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Supporting Information
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X-Linked Variation in Immune Response in *Drosophila melanogaster*

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ACCTTCATATTGTCGGTCTGTTTGCNCGCAACGCAGAAAAAAAAAGAAACGGCGGAGGTCTG
TTGGCTGCGAGCGCAGGGTTGAAAA

>Rps6Exon3_01
TTGGACTCCTTCTTGCGCTGCACCAACAGNTTGGCGTAGTCGGCGGAAGCCTCCTTGGAAG
CGATCTGGCGCTTCTTCTTCAGCGCAATGCGACGGTGCTTGCGCTGCAGCACAACGGG[G/T]
GTGATCAGGCGCTGAATTTTGGGGGCCTTGGAGGTGGCCTTCTTGTTGTCCTTGGCGGGCAA
AGGGCGACGCACAACGAAGCGACGCACATCATCTTCCTT

>Ser75inter_01

CTGGAAGCGCGATTGGAAGGCGGCAACGGGTTTTNCCGCCCAGCCGCAATCAATGAGAATC
GATCCGATCGTAGCTAATCAACGCAGCGTCGGCGATGGAAAAG[G/C]CAAATCAAAAGCCAA
TCTCTGAGATTCAAAAAGCTTCCGAGGGTCGCGGCTTGAGGTTGCCGATCGCCAGTAGATCA
GTAGTTGATTGCCAGCCACCGGGGACGC

>Ser7Exon3_01
TGAACTGGCTGCAGATGCAGAATCTGGAGCCCGTCTGTTTGCCACCGCAGAGGGGCAGGTA
TGCCAATCAGCTGGCCGGCTCAGCNGCCGATGTTTCCGGCTGGGGC[A/C]AGACCGAGTCC
AGCGGCAGCAGCAAGATCAAGCAAAAGGCNATGCTGCACATCCAGCCGCAGGATCAGTGCC
AGGAGGCNTTTTACAAGGACACCAAGATTACGCTCGCCGATAGTC

>Ser7Exon3_02
CGGCAATCGATATGTCTATCTGGCCGGCGTGGTCTCCATTGGACGGAAACACTGTGGCACAG
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ACCCATAACGCAAAGTCAAGCTCATTGTGACCTT

>Tak15UTR_01
GCGCTATTTTGGTAGAATTACNGGGATTTCGCCTTTTTAGTGGCTACGATTCCGTGGGTTCCC
GATTTCATTGCTGGCTAACTGTGCCTTTGGTTCCCTCTTGGG[G/T]ACAGAGTTTTCGGAATC
TTTGCAAGATCTAGACCTGGATTCATCATAAAGTTTCTNGCCTTTGTATAGATTGCGACTGAC
AACTTTTACCACGTCATTT

>Tak1Intron1_01
TGGGTTTTTTAACNGAGCTGTTACNAAGCATACACTTTTAAAACGAAAAAATAACCGNTTATA
GATTAAAACATGCTTTNTGAAAGTGCGATAATCGTCT[G/T]ACTAACTAAGAATGAGTACTTG
CTCTGCCCTAAATGGTATATGATTACTGGTTGTTTATCGTTTCAAGATTGCGTATACGTATAC
ACCAATAGGAGCTCTAGACTTT

>Tak1Exon2_01
ACGCGCGACAACTGCTTCACCTCCTTCTCGATGTCCTTCTGCTCGGCGCTGGCGAAGAACT
CCTTGACGGCAACCAGCTTGTCGCGCCAAACGGCCTTGCAGACCAC[T/A]CCGTAGGACCC
ATGGCCGACTTTCTGCGGGGNAAAAGATTATTAGATCTGANTCAACAGTTGTACCCTCNTTG
NGCANNACTCCTCAATACNNANTATACGTTATACANCTTG

>Tak1Exon3_01
GCTTCCTGGACAGAACCTCCCATAGAACAATGGCCCAGCTNAAAATGTCACACTTCTCCGTA
TACTTGGAGCCTTCGAAGACCTCGGGCGCCATCCAAGCGGCACT[G/A]CCGCGATTGTTGGT
CATCATGGTCGACTTGTCCGCCACCGTGCCGAAGTCNCATATCTTCAGATTGNNTCCCTTGT
NRRTCAAGAGCAGGTT

>Tak1Exon4_01 (Tak1Intron4_01)
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ACCTGTTGATTAACAAANGTGTATTCCAGGGCCTTGTCCGCCCCCGTATAGTCCTTGACGAT
CTCGTGCATAACGCCCACTATGTACTGCATCGACGGG

>Traf2Exon1_01
GGATGCACCATGCACAACTTGATGCGACCCTTGAAGGGCCAGTCCAAGTGGTAATCGTTCTC
CGACTGCATCAGATGCACATGCAAGCTGAGCACATGCGGTTT[C/T]CGCGGCTGAATGTTCA
GCCGCGCACAGAANTTGTAGCCATGNGGCGAGGTGTAGCACTCGTGCGAGTACACTTGATT
GTTGGCATTNGNCCGCAGGCG

