O₃₊₄) A.....C.....TACA..TAC.....TCC..TC..G..AT.....TT.....CCC.....G..AC..T..G.....T..T.....
 P22-33 (O₃₊₄) A.....CA..AC.....C..T.....T.....TTT.....CCC.....T..T.....A.....T..T.....
 P22-36 (O₃₊₄) A.....TACA..AC.....C..T.....T.....TT.....CCC.....A..CG..G..AC..T.....A.....
 P22-MAD A.....CT..T.....CA..AC.....T..C.....T.....TG.....AC..T..A.....G..GC.....TGCT

P22 gene region (cont.)

P22-01 (Ost) GAGGATGTCGGCCCCGACAGGCGCGAGAAT
P22-02 (Ost)CA.....A..C..CT.
P22-03 (Ost)C.....G.....
P22-04 (Ost)C.....CT.
P22-05 (Ost)C.....A..A..C....
P22-06 (Ost)CA.....T...C..A..AC....
P22-07 (Ost)C.....C.....
P22-08 (Ost)CA.....A..C....
P22-09 (Ost)C.....
P22-10 (Ost)CA.....
P22-11 (Ost)CA.....A..C...A
P22-12 (Ost)CA.....A..C....
P22-13 (Ost)C.....G.....
P22-14 (Ost)CA.....A..C....
P22-21 (O₃₊₄)C..A...TGAGA.....
P22-22 (O₃₊₄)C..A...TGAGA.....
P22-23 (O₃₊₄)C..C...TGAGA...A..CA...
P22-24 (O₃₊₄)C..C...TGAGA...A..CA...
P22-25 (O₃₊₄) .C...C...TGAGA...A.....
P22-26 (O₃₊₄) .C...C..C...TGAGA...A..CA...
P22-27 (O₃₊₄) .C...C...TGAGA...A..C...A
P22-28 (O₃₊₄) ..A..CC..CA..TGAGA.....
P22-29 (O₃₊₄) .C...C...TGAGA.....A
P22-30 (O₃₊₄)C...TGAGA...A..CA...
P22-31 (O₃₊₄) .C...C..C...TGAGA...A.....A
P22-32 (O₃₊₄)C...TGAGA...G..A...
P22-33 (O₃₊₄) .C...C...TGAGA...A..C....
P22-36 (O₃₊₄)C..C...TGAGA...A..CA...
P22-MAD A--AT.C..C..TT.....GA..C....

