

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

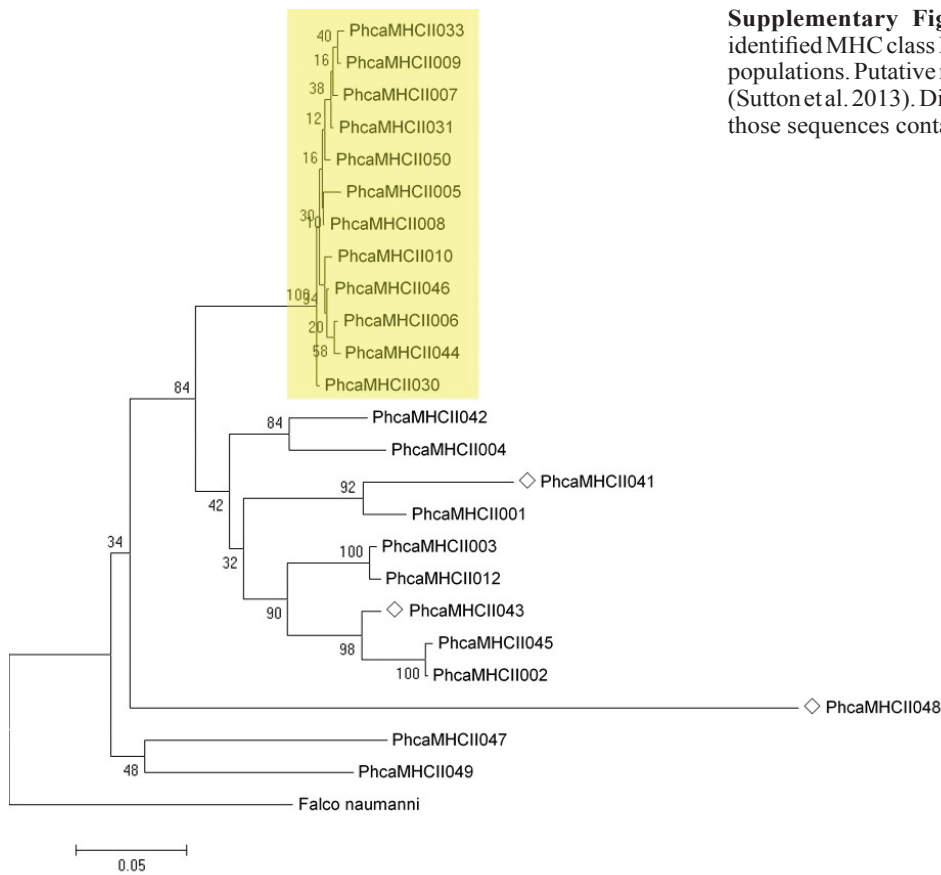
Locus	P/M	Source
2F9	M	Lambert et al. 2005
2H8	M	Lambert et al. 2005
3A11	M	Lambert et al. 2005
3B6	P	Lambert et al. 2005
4E8	M	Lambert et al. 2005
4G9	M	Lambert et al. 2005
4H2	M	Lambert et al. 2005
6E4	P	Lambert et al. 2005
Ase18	P	Richardson et al. 2000
CK5A4B	P	Tarr & Fleischer 1998
Hru6	P	Primmer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

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

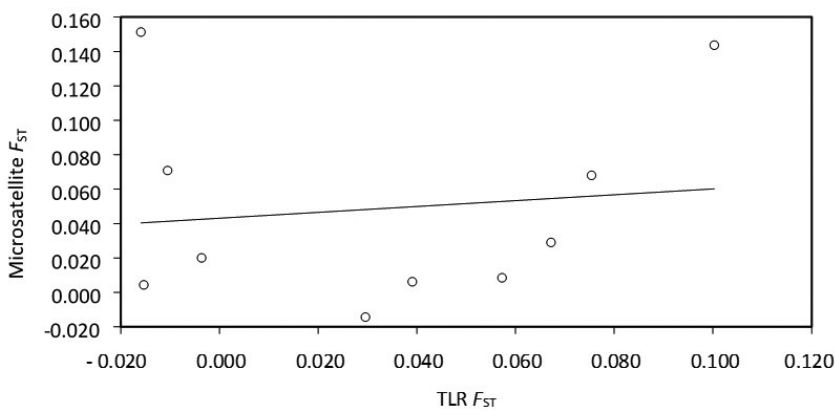
Codon	FEL d_N/d_S	FEL p-value	REL dN/d_S	REL Bayes Factor
5	1.770e14	0.009	6.422e14	60866.1
47	1.314e13	0.048	4.032e14	7081.93
64	8.744e12	0.054	6.774e14	3758.11

Supplementary 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.

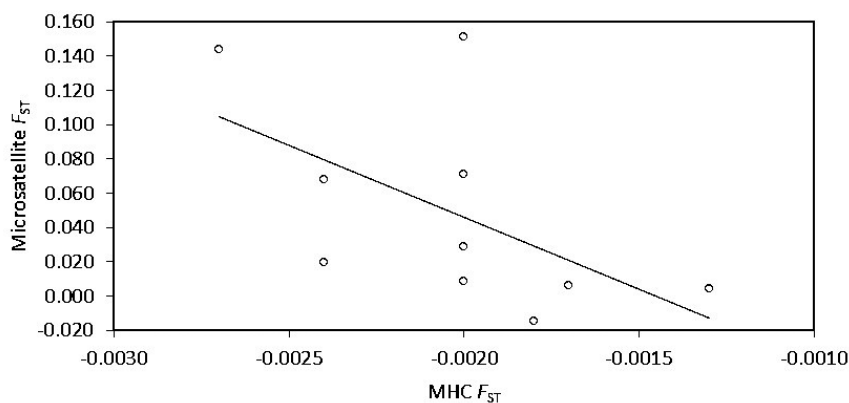
a					
	1	2	3	4	5
1	0.000				
2	0.113	0.000			
3	0.056	0.192	0.000		
4	0.023	0.143	0.001	0.000	
5	0.064	0.166	0.001	0.005	0.000
b					
	1	2	3	4	5
1	0.000				
2	0.100	0.000			
3	-0.004	0.075	0.000		
4	0.057	-0.010	0.030	0.000	
5	0.067	-0.016	0.039	-0.015	0.000
c					
	1	2	3	4	5
1	0.000				
2	-0.003	0.000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

