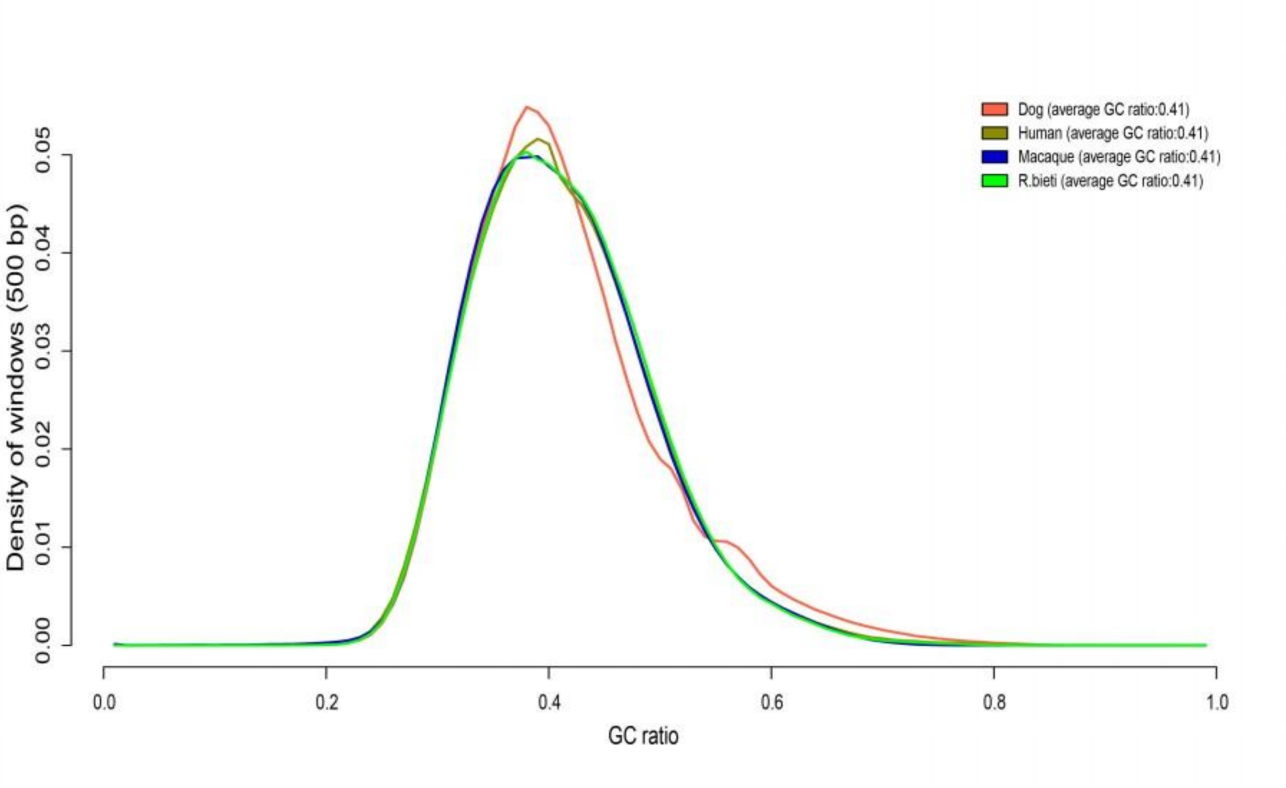
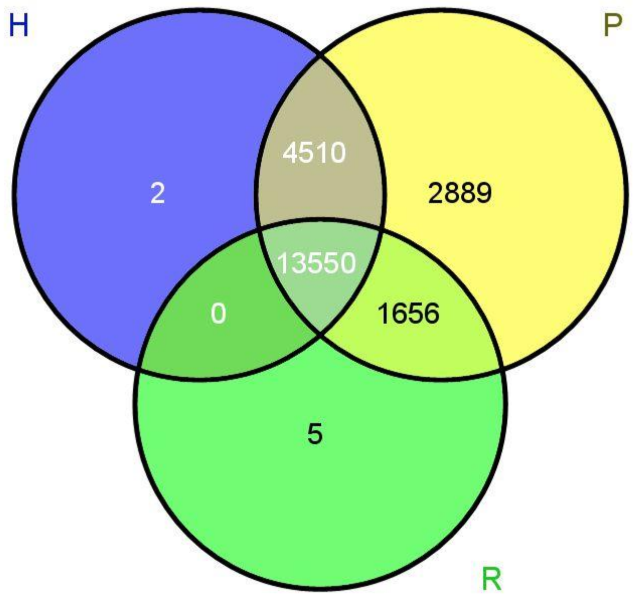


Supplementary Figure 1

GC content of the *R. bieti* genome.

Distribution of GC content in the *R. bieti* (green), macaque (blue), human (brown), and dog (red) genomes. The proportion of 500-bp non-overlapping sliding windows with a given GC content is shown.