P154 gene region

P154-01 (Ost) GGTGGGCTTACATCACTTCATCGACCATCAGCCAGGGGGAGGTGTGTATTTCGAGCTTAAATTTGGGGCACCTTCTACATGGTGCCCATTCAGGATAAGGT
P154-02 (Ost)T.....TT.....TC..T.....T.AT...C.....T..A.....
P154-03 (Ost)TC..T.....C..A..T.AT.....T..A.....
P154-04 (Ost)AAG...T.T..TT.....T.....C..A..T.AT...C.....T..A.....
P154-05 (Ost)T.....T.....C.....
P154-06 (Ost)TT.....C.....T..TG.CC..C.....T.....T..A.....
P154-07 (Ost)AT.A..TCC..C.....AT.....
P154-08 (Ost) .T.....T.....T.T.TTT...T.....T...TCC..C..A.....T.....T..A.GT....
P154-09 (Ost)T.T.TTT.....T.....C.A.....T.....T..A.GT....
P154-10 (Ost)C.....G.T.....C.....T.....
P154-11 (Ost)TT.....C.....T.....C.....G..T..A.....
P154-12 (Ost)T.....TC..T.....C.....T.....
P154-13 (Ost)T.....T.....TC..T.....AT.....T.....
P154-14 (Ost)TT.....T.....C.....T.AT.....T..A.....
P154-21 (O₃₊₄) A.C...T..TA.G...G..G.AAG...C..TT.TT..AA.....T.C.A...T...G.CA..C.....T.....A...A.GC..GAA.G.T.AA
P154-22 (O₃₊₄)TAGG...GA.G.AAG...TT.TT.....C.....T...G.CC..C.....T.....A...GC..GAA.G.T.AA
P154-23 (O₃₊₄) A.CCTTT..TA.G...G..GCAAG...TTT.TT.....CC.....T...G.CCGTC.....T.....A...GC..GAA.G.T.AA
P154-24 (O₃₊₄)TA.G...G..GCAAG...TTT.TT.....C.....T...G..C..C.....T.....A...GC..GAA.G.T.AA
P154-25 (O₃₊₄) A.C...T..TA.G...G..G.AAG...TT.TT.T.....C.....T...G.CC..C.....T.....A...GC..GAA.G.T.AA
P154-26 (O₃₊₄)A.TA.G...G...AAG...TTT.TT.....C.....T...G.CC..C.....T.....ACAA..GC..GAA.G.T.AA
P154-27 (O₃₊₄)TA.G...G..G.AAG...T..TT...A.A..AC.....T...G.CA..CT.....T.....C..GAA.G.T.AA
P154-28 (O₃₊₄)TA.G..AG..G.AAG...TT.TT.....C.....T...TG.CC..C.....T...G..ACAA..GC..GAA.G.T.AA
P154-29 (O₃₊₄)TA.G...G.TG.AAG...TT.TT.....C.....T...G.CC..C.....T.....GC..GAA.G.T.AA
P154-30 (O₃₊₄) A.C...T..TAGG...GA.G.AAG...TTT.TT.....T..C.....T...G.CC..C.....T.....A...GC..GAA.G.T.AA
P154-31 (O₃₊₄)TA.G..AG..G.AAG...TT.TT.....C.....T...G.CC..C.....T.....AA...GC..GAA.G.TTAA
P154-32 (O₃₊₄)TA.G..AG..G.AAG.G.....TT...G...C..C.....T...G.CC..C.....T.....ACAA..GC..GAA.G.T..A
P154-33 (O₃₊₄) ..C...T.CTAGG...GA.G.AAG...TT.TT.....C.....T...G.CC..C.....T.....ACAA..GC..GAA.G.T.AA
P154-36 (O₃₊₄)TA.G..AG..G.AAG...TT.TT.....C..C.....TA..G.CC..C.....T.....A...GC..GAA.G.TTAA
P154-MADG.G.....GA.G.....T.....T.....CC..C...TT.C.TATG...A...GCC.G.AG..T...

P154 gene region (cont.)

P154-01 (Ost) CTAAGCTCCCAGTCGCAAA
P154-02 (Ost) A.....C.....
P154-03 (Ost)C.....
P154-04 (Ost)
P154-05 (Ost)C...C.....GCT
P154-06 (Ost)C.....
P154-07 (Ost)C...C.....
P154-08 (Ost)C...C.....
P154-09 (Ost)C...C.....
P154-10 (Ost)C...C.....
P154-11 (Ost)C.....
P154-12 (Ost)C...C.....
P154-13 (Ost)C.....
P154-14 (Ost)C.....
P154-21 (O_{3+4}) ..T...C...C.....
P154-22 (O_{3+4}) ..TT...C...C.....
P154-23 (O_{3+4}) .GT...C.G.C.....
P154-24 (O_{3+4}) ..T...C...C.....
P154-25 (O_{3+4}) ..T...C...C.....
P154-26 (O_{3+4}) ..T...C...C.....
P154-27 (O_{3+4}) ..T...C...C.....
P154-28 (O_{3+4}) ..T...C...C.....
P154-29 (O_{3+4}) ..T...C.G.C..T.....
P154-30 (O_{3+4}) ..T...C...C.....
P154-31 (O_{3+4}) ..T.C.C.G.C.....
P154-32 (O_{3+4}) ..T...C...TC...A...
P154-33 (O_{3+4}) ..T...C.G.C.....
P154-36 (O_{3+4}) ..T...CT..C.....
P154-MADGC...CAC.C.....

