Table S1. Animals and specimens included in external morphology examination and all sequences used for phylogenetic reconstructions

Resources	ID	Taxon	CYTB	D-Loop	complete mitogenome	Locality	Description
Wild animals	SDAM	*H. tianxing*				Sudian,Yingjiang, China	Adult male in Lamahe group
Wild animals	ZNA1	*H. tianxing*				Zhina, Yingjiang, China	Adult male in Xiangbai group A
Wild animals	ZNB1	*H. tianxing*				Zhina, Yingjiang, China	Adult male in Xiangbai group B
Wild animals	ZNA2	*H. tianxing*				Zhina, Yingjiang, China	Old adult female in Xiangbai group A
Wild animals	ZNA3	*H. tianxing*				Zhina, Yingjiang, China	Young adult female in Xiangbai group A
Wild animals	ZNJ	*H. tianxing*				Zhina, Yingjiang, China	Juvenile in Xiangbai group A
Wild animals	NA1	*H. tianxing*	Y	Y	**NGS**	Nankang, Gaoligongshan, China	adult male in group NA
Wild animals	NA2	*H. tianxing*	Y	NO	**NGS**	Nankang,	adult female in

					(partial)	Gaoligongshan, China	group NA
Wild animals	NA3	*H. tianxing*				Nankang, Gaoligongshan, China	Juvenile in group NA
Wild animals	NB	*H. tianxing*				Nankang,Gaoligongshan, China	Adult solitary female
Wild animals	BB1	*H. tianxing*	Y	Y		Banchang, Gaoligongshan, China	Adult male in group BB
Wild animals	BB2	*H. tianxing*	Y	Y		Banchang, Gaoligongshan, China	Adult female in group BB
Wild animals	BB3	*H. tianxing*				Banchang, Gaoligongshan, China	Subadult male in group BB, dispersed in 2013
Wild animals	BB4	*H. tianxing*	Y	Y		Banchang, Gaoligongshan, China	Subadult male in group BB
Captive animals	Baimei (BA)	*H. leuconedys*	Y	Y	**partial**	Kunming Zoo, China	Adult female, possibly exported from Myanmar
Captive animals	Dabaimei	*H. leuconedys*				Kunming Zoo, China	Adult female, transferred from Gejiu Zoo in 2015.
Captive animals	Nana	*H. leuconedys*	Y	Y	**NGS**	Dulongjiang	Juvenile female, exported from Myanmar (3

							years old), private pet
Captive animals	Beibei-F	*H. leuconedys*	Y	Y		Yunnan safari park	Sex unknown, exported from Myanmar
Captive animals	Dangdang	*H. leuconedys*	Y	Y	**NGS**	Yunnan safari park	Sex unknown, exported from Myanmar
Captive animals	?	*H. leuconedys*				Yunnan safari park	Adult male, transferred to Simao Zoo in 2014
Captive animals	BSF	*H. leuconedys*	Y	Y	**NGS**	Taibao park, Baoshan, China	Adult female, confiscated by border police
Captive animals	Jingjing (BSJJ)	*H. leuconedys*	Y	Y		Taibao park, Baoshan, China	Jingjing, 2 years old juvenile, confiscated by border police
Captive animals	Lingling (BSJO)	*H. leuconedys*	Y	Y	**NGS**	Taibao park, Baoshan, China	Jiaojiao, 2 years old juvenile, confiscated by border police
Captive animals	DH1	*H. leuconedys*	Y	Y		Dehong Wildlife Rescue Center, China	Subadult female,changing color, donated