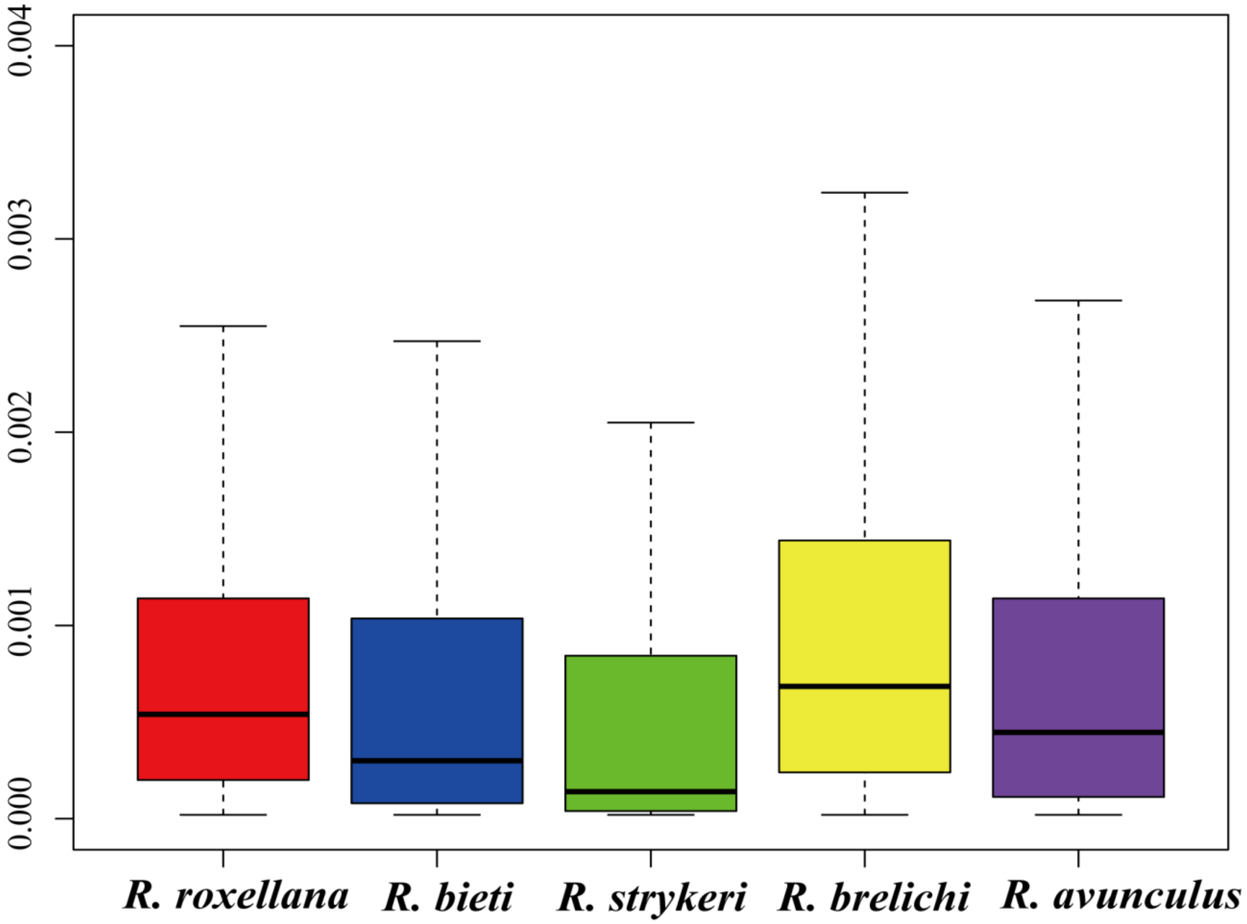
Nature Genetics: doi:10.1038/ng.3615



Supplementary Figure 2

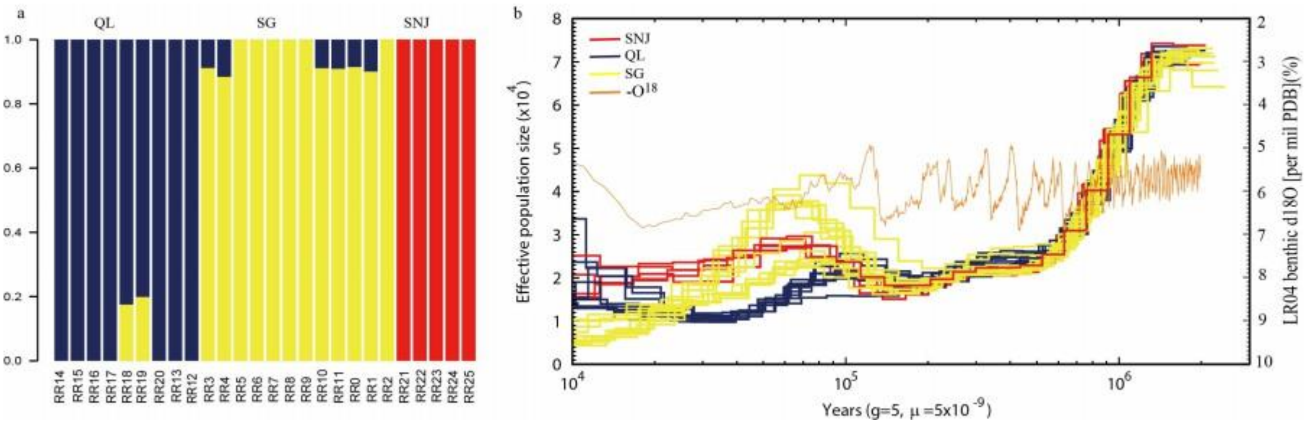
Summary of the evidence for gene models merged from three types of gene sources.

P, *ab initio* prediction; H, homology based; R, RNA-seq.



Supplementary Figure 3

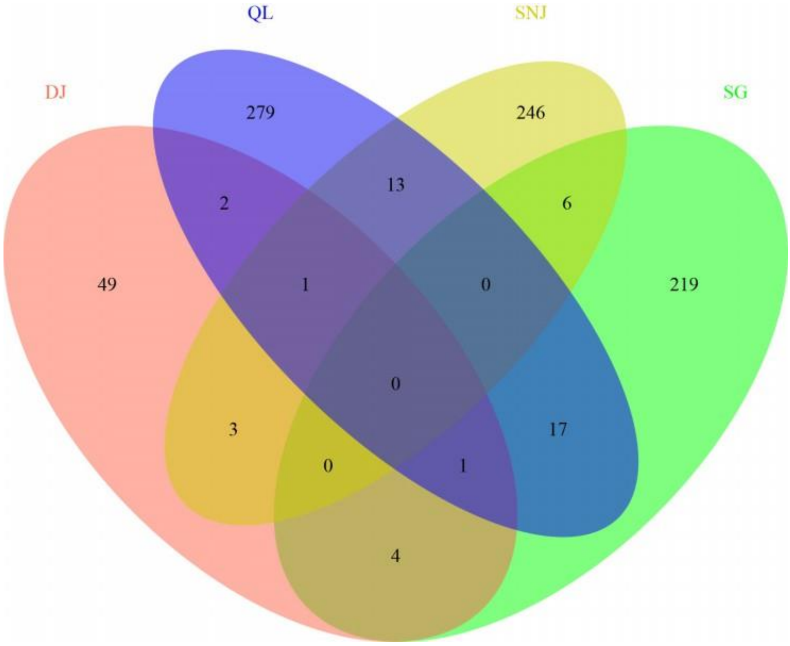
Genetic diversity among snub-nosed monkeys calculated using 50-kb windows.



Supplementary Figure 4

Population genomic analysis of *R. roxellana*.

(**a**) Population structure analysis of 26 *R. roxellana* individuals (*K* = 3). (**b**) Demographic history of *R. roxellana* reconstructed using the PSMC model. Blue lines represent the QL population, red lines represent the SNJ population, yellow lines represent the SG population, and orange line represents negative O^{18}. O^{18} is inversely proportional to temperature.



Supplementary Figure 5

Genes under selection identified by the genome scans in one *R. bieti* population (DJ) and three *R. roxellana* populations (SG, QL, and SNJ).

Genes identified by at least two of the three scan methods (Z_H, LSBL, and $\theta\pi$ scans) are shown as candidate genes under selection.

Supplementary Tables

Supplementary Table 1: Reads and libraries used in the *de novo* sequencing of the *R. bieti* genome.

Libraries	Insert size (bp)	Read length (bp)	Raw reads			Qualified reads[a]		
			Total data(Gb)	Sequence coverage(X)[b]	Physical coverage(X)[b]	Total data(Gb)	Sequence coverage(X)[b]	Physical coverage(X)[b]
Illumina reads	200bp	100	39.6	11.3	10.8	38.5	10.9	10.6
	300bp	100	31.1	8.8	12.7	29.3	8.3	12.3
	400bp	100	40.9	11.6	22.6	39.3	11.2	21.9
	600bp	100	52.5	14.9	41.7	50.9	14.5	40.6
	5kb	100	37.6	10.6	320.6	19.5	5.5	166.2
	10-15kb	100	26.4	7.5	477.8	4.2	1.2	78.2
	>15kb	100	41.4	11.76	921.3	6.6	1.9	155.4
Total	-	-	269.5	76.6	1807.4	188.3	53.5	485.2

[a] Qualified reads were generated by filtering the single reads, low quality reads, base-calling duplicates and adapter contamination from the raw data.

[b] Coverage was calculated under the assumption of a genome size of 3.52 Gb. Sequence coverage refers to the total length of generated reads, and physical coverage refers to the total length used for the paired reads.

Supplementary Table 2: *R. bieti* whole-genome assembly statistics.

	Contig[a]		Scaffold[b]	
	Size (bp)	**Number**	**Size (bp)**	**Number**
Total Size	2,779,866,736		2,977,333,459	
Total Number (> 100bp)	321,567		123,387	
Total Number (> 2kb)	201,468		17,335	
Longest	247,741		14,865,877	
N50	20,489	38,892	2,223,895	380
N90	4,689	145,115	197,251	1,787

[a] Contig represents the final contig after filling the gap in the intra-scaffold.

[b] The scaffolds with a length of < 100bp were not included in the statistics.

Supplementary Table 3: Significant enrichment (p<0.01 by Fisher exact test) in protein domain that may be related to high-altitude adaptation of *R. bieti* using InterPro prediction.

InterProScanID	**Candidate Gene Number[a]**	***R bieti* Gene Number**	**Bos Gene Number**	**Canis Gene Number**	**Homo Gene Number**	**Macaca Gene Number**	**P value**	**Bos P value**	**Canis P value**	**Homo P value**	**Macaca P value**	**Description**
DNA repair and damage response												
IPR014721	21	45	23	27	21	42	3.51E-09	4.77E-13	7.69E-12	8.00E-14	9.39E-10	Ribosomal protein S5 domain 2-type fold, subgroup
IPR020568	26	62	35	36	34	57	3.65E-06	3.29E-09	8.87E-09	5.32E-10	9.70E-07	Ribosomal protein S5 domain 2-type fold
IPR009071	23	66	56	52	57	64	5.31E-08	5.14E-09	3.52E-09	1.27E-09	2.32E-08	High mobility group box domain
IPR017967	6	6	8	3	3	10	8.84E-05	2.64E-04	1.27E-05	6.11E-06	5.35E-04	HMG box A DNA-binding domain, conserved site
IPR001846	8	34	14	18	27	17	9.38E-03	9.75E-05	4.77E-04	1.77E-03	2.24E-04	von Willebrand factor, type D domain
IPR022617	10	11	6	6	5	10	6.27E-07	2.14E-08	3.12E-08	3.69E-09	2.92E-07	Rad60/SUMO-like domain
Oxidative phosphorylation progress												
IPR015875	5	5	4	4	4	4	3.60E-04	1.99E-04	2.39E-04	1.31E-04	1.74E-04	IMP dehydrogenase / GMP reductase, conserved site
IPR001093	12	13	4	4	4	7	4.10E-08	2.90E-11	4.58E-11	1.04E-11	4.75E-10	IMP dehydrogenase/GMP reductase
IPR015878	9	10	3	3	3	7	2.46E-06	1.00E-08	1.41E-08	4.63E-09	3.14E-07	S-adenosyl-L-homocysteine hydrolase, NAD binding domain
IPR003096	15	17	8	11	10	15	1.22E-09	2.21E-12	4.92E-11	3.65E-12	2.92E-10	Smooth muscle protein/calponin
IPR000043	10	11	3	3	3	7	6.27E-07	9.39E-10	1.38E-09	3.98E-10	3.74E-08	Adenosylhomocysteinase
IPR018170	13	14	17	8	10	14	1.05E-08	5.60E-08	2.88E-10	2.95E-10	8.28E-09	Aldo/keto reductase, conserved site
IPR020471	12	13	19	8	10	19	4.10E-08	8.04E-07	2.38E-09	2.53E-09	5.98E-07	Aldo/keto reductase subgroup

IPR023210	17	28	25	14	17	25	5.63E-09	1.80E-09	7.56E-12	7.37E-12	1.18E-09	NADP-dependent oxidoreductase domain
IPR011613	8	8	3	3	3	3	5.50E-06	1.04E-07	1.41E-07	5.25E-08	8.38E-08	Glycoside hydrolase family 15
IPR006103	6	9	2	2	2	4	3.96E-04	3.61E-06	4.54E-06	2.16E-06	2.03E-05	Glycoside hydrolase, family 2, TIM barrel

[a] The candidate genes represent the genes that were included in the expanded gene family and contained the corresponding InterPro protein

Supplementary Table 4: Tissues and sequencing throughputs for *R. bieti* and *M. mulatta* RNA sequencing.