P2 gene region

P2-01 (Ost) CCGGTTGTTCTCGAGTGCCTGTTCCACGCTCGAAATCATCTACTCATCCGTCGATCTTCCCTACAGTGCGAAGGGCATGACCAATCTGGTG--TGGATA
 P2-02 (Ost) G.C.....C.....T.....GGA..C.....A.....--.....
 P2-03 (Ost)C.....T.....G.A.....--.....
 P2-04 (Ost)C.....T.....G.A..C.....A.....--.....
 P2-05 (Ost) ..T.....C.....CT.....G.A..CA.....A.....A.....--.....
 P2-06 (Ost)C.....T...G...G.A..C.....A.....T.....--G.T...
 P2-07 (Ost)C.....T.....G.A.....A.....T.....--T...
 P2-08 (Ost)C.....T.....G.A..C.....A...A.....--.....
 P2-09 (Ost)G.A..C.....A.....--.....
 P2-10 (Ost)T.....G.A.....--.....
 P2-11 (Ost) ..T.....C...T.....T.....G...C.....A.....A...T.....--.....
 P2-12 (Ost) ..T.....C.....AT.....G.A.....A...A.....C.--.....
 P2-13 (Ost) .A.T.....C.....T.....G.A..C.....A.....--.....
 P2-14 (Ost) ..T.....T.....G.T.....G.....--.....
 P2-21 (O₃₊₄) ...CCA.....C.....C.....C...ATCC...C..G-AC.....AT.T.T.C.....C...A...A.....G...C.A...AT...C.
 P2-22 (O₃₊₄) ...CC.....C.....ATCC...C..G-A.....AT.T...C...GA...A...A.....C...A...CT...C.
 P2-23 (O₃₊₄) ...CC.....A.....C...ATCC...C..G-A.....A.....A.A...A.....G.A...CC...G
 P2-24 (O₃₊₄) ...CC...T...A.....C.A.AT.....CC.G-ACT...TAT...C.....A...A.....C...C.A...--...C.
 P2-25 (O₃₊₄) ...CC.....C...ATCC...C..G-AC.....AT.T.T.C...GA...A...A...A.....C.A...CT...G
 P2-26 (O₃₊₄) ...CC.....C...AT.....C..G-AC.....AT.T...C.....A...A.....TG...A...T--...C.
 P2-27 (O₃₊₄) ...CC.....C.....C...AT.....C..G-AC.....A...T...C.....A.....G...C.A...CT...C.
 P2-28 (O₃₊₄) ...CC.....T...C...ATCC...C..G-A.....AT.T.T.C...GA...A...A.....C...A...CT...C.
 P2-29 (O₃₊₄) ...CC.....C...TATCC...C..G-AC.....AT.T...C...GA...A...A.....C...A...CT...C.
 P2-30 (O₃₊₄) ...CC.....C.....C...ATCC...C..G-A.....A.....C.T.C...A...A.....G...C.A...CT...G
 P2-31 (O₃₊₄) ...CC...G.....A.....C...ATCC...C..G-AC...A.AT.T...C.....A...A.....AAG...T--...
 P2-32 (O₃₊₄) ...CC.....T.C.....C...ATCC...C..G-A.....AT...CT.T...A...A.....C.A...T--...C.
 P2-33 (O₃₊₄) ...CC...C.....A...C...ATCC...C..G-A.....AT.TCT.C...A...A.....C.A...--...T.G
 P2-36 (O₃₊₄) ...CC.....C...AT.....C..G-A.....AT.T...C.....A...A.....C.A...T--...
 P2-MAD ...C..AA.....C..C.TGCT..AT..CT.T..GG-A..C.G.....AAA.CG...C..AG...CC.----

P2 gene region (cont.)