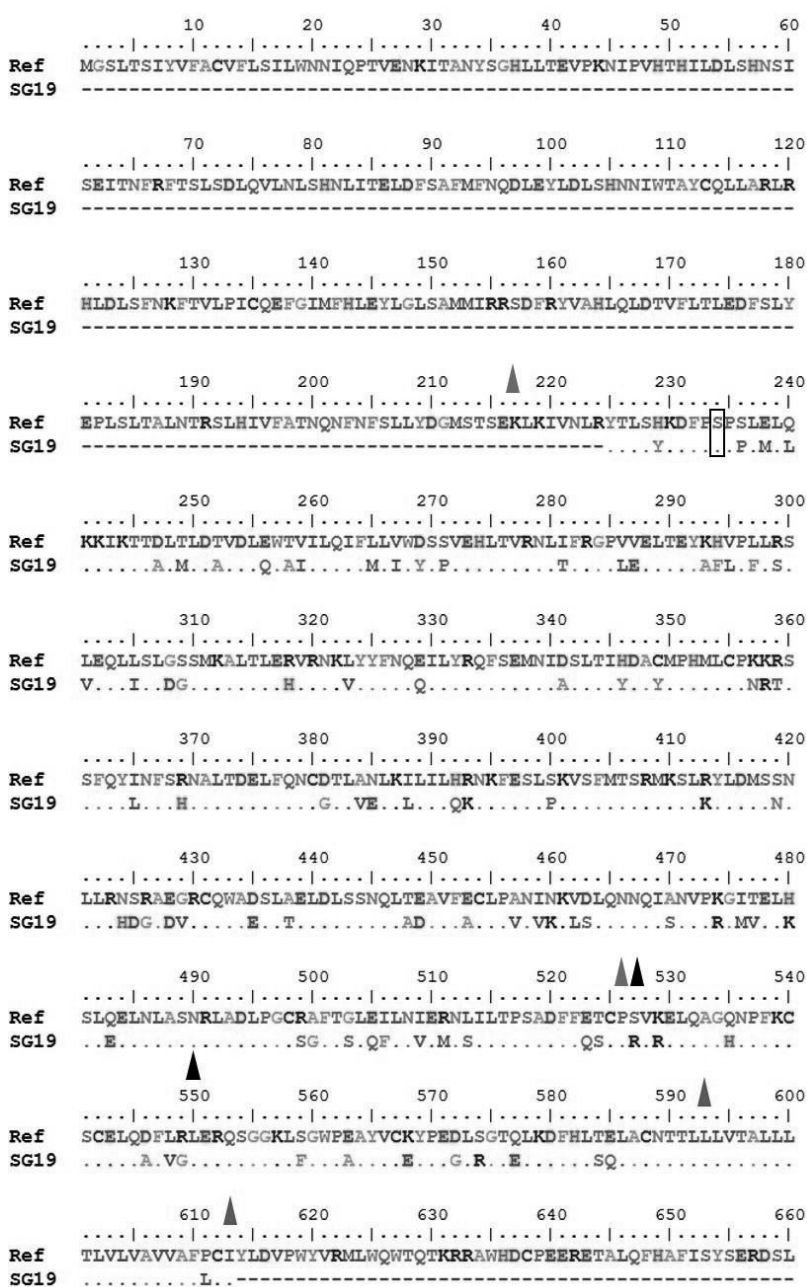


Supplementary Figure S1. Neighbour-Joining tree of 24 identified MHC class II alleles across five South Island saddleback populations. Putative non-classical MHC loci are shaded in yellow (Sutton et al. 2013). Diamond symbol next to allele names indicates those sequences contained stop codons.



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





Supplementary Figure S3. PhcaTLR1LA1 (SG19) aligned against *Gallus gallus* toll-like receptor 1 (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.

References

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- Lambert DM, King T, Shepherd LD, Livingston A, Anderson S, Craig JL 2005. Serial population bottlenecks and genetic variation: translocated populations of the New Zealand saddleback (*Philesturnus carunculatus rufusater*). *Conservation Genetics* 6: 1–14.
- Primmer CR, Moller AP, Ellegren H 1995. Resolving genetic relationships with microsatellite markers: a parentage testing system for the swallow *Hirundo rustica*. *Molecular Ecology* 4: 493–498.
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- Sutton JT, Robertson BC, Grueber CE, Stanton J-AL, Jamieson IG 2013. Characterization of MHC class II B polymorphism in bottlenecked New Zealand saddlebacks reveals low levels of genetic diversity. *Immunogenetics* 65: 619–633.
- Tarr CL, Fleischer RC 1998. Primers for polymorphic GT microsatellites isolated from Mariana crow, *Corvus kubaryi*. *Molecular Ecology* 7: 253–255.