Species	Tissue	Raw data (Gb)	Source
R. bieti (Rb0)	blood	5.9	this study
	stomach	7.0	this study
	large intestine	6.8	this study
	small intestine	11.7	this study
	spleen	7.7	this study
	kidney	8.6	this study
	testicle	7.0	this study
	liver	6.1	this study
	brain	6.4	this study
	heart	8.7	this study
	lung	7.2	this study
	muscle	6.6	this study
M. mulatta	stomach	5.9	this study
	large intestine	5.6	this study
	small intestine	5.9	this study
	spleen	15.6	download
	kidney	17.4	download
	testicle	18.5	download
	liver	18.1	download
	brain	17.2	download
	heart	17.5	download
	lung	18.0	download
	muscle	18.4	download

Supplementary Table 5: Sequencing Statistics of five snub-nosed monkeys.

species	data size (bp)	reads number	reads number after duplication removal	Homozygous SNP	Heterozygous SNP	Heterozygous Rate (%)
R. strykeri	97,012,702,866	959,240,676	905,345,888	1,876,488	416,076	0.0151
R. brelichi	117,801,130,200	1,178,011,302	1,053,517,166	7,189,626	171,0421	0.0621
R. avunculus	115,457,855,112	1,143,053,318	910,514,045	3,210,004	1,147,093	0.0416
R. bieti[a]	162,300,853,600	1,623,008,536	1,523,642,072	-	839,865	0.0305
R. roxellana[a]	288,129,863,200	2,881,298,632	2,495,902,973	7,855,574	1,191,986	0.0433

[a] Only short reads were used for alignment.

Supplementary Table 6: 20 common amino acid substitutions in 18 genes observed in high-altitude snub-nosed monkeys.

OSBPL3	Amino acid position 506 in the CDS of ENSG00000070882									
R.roxellana	**L**	**E**	**S**	**G**	**A**	**E**	**A**	**K**	**S**	**R**
R.brelichi	**L**	**E**	**S**	**G**	**G**	**E**	**A**	**K**	**S**	**R**
R.bieti	**L**	**E**	**S**	**G**	**A**	**E**	**A**	**K**	**S**	**R**
R.strykeri	**L**	**E**	**S**	**G**	**A**	**E**	**A**	**K**	**S**	**R**
R.avunculus	**L**	**E**	**S**	**G**	**G**	**E**	**A**	**K**	**S**	**R**
Macaque	**L**	**E**	**S**	**G**	**G**	**E**	**A**	**K**	**S**	**R**
Human	**L**	**D**	**S**	**G**	**R**	**E**	**A**	**K**	**S**	**R**
Dog	**L**	**E**	**S**	**G**	**G**	**E**	**A**	**K**	**S**	**R**

DNAH11	Amino acid position 466 in the CDS of ENSG00000105877									
R.roxellana	**C**	**R**	**F**	**D**	**E**	**F**	**L**	**D**	**R**	**L**
R.brelichi	**C**	**R**	**F**	**D**	**K**	**F**	**L**	**D**	**R**	**L**
R.bieti	**C**	**R**	**F**	**D**	**E**	**F**	**L**	**D**	**R**	**L**
R.strykeri	**C**	**R**	**F**	**D**	**E**	**F**	**L**	**D**	**R**	**L**
R.avunculus	**C**	**R**	**F**	**D**	**K**	**F**	**L**	**D**	**R**	**L**
Macaque	**C**	**R**	**F**	**D**	**K**	**F**	**L**	**D**	**R**	**L**
Human	**C**	**R**	**F**	**D**	**K**	**F**	**L**	**D**	**R**	**L**
Dog	**C**	**R**	**F**	**D**	**K**	**F**	**L**	**D**	**R**	**F**

AKNA	Amino acid position 1018 in the CDS of ENSG00000106948									
R.roxellana	**G**	**L**	**A**	**A**	**K**	**M**	**A**	**V**	**P**	**G**
R.brelichi	**G**	**L**	**A**	**A**	**E**	**M**	**A**	**V**	**P**	**G**
R.bieti	**G**	**L**	**A**	**A**	**K**	**M**	**A**	**V**	**P**	**G**
R.strykeri	**G**	**L**	**A**	**A**	**K**	**M**	**A**	**V**	**P**	**G**
R.avunculus	**G**	**L**	**A**	**A**	**E**	**M**	**A**	**V**	**P**	**G**
Macaque	**G**	**P**	**S**	**A**	**S**	**L**	**A**	**V**	**P**	**G**
Human	**G**	**P**	**A**	**A**	**E**	**M**	**A**	**V**	**P**	**G**
Dog	**S**	**P**	**V**	**A**	**E**	**M**	**E**	**V**	**P**	**G**

TTF2	Amino acid position 834 in the CDS of ENSG00000116830									
R.roxellana	**R**	**P**	**L**	**V**	**T**	**L**	**P**	**Q**	**R**	**K**
R.brelichi	**R**	**P**	**L**	**V**	**I**	**L**	**P**	**Q**	**R**	**K**
R.bieti	**R**	**P**	**L**	**V**	**T**	**L**	**P**	**Q**	**R**	**K**
R.strykeri	**R**	**P**	**L**	**V**	**T**	**L**	**P**	**Q**	**R**	**K**
R.avunculus	**R**	**P**	**L**	**V**	**I**	**L**	**P**	**Q**	**R**	**K**
Macaque	**R**	**P**	**L**	**V**	**I**	**L**	**P**	**Q**	**R**	**K**
Human	**R**	**P**	**L**	**V**	**I**	**L**	**P**	**Q**	**R**	**K**
Dog	**K**	**P**	**L**	**V**	**M**	**L**	**P**	**Q**	**R**	**Q**

TEP1	Amino acid position 317 in the CDS of ENSG00000129566									
R.roxellana	**A**	**F**	**L**	**P**	**T**	**C**	**R**	**P**	**H**	**L**
R.brelichi	**A**	**F**	**L**	**P**	**A**	**C**	**R**	**P**	**H**	**L**
R.bieti	**A**	**F**	**L**	**P**	**T**	**C**	**R**	**P**	**H**	**L**
R.strykeri	**A**	**F**	**L**	**P**	**T**	**C**	**R**	**P**	**H**	**L**
R.avunculus	**A**	**F**	**L**	**P**	**A**	**C**	**R**	**P**	**H**	**L**
Macaque	**A**	**F**	**L**	**P**	**A**	**C**	**R**	**P**	**H**	**L**
Human	**A**	**F**	**L**	**P**	**A**	**C**	**R**	**P**	**H**	**L**
Dog	**A**	**L**	**L**	**P**	**V**	**C**	**R**	**P**	**Y**	**L**

ARMC2	Amino acid position 835 in the CDS of ENSG00000118690									
R.roxellana	**N**	**Y**	**H**	**K**	**F**	**H**	**W**	**E**	**T**	**E**
R.brelichi	**N**	**Y**	**H**	**K**	**L**	**H**	**W**	**E**	**T**	**E**
R.bieti	**N**	**Y**	**H**	**K**	**F**	**H**	**W**	**E**	**T**	**E**
R.strykeri	**N**	**Y**	**H**	**K**	**F**	**H**	**W**	**E**	**T**	**E**
R.avunculus	**N**	**Y**	**H**	**K**	**L**	**H**	**W**	**E**	**T**	**E**
Macaque	**N**	**Y**	**H**	**K**	**L**	**H**	**W**	**E**	**T**	**E**
Human	**N**	**Y**	**H**	**K**	**L**	**H**	**W**	**E**	**T**	**E**
Dog	**N**	**Y**	**H**	**K**	**L**	**H**	**W**	**E**	**T**	**E**

EDAR	Amino acid position 474 in the CDS of ENSG00000135960									
R.roxellana	V	P	P	A	T	Q	P	H	A	A
R.brelichi	V	P	P	A	S	Q	P	H	A	A
R.bieti	V	P	P	A	T	Q	P	H	A	A
R.strykeri	V	P	P	A	T	Q	P	H	A	A
R.avunculus	V	P	P	A	S	Q	P	H	A	A
Macaque	V	P	P	A	S	Q	P	H	A	A
Human	V	P	P	A	S	Q	P	H	A	A
Dog	V	P	P	A	S	Q	P	P	A	T