P2-01 (Ost) GCGGCCGCGCCG-TGGCTTGTGCATACGCCCTATCTGTGCGAGAACAA
P2-02 (Ost)ATAAT.....C.....TGC.....GC
P2-03 (Ost)AT.A-.....C.....T.....AG.....
P2-04 (Ost)AT.AC.....T...T.C.....
P2-05 (Ost) ...ATTTAT..C.....T.....
P2-06 (Ost) ...ATTTAT.AT.....G.....CAA.....
P2-07 (Ost)AT.AC.....C.....T.C.....
P2-08 (Ost)AT.AT.....G.....
P2-09 (Ost)TAT.A-.....G.....T.C..T.....
P2-10 (Ost)AT.A-C.TG.....G.....CAA.....
P2-11 (Ost)AT.A-.....T.....
P2-12 (Ost)AT.AT.....C..G.....T.....
P2-13 (Ost)AT.AT.....CAA.....
P2-14 (Ost)AT.AT.....G.....
P2-21 (O₃₊₄) C.A...AT.A-...G..C...AG.T.....
P2-22 (O₃₊₄) C..A...AT.A-...G..C...C.AG.T.....
P2-23 (O₃₊₄) CT....AT.A-.C..G..C...AG.T.....--.....
P2-24 (O₃₊₄) C..ATT.AT.AC...GA.C...AG.T.....G...
P2-25 (O₃₊₄) CT....AT.AC...G..C.T...AG.T..T.....AG...
P2-26 (O₃₊₄) C..ATT.AT.A-...G..C...A.GT.....G.....
P2-27 (O₃₊₄) C..ATT.AT.A-.....C...AG.T.....C.....
P2-28 (O₃₊₄) C..ATT.AT.AC.....CA...AG.T.....
P2-29 (O₃₊₄) C..ATT.AT.A-...G..C...A..T.....AG...
P2-30 (O₃₊₄) CT...T.AT.A-.....CA...AG.T.....T...
P2-31 (O₃₊₄) C...TT.AT.A-.....C...AG.T.....A.-----
P2-32 (O₃₊₄) C..ATT.AT.A-...G..C...A.GT...A.....AG...
P2-33 (O₃₊₄) CT..T-.AT.A-.....C.....T.....G.....
P2-36 (O₃₊₄) C..ATT.AT.A-.....AC.....AG.T.....AG...
P2-MAD -----

S1 gene region

S1-01(Ost) GATTGGCCCTACCTCTATTCTGACTAAGCCAGGCGCTAGTCCCTCATGTTACTATAACCAC
S1-02(Ost)T.....
S1-03(Ost)G.....A.....
S1-04(Ost)A.....C.....G.....A
S1-05(Ost)T.....A
S1-06(Ost)C.....TC.....
S1-07(Ost)A.....A
S1-08(Ost) ..C.....A...G.....T.....
S1-09(Ost)C.....C.....TC.....
S1-10(Ost)C...A...G.....A.....A
S1-11(Ost)AT.....C.....T.....
S1-12(Ost)T.....A.....
S1-13(Ost)T.....A.....A.....
S1-14(Ost)A.....T.....A
S1-21(O₃₊₄) .C.C.T.A.T.T.C.T.....C.....T.G...C.G..AA.....A..
S1-22(O₃₊₄) .C.C...TA..C.C...CA.....C.....T.G...C.G...A.....A..
S1-23(O₃₊₄) .C...A..TA..T.....C.....C.....C.....C.G.T.A.....A..
S1-24(O₃₊₄) .C.....TA..C.C...GCA.....T.AC.....C.....C.G.T.A.....A..
S1-25(O₃₊₄) .C.C...TA..T.....C.....C.....T.G...C.G...A.....AG..
S1-26(O₃₊₄) .C.....TA..T.....C.....C.....T.G...C.G.T.AC.C.....A..
S1-27(O₃₊₄) .C.C...TA..C.C...C.T.....C.....T.G...C.G...A.....A..
S1-28(O₃₊₄) .C...A..TA..C.C...A.....C.....T.GTT.C.G...A...G...A..
S1-29(O₃₊₄) AC...A...A...CTC...A.A...T.C.....T.G...C.G.-.A.....C.A..
S1-30(O₃₊₄) .C...A..TA..T.....C.....C.....T.GT...C.G...A.....A..
S1-31(O₃₊₄) .C...A..TA..T.....C.....C.....T.G...C.G.T.A.....
S1-32(O₃₊₄) AC...A...AT.T.....C.....C.....C.....C.G...A.....A..
S1-33(O₃₊₄) .C.C...TA..C.C...C.T.....C.....T.G...C.G.T.A.....A..
S1-36(O₃₊₄) AC.CT...TA.T.C.C...C.....C.....T.G...C.G.T.A.....T..A..
S1-MAD .C...A.....AA..A.AAG...CT.....A...CTGGT.....A..T.G.

