

- 1 **Table S1** Primer sequences for the PCR amplification of MHC class I and class II DRB loci
 2 in the Alpine marmot (*Marmota marmota*).

Primers	Primer sequence (5' – 3')
MHC class I 2 nd exon	
MarmMF1	AyCTCCGTGTCCCGGCC
MarmMR1	GCGCTCTGGTyGTAGTAGC
MarmR1	CksGCAGGkTGTTGAGGCT
MarmR2	GCAGGTTGCTCAGGCCCACTT
MarmR3	GGTTATTCAAGTTCACTCGT
MarmR4	GCGCAGGGTGTTCAAGCACAT
MHC class II DRB 2 nd exon	
SusL1	GAGTGTCATTTCTCCAACGGGA
SusR2	TCACCTCTCCKCTCCACAGTGAA
EV2F	TGGCAGCTGTGRTCCTG
EV1R	CAGACCAGGAGGTTGTGRTG
MM_DRB_F1	GAGTGTCATTTCTCCAACsrGA
MM_DRB_R3	TyAmCTCTCCKCTCCACAGTGAA
MM_DRB_F2	GAGTGTCATTTTTTCAATrGGA
MM_DRB_R2	TTCGGCTTAACTCTCCGCTTTGA

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3 **Table S2** The PCR conditions and polymorphism characterization of MHC class I and class II DRB loci in *Marmota marmota*.

Primer pair	Putative locus name	Primer concentration (μM)	Annealing temperature (°C)	Fragment size (bp)	Allelic polymorphism	Amino acid polymorphism	Accession number
MarmMF1/Mar		100	55	199-202			
mMR1 MarmMF1/Mar	<i>MhcMama-UA</i>	20	55	175	1	1	
mR1 MarmMF1/Mar	<i>MhcMama-UB</i>	20	55	175	2	1	
mR2 MarmMF1/Mar	<i>MhcMama-UC</i>	100	50	176	1	1	
mR3 MarmMF1/Mar	<i>MhcMama-UD</i>	20	50	180	3	2	
mR4 SusL1/SusR2		100	55	203			
EV2F/EV1R		100	55	366			
MM_DRB_F1/M	<i>MhcMama-DRB1</i>	20	55	203-204	8	7	
M_DRB_R3 MM_DRB_F2/M	<i>MhcMama-DRB2</i>	20	50	203	3	1	
M_DRB_R2							

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7 **Table S3** The allele frequencies of four polymorphic loci in *Marmota marmota*.

Allele	Total sample
	(n = 38)
<i>Mama-UB*01</i>	0.71
<i>Mama-UB*02</i>	0.29
<i>Mama-UD*01</i>	0.68
<i>Mama-UD*02</i>	0.18
<i>Mama-UD*03</i>	0.13
<i>Mama-DRB1*01</i>	0.43
<i>Mama-DRB1*02</i>	0.26
<i>Mama-DRB1*03</i>	0.08
<i>Mama-DRB1*04</i>	0.07
<i>Mama-DRB1*05</i>	0.07
<i>Mama-DRB1*06</i>	0.05
<i>Mama-DRB1*07</i>	0.03
<i>Mama-DRB1*08</i>	0.01
<i>Mama-DRB2*01</i>	0.49
<i>Mama-DRB2*02</i>	0.37
<i>Mama-DRB2*03</i>	0.14

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10 **Table S4** Observed (H_o), expected (H_e) heterozygosities and allelic richness (R) per putative locus per population. H_o – observed heterozygosity, H_e – expected
 11 heterozygosity, P – probability of deviation from Hardy-Weinberg equilibrium. Asterisk denotes significant deviation from Hardy-Weinberg expectations after
 12 Bonferroni correction. R – allelic richness.

Population		<i>MhcMama- DRB1</i>	<i>MhcMama- DRB2</i>	<i>MhcMama- UB</i>	<i>MhcMama- UD</i>
Les Ecrins	H_o	0.60	0.60	0.50	0.70
	H_e	0.54	0.54	0.52	0.61
	P	1.00	1.00	1.00	0.60
	R	3	3	2	3
La Maurienne	H_o	0.60	0.30	0.20	0.10
	H_e	0.70	0.51	0.19	0.42
	P	0.54	0.13	1.00	<0.01*
	R	4	3	2	3
La Sassiere	H_o	0.83	0.67	0.39	0,44
	H_e	0.78	0.63	0.39	0,37
	P	0.91	0.17	1.00	1.00
	R	6.4	3	2	2.8

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26 **Table S6** The average pairwise nucleotide distances (Kimura 2-parameter models, K2P),
 27 Poisson-corrected amino acid distances, the average rates of synonymous (d_s) and
 28 nonsynonymous (d_N) substitutions per site and the results of Z-test of positive selection for
 29 polymorphic putative MHC loci in the Alpine marmot.