GPR114	Amino acid position 480 in the CDS of ENSG00000159618									
R.roxellana	S	F	G	V	L	L	L	P	Q	L
R.brelichi	S	F	G	V	F	L	L	P	Q	L
R.bieti	S	F	G	V	L	L	L	P	Q	L
R.strykeri	S	F	G	V	L	L	L	P	Q	L
R.avunculus	S	F	G	V	F	L	L	P	Q	L
Macaque	S	F	G	I	F	L	L	P	Q	L
Human	S	F	G	V	F	L	L	P	Q	L
Dog	S	F	G	V	F	L	L	P	Q	L

FCRL4	Amino acid position 239 in the CDS of ENSG00000163518									
R.roxellana	V	I	L	S	N	W	S	R	S	R
R.brelichi	V	I	L	S	D	W	S	R	S	Q
R.bieti	V	I	L	S	N	W	S	R	S	R
R.strykeri	V	I	L	S	N	W	S	R	S	R
R.avunculus	V	I	L	S	D	W	S	R	S	Q
Macaque	V	T	L	S	D	W	S	P	S	R
Human	V	I	L	S	D	W	S	T	Y	P
Dog	V	M	L	S	D	W	S	R	S	P

FCRL4	Amino acid position 290 in the CDS of ENSG00000163518									
R.roxellana	V	S	G	V	V	L	E	T	Q	P
R.brelichi	V	S	G	V	L	L	E	T	Q	P
R.bieti	V	S	G	V	V	L	E	T	Q	P
R.strykeri	V	S	G	V	V	L	E	T	Q	P
R.avunculus	V	S	G	V	L	L	E	T	Q	P
Macaque	V	S	G	V	L	L	E	T	Q	P
Human	V	S	G	V	L	L	E	T	Q	P
Dog	V	S	G	V	L	L	E	T	Q	P

TMEM71	Amino acid position 203 in the CDS of ENSG00000165071									
R.roxellana	G	G	N	T	D	G	L	S	P	Q
R.brelichi	G	G	N	T	H	G	L	S	P	Q
R.bieti	G	G	N	T	D	G	L	S	P	Q
R.strykeri	G	G	N	T	D	G	L	S	P	Q
R.avunculus	G	G	N	T	H	G	L	S	P	Q
Macaque	G	G	N	T	H	S	L	S	P	Q
Human	G	G	N	S	H	S	L	S	L	Q
Dog	R	Q	N	T	H	N	G	A	L	Q

CDT1	Amino acid position 537 in the CDS of ENSG00000167513									
R.roxellana	T	A	R	L	V	R	Q	A	R	A
R.brelichi	T	A	R	L	A	R	Q	A	R	A
R.bieti	T	A	R	L	V	R	Q	A	R	A
R.strykeri	T	A	R	L	V	R	Q	A	R	A
R.avunculus	T	A	R	L	A	R	Q	A	R	A
Macaque	T	A	R	L	A	R	Q	A	R	A
Human	T	A	R	L	A	H	Q	T	R	A
Dog	I	M	R	L	A	H	L	A	L	A

PARP15	Amino acid position 346 in the CDS of ENSG00000173200									
R.roxellana	A	A	G	P	T	V	E	N	E	C
R.brelichi	A	A	G	P	A	V	E	N	E	C
R.bieti	A	A	G	P	T	V	E	N	E	C
R.strykeri	A	A	G	P	T	V	E	N	E	C
R.avunculus	A	A	G	P	A	V	E	N	E	C
Macaque	G	A	G	Q	A	V	E	N	E	C
Human	G	A	G	Q	A	V	E	S	E	C
Dog	G	A	G	P	A	V	E	N	E	C

ZBBX	Amino acid position 97 in the CDS of ENSG00000169064									
R.roxellana	S	A	G	K	A	K	L	K	L	L
R.brelichi	S	A	G	K	V	K	L	K	L	L
R.bieti	S	A	G	K	A	K	L	K	L	L
R.strykeri	S	A	G	K	A	K	L	K	L	L
R.avunculus	S	A	G	K	V	K	L	K	L	L
Macaque	S	A	G	K	V	K	L	K	L	L
Human	S	A	G	K	V	K	L	K	L	L
Dog	S	A	G	K	V	K	L	K	L	L

NT5DC1	Amino acid position 393 in the CDS of ENSG00000178425									
R.roxellana	T	E	D	S	F	V	Y	T	W	S
R.brelichi	T	E	D	S	L	V	Y	T	W	S
R.bieti	T	E	D	S	F	V	Y	T	W	S
R.strykeri	T	E	D	S	F	V	Y	T	W	S
R.avunculus	T	E	D	S	L	V	Y	T	W	S
Macaque	T	E	D	S	L	V	Y	T	W	S
Human	T	E	D	S	L	V	Y	T	W	S
Dog	T	E	D	S	L	V	Y	T	W	S

MACC1	Amino acid position 586 in the CDS of ENSG00000183742									
R.roxellana	G	E	G	K	I	K	A	I	G	Q
R.brelichi	G	E	G	K	V	K	A	I	G	Q
R.bieti	G	E	G	K	I	K	A	I	G	Q
R.strykeri	G	E	G	K	I	K	A	I	G	Q
R.avunculus	G	E	G	K	V	K	A	I	G	Q
Macaque	G	E	G	K	V	K	A	I	G	Q
Human	G	E	G	K	V	K	A	I	G	Q
Dog	G	E	G	K	V	K	A	I	G	Q

RNASE4	Amino acid position 89 in the CDS of ENSG00000258818									
R.roxellana	C	S	T	T	K	I	Q	C	K	N
R.brelichi	C	S	T	T	N	I	Q	C	K	N
R.bieti	C	S	T	T	K	I	Q	C	K	N
R.strykeri	C	S	T	T	K	I	Q	C	K	N
R.avunculus	C	S	T	T	N	I	Q	C	K	N
Macaque	C	S	T	T	N	I	Q	C	K	N
Human	C	S	T	T	N	I	Q	C	K	N
Dog	C	S	T	T	N	I	Q	C	K	N

RNASE4	Amino acid position 128 in the CDS of ENSG00000258818									
R.roxellana	A	M	A	S	I	R	R	V	V	I
R.brelichi	A	M	A	S	T	R	R	V	V	I
R.bieti	A	M	A	S	I	R	R	V	V	I
R.strykeri	A	M	A	S	I	R	R	V	V	I
R.avunculus	A	M	A	S	T	R	R	V	V	I
Macaque	A	M	A	S	T	R	R	V	V	I
Human	A	I	A	S	T	R	R	V	V	I
Dog	A	S	A	S	T	R	H	V	V	I

D2HGDH	Amino acid position 232 in the CDS of ENSG00000180902									
R.roxellana	**V**	**V**	**L**	**A**	**N**	**G**	**T**	**I**	**L**	**D**
R.brelichi	**V**	**V**	**L**	**A**	**D**	**G**	**T**	**I**	**L**	**D**
R.bieti	**V**	**V**	**L**	**A**	**N**	**G**	**T**	**I**	**L**	**D**
R.strykeri	**V**	**V**	**L**	**A**	**N**	**G**	**T**	**I**	**L**	**D**
R.avunculus	**V**	**V**	**L**	**A**	**D**	**G**	**T**	**I**	**L**	**D**
Macaque	**V**	**V**	**L**	**A**	**D**	**G**	**T**	**I**	**L**	**D**
Human	**V**	**V**	**L**	**A**	**D**	**G**	**T**	**V**	**L**	**D**
Dog	**V**	**V**	**L**	**A**	**D**	**G**	**T**	**V**	**L**	**N**

RTEL1	Amino acid position 234 in the CDS of ENSG00000258366									
R.roxellana	**L**	**D**	**A**	**K**	**N**	**R**	**R**	**A**	**H**	**S**
R.brelichi	**L**	**D**	**A**	**K**	**S**	**R**	**R**	**A**	**H**	**S**
R.bieti	**L**	**D**	**A**	**K**	**N**	**R**	**R**	**A**	**H**	**S**
R.strykeri	**L**	**D**	**A**	**K**	**N**	**R**	**R**	**A**	**H**	**S**
R.avunculus	**L**	**D**	**A**	**K**	**S**	**R**	**R**	**A**	**H**	**S**
Macaque	**L**	**D**	**A**	**K**	**S**	**R**	**R**	**A**	**H**	**S**
Human	**L**	**D**	**A**	**K**	**S**	**R**	**R**	**A**	**H**	**N**
Dog	**L**	**D**	**T**	**K**	**S**	**R**	**R**	**A**	**H**	**S**

Supplementary Table 7: Common amino acid substitutions in coding genes that were also identified as evolving under positive selection along the lineage containing *R. bieti* and *R. strykeri* and the lineage leading to *R. roxellana*.