>Traf2Exon1_02
TATTCTCCAGTCGCGTNTCCTGCTCGCGNNTNNNNTNTTCCAAAACCACAATTNNCTGGNA
CATCGTTTGCACAATCTGCTCATCCACACCATTGGCATATTGCG[G/A]CGGTGGCGGCAGCT

GCTGCTGGCCATGACCNTTNTCCACGGCGGCGCCACTTGTGCTGGGCTTGTGNGGCTGCCA
GGTGGCAATGGCTGTCTGCTGGAATGCCTGCA

>Traf2Exon1_03
AGATGTCGTGCTCGGCGGACAGACGCTTGTTGTCCATGGGGCAGCATTGATTGTTCTTTTGC
ATCCAGGCGGTGAGGCAGCTGCGACAAAATCGATGGCCGCACGA[C/T]GTCAACACCGGCT
CATTTAGCCAATCGATGCAAATGGCGCACTCGTATCGCGAGTCCAGCAGCTCCTCCTCCTGT
TCCCCGGATGTATCCGAACCNGGTGCAT

>Traf25inter_01
TANCGTGTTAATTGTGCTAAATTTAGTTNTTATTTTACANNTAANANNAAATCAATGTAAAAC
CATCACTTGTATAGTTTANTTGGTTGTTAGAAGCTGATA[G/A]CGTGTAAACAACATGGCCTG
CGCAGATGCAGGCCAGTGTGAACACNCTCGTTTNGTTTTGGCGGCGGTGGGCGAGCATATA
AAACGGCAGTGTTTTTCGGATTGGCGAGC

>Traf3Exon2_01
TCCCATNTGAAGGAGTGTCCACGCAACCAGCACAATCTGAGCAATCAGCAACGCATGAGTG
TCAGCATGGATCGCCTGGATAGGCAGTCGGATCAGCGTCT[C/G]CTGGTCATTGAACAGGAC
GTGGGCACCATTCGGTCCGTTCTCAACGAGGAGATACGACAGCGTTTGCATCTCATTACCGA
TGTGGGCAACATACGGAAGCAGAACCA

>Traf3Exon3_01
TGAGAACGAGNGNCTCAACNGGGAGAAGTTCTTTCAGATCGAGGAGTTNCTGCAGCAAGAT
CAATGAGGACATCAAAACAAAGCTGGGCAACAGTGACTATGTGACGTC[A/G]AAGCAGGCCA
CATTGGACTANGAGGTGAAGAATGTGAAGAACATTGTGTGCGAAACGGAGGAACGTTGCGAT
AAATTGGATCGAGCACTTCACCAGACCATGCAG

>Tsf15inter_01
TAGCATACTAATTGATTTGCGAAAATCGCATTTAATGGCATAGCCATATATCAGTGTCGNAAA
CTCGTTTGCCGGAGTATATAGGCCTGGATTGCCGCCCACTCA[C/T]GCCTTTCCTCGGGGAA
AAACCGGTCGCCTGGACTGTCTTTCTTTCTTTATTGTTATGATTGCTATTNTTATTATTATTAC
TATTATTATTGGTATTGGTATTGGTATTA

>Tsf1Exon2_02
TGGAGTGCGTGGCTGGACGGGATCGAGTGGACTGCCTGGAGCTGATCGAGCAGCGCAAGGC
CGATGTGCTGGCCACCGAGCCGGAGGACATGTACATCGCCTA[T/C]CATCGCAAGAACGAG
GANTATCGCGTGATCTNTGAGATCCGAACGCAGCAGGACAAGGATGGTAAGTGGTGCANAT
GCTCGTGGGAGCAAAA

>Tsf1Exon3_01
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CACGCACGTCCTGAAGGTGTCCGCCGATCCGCAGATCTCCGC[T/C]ACGGAGCGCGAACTG
AAGTCGCTGTCCGAGTTCTTCACGCAGTCGTGNCTGGTGGGCACCTACTCCACGCATCCGG
AAACGGATCGCCTGCTGAAGAAGAAGTAC

>Tsf1Exon3_02
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CCATCTGCTCATCCAGCCGAATGCCGTGTACCACAGCAAGGATGC[T/C]GCCATCGATCCCA
AGGTCTATTTGGAGCGTGCCGGCTACAAGGATGTGATCGAGCGTGATGGCAGTGCCATCAGG
AAGATCCGCTTGTGNGCCCAGAACGACGA

>Tsf1Exon3_03
CCATCGATCCCAAGGTCTATTTGGAGCGTGCCGGCTACAAGGATGTGATCGAGCGTGATGGC
AGTGCCATCAGGAAGATCCGCTTGTGNGCCCAGAACGACGA[C/A]GAGTTCGCCAAATGCCA
GGCGCTGCACCAGGCTGCCTACGCCCGCNACGCTCGTCCGGAACTCGAGTGCGTTCAGTC
CACCGATTGTGTGGTGGCTCTGACCAAGAAG