Sites	No.	K2P	aa	d_N	d_s	Z	P
	codons	distance	distance				
<i>Cluster MhcMama-UD</i>							
All	58	0.8 (0.5)	1.2 (1.1)	0.5 (0.5)	1.7 (1.8)	-0.654	1.000
ABS	7	0.0	0.0	0.0	0.0	0.000	1.000
Non-ABS	51	0.9 (0.6)	1.3 (1.3)	0.6 (0.6)	2.0 (2.0)	-0.661	1.000
<i>Cluster MhcMama-DRB1</i>							
All	67	4.3 (1.0)	10.3 (2.8)	5.3 (1.5)	1.7 (1.4)	2.273	0.012
ABS	15	11.5 (3.7)	28 (10.4)	14.3 (5.3)	2.2 (2.5)	2.064	0.021
Non-ABS	52	2.5 (0.9)	5.9 (2.4)	2.8 (1.1)	1.5 (1.6)	1.140	0.128

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31 **Table S7** The evaluation of the fit of various models of codon evolution. The parameter
 32 descriptions are: ω – d_N/d_S per all sites; ω_1 – estimated value of ω for sites under positive
 33 selection, p_0 – proportion of sites with $\omega \leq 1$; and p_1 – proportion of sites with $\omega > 1$.

Model	$\ln L$	ΔAIC	Parameters
<i>MHC class I – all alleles</i>			
M0	-544.6	5.0	$\omega = 0.302$
M7	-541.1	Best	
M8	-540.8	3.4	$\omega_1 = 1.000, p_0 = 0.697, p_1 = 0.303$
<i>MHC class II DRB – all alleles</i>			
M0	-574.9	29.6	$\omega = 0.323$
M7	-559.1	Best	
M8	-557.2	0.3	$\omega_1 = 3.628, p_0 = 0.903, p_1 = 0.097$
<i>Mama-DRB1 cluster</i>			
M0	-386.1	12.0	$\omega = 1.408$
M7	-382.7	7.4	
M8	-377.1	Best	$\omega_1 = 15.014, p_0 = 0.732, p_1 = 0.268$

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36 **Table S8** *Marmota marmota* MHC class I sequences.

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38 >Mama-UA*01

39 GGCGGGGAGCCCCGCTTCATCTCCGTGGGCTACGTGGACGACACGCAGTTCGTGC

40 GCTTCGACAGCTACACCGAGAATCCCAGGATGGAGCCCCGGGCGCCCTGGATGGA

41 GAAGGTGGGACCCAAGTATTGGGAACGGGAGACACAGACCGCCAAGGACAATGC

42 ACAGAGTGACC

43 >Mama-UB*01

44 GGAGGGGAGCCCCGGCATATGGAAGTGGGCTATGTGGAGGACACGCAGTTCGTGC

45 GCTTTGACAGCGACGCCCCGAAGCCGAGGATGGAGCCGCGAGCGCCATGGATAGA

46 GCAGGAGGGGCGGGGTATTGGAAACGGAACACACGGATTGCCAAGGGCAATGC

47 ACAGAGTGACC

48 >Mama-UB*02

49 GGAGGGGAGCCCCGGCATATGGAAGTGGGCTATGTGGAGGACACGCAGTTCGTGC

50 GCTTTGACAGCGACGCCCCGAAGCCGAGGATGGAgCCGCGAGCGCCGTGGATAGA

51 GCAGGAGGGGCGGGGTATTGGAAACGGAACACACGGATTGCCAAGGGCAATGC

52 ACAGAGTGACC

53 >Mama-UC*01

54 GGCCACGGGGAGCCCCGCTTCATCTCCGTGGGCTACGTGGACCACACGCAGTTCG

55 TGCCTTGGACAGCGACGCTGAGAATCCCAGGGAGGAGCCGCGGGGCGCCGTGGA

56 TAGAGCAGGAGGGGTTCGGATTATTGGGTTAGGAACACACAGAAAGCCAAGAACG

57 CCGCACAGATTGA

58 >Mama-UD*01

59 GGCTCCGGGAGTCCCGCTTCATCTCCGTGGGCTACGTGGACGACACCCAGTTCAT

60 GCGCTTCGACAGCGACGCGAAGAATCCCAGACAGGAGCCGCGGGGCGCCGTGGAT

61 GGGGCTGGAGGGTCCGGAGTATTGGGAGCAAAACACACGGATTTCCGAGAACTCT

62 GCACAGAATCACCGA

63 >Mama-UD*02

64 GGCTCCGGGAGTCCCGCTTCATCTCCGTGGGCTACGTGGACAACACCCAGTTCAT

65 GCGCTTCGACAGCGACGCGAAGAATCCCAGACAGGAGCCGCGGGGCGCCGTGGAT

66 GGGGCTGGAGGGTCCGGAGTATTGGGAGCAAAACACACGGATTTCCGAGAACTCT

67 GCACAGAATCACCGA

68 >Mama-UD*03

69 GGCCTCCGGGAGTCCCGCTTCATCTCCGTGGGCTACGTGGACGACACCCAGTTCAT
70 GCGCTTCGACAGCGACGCaAAGAATCCCAGACAGgAgCCGCGGGCGCCGTGGATG
71 GGGCTGGAGGGTCCGGAGTATTGGGAGCAAAACACACGGATTTCCGAGAACTCTG
72 CACAGAATCACCGA