Gene	P value	Position[a]	Common amino acid substitution	BEB value[b]
RNASE4	2.13E-05	89	Asn→Lys	0.999**
		128	Thr→Ile	0.998**
EDAR	5.51E-04	474	Ser→Thr	0.996**
TMEM71	2.37E-03	203	His→Asp	0.900
DNAH11	6.07E-03	466	Lys→Glu	0.937
ZBBX	1.63E-03	97	Val→Ala	0.990*
CDT1	1.26E-02	537	Ala→Val	0.981*
GPR114	1.18E-03	480	Phe→Leu	0.994**
TEP1	6.56E-03	317	Ala→Thr	0.710
MACC1	1.01E-02	586	Val→Ile	0.936
AKNA	1.99E-02	1018	Glu→Lys	0.709
RTEL1	9.11E-03	234	Ser→Asn	0.954*
PARP15	2.12E-02	346	Ala→Thr	0.847
FCRL4	1.84E-05	239	Asp→Asn	0.975*
		290	Leu→Val	0.972*
ARMC2	1.16E-03	835	Leu→Phe	0.955*
NT5DC1	5.37E-04	393	Leu→Phe	0.990**
D2HGDH	1.64E-02	232	Asp→Asn	0.980*

[a] Position of the amino acid substitution within the encoded product of the human gene sequences.

[b] *p<0.05, **p<0.01

Supplementary Table 8: The comparison parameters for the dN/dS of PSGs and non-PSGs in the snub-nosed monkeys.

Snub-nosed monkeys	The average dN/dS of PSGs	The average dN/dS of other genes	P_dN/dS[a]	P_dS[b]
R. roxellana	0.6220	0.1076	5.1014E-08	4.3828E-01
R. bieti	0.3640	0.2175	3.4488E-06	1.0206E-01
R. strykeri	0.4309	0.2150	3.8368E-03	9.1170E-02
R. brelichia	0.3974	0.1801	6.2914E-02	2.3582E-02
R. avunculus	0.3710	0.1672	9.5544E-02	4.2658E-03

[a] P_dN/dS was the *P* values got by the Wilcoxon Rank Sum Test using the dN/dS data.

[b] P_dS was the *P* values got by the Wilcoxon Rank Sum Test using the dS data.

Supplementary Table 9: The examination of the common amino acid substitutions of *ARMC2*, *NT5DC1*, *RNASE4*, *CDT1*, *RTEL1* and *DNAH11* genes from more mammalian species.

ARMC2	Amino acid position 835 in the CDS of ENSG00000118690									
R.roxellana	**N**	**Y**	**H**	**K**	**F**	**H**	**W**	**E**	**T**	**E**
R.brelichi	**N**	**Y**	**H**	**K**	**L**	**H**	**W**	**E**	**T**	**E**
R.bieti	**N**	**Y**	**H**	**K**	**F**	**H**	**W**	**E**	**T**	**E**
R.strykeri	**N**	**Y**	**H**	**K**	**F**	**H**	**W**	**E**	**T**	**E**
R.avunculus	**N**	**Y**	**H**	**K**	**L**	**H**	**W**	**E**	**T**	**E**
Macaque	**N**	**Y**	**H**	**K**	**L**	**H**	**W**	**E**	**T**	**E**
Human	**N**	**Y**	**H**	**K**	**L**	**H**	**W**	**E**	**T**	**E**
Tree shrew	**N**	**Y**	**H**	**K**	**L**	**H**	**W**	**E**	**T**	**E**
Mouse	**S**	**Y**	**H**	**R**	**L**	**H**	**W**	**E**	**T**	**E**
Rabbit	**E**	**E**	**A**	**P**	**V**	**P**	**W**	**E**	**A**	**L**
Dolphin	**N**	**Y**	**H**	**K**	**L**	**H**	**W**	**E**	**T**	**E**
Cow	**N**	**Y**	**H**	**K**	**L**	**H**	**W**	**E**	**T**	**E**
Horse	**N**	**Y**	**H**	**R**	**L**	**H**	**W**	**E**	**T**	**E**
Dog	**N**	**Y**	**H**	**K**	**L**	**H**	**W**	**E**	**T**	**E**
Microbat	**N**	**Y**	**H**	**K**	**L**	**H**	**W**	**E**	**T**	**E**
Elephant	**N**	**Y**	**H**	**R**	**V**	**H**	**W**	**E**	**T**	**E**
Armadillo	**N**	**Y**	**H**	**K**	**L**	**H**	**W**	**E**	**T**	**E**
Sloth	**-**	**-**	**-**	**K**	**L**	**H**	**W**	**E**	**T**	**E**
Wallaby	**-**	**Y**	**N**	**K**	**L**	**Y**	**W**	**E**	**I**	**E**

DNAH11	Amino acid position 466 in the CDS of ENSG00000105877									
R.roxellana	**C**	**R**	**F**	**D**	**E**	**F**	**L**	**D**	**R**	**L**
R.brelichi	**C**	**R**	**F**	**D**	**K**	**F**	**L**	**D**	**R**	**L**
R.bieti	**C**	**R**	**F**	**D**	**E**	**F**	**L**	**D**	**R**	**L**
R.strykeri	**C**	**R**	**F**	**D**	**E**	**F**	**L**	**D**	**R**	**L**
R.avunculus	**C**	**R**	**F**	**D**	**K**	**F**	**L**	**D**	**R**	**L**
Macaque	**C**	**R**	**F**	**D**	**K**	**F**	**L**	**D**	**R**	**L**
Human	**C**	**R**	**F**	**D**	**K**	**F**	**L**	**D**	**R**	**L**
Tree shrew	**C**	**R**	**F**	**D**	**Q**	**F**	**L**	**D**	**R**	**L**
Mouse	**G**	**R**	**F**	**N**	**K**	**F**	**L**	**D**	**R**	**L**
Rabbit	**C**	**R**	**F**	**D**	**K**	**F**	**L**	**D**	**R**	**L**
Dolphin	**L**	**R**	**F**	**D**	**K**	**F**	**L**	**D**	**R**	**F**
Cow	**H**	**R**	**F**	**D**	**K**	**F**	**L**	**D**	**R**	**F**
Horse	**C**	**R**	**F**	**D**	**K**	**F**	**L**	**D**	**R**	**F**
Dog	**C**	**R**	**F**	**D**	**K**	**F**	**L**	**D**	**R**	**F**
Microbat	**C**	**R**	**F**	**D**	**K**	**F**	**L**	**D**	**R**	**C**
Elephant	**C**	**R**	**F**	**D**	**K**	**F**	**L**	**D**	**R**	**L**
Armadillo	**C**	**R**	**F**	**D**	**K**	**F**	**L**	**D**	**R**	**L**
Opssum	**R**	**R**	**F**	**D**	**K**	**F**	**L**	**N**	**H**	**M**
Wallaby	**W**	**R**	**Y**	**D**	**K**	**F**	**F**	**D**	**R**	**L**

NT5DC1	Amino acid position 393 in the CDS of ENSG00000178425									
R.roxellana	**T**	**E**	**D**	**S**	**F**	**V**	**Y**	**T**	**W**	**S**
R.brelichi	**T**	**E**	**D**	**S**	**L**	**V**	**Y**	**T**	**W**	**S**
R.bieti	**T**	**E**	**D**	**S**	**F**	**V**	**Y**	**T**	**W**	**S**
R.strykeri	**T**	**E**	**D**	**S**	**F**	**V**	**Y**	**T**	**W**	**S**
R.avunculus	**T**	**E**	**D**	**S**	**L**	**V**	**Y**	**T**	**W**	**S**
Macaque	**T**	**E**	**D**	**S**	**L**	**V**	**Y**	**T**	**W**	**S**
Human	**T**	**E**	**D**	**S**	**L**	**V**	**Y**	**T**	**W**	**S**
Tree shrew	**T**	**D**	**T**	**S**	**L**	**V**	**Y**	**T**	**W**	**S**
Mouse	**A**	**E**	**D**	**S**	**V**	**V**	**Y**	**T**	**W**	**S**
Rabbit	**T**	**G**	**D**	**S**	**L**	**V**	**Y**	**T**	**W**	**S**
Dolphin	**T**	**E**	**D**	**S**	**L**	**I**	**Y**	**T**	**W**	**S**
Cow	**R**	**E**	**D**	**S**	**L**	**V**	**Y**	**T**	**W**	**S**
Horse	**T**	**E**	**D**	**S**	**L**	**V**	**Y**	**T**	**W**	**S**
Dog	**T**	**E**	**D**	**S**	**L**	**V**	**Y**	**T**	**W**	**S**
Hedgehog	**T**	**E**	**D**	**S**	**L**	**I**	**H**	**T**	**W**	**S**
Opssum	**M**	**E**	**N**	**L**	**L**	**T**	**F**	**T**	**W**	**S**
Tasmanian devil	**V**	**E**	**T**	**S**	**L**	**I**	**I**	**S**	**W**	**L**