>Tsf1Exon3_04
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GGCTCAGGATGATGTCCTTGTGGCGGTCGCAGCACCCGGCGTTACACGGGAG[G/T]CTCTCC
AGAAGGCCAGCATGTAAGTGGAATCCCTCGATCATCCGTAGCANATTAGCTACATATACTAT
CAATATTCCGCAGCAANTTCAATGNGANTTGCGAACGATCCCGTGCTGCTGCCGCC

>upd2Exon1_01
GATGATGAGGATGACGATGACGACGAGGAAGATCGGCCGGAGTTGTCCTCGTCGTAGGNGT
AGTCCAGTGCCACCTGGTCGCGCAAGTGTCGCGCCTTGGT[G/A]AATGGCATCACGACGCTC
AGGATCATGATCACTAGCAGCACCTGCCGGNTGTGGCAGCTCCAGCTGCTGTGTGCACTCC
TGCTGCTGCGGCTGCTTTGGCTNTGTTGGCTG

>upd2Intron1_01
GAAATCGATGAGTAATGCATATTGGCTGTGTGACAGAATTTCTCGAACGTTTCGGGTTCAACT
AACTGCCTAAGTANCTGTCCTGCNAAAGATGCTAACAGGACAC[A/G]CAACGCACAAAAGTA
TCTATGTATCTTAGTATCTATGAAGNTGCNTTGCGACTATGTAAATATAAACTGTTATCAAAC
AATGTAAGAAAAGCTTGGTGTAGGTTGCTTTCCTC

>upd2Exon3_01
TCGCCGCAGGACACGGTGCAGGGTCTTCCACACGTTGTTCAGATACTGGAAGTACAGCTCCT
TGCTGACCTTCAGGTCGCGCTGGTCCGCCTCCATGGATCCGTTGGC[T/G]GGCGTGTGAAAG
TTGAGACGCTCCTCCATCGCCTGCCGGCTAACGCGGCTCAGCTTCGCACCATTGCTGTTCG
GATAGGAGGCGTTTATGGTCAACTCGA

>upd2Exon3_02
TGCCGAGGGCTCAAGACTCATTGGATCCGCCATCGGAGCCGGAACTGCCACCGGATCCGTT
CGAGGAGCCCACGTCGAGCATTTCCGAGCTGCCCGCCCGCAG[C/G]CCGCTCGCACCAGTT
CCGTGAATCGCCGCCAGGTGTCGCCGCTCGGCACTATTGCGTCGCGGTCGCCGCAGGACAC
GGTGCAGGGTCTTCCACACGTTGTTCAGATACTGGAAGTA

>(upd3Exon1_01)upd35inter_01
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ACCAGTGTGCCTCGTACAATGGTTTAAAAATAGCTCGGCCAAATCAT[G/A]ACACCGATCAC
CATCCGTAAGTTTGGCCGCCANCGGTGNGCGTTGGGCGGCNGACGGCGAGTGGGAGTGGC
AGTGGCAGTGAGCGGTACACGGTACATGGTAC

>(upd3Intron1_01)upd35inter_02
CGGTGGAGCGTAGTCGGCAANCATGAATGAATCGCCGTGTCTGCGAGCGTGAGAGCCCGGC
TCGCGGTTGAACAAATCGTGTCGTCATTGACGGCTGTCG[G/T]CGGCCGACGGAGCGTATGA
GTAATATTCTTGTGAAATTGAACGGAAATAANTGAAATTCATGCCAACCCCCATAAATTGCCG
ACTATTTGCGGGGGNTACTTCGGAACG

>upd3Exon2_04
CAGAGCGGCCAACTTCCGGCTGACNTTCCAGCAGAAANTNAATGCCAGCAGTACGCATCTG
GACTGGGAGAACACCTGCAATCTGAAGCCCACGGGTCTGAACGAAACGCA[C/T]AGCAAGG
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NATNNDTNGGCACAACTAATTCACACACTATTATCTATA

>upd3Exon3_01
TGCAGAANCTACAGAACCAAACGGGCCGCGAGCTGCGGGGCATCCAGGCCGAGGACAAGG
CCAGGATCACCACCAATGCGGACAAGCTGGCCACAGTGAGCACCAA[G/A]ACTCTGGACATT
GTCGAGAAGAACAAGTGGCGATTCTATAAGGGAAACTACAGATTCCTGCCCCGTNTGAATCT
CACTAGCAAACAGGTGAGTGT