P21 gene region

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P21-01 (Ost) CTAAGGCTATCAAGCCTGCGAAAATGCAATCCTCAATTGCCCGTCCCCCGGATACCCCCCTGCCAGGGCCTAGTAATCTCGGGTCGGCTAGAACAACGG
P21-02 (Ost) .CG.....A.....A.TCG.....C...CT.....
P21-03 (Ost) .CG.T.G.....A.TCG.....C...CT...G.....
P21-04 (Ost) A.....T.....CT.....
P21-05 (Ost) .CG.T.G.....C...A.TCG.....CT.....
P21-06 (Ost) .CG.....A.TCGG.....G.....
P21-07 (Ost) .CG.....C.....T.....T.....
P21-08 (Ost) .C.....G.....T.....T.....A.TCG.....A.....G.....
P21-09 (Ost) A.....C.....A.....T.....T.....
P21-10 (Ost) A.G.T.G.....A.TCG.....CT..AG.....
P21-11 (Ost) .CG.....C...A.TCG.....CT.....
P21-12 (Ost) A.....C.....A.....T.....AGTCG.....G.....
P21-13 (Ost) .CG.T.G.....C...A.TCG.....CT.....
P21-14 (Ost) .C.....G.....A.TCG.....CT...G.....
P21-21 (O3+4) .CGG.T...ACG...AT.....T.....T.....A.....T..C.....G.A.T...
P21-22 (O3+4) .CGG.T...AT.....T..AT.....G.C...T..C...T..G...T.....C.....G..C...
P21-23 (O3+4) .CG.....AC...AT.....CAT.....T.....T.....A..T..C.....G.A...
P21-24 (O3+4) .CG..T...CG...AT.....AT.CGA.....T..C.....T.....C.....T.G...A..
P21-25 (O3+4) .CG.....C..AT.....A.....AT.C...TT.....T.....T.....A...C.....G.A...
P21-26 (O3+4) .CG..T...CG...AT.....AT.C.....T...T...C...T...T...T.....C.A...G.A...
P21-27 (O3+4) .CG..T...CG...AT...T.....AT.....T.....CT.TC.....G.A.T...
P21-28 (O3+4) .CG..T...C.CG...AT.....T.....T.T.....A.....T..C.....G.A.T...
P21-29 (O3+4) .CG..T...C.CG...AT.....T..A.....T.T.....A.....T..C.....G.A.T...
P21-30 (O3+4) .CG.....AT.....AT.....G.C...T...C..A...--T..T.....C.....G.A...
P21-31 (O3+4) .CG.....C..AT.....AT..A.....C...T.T.T.....T.....C.....C..G.A...T.
P21-32 (O3+4) .CG..T...ACG...AT.....A.....T.T.....T.....T..C.....G.A.T...
P21-33 (O3+4) .CG..T...CG...ATAA.....G.C...T...C...T..G...T.....T..C.....G.A.T...
P21-36 (O3+4) .CG..T...C.CG...AAT.....A.....AT.CG...A...T...C...T...TA.....A...C.....G.A.T...
P21-MAD      ACG...C.....T.AT...C.CC..CG.....T.....AAAT...TA.T...T...TG.T...A.....A...T...G.....A

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P21 gene region (cont.)

P21-01 (Ost) TGCCCCCCAAT
P21-02 (Ost) ..T.....
P21-03 (Ost) ..T.....
P21-04 (Ost) ..T.....
P21-05 (Ost) ..T.....
P21-06 (Ost) ..T.A.....
P21-07 (Ost) ..T.....
P21-08 (Ost) ..T.....
P21-09 (Ost) ..T.....
P21-10 (Ost) ..T.....
P21-11 (Ost) ..T.....
P21-12 (Ost) ..T.....
P21-13 (Ost) ..T.....
P21-14 (Ost) ..T.....
P21-21 (O₃₊₄) ..T..T..A...
P21-22 (O₃₊₄) ..T..T..A...
P21-23 (O₃₊₄) .AT..T..A...
P21-24 (O₃₊₄) .AT..T..A...
P21-25 (O₃₊₄) .AT..T..A...
P21-26 (O₃₊₄) ..T..T..A...
P21-27 (O₃₊₄) ..T..T..A...
P21-28 (O₃₊₄) ..T..T..A...
P21-29 (O₃₊₄) ..T..T..A...
P21-30 (O₃₊₄) ..T..TG.A...
P21-31 (O₃₊₄) ..T..T.TA...
P21-32 (O₃₊₄) .AT..T..A...
P21-33 (O₃₊₄) ..TA.T..A...
P21-36 (O₃₊₄) ..T..T..A...
P21-MAD A.T..T...CTG