CDT1	Amino acid position 537 in the CDS of ENSG00000167513									
R.roxellana	**T**	**A**	**R**	**L**	**V**	**R**	**Q**	**A**	**R**	**A**
R.brelichi	**T**	**A**	**R**	**L**	**A**	**R**	**Q**	**A**	**R**	**A**
R.bieti	**T**	**A**	**R**	**L**	**V**	**R**	**Q**	**A**	**R**	**A**
R.strykeri	**T**	**A**	**R**	**L**	**V**	**R**	**Q**	**A**	**R**	**A**
R.avunculus	**T**	**A**	**R**	**L**	**A**	**R**	**Q**	**A**	**R**	**A**
Macaque	**T**	**A**	**R**	**L**	**A**	**R**	**Q**	**A**	**R**	**A**
Human	**T**	**A**	**R**	**L**	**A**	**H**	**Q**	**T**	**R**	**A**
Mouse	**T**	**A**	**R**	**L**	**A**	**H**	**H**	**V**	**H**	**A**
Rabbit	**M**	**A**	**R**	**L**	**A**	**H**	**Q**	**A**	**R**	**I**
Cow	**M**	**E**	**Q**	**L**	**A**	**H**	**L**	**A**	**R**	**A**
Horse	**I**	**A**	**Q**	**L**	**A**	**H**	**L**	**A**	**R**	**A**
Dog	**I**	**M**	**R**	**L**	**A**	**H**	**L**	**A**	**L**	**A**
Microbat	**T**	**A**	**Q**	**L**	**A**	**R**	**L**	**A**	**R**	**A**
Hedgehog	**T**	**E**	**Q**	**L**	**A**	**R**	**L**	**T**	**Q**	**A**
Elephant	**T**	**V**	**R**	**L**	**A**	**R**	**L**	**A**	**R**	**T**
Armadillo	**T**	**A**	**R**	**L**	**A**	**L**	**L**	**A**	**R**	**A**
Opssum	**A**	**E**	**R**	**L**	**A**	**R**	**I**	**T**	**Q**	**E**
Wallaby	**S**	**E**	**R**	**L**	**A**	**R**	**I**	**T**	**Q**	**E**
Tasmanian devil	**S**	**E**	**R**	**L**	**A**	**R**	**V**	**T**	**Q**	**Q**

RTEL1	Amino acid position 234 in the CDS of ENSG00000258366									
R.roxellana	**L**	**D**	**A**	**K**	**N**	**R**	**R**	**A**	**H**	**S**
R.brelichi	**L**	**D**	**A**	**K**	**S**	**R**	**R**	**A**	**H**	**S**
R.bieti	**L**	**D**	**A**	**K**	**N**	**R**	**R**	**A**	**H**	**S**
R.strykeri	**L**	**D**	**A**	**K**	**N**	**R**	**R**	**A**	**H**	**S**
R.avunculus	**L**	**D**	**A**	**K**	**S**	**R**	**R**	**A**	**H**	**S**
Macaque	**L**	**D**	**A**	**K**	**S**	**R**	**R**	**A**	**H**	**S**
Human	**L**	**D**	**A**	**K**	**S**	**R**	**R**	**A**	**H**	**N**
Mouse	**L**	**D**	**A**	**K**	**S**	**R**	**K**	**A**	**H**	**S**
Rabbit	**L**	**D**	**A**	**K**	**S**	**R**	**R**	**A**	**H**	**S**
Dolphin	**L**	**D**	**A**	**K**	**S**	**R**	**R**	**A**	**Y**	**G**
Cow	**L**	**D**	**A**	**K**	**S**	**R**	**R**	**A**	**H**	**G**
Horse	**L**	**D**	**A**	**K**	**S**	**R**	**R**	**A**	**H**	**S**
Dog	**L**	**D**	**T**	**K**	**S**	**R**	**R**	**A**	**H**	**S**
Microbat	**L**	**D**	**A**	**K**	**S**	**R**	**R**	**A**	**Q**	**G**
Elephant	**L**	**D**	**P**	**K**	**S**	**R**	**R**	**A**	**H**	**S**
Platypus	**L**	**D**	**S**	**K**	**S**	**R**	**R**	**A**	**H**	**N**
Opssum	**L**	**D**	**S**	**K**	**T**	**R**	**R**	**A**	**H**	**N**
Tasmanian devil	**L**	**D**	**S**	**K**	**T**	**R**	**R**	**A**	**H**	**N**

RNASE4	Amino acid position 89 in the CDS of ENSG00000258818									
R.roxellana	**C**	**S**	**T**	**T**	**K**	**I**	**Q**	**C**	**K**	**N**
R.brelichi	**C**	**S**	**T**	**T**	**N**	**I**	**Q**	**C**	**K**	**N**
R.bieti	**C**	**S**	**T**	**T**	**K**	**I**	**Q**	**C**	**K**	**N**
R.strykeri	**C**	**S**	**T**	**T**	**K**	**I**	**Q**	**C**	**K**	**N**
R.avunculus	**C**	**S**	**T**	**T**	**N**	**I**	**Q**	**C**	**K**	**N**
Macaque	**C**	**S**	**T**	**T**	**N**	**I**	**Q**	**C**	**K**	**N**
Human	**C**	**S**	**T**	**T**	**N**	**I**	**Q**	**C**	**K**	**N**
Tree shrew	**C**	**S**	**T**	**T**	**N**	**I**	**A**	**C**	**K**	**N**
Mouse	**C**	**S**	**T**	**T**	**N**	**I**	**L**	**C**	**K**	**N**
Rabbit	**C**	**S**	**T**	**T**	**S**	**I**	**R**	**C**	**K**	**N**
Cow	**C**	**S**	**T**	**T**	**N**	**I**	**Q**	**C**	**K**	**N**
Horse	**C**	**S**	**T**	**T**	**S**	**I**	**Q**	**C**	**K**	**N**
Dog	**C**	**S**	**T**	**T**	**N**	**I**	**Q**	**C**	**K**	**N**
Hedgehog	**C**	**S**	**T**	**A**	**N**	**I**	**Q**	**C**	**K**	**N**
Elephant	**C**	**S**	**T**	**T**	**N**	**I**	**Q**	**C**	**K**	**N**
Armadillo	**C**	**S**	**T**	**T**	**S**	**I**	**M**	**C**	**K**	**N**
Platypus	**C**	**S**	**T**	**D**	**S**	**I**	**S**	**C**	**K**	**N**
Opssum	**C**	**R**	**T**	**T**	**D**	**I**	**R**	**C**	**K**	**N**
Tasmanian devil	**C**	**H**	**T**	**T**	**D**	**I**	**K**	**C**	**K**	**N**

RNASE4	Amino acid position 128 in the CDS of ENSG00000258818									
R.roxellana	**A**	**M**	**A**	**S**	**I**	**R**	**R**	**V**	**V**	**I**
R.brelichi	**A**	**M**	**A**	**S**	**T**	**R**	**R**	**V**	**V**	**I**
R.bieti	**A**	**M**	**A**	**S**	**I**	**R**	**R**	**V**	**V**	**I**
R.strykeri	**A**	**M**	**A**	**S**	**I**	**R**	**R**	**V**	**V**	**I**
R.avunculus	**A**	**M**	**A**	**S**	**T**	**R**	**R**	**V**	**V**	**I**
Macaque	**A**	**M**	**A**	**S**	**T**	**R**	**R**	**V**	**V**	**I**
Human	**A**	**I**	**A**	**S**	**T**	**R**	**R**	**V**	**V**	**I**
Tree shrew	**A**	**K**	**A**	**S**	**T**	**R**	**R**	**I**	**V**	**I**
Mouse	**A**	**R**	**T**	**S**	**T**	**R**	**R**	**V**	**V**	**I**
Rabbit	**A**	**A**	**A**	**S**	**T**	**R**	**R**	**V**	**V**	**I**
Cow	**A**	**K**	**A**	**S**	**T**	**R**	**R**	**V**	**V**	**I**
Horse	**A**	**M**	**T**	**S**	**T**	**R**	**R**	**V**	**V**	**V**
Dog	**A**	**S**	**A**	**S**	**T**	**R**	**H**	**V**	**V**	**I**
Hedgehog	**A**	**L**	**A**	**S**	**T**	**R**	**R**	**V**	**V**	**I**
Elephant	**A**	**K**	**T**	**S**	**T**	**R**	**R**	**V**	**V**	**I**
Armadillo	**A**	**M**	**A**	**S**	**T**	**R**	**R**	**V**	**V**	**I**
Platypus	**A**	**Q**	**V**	**S**	**T**	**R**	**R**	**V**	**V**	**I**
Opssum	**A**	**M**	**T**	**R**	**T**	**R**	**H**	**V**	**V**	**I**
Tasmanian devil	**A**	**L**	**A**	**R**	**T**	**R**	**H**	**V**	**V**	**I**

Supplementary Table 10: *R. bieti* population-level sample information and SNP statistics. 20 individuals were used in our population genomic study.