FIGURE S1.—Sequences used to detect each SNP using SNPlex

TABLE S1

Results of Autosomal Genotyping

Line	2nd chromosome				3rd chromosome			
	Dro,AttAB	imd	Tehao	cact	PGRP-LC	DrsL	BG4	AttD
proportion consistent	0.9875	0.98125	1	1	1	1	1	1
FM7a		uncut	cut	cut	cut	uncut		cut
X2	cut	uncut	cut	cut	cut	uncut		cut
X3	cut	uncut	cut	cut	cut	uncut	cut	cut
X4	cut	uncut	cut	cut	cut	uncut	cut	cut
X6	cut	uncut	cut	cut	cut	uncut	cut	cut
X7	uncut	uncut	cut	cut	cut	uncut	cut	cut
X9	cut	uncut	cut	cut	cut	uncut	cut	cut
X10	cut	uncut	cut	cut	cut	uncut	cut	cut
X11	cut	uncut	cut	cut	cut	uncut	cut	cut
X12	cut	uncut	cut	cut	cut	uncut	cut	cut
X13	cut	uncut	cut	cut	cut	uncut	cut	cut
X14	cut	uncut	cut	cut	cut	uncut	cut	cut
X15	cut	uncut	cut	cut	cut	uncut	cut	cut
X16	cut	uncut	cut	cut	cut	uncut	cut	cut
X17	cut	uncut	cut	cut	cut	uncut	cut	cut
X22	cut	uncut	cut	cut	cut	uncut	cut	cut
X23	cut	uncut	cut	cut	cut	uncut	cut	cut
X24	cut	uncut	cut	cut	cut	uncut	cut	cut
X25	cut	uncut	cut	cut	cut	uncut	cut	cut
X26	cut	uncut	cut	cut	cut	uncut	cut	cut
X27	cut	uncut	cut	cut	cut	uncut	cut	cut
X28	cut	uncut	cut	cut	cut	uncut	cut	cut
X29	cut	uncut	cut	cut	cut	uncut	cut	cut
X31	cut	uncut	cut	cut	cut	uncut	cut	cut
X33	cut	uncut	cut	cut	cut	uncut	cut	cut
X34	cut	uncut	cut	cut	cut	uncut	cut	cut
X35	cut	uncut	cut	cut	cut	uncut	cut	cut
X36	cut	uncut	cut	cut	cut	uncut	cut	cut
X37	cut	uncut	cut	cut	cut	uncut	cut	cut
X38	cut	uncut	cut	cut	cut	uncut	cut	cut
X39	cut	uncut	cut	cut	cut	uncut	cut	cut
X40	cut	uncut	cut	cut	cut	uncut	cut	cut

X41	cut	uncut	cut	cut	cut	uncut		cut
X42	cut	uncut	cut	cut	cut	uncut	cut	cut
X43	cut	uncut	cut	cut	cut	uncut		cut
X44	cut	uncut	cut	cut	cut	uncut	cut	cut
X46	cut	uncut	cut	cut	cut	uncut	cut	cut
X47	cut	uncut	cut	cut	cut	uncut	cut	cut
X48	cut	uncut	cut	cut	cut	uncut	cut	cut
X49	cut	uncut	cut	cut	cut	uncut		cut
X50	cut	uncut	cut	cut	cut	uncut		cut
X51	cut	uncut	cut	cut	cut	uncut		cut
X52	cut	uncut	cut	cut	cut	uncut	cut	cut
X53	cut	uncut	cut	cut	cut	uncut	cut	cut
X54	cut	uncut	cut	cut	cut	uncut	cut	cut
X55	cut	uncut	cut	cut	cut	uncut	cut	cut
X56	cut	uncut	cut	cut	cut	uncut	cut	cut
X57	cut	uncut	cut	cut	cut	uncut	cut	cut
X58	cut	uncut	cut	cut	cut	uncut	cut	cut
X59	cut	uncut	cut	cut	cut	uncut	cut	cut
X60	cut	uncut	cut	cut	cut	uncut	cut	cut
X61	cut	cut	cut	cut	cut	uncut	cut	cut
X62	cut	uncut	cut	cut	cut	uncut	cut	cut
X63	cut	uncut	cut	cut	cut	uncut	cut	cut
X64	cut	uncut	cut	cut	cut	uncut	cut	cut
X65	cut	uncut	cut	cut	cut	uncut	cut	cut
X68	cut	uncut	cut	cut	cut	uncut	cut	cut
X69	cut	cut	cut	cut	cut	uncut	cut	cut
X70	cut	uncut	cut	cut	cut	uncut	cut	cut
X71	cut	uncut	cut	cut	cut	uncut	cut	cut
X73	cut	cut	cut	cut	cut	uncut	cut	cut
X74	cut	uncut	cut	cut	cut	uncut	cut	cut
X75	cut	uncut	cut	cut	cut	uncut	cut	cut
X76	cut	uncut	cut	cut	cut	uncut	cut	cut
X79	cut	uncut	cut	cut	cut	uncut	cut	cut
X80	cut	uncut	cut	cut	cut	uncut	cut	cut
X81	cut	uncut	cut	cut	cut	uncut		cut
X83	cut	uncut	cut	cut	cut	uncut		cut
X84	cut	uncut	cut	cut	cut	uncut	cut	cut
X86	cut	uncut	cut	cut	cut	uncut		cut
X87	cut	uncut	cut	cut	cut	uncut	cut	cut

