

Table**Table S1 Information of 11 microsatellite loci in *Rhinopithecus bieti***

Locus	Forward primer sequence (5'-3')	Reverse primer sequence (5'-3')	T _A (°C)	Reference
D1s207	CACTTCTCCTTGAATCGCTT	GCAAGTCCTGTTCCAAGTCT	50	(Liu et al. 2008)
D1S533	CATCCCCCCCCAAAAAATATA	TTGCTTAATCAAATAACAATGGG	50	(Liu et al. 2008)
D2S1326	AGACAGTCAAGAATAACTGCC	CTGTGGCTAAAAGCTGAAT	55	(Liu et al. 2008)
D6S474	ATCCCAACTCTTAAATGGGC	TTCCATGGCAGAAATTGTTT	52	(Liu et al. 2008)
D6S493	ATCCCAACTCTTAAATGGGC	TTCCATGGCAGAAATTGTTT	50	(Liu et al. 2008)
D8S505	CAAAAGTGAACCCAAACCTA	AGTGCTAAGTCCCAGACCAA	58	(Liu et al. 2008)
D11S2002	CATGCCCTTCTTCATAG	AATGAGGTCTTACTTGTGCC	55	(Liu et al. 2008)
D17S1290	GCCAACAGAGCAAGACTGTC	GGAAACAGTTAAATGCCAA	55	(Liu et al. 2008)
GM108	CAGCGTAAGCCAGTTGCC	GGAAAAGTCTGAAACCCACGA	51	(Hao et al. 2007)
GM109	GGTGGAGGAGGGCCTAAC	CTGATGTCCATAGGCGACCAT	64	(Hao et al. 2007)
GM214	GGGCAACAGAGCGAGACTG	TGCAAAGATGTGAACGGAAAT	58	(Hao et al. 2007)

Table S2 Homologous sequences for *Rhinopithecus bieti* MHC genes from closely related species and an outgroup sequence from *Mus musculus* for phylogenetic reconstruction

Species	Allele	GenBank number
<i>Mus musculus</i>	<i>Mumu-H2-Aa</i>	NM_010378.3
<i>Rhinopithecus roxellana</i>	<i>Rhro-DQA1*02</i>	JQ217108.1
	<i>Rhro-DQA1*05</i>	JQ217111.1
	<i>Rhro-DQA1*07</i>	JQ217113.1
	<i>Rhro-DQB1*10</i>	JQ217125.1
	<i>Rhro-DQB1*17</i>	KU184585.1
	<i>Rhro-DQB1*06</i>	JQ217121.1
	<i>Rhro-DPB1*02</i>	PP871676
	<i>Rhro-DPB1*06</i>	PP871680
	<i>Rhro-DPB1*01</i>	PP871675
	<i>Rhro-DRB*10</i>	JQ863331.1
	<i>Rhro-DRB*20</i>	JQ863341.1
	<i>Rhro-DRB*37</i>	JQ863358.1
<i>Papio anubis</i>	<i>Paan-DQA1*01:05</i>	OP375770.1
	<i>Paan-DQA1*05:01</i>	LT607037.1
	<i>Paan-DQB1*18:01:01</i>	LT546107.1
<i>Pan troglodytes</i>	<i>Patr-DQA1*01</i>	DQ924453.1
	<i>Patr-DQA1*05:02:02</i>	LT622882.1
	<i>Patr-DQB1*03:06</i>	LT908065.1
	<i>Patr-DPB1*12</i>	AB183470.1
	<i>Patr-DRB1*02</i>	LR216144.1
	<i>Patr-DRB1*07:01</i>	DQ655659.1
	<i>Patr-DRB5*03</i>	LR216147.1
<i>Macaca mulatta</i>	<i>Mamu-DQA1*26:02:02</i>	OX377330.1
	<i>Mamu-DQB1*15:09</i>	HQ215939.1
	<i>Mamu-DPB1*03</i>	EF426707.1
	<i>Mamu-DRB1*03:12</i>	AM910416.1
	<i>Mamu-DRB5*03:06</i>	HM594300.1
	<i>Mamu-DQA1*01:02</i>	KC428065
<i>Macaca fascicularis</i>	<i>Mafa-DQA1*26:02</i>	AM086060.1
	<i>Mafa-DQA1*01:10</i>	AB764109
	<i>Mafa-DQB1*06:08</i>	AB764119
	<i>Mafa-DQB1*28:02</i>	HG994112.1
	<i>Mafa-DPB1*03:04</i>	AB764135
	<i>Mafa-DPB1*22</i>	AM086165.1
	<i>Mafa-DRB1*03:01</i>	AY340675
<i>Homo sapiens</i>	<i>HLA-DQA1*04:02</i>	HF674388.2
	<i>HLA-DQB1*06</i>	LR777803.1