Sample ID	Origin	#of all SNPs	#of homozygous SNPs	#of heterozygous SNP	#of heterozygosity
Rb0[a]	Weixi, Yunnan, China	1,251,847	69,865	1,181,982	3.97E-04
Rb1	Weixi, Yunnan, China	1,623,950	415,626	1,208,324	4.06E-04
Rb2	Weixi, Yunnan, China	1,493,375	270,423	1,222,952	4.10E-04
Rb3	Weixi, Yunnan, China	1,485,962	306,023	1,179,939	3.96E-04
Rb4	Weixi, Yunnan, China	1,678,191	492,064	1,186,127	3.98E-04
Rb5	Weixi, Yunnan, China	1,432,994	343,525	1,089,469	3.66E-04
Rb6	Weixi, Yunnan, China	1,690,030	498,609	1,191,421	4.00E-04
Rb7	Weixi, Yunnan, China	1,678,015	497,565	1,180,450	3.96E-04
Rb8	Weixi, Yunnan, China	1,670,564	509,101	1,161,463	3.90E-04
Rb9	Weixi, Yunnan, China	1,689,658	493,854	1,195,804	4.01E-04
Rb10	Weixi, Yunnan, China	1,710,090	466,085	1,244,005	4.17E-04
Rb11	Weixi, Yunnan, China	1,691,631	510,108	1,181,523	3.97E-04
Rb12	Weixi, Yunnan, China	1,700,420	515,775	1,184,645	3.98E-04
Rb13	Weixi, Yunnan, China	1,690,259	504,313	1,185,946	3.98E-04
Rb14	Weixi, Yunnan, China	1,699,112	488,076	1,211,036	4.06E-04
Rb15	Weixi, Yunnan, China	1,686,614	498,565	1,188,049	3.99E-04
Rb16	Weixi, Yunnan, China	1,685,389	487,517	1,197,872	4.02E-04
Rb17[b]	Weixi, Yunnan, China	1,692,730	486,481	1,206,249	4.05E-04
Rb18	Weixi, Yunnan, China	1,663,095	503,661	1,159,434	3.89E-04
Rb19	Weixi, Yunnan, China	1,684,221	486,000	1,198,221	4.02E-04

[a] Sequencing data from a short paired-ended library of 560bp from the *de novo* genome sequencing of Rb0 was used for our population genomic analyses.

[b] Sequencing data of Rb17 was obtained from Zhou et al. (2014).

Supplementary Table 11: *R. roxellana* population-level sample information and SNP statistics. 26 individuals were used in the population genomic study.

Sample ID	Origin	#of all SNPs	#of homozygous SNPs	#of heterozygous SNP	#Ratio of heterozygosity
RR0	Sichuan, China	2,480,354	1,377,413	1,102,941	3.80E-04
RR1	Gansu, China	2,827,326	1,163,510	1,663,816	5.74E-04
RR2[a]	Beijing Zoo, China	1,461,125	116,987	1,344,165	4.64E-04
RR3	Gansu, China	2,707,134	1,380,329	1,326,805	4.58E-04
RR4	Gansu, China	2,722,575	1,354,196	1,368,379	4.72E-04
RR5	Gansu, China	2,491,651	928,554	1,563,097	5.39E-04
RR6	Gansu, China	2,688,959	760,086	1,928,873	6.65E-04
RR7	Gansu, China	2,446,334	899,197	1,547,137	5.34E-04
RR8	Gansu, China	2,510,713	912,507	1,598,206	5.51E-04
RR9	Gansu, China	2,504,864	894,582	1,610,282	5.55E-04
RR10	Gansu, China	2,707,165	1,357,520	1,349,645	4.65E-04
RR11	Gansu, China	2,731,027	1,314,618	1,416,409	4.88E-04
RR12	Shaanxi, China	2,627,141	1,433,860	1,193,281	4.12E-04
RR13	Shaanxi, China	2,676,020	1,408,354	1,267,666	4.37E-04
RR14	Shaanxi, China	2,632,498	1,478,215	1,154,283	3.98E-04
RR15	Shaanxi, China	2,604,409	1,476,125	1,128,284	3.89E-04
RR16	Shaanxi, China	2,617,633	1,492,262	1,125,371	3.88E-04
RR17	Shaanxi, China	2,634,953	1,469,718	1,165,235	4.02E-04
RR18	Shaanxi, China	2,878,833	1,173,180	1,705,653	5.88E-04
RR19	Shaanxi, China	2,689,933	1,377,719	1,312,214	4.53E-04
RR20	Shaanxi, China	2,638,788	1,479,264	1,159,524	4.00E-04
RR21	Shennongjia, China	2,930,894	1,590,391	1,340,503	4.62E-04
RR22	Shennongjia, China	2,953,354	1,527,790	1,425,564	4.92E-04
RR23	Shennongjia, China	2,951,237	1,529,910	1,421,327	4.90E-04
RR24	Shennongjia, China	2,969,358	1,532,230	1,437,128	4.96E-04
RR25	Shennongjia, China	2,958,177	1,520,252	1,437,925	4.96E-04

[a] The sequencing data of a short paired-ended library of 500bp from the published *de novo* genome sequence of RR2 was used for our population genomic analyses. Our population structure analysis suggested that this individual (RR2) belong to SG population.

Supplementary Table 12: Reads mapping statistics of *R. bieti*. The genome-wide resequencing data for 20 samples (Rb1-19) that were mapped to the *de novo* assembly genome (Rb0).

Sample ID	The Number Whole of Raw Reads	The Number of Whole Raw Bases	The Number of Non-redundant Reads	The Number of Non-redundant Mapped Reads	The Percentage of Non-redundant Mapped Reads	Mapping Depth
Rb0[a]	373,978,334	37,771,811,734	355,880,848	332,580,978	93.45	9.49
Rb1	314,868,232	32,746,296,128	292,748,008	276,656,046	94.50	8.68
Rb2	303,030,408	31,394,092,032	282,037,920	265,930,011	94.29	8.21
Rb3	295,014,106	30,449,967,176	280,076,625	267,460,050	95.50	8.34
Rb4	345,271,064	35,751,281,216	322,789,262	297,683,738	92.22	8.51
Rb5	324,372,912	33,734,782,848	303,940,515	283,577,409	93.30	8.22
Rb6	293,445,726	30,415,878,680	261,555,762	245,347,399	93.80	7.67
Rb7	300,069,190	31,095,703,896	270,525,874	253,554,169	93.73	7.93
Rb8	361,729,556	37,272,925,670	345,644,719	325,081,035	94.05	9.11
Rb9	331,975,332	34,200,059,436	316,836,946	296,985,028	93.73	8.27
Rb10	408,592,580	42,138,682,792	386,849,813	355,194,661	91.82	10.41
Rb11	345,735,828	35,162,892,016	325,030,858	299,602,303	92.18	8.63
Rb12	336,086,282	34,296,594,696	323,185,338	306,856,361	94.95	8.97
Rb13	319,565,754	32,720,581,086	307,192,903	292,734,875	95.29	8.81
Rb14	357,775,204	36,949,407,380	340,572,731	320,110,479	93.99	9.02
Rb15	363,963,948	37,437,792,536	342,946,044	318,615,787	92.91	8.99
Rb16	401,505,568	41,756,579,072	380,609,528	352,141,649	92.52	10.39
Rb17[b]	352,494,338	35,249,433,800	336,916,742	318,479,742	94.53	9.56
Rb18	332,447,746	34,235,168,544	310,020,163	287,939,250	92.88	8.30
Rb19	380,398,776	39,561,472,704	358,225,956	333,744,276	93.17	9.91

[a] Sequencing data from a short paired-ended library of 560bp from the *de novo* genome sequencing of Rb0 was used for our population genomic analyses.

[b] Sequencing data of Rb17 was obtained from Zhou et al. (2014).

Supplementary Table 13: Reads mapping statistics of *R.roxellana*. The genome-wide resequencing data for 26 samples (RR0-25) that were mapped to the published *R. roxellana* genome (RR2).