X88	cut	uncut	cut	cut	cut	uncut		cut
X89					cut			
X90	cut	uncut	cut	cut	cut	uncut		cut
X91	cut	uncut	cut	cut	cut	uncut	cut	cut
X92	cut	uncut	cut	cut	cut	uncut	cut	cut
X93	cut	uncut	cut	cut	cut	uncut	cut	cut
X94	cut	uncut	cut	cut	cut	uncut	cut	cut
X95	cut	uncut	cut	cut	cut	uncut	cut	cut
X96	cut	uncut	cut	cut	cut	uncut	cut	cut
X97	cut	uncut	cut	cut	cut	uncut		cut
X98	cut	uncut	cut	cut	cut	uncut	cut	cut
X99	cut	uncut	cut	cut	cut	uncut	cut	cut
X101	cut	uncut	cut	cut	cut	uncut		cut
X102	cut	uncut	cut	cut	cut	uncut		cut
X103	cut	uncut	cut	cut	cut	uncut	cut	cut
X104	other	uncut	cut	cut	cut	uncut	cut	cut
X105	cut	uncut	cut	cut	cut	uncut	cut	cut
X106	cut	uncut	cut	cut	cut	uncut	cut	cut
X107	cut	uncut	cut	cut	cut	uncut		cut
X108	cut	uncut	cut	cut	cut	uncut	cut	cut
X109	cut	uncut	cut	cut	cut	uncut	cut	cut
X110	cut	uncut	cut	cut	cut	uncut	cut	cut
X111	cut	uncut	cut	cut	cut	uncut	cut	cut
X112	cut	uncut	cut	cut	cut	uncut		cut
X113	cut	uncut	cut	cut	cut	uncut		cut
X114	cut	uncut	cut	cut	cut	uncut		cut
X115	cut	uncut	cut	cut	cut	uncut		cut
X116	cut	uncut	cut	cut	cut	uncut		cut
X117	cut	uncut	cut	cut	cut	uncut		cut
X119	cut	uncut	cut	cut	cut	uncut		cut
X122	cut	uncut	cut	cut	cut	uncut		cut
X123	cut	uncut	cut	cut	cut	uncut		cut
X125	cut	uncut	cut	cut	cut	uncut		cut
X126	cut	uncut	cut	cut	cut	uncut		cut
X127	cut	uncut	cut	cut	cut	uncut		cut
X128	cut	uncut	cut	cut	cut	uncut		cut
X130	cut	uncut	cut	cut	cut	uncut		cut
X131	cut	uncut	cut	cut	cut	uncut		cut
X134	cut	uncut	cut	cut	cut	uncut		cut

X136	cut	uncut	cut	cut	cut	uncut	cut
X137	cut	uncut	cut	cut	cut	uncut	cut
X138	cut	uncut	cut	cut	cut	uncut	cut
X139	cut	uncut	cut	cut	cut	uncut	cut
X140	cut	uncut	cut	cut	cut	uncut	cut
X142	cut	uncut	cut	cut	cut	uncut	cut
X143	cut	uncut	cut	cut	cut	uncut	cut
X144	cut	uncut	cut	cut	cut	uncut	cut
X145	cut	uncut	cut	cut	cut	uncut	cut
X146	cut	uncut	cut	cut	cut	uncut	cut
X148	cut	uncut	cut	cut	cut	uncut	cut
X149	cut	uncut	cut	cut	cut	uncut	cut
X151	cut	uncut	cut	cut	cut	uncut	cut
X152	cut	uncut	cut	cut	cut	uncut	cut
X153	cut	uncut	cut	cut	cut	uncut	cut
X154	cut	uncut	cut	cut	cut	uncut	cut
X155	cut	uncut	cut	cut	cut	uncut	cut
X158	cut	uncut	cut	cut	cut	uncut	cut
X160	cut	uncut	cut	cut	cut	uncut	cut
X164	cut	uncut	cut	cut	cut	uncut	cut
X166	cut	uncut	cut	cut	cut	uncut	cut
X167	cut	uncut	cut	cut	cut	uncut	cut
X168	cut	uncut	cut	cut	cut	uncut	cut
X169	cut	uncut	cut	cut	cut	uncut	cut
X172	cut	uncut	cut	cut	cut	uncut	cut
X173	cut	uncut	cut	cut	cut	uncut	cut
X174	cut	uncut	cut	cut	cut	uncut	cut
X201	cut	uncut	cut	cut	cut	uncut	cut
X202	cut	uncut	cut	cut	cut	uncut	cut
X203	cut	uncut	cut	cut	cut	uncut	cut
X204	cut	uncut	cut	cut	cut	uncut	cut
X205	cut	uncut	cut	cut	cut	uncut	cut
X206	cut	uncut	cut	cut	cut	uncut	cut
X207	cut	uncut	cut	cut	cut	uncut	cut
X208	cut	uncut	cut	cut	cut	uncut	cut
X209	cut	uncut	cut	cut	cut	uncut	cut
X210	cut	uncut	cut	cut	cut	uncut	cut
X211	cut	uncut	cut	cut	cut	uncut	cut
X212	cut	uncut	cut	cut	cut	uncut	cut