Figure S3

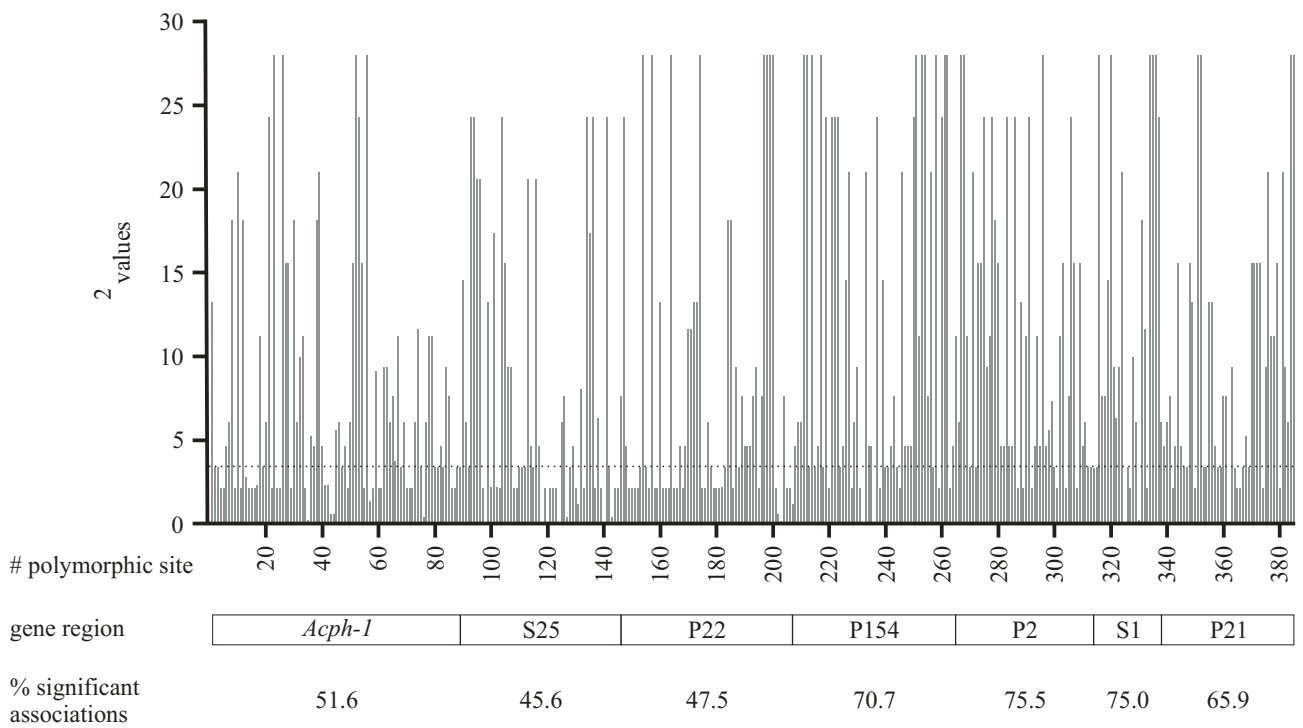


Figure S3

Association between each of the 385 informative polymorphic sites present in the concatenated data set and chromosomal arrangement (O_{ST} vs. O_{3+4}). Vertical grey bars indicate χ^2 values for each polymorphic site. The dotted horizontal line corresponds to the critical value for 1 d.f.. Boxes below polymorphic sites indicate gene regions, which are arranged in the same order as they are in the O_{ST} chromosomal arrangement. Numbers below boxes indicate the percentage of significant associations ($P < 0.05$) obtained by the χ^2 test for each gene region.