	<i>HLA-DQB1*05</i>	LR778295.1
	<i>HLA-DPB1*02</i>	LT630703.1
	<i>HLA-DPB1*16</i>	LT882730.1
	<i>HLA-DRB1*10</i>	AJ920405.1
	<i>HLA-DRB1*13</i>	AJ920408.1
<i>Gorilla gorilla</i>	<i>Gogo-DQB1*05:02</i>	KP872253
	<i>Gogo-DPB1*01</i>	KP872242
	<i>Gogo-DRB5*05:01</i>	KP872282
<i>Chlorocebus sabaeus</i>	<i>Chsa-DQA1*01:01</i>	KA650601
	<i>Chsa-DQA1*05:01</i>	KA650600
	<i>Chsa-DQB1*06:01</i>	KA650615
	<i>Chsa-DQB1*15:01</i>	KA650616
	<i>Chsa-DPB1*09:01</i>	KA650617
	<i>Chsa-DRB1*03:01</i>	KA650612
	<i>Chsa-DRB5*01:01</i>	KA650607

Table S3 Rate of non-synonymous substitutions (d_N) and synonymous substitutions (d_S) of five *Rhinopithecus bieti* MHC loci

Locus		N	d_N	d_S	$\omega (d_N/dS)$	Z	P
<i>DPB1</i>	ABS	15	0.244 ±0.090	0.266 ±0.198	0.917	-0.095	0.924
	Non-ABS	72	0.070 ±0.017	0.157 ±0.050	0.446	-1.628	0.106
	All	87	0.098 ±0.020	0.172 ±0.047	0.570	1.390	0.084
<i>DQA1</i>	ABS	19	0.227±0.107	0.228±0.216	0.996	-0.004	0.997
	Non-ABS	63	0.130±0.030	0.226±0.085	0.575	-0.986	0.326
	All	82	0.150 ±0.031	0.227±0.078	0.661	0.855	0.197
<i>DQB1</i>	ABS	21	0.229±0.102	0.000±0.000	≥1	0.004	0.498
	Non-ABS	68	0.097±0.030	0.108±0.053	0.898	-0.181	0.857
	All	89	0.127 ±0.033	0.085±0.040	1.494	0.778	0.438
<i>DRB1</i>	ABS	20	0.207±0.096	0.125±0.118	1.656	0.587	0.559
	Non-ABS	69	0.053±0.020	0.042±0.032	1.262	0.324	0.747
	All	89	0.085±0.025	0.058±0.032	1.466	0.739	0.231
<i>DRB5</i>	ABS	20	0.294±0.112	0.090±0.092	3.267	1.314	0.191
	Non-ABS	69	0.019±0.011	0.114±0.059	0.167	-1.430	0.155
	All	89	0.073±0.023	0.109±0.047	0.670	0.641	0.262

Table S4 likelihood ratio test of codon evolution for the second exons of five *Rhinopithecus bieti* MHC loci

	Models compared	df	Test statistic	Significance(<i>P</i>)
<i>DQA1</i>	M2a vs. M1a	2	1.474	> 0.05
	M3 vs. M0	4	2.026	> 0.05
	M8 vs. M7	2	1.504	> 0.05
<i>DPB1</i>	M2a vs. M1a	2	0.000	> 0.05
	M3 vs. M0	4	3.694	> 0.05
	M8 vs. M7	2	0.000	> 0.05
<i>DQB1</i>	M2a vs. M1a	2	7.160	< 0.05
	M3 vs. M0	4	11.156	< 0.05
	M8 vs. M7	2	7.160	> 0.05
<i>DRB1</i>	M2a vs. M1a	2	10.816	< 0.01
	M3 vs. M0	4	16.144	< 0.01
	M8 vs. M7	2	11.174	< 0.01
<i>DRB5</i>	M2a vs. M1a	2	1.472	> 0.05
	M3 vs. M0	4	7.46	> 0.05
	M8 vs. M7	2	1.474	> 0.05

1. Hao Y.L., Liu Z.J., Wu H., Ren B.P., Wei F.W. & Li M. (2007) Isolation and characterization of 11 microsatellite loci for the Sichuan snub-nosed monkey, *Rhinopithecus roxellana*. Conservation Genetics 8, 1021-4.
2. Liu Z.J., Ren B.P., Hao Y.L., Zhang H.R., Wei F.W. & Li M. (2008) Identification of 13 human microsatellite markers via cross-species amplification of fecal samples from <i>*Rhinopithecus bieti*</i>. International Journal of Primatology 29, 265-72.