X213	cut	uncut	cut	cut	cut	uncut	cut
X214	cut	uncut	cut	cut	cut	uncut	cut
X215	cut	uncut	cut	cut	cut	uncut	cut
X216	cut	uncut	cut	cut	cut	uncut	cut
X217	cut	uncut	cut	cut	cut	uncut	cut
X218	cut	uncut	cut	cut	cut	uncut	cut
X219	cut	uncut	cut	cut		uncut	cut
X220	cut	uncut	cut	cut	cut		cut
X221	cut	uncut	cut	cut	cut	uncut	cut
X222	cut	uncut	cut	cut	cut	uncut	cut
X223	cut	uncut	cut	cut	cut	uncut	cut
X224	cut	uncut	cut	cut	cut	uncut	cut
X225	cut	uncut	cut	cut	cut	uncut	cut

TABLE S2

Resequencing Primers

Gene	Location	Primer Sequence	Direction
dome	322868	GCGCGCATATACGTCCATA	reverse
	323949	CCATTCCACAATCTCGGTTC	forward
	324467	GTCCAGACTCGTCCGTCAG	forward
	328272	GACGCCTGTTGTCTGCTGTA	reverse
	328437	ACTGGCGTGCATGTGTGTA	reverse
	329307	TGAAGCGCTTGTAGTTGTCG	reverse
	329494	CTGCCTGGACTACGACTTCC	forward
	330487	GTCGACAGGTAGCCCCAGT	forward
	330520	GTTTGGCACCTATCGCATTT	forward
Dredd	103613	TGACGAAGTGGTTGTGAGGT	reverse
	103626	ACCCCAATAAGAAACCTTACAAT	reverse
	104818	TCTCTTGCTTGACTGCCATC	reverse
	105060	CAGGAGATCCACTTCGCTTC	forward
	105694	ATAGCCGTGGCCTGAAGAG	reverse
	106354	TCGAATTTTTCGCCAGTTTT	forward
	106399	AAAAGAAGGAAACACCCCAAT	forward
Dsor1	198092	AATGAGTGGGGTGGGAGAGT	forward
	199438	TCAAATCCCATCCATTGCTT	forward
	199836	GTGCGGGAAATTACATTCGT	reverse
	201052	AAAGATAATCCTCCAATGCAAA	reverse
hep	152490	CACAGCCAAGCATAACAGGA	reverse
	152909	TTTGAATTGTCGCTTGTTGC	reverse
	154130	AATCTGCTGGAGCTGAGTGG	forward
	154513	GTGGCAAACTGTCGCTTC	forward
	154506	AACATAGGTGGCAAACTGTCG	reverse
	154642	CTGCACCATCACCATGAAAC	reverse
	155193	CCGCTCCAAAGTGACCAG	reverse
	155406	AGCACGAATCCGTTTCACAG	forward
	156340	TGGCTGATTGCATGAAAAAC	reverse
	156532	ACTGGAAGTGCGATCGGTTC	forward
	156340	TGGCTGATTGCATGAAAAAC	reverse
	156865	TGAGTGAGTTTTGCGTGTGA	reverse
	156998	GGAAAGCCATCATGAGCAAA	forward
	159226	GGGCTCTGTACAAGCGACA	reverse
	159965	ATGTTCGAGGGCTTCACATC	reverse

	160154	GCTCAAGCTGTCCAAGAAGC	forward
	161016	CAATGTCCGATGAACGAATG	reverse
	161527	TTGCTCGCTCATTATGTACCA	reverse
	161631	TAGTTTCCGCGAATTTCAGG	forward
	161638	TGGTTAATAGTTTCCGCGAAT	forward
	162286	CGATTTTTCTCAGCCCACTT	reverse
	163439	TCAGCGACAAAACAAACAGG	forward
	163959	GTTTCTGAGGTGCCGATGTT	forward
hop	274275	CCATCCCTTTCGTTTTCGTA	reverse
	275322	GGCGACTGGTGTCCATCT	reverse
	275449	TACGACCTGATGCAGCTGTG	forward
	275469	CCAGTTGTCCCGATTTCATT	forward
	275804	ACGCTTGCTTTTCGCATAGT	reverse
	276983	CGCAACGAGTAAGTTGAGCA	forward
	277393	ATGACCCAACCGAGAAGATG	reverse
	277510	GATCCGAATTCGTACGTGCT	forward
	277896	ATCGAATCTGCGCAAAAGAC	reverse
	279132	CAGTGCTTGAAATGCTTGCT	forward
	279489	CCTTCTCCGTCTGAAACTGC	reverse
	279616	TCTGCAGTGGATCCTTGTTG	forward
	280013	AGTGCAACGGAATTGGTGTT	reverse
	281669	GAACTAGAACCTCGCGTTGC	forward
lz	235452	AAACGATTGGATTCGACTCAG	forward
	236290	TTTGCACTTCACTCGGCTAA	reverse
	237836	TGTCCTTCAAAATCAAAGTGAA	forward
	240167	CGGGTGCACAAAAAGAAAAT	reverse
	244400	GTTAATCGAACTGCGCGATG	forward
	245283	GCGTTTTGGGTTACCGATT	forward
	245450	TTGGAAAGTGGGGATTAGGG	reverse
	246318	AGGGGAAGCCATCGATGTAG	reverse
	253049	GCACCTGCAACACCAGATG	forward
	254073	CAACTTGCAGATATTTTGGGATT	reverse
mxc	194219	CTTTTCGCCTTGCCTTTCTT	forward
	194244	TTTCGCTTGCAAGACTTTAGG	forward
	195025	CAAATGCCTCTTCCTTTTGC	reverse
	194897	GCGACATCAGCGGAGAAA	forward
	197005	ATCTAGCACAATTCTTTGATCGT	reverse
Ntf2	113279	CAAATGGCAATGAATATTTAATTTTAG	forward
	113327	TGCTTTTCCGAATGTGAAGA	forward