Sample ID	The Number of Whole Raw Reads	The Number of Whole Raw Bases	The number of Non-redundant Reads	The number of Non-redundant Mapped Reads	The Percentage of Non-redundant Mapped Reads	Mapping Depth
RR0	385,427,102	38,542,710,200	349,067,969	339,277,169	97.20	10.33
RR1	363,100,928	35,946,991,872	336,040,474	324,297,014	96.51	9.73
RR2[a]	428,410,476	42,841,047,600	377,287,622	288,312,395	76.42	8.68
RR3	462,431,400	46,243,140,000	382,153,957	370,302,876	96.90	11.26
RR4	369,355,988	36,935,598,800	339,764,358	325,729,396	95.87	10.00
RR5	392,454,862	39,245,486,200	358,060,064	349,255,633	97.54	10.64
RR6	419,300,640	41,930,064,000	357,614,999	346,873,839	97.00	10.56
RR7	292,857,444	29,285,744,400	274,020,566	267,493,290	97.62	8.23
RR8	446,398,120	44,639,812,000	372,145,944	362,183,104	97.32	11.08
RR9	366,085,334	36,608,533,400	303,506,549	294,586,169	97.06	9.04
RR10	338,304,140	33,830,414,000	314,867,885	307,520,904	97.67	9.47
RR11	307,644,708	38,455,588,500	291,699,759	282,438,417	96.83	10.76
RR12	322,730,778	33,460,412,880	309,932,612	294,816,839	95.12	8.58
RR13	362,285,728	36,228,572,800	336,557,140	310,545,802	92.27	8.84
RR14	380,161,224	38,016,122,400	352,062,968	344,158,712	97.75	10.61
RR15	391,848,488	39,184,848,800	335,885,804	322,911,698	96.14	9.93
RR16	415,470,808	41,547,080,800	366,083,317	355,501,018	97.11	10.83
RR17	356,828,928	35,682,892,800	323,644,993	314,151,490	97.07	9.51
RR18	293,823,530	29,382,353,000	272,979,080	260,313,944	95.36	7.92
RR19	306,519,784	30,651,978,400	285,997,234	279,124,030	97.60	8.56
RR20	455,900,714	45,590,071,400	381,333,687	363,243,728	95.26	11.03
RR21	358,918,826	36,968,639,078	337,553,428	327,500,611	97.02	10.16
RR22	319,640,194	32,872,284,248	307,457,480	295,966,904	96.26	8.61
RR23	318,034,252	32,528,731,168	307,713,549	297,463,397	96.67	8.79
RR24	351,368,462	43,921,057,750	329,846,991	320,753,590	97.24	12.07
RR25	319,880,868	39,985,108,500	303,535,266	289,226,350	95.29	10.89

[a] Sequencing data from a short paired-end library of 500bp from the published *de novo* genome sequence of RR2 was used for our population genomic analyses.

Supplementary Note

Genome size estimation.

Blood cells from *R. bieti* (Rb0) and two internal standards are diluted with buffered Phosphate Buffered Saline (PBS) solution and stained using propidium iodide (PI). DNA content of 5,000-10,000 stained nuclei was determined using FACSDiVa-14F (BD, USA) flow cytometer with a 495-nm blue solid state laser. Flow cytometry data was analyzed by WinMDI 2.8 software. The C-value experiment utilized 3 different PBS solution concentrations and was repeated 4 times to calibrate the *R. bieti*'s value. The average value of all repeats was used. The monoploid C-value (1C) was calculated and expressed in Mb using the conversion factor 1 pg DNA=978 Mb[1].

Transcriptome data of *M. mulatta*.

RNA-seq data from 11 tissues of *M. mulatta* includes those publicly available from 8 tissues (spleen, kidney, testicle, liver, brain, heart, and lung, muscle) (NCBI Gene Expression Omnibus, accession no. GSE41637)[2], and those newly produced from 3 tissues (large intestine, small intestine, stomach) **(Supplementary Table 4)**. The 3 tissues were collected from a single adult male *M. mulatta* individual that was caught in the wild and kept in the Centre of Experimental Primates at Kunming Institute of Zoology.

Transcriptomic analysis of *R. bieti* and *M. mulatta*

After quality trimming of the RNA-Seq library by cutadapt[3] and filtering residual reads by TrimmomaticPE[4], we aligned the high-quality RNA-seq reads from *M.mulatta*, and those from *R. bieti* to their respective genomes (rhemac Ensemble release 72 and *R. bieti de novo*) using Tophat[5] with default parameters. Expression levels of each gene in each RNA-seq library of *R. bieti* and *M. mulatta* were measured using Cufflinks[6]. The top 500 most highly expressed one-to-one orthologous genes in each tissue were selected and then merged. All of these were then clustered hierarchically using the Pearson's correlations as distances. Species-specific expressed orthologous genes were selected only if the genes clustered in a clade in which the correlation between tissues of the same species was higher than between species of the same tissue. The clustering and heat map of the selected genes' FPKM was performed by pheatmap package in R.

Resequencing Data Process and SNP Calling

The mapping for the re-sequencing data to the reference *de novo* genome was done by BWA software with parameters ‘bwa aln –q 20’[7]. Redundant sequences resulting from PCR amplification were removed with PICARD (http:// picard.sourceforge.net). InDel realignment was done to generate final mapping BAM files using GATK[8, 9]. The genome-wide single nucleotide polymorphisms (SNPs) were identified using conjugated mapping BAM files by SAMtools package[10] with commands ‘samtools mpileup -q 20 -Q 20 -C 50 –uDEf’. We then filtered SNPs with the following criteria: (1) SNPs located nearby insert and deletions (INDELS) within 5 bp were filtered out; (2) For population genomic analyses, those of each SNP position, at which if the ratio of individuals non-sequenced bigger than 20%, was excluded out. For comparative genomic analyses of five snub-nosed monkeys and macaque, the ratio is set to be 0 for each SNPs; (3) INDELS were filtered out; (4) All SNPs were sorted by their depths. SNPs with depths ranged from 2.5% to 97.5% in depth quantile and the Quality value bigger than 40 was reserved.

Divergence Time Estimation

We implemented a Bayesian Markov Chain Monte Carlo (MCMC) algorithm for divergence time estimation using program MCMCtree from the PAML package[11]. The calibration point from the fossil record for the origin of genus *Rhinopithecus* (1-4 mya)[12] was applied. We assumed a GTR model of DNA substitution[13, 14]. The means and standard deviations were used for kappa gamma (3.46, 1.73), alpha_gamma (1, 1) and rgene_gamma (1, 6.67).

Ortholog identification and alignment

Orthologous gene sequences from *R. bieti, R. roxellana, Macaca mulatta* (macaque), *Homo sapiens* (human) and *Canis lupus familiaris* (dog) genomes were identification based on bidirectional best-hit (BBH) identification, we used NCBI BLAST version 2.2.26 and applied the following thresholds: E-value < 10^{-10} and identity >30%. Protein sequences of *R. strykeri, R. brelichi*, and *R. avunculus* were predicted by aligning and substituting the raw reads to *R. bieti* scaffolds. Orthologous genes from the eight species were aligned using the Prank program[15, 16] with the option “-codon”, and the alignments were trimmed by the Gblocks program[17], with potentially unreliable regions removed using the default settings ("-t=c”). After trimming, any alignment that was shorter than 100bp was discarded[18].

Examination of common amino acid substitutions in more mammalian species

We used the Ensembl ortholog_one2one gene database[19] of *ARMC2*, *NT5DC1*, *RNASE4*, *CDT1*, *RTEL1* and *DNAH11* genes for each pair of species with the genomics publicly available, including the tree shrew, mouse, rabbit, dolphin, cow, horse, microbat, hedgedog, elephant, armadillo, sloth, platypus, opossum, wallaby, and Tasmanian devil. Some genes were not found in some of these species.

Selection scans for *R. bieti* and *R. roxellana* populations

Only scaffolds bigger than 100k were used in the genome-wide selection scan analyses. These scaffolds occupied about 92.5% of *R. bieti* genome and 93.9% of *R. roxellana* genome. We used three selection scan methods. $\theta\pi$ scan was used to identify the genomic region as outliers in the populations with VCFtools v0.1.11[20] and the window size was set to be 20k bp without steps. Windows with values lower than the 1% quantile of $\theta\pi$ were considered as outlier regions and retained. Standardized heterozygosity (Z_H) and locus-specific branch-length (LSBL) scans were processed as described in Ai et al. (2015)[21] with slipped windows strategy (20k window size and 10k step size). For Z_H scan, windows with Z_H lower than 1% quantile were retained. For LSBL scan, the pairwise fixation index (Fst) was first estimated using VCFtools for three populations of *R. roxellana* (it cannot be applied for *R. bieti* because *R. bieti* consists of only one population). Windows with values bigger than 99% quantile of LSBL were considered as outlier regions and retained. Those detected by at least two of the three scan methods were identified as the candidate genes under selection.

Pairwise sequentially Markovian coalescence (PSMC) analysis

We used those loci that is more than a third and less than the twice of the average depth to do the PSMC analysis[22]. The PSMC parameters were set as follows: -N25 -t15 -r5 -p “4+25*2+4+6”. We performed the PSMC correction by adjusting the options “-N” (false negative rate) by reference to the assembled genome[23]. The mutation rate used in PSMC analysis is based on the generation of snub-nosed monkeys (g=5 years)[24, 25] and the mutation rate of macaque (1×10^{-9} per nucleotide per year)[26, 27].

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