Locus	P/M	Source		
2F9	М	Lambert et al. 2005		
2H8	Μ	Lambert et al. 2005		
3A11	Μ	Lambert et al. 2005		
3B6	Р	Lambert et al. 2005		
4E8	М	Lambert et al. 2005		
4G9	М	Lambert et al. 2005		
4H2	М	Lambert et al. 2005		
6E4	Р	Lambert et al. 2005		
Ase18	Р	Richardson et al. 2000		
CK5A4B	Р	Tarr & Fleischer 1998		
Hru6	Р	Primmer et al. 1995		
IB4	М	Lambert et al. 2005		
ID6	М	Lambert et al. 2005		
Pcc02	М	T. King, pers. comm.		
Pcc04	М	T. King, pers. comm.		
POCC1	М	Bensch et al. 1997		
POCC6	М	Bensch et al. 1997		
POCC8	М	Bensch et al. 1997		

**Supplementary Table S1.** Polymorphic and monomorphic (P/M) microsatellite loci amplified in this study and their corresponding references.

**Supplementary Table S3.** Pairwise  $F_{ST}$  values for microsatellite (a), MHC (b) and TLR (c) loci. Populations SG, SK, SM2002, SM2004 and SM2012 are numbered 1–5, respectively.

a					
	1	2	3	4	5
1	0.000				
2	0.113	0.000			
3	0.056	0.192	0.000		
4	0.023	0.143	0.001	0.000	
5	0.064	0.166	0.001	0.005	0.000
b					
	1	2	3	4	5
1	0.000				
2	0.100	0.000			
3	-0.004	0.075	0.000		
4	0.057	-0.010	0.030	0.000	
5	0.067	-0.016	0.039	-0.015	0.000
с					
	1	2	3	4	5
1	0.000				
2	-0.003	0.000			
3	-0.003	-0.003	0.000		
4	-0.002	-0.002	-0.002	0.000	
5	-0.002	-0.002	-0.002	-0.001	0.000

**Supplementary Table S2.** Positively selected sites on MHC loci as identified by FEL and REL analyses.

Codon	$\begin{array}{c} \text{FEL} \\ d_N \! / \! d_S \end{array}$	FEL p-value	REL dN/d <sub>S</sub>	REL Bayes Factor
5	1.770e14	0.009	6.422e14	60866.1
47	1.314e13	0.048	4.032e14	7081.93
64	8.744e12	0.054	6.774e14	3758.11



**Supplementary Figure S1.** Neighbour-Joining tree of 24 identified MHC class II alleles across five South Island saddleback populations. Putative non-classical MHC loci are shaded in yellow (Sutton et al. 2013). Diamond symbol next to allele names indicates those sequences contained stop codons.



**Supplementary Figure S2a.** Relationships between pairwise MHC/microsatellite (y = -83.906x - 0.122, R<sup>2</sup> = 0.322, p = 0.070) and TLR/microsatellite (y = 0.170 + 0.043, R<sup>2</sup> = 0.015, p=0.390)  $F_{ST}$  values. **S2b.** Relationship between TLR and MHC loci pairwise  $F_{ST}$  among five South Island saddleback populations (y = -0.005x - 0.002, R<sup>2</sup> = 0.296, p = 0.030).

ς	3	2	•
r,	)	2	,

		10	20	30	40	50	60
,	MGSLTSI	YVFACVFLS	ILWNNIQPTVE	NKITANYSGE	ILLTEVPKNIE	PVHTHILDLSH	INSI
	]	70	80 • • •   • • • •   • •	90 ••• •••• ••	100	110	120 •••
,	SEITNFE	RETSLSDLQV	LNLSHNLITEI	DFSAFMFNQI	DLEYLDLSHNN	VIWTAYCQLLA	RLR
		130	140	150	160	170	180
	HLDLSF	KFTVLPICQ	EFGIMFHLEYI	GLSAMMIRRS	DFRYVAHLQI	DTVFLTLEDE	SLY
	EPLSLT	190 	200   . FATNQNFNFSI	210    LYDGMSTSER	220    KLKIVNLRYTI	230 	240 ••  ELQ
		250	260	270	280	290	M.L 300
	KKIKTTI	LTLDTVDLE A.M A Q	WTVILQIFLLV .AIM.J	WDSSVEHLTV	/RNLIFRGPVV	/ELTEYKHVPI AFL.H	 LRS
	LEQLLSI VI.	310   . GSSMKALTL DG	320    ERVRNKLYYFN .HV	330    IQEILYRQFSE .Q	340 	350 	360   KRS IRT.
	SFQYINE	370   . FSRNALTDEL .H	380    FQNCDTLANLF GVE	390 	400 	410 	420   ISSN .N.
	LLRNSR2	430   . AEGRCQWADS: DVE.	440   . LAELDLSSNQI .T	450 	460 	470 	480   TELH
	SLQELNI	490   . LASNRLADLP	500   . G <b>CR</b> AFTGLEII SGS.QF.	510 	520 	530 	540 ••  ?FKC
	SCELQDI	550   . FLRLERQSGG	560    KLSGWPEAYVC FA	570    XYPEDLSGTÇ EG.RE	580    2LKDFHLTEL7	590	600 ••  LLL
		610	620   . VPWYV <b>R</b> MLWQV	630 	640 	650 	660   DSL
•		L					

**Supplementary Figure S3.** PhcaTLR1LA1 (**SG19**) aligned against *Gallus gallus* toll-like receptor1 (**Ref**; GenBank Accession NP\_001007489) sequence. Grey triangles represent the start (217) and stop (526) position of leucine-rich repeats. Black triangles represent start (527) and stop (550) positions of potential LRR C-terminal regions. Blue triangles represent start (593) and stop (613) positions of potential transmembrane domain. The black box indicates the position of the non-conservative amino acid substitution.

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