	114294	TTCTCGAAGTTTCGGGTGAC	forward
	114483	TGAATTGATTGAAACTAATGAAACA	reverse
	115273	CCCGTTACTAGTGCAGTTAAAGA	forward
	115410	TCCTGAGATCTCGACGTTCAT	reverse
	115577	TCAAAACAAGAGAGAATGCTATGG	reverse
	115955	CGGCAGTTTCTTTGTGCAG	forward
	117037	GCACTGCAAAGGAATGAAATC	reverse
	117613	AAACTTATGTAGGCGATGATCC	reverse
os	152853	CCTCAAAATGGGAAGTACGAA	reverse
	152869	ACGAAGTTCTTTTCCATCATAAA	reverse
	154156	GCGTCTCGAGATGAACAAGC	forward
	154028	TGCTTCACAAAGCGCATATC	reverse
	155238	CGCAGAAGAGAAAGTGGCTA	forward
	155085	CGCTATCGATAACCGTTAGACC	reverse
	155849	CCCGCCCTCAATATACACAC	forward
PGRP-LE	95395	AAACTGCCAGTAGCTGGAAAA	reverse
	95994	AGCTGTGTGTACTGCGTGGT	reverse
	97097	TAAGGTGGACACGACACGAA	forward
	97607	TTTTCGGATCTGGACAAAGC	forward
PGRP-SA	191815	TTTTTCCTCGCCCTCTTTTT	forward
	193314	CGACACATTTTTGTAAATTATGACAG	reverse
phl	273661	GCCTATGCACGCCATCTATT	forward
	273273	TGGAAAGGATACAAGCCAGAA	forward
	275609	CTCGAAGCCACCATCTTCAT	forward
	275729	TGTGACCGATCGAATGTTGT	reverse
	276530	TCCGTGAAGATAGGCGACTT	forward
	276690	AAGGCATAAACGTCCGACTG	reverse
	277575	GAACCTTGTGTGTAAACATAAACCA	reverse
	277615	TGAATATACGGCTGGGTGGT	reverse
Pvf1	74559	CGGATTGGATGTGAGTGTTG	forward
	75186	GTGTTCTGGTTTTGCTCGAA	reverse
	76087	CTACTGCTCCCCCGTCTACA	forward
	76833	ACCACAGGGAGACGGATAGA	reverse
	79380	CGTACCCTCGGAGTGATGAT	forward
	79800	CTTCGCGGCTTTGAAGAAT	forward
	80882	TTTCGCTGCGTGAGAATATG	reverse
	80713	CGTTTTGTTTGCAGCTTGAT	forward
	81346	CGGCGAGAAATACTCGTATGTAA	forward
	81484	AACCGATTCCCCACTTGTTT	reverse

	81858	CGTTATTATCACGGCGGTTAG	forward
	82943	TGGTACACGTTGCAGTCCTC	reverse
	82768	GGATCCACGCTGATCTCCT	forward
	83430	GGAATTCGCGCAGTATGAAT	reverse
	83287	CCCAACAAGTTCCTCGCTTA	forward
	84226	CACCCATCGATGTCTTGGA	reverse
	84386	CCTTCTCAGTACTCGGGGATT	reverse
	85062	CGTGGAACTCGACTACAGCA	reverse
Rps6	100048	GCTGGCTAGCTCATAACCAAA	reverse
	100808	GTGTCCCTTCTTCAGGAGCA	reverse
	102386	GGCTTTTCGATAGGCTTGTG	forward
Ser7	236140	TCAATAGCACCAATGCAAAGA	forward
	236901	GAATTCCACCGAGTTGCAGT	reverse
	236787	CAGCAATTTGGCAGTGAGTT	forward
	237893	TTATCACGTCCGGTGAACTG	forward
	238577	AGGGATTTGGAATGCTTTGA	reverse
Tak1	196554	TTAAGGTCGTCGGCAATAAA	reverse
	196578	GGTCGTCGGCAATAAATAGAA	reverse
	196911	AAACAAAGTGCTATGGTTAATCG	reverse
	197877	TTTGCTGCAATGACAATTCC	reverse
	197098	AGAAGGCTGGGTGGTCATC	forward
	198605	TGTGTTGGAGTGTGGAGCAT	forward
	201271	AAAAGATTCCTTGTGCATTCG	reverse
	201992	CAGCACGAACGGTGAGTTT	forward
	201849	GCCATTGTGTCTCTGAACGA	reverse
	202939	TCTGCCCGTCTTTAAAACCT	forward
	202794	GACAATCTGCGAGCAGTTCA	reverse
	203374	CCGTATACTTGGAGCCTTCG	reverse
	203437	TCATCATGGTCGACTTGTCC	reverse
	203499	ACAAGGGACGCAATCTGAAG	forward
	204115	TTCTGCGGGGAAAAAGATTA	reverse
	204256	ATCACAATGCGTTCGTGTGT	forward
	205112	TGCGACTGACAACTTTTACCA	reverse
	205249	ATCCACTAGGGTTGGCATCA	forward
	205727	TTATCGTTATCGGCGAGTCC	forward
	205767	TCCATTGATGTCGCTGGAAT	forward
Traf2	38316	GTTCCAAATTGCGCCATAAT	reverse
	39038	CAAAAGTCAATGCAGATCACG	forward
	39572	GATCCACCTTGGTGCAAACT	reverse

	39688	GATCGGCTGCTCATCAAGA	forward
	40081	CAATCGTGCCATTGCTGTAG	reverse
	40916	ACTGCTACTGGCCGCAAT	reverse
	41011	GCGCACAGTTTGCAGCAT	forward
	41679	GATTCGATTTCGCTTTGAGG	forward
Traf3	81982	ACTTCAATCCCGATCCACAT	forward
	82520	TTTGGCTGAGTTTAGTGTGCAT	forward
	83247	TGGATGTCCAGTACTGCTGTG	forward
	84911	CATACAAGAACACGCCAACG	reverse
Tsf1	234903	TCACTGCAATTTTTCCAGCTT	forward
	235473	GGGAAAGAAGCAGCACATCT	forward
	236278	AGCCAGTGTGGCAGGACTT	reverse
	236581	GCCTTCTCCAAGGTGCAGTA	forward
	236694	GCCATCCTCGCACAGATATT	reverse
	237205	AGGGCTCAGGATGATGTCC	forward
	238054	GGAAACTTTGTAGCATTGTATTTGG	reverse
	238059	GGCTGGGAAACTTTGTAGCA	reverse
upd2	88810	TGGTCCTCTATTTGGCTTGG	reverse
	89315	AACTCGATCTCGCAGAGCATA	reverse
	90057	GCTTTCCTCCATTGCCCTTA	reverse
	90303	CCACAACCTGCGACTCTTCT	forward
	91399	CGGAAGTCGTGAATCGAAAT	forward
upd3	122615	GAGAAAGTTCTTCCCCTCGAA	forward
	123203	CCGATCACCATCCGTAAGTT	forward
	123349	GACGTCTCCGTTTTGTCGTT	reverse
	124190	CCAAATATTGGTCTCAATCGAA	forward
	124343	TACGCTGAAGAAAGCATGGA	reverse
	124817	TGGAGTGGAGTGTTGTGGAG	reverse
	126451	TGCGATTATATTTATATGTGTGCGTA	forward
	126465	TATGTGTGCGTATGGGTTTG	forward
	127477	CAAGAAACGCCAAAGGGTAA	forward
	127624	GCCCGTTTGGTTCTGTAGAT	reverse
	128460	TCCAGCGATCACGTTTTATG	forward
	128576	CGAATTGAGATTCGGATTGA	reverse

TABLE S3

Genotypes for Each SNP

Table S3 is available for download as an Excel file at http://www.genetics.org/cgi/content/full/genetics.109.093971/DC1.

TABLE S4

TaqMan Primer and Probe Sequences

Gene	Oligo	Sequence
Def	MGB probe	AGGATGCCCACCAGGA
	forward primer	GAGGATCATGTCCTGGTGCAT
	reverse primer	TCGCTTCTGGCGGCTATG
DptA	MGB probe	TTTGCAGTCCAGGGTC
	forward primer	GCGGCGATGGTTTTGG
	reverse primer	CGCTGGTCCACACCTTCTG
Mtk	MGB probe	GCTGGGTGTGATGG
	forward primer	AACTTAATCTTGGAGCGATTTTTCTG
	reverse primer	ACGGCCTCGTATCGAAAATG
PGRP-SA	MGB probe	CGAAGGCACTGGTTG
	forward primer	TCGGCAACGATGGTATCGTA
	reverse primer	GGCACCGCGCAATCC
Tsf1	MGB probe	AGTGCCGCCTTCC
	forward primer	GAACGCAGCAGGACAAGGA
	reverse primer	CTGCTGCAGGGTGCGAAT
RpL32	MGB probe	AGCTGTCGCACAAAT
	forward primer	AGGCCCAAGATCGTGAAGAA
	reverse primer	GACGCACTCTGTTGTCGATACG