Captive animals	DH2	*H. leuconedys*	Y	Y	**NGS**	Dehong Wildlife Rescue Center, China	Adult female, donated
Captive animals	DH3	*H. leuconedys*	Y	Y	**NGS**	Dehong Wildlife Rescue Center, China	Adult male, donated
Captive animals	PM	*H. leuconedys*	Y	NO		Pianma Ranger Station, China	1 year old infant, confiscated by border police
Captive animals	ZZ822	*H. leuconedys*	Y	NO		Zhengzhou Zoo, China	Subadult female, changing color, origin unknown
Captive animals	Beibei-M	*H. leuconedys*	Y	NO		Beijing Zoo, China	Adult male, wild born
Captive animals	Dashuang	*H. tianxing*	Y	Y		Kunming Zoo, China	Adult male, born in 1994 in Yunnan
Captive animals	Maomao	*H. tianxing*				Kunming Zoo, China	Adult female, died in 1997
Captive animals	Linlin	*H. tianxing*	Y	NO		Beijing Zoo, China	Adult male, borin in 20040106 in Beijing Zoo by a wild born male (99-1 from Ruili) and a

							wild born female (93-6)
Captive animals	Dandan	*Hybrid (H. leuconedys x H. tianxing)*	Y	Y	**NGS**	Kunming Zoo, China	Adult male, born in 2003 in Kunming Zoo by a wild born female (Maomao) and a wild born male (Hehe)
Captive animals	Xiaobao (BD)	*Hybrid (H. leuconedys x H. tianxing)*	Y	Y		Kunming Zoo, China	Adult male, born in 1997 in Kunming Zoo by a wild born female (Maomao) and a wild born male (Hehe)
Captive animals	Jiaojiao	*Hybrid F2*	Y	Y		Kunming Zoo, China	Juvenile female, born in 2015 in Kunming Zoo by a wild born female (Baimei) and a captive born male

							(Xiaobao)
Captive animals	Yuanyuan	*Hybrid F2*	Y	Y	**NGS (partial)**	Kunming Zoo, China	Juvenile male, born in 2010 in Kunming Zoo by a wild born female (Baimei) and a captive born male (Xiaobao)
Voucher specimens	2007090801 (Xinxin)	*hybrid (H. leuconedys x H. tianxing)*	Y	NO		Kunming Natural History Museum of Zoology, China	Skin Specimen. Name is xinxin, born in 2000 in Kunming Zoo by a wild born female (Maomao) and a wild born male (Hehe) died in 20070908,
Voucher specimens	LS970114	*H. leuconedys*	Y	NO		Kunming Natural History Museum of Zoology, China	Adult female, skin from Tengchong
Tissue sample	KIZ90218106	*H. leuconedys*	Y	Y	**NGS**	Kunming Natural History Museum of	a muscle sample from Kunming

						Zoology, China	Natural History Museum of Zoology
GenBank	HHO1	*Hoolock hoolock*	GU321286			Dhaka Zoo, Bangladesh	unknown identity
GenBank	**HHO2**	***Hoolock hoolock***	**GU321287**		**Sanger**	**Dhaka Zoo, Bangladesh**	**unknown identity**
GenBank	HLE1	*Hoolock leuconedys*	GU321288			Perth Zoo, Australia	unknown identity
GenBank	HLE2	*Hoolock leuconedys*	GU321289			Beijing Zoo, China	unknown identity
GenBank	HLE3	*Hoolock leuconedys*	GU321290		**Sanger**	Beijing Zoo, China	unknown identity
GenBank	Horace	*Hoolock hoolock*	Y13304			Perth Zoo, Australia	Perth Zoo House Name: Horace
GenBank	P01	*Hoolock hoolock*	Y13305			Beijing Center for Breeding Endangered Animals, China	unknown identity
GenBank	T16	*Hylobates lar*	HQ622772				
GenBank	J12	*Hylobates muelleri*	HQ622781				
GenBank	1230	*Hylobates moloch*	HQ622782				
GenBank	N.A.	*Hylobates klossii*	HQ622788				

GenBank	N.A.	*Hylobates pileatus*	AB504749				
GenBank	N.A.	*Symphalangus syndactylus*	AB504750				
GenBank	N.A.	*Nomascus siki*	AB504751				
GenBank	N.A.	*Nomascus leucogenys*	KC757404				
GenBank	N.A.	*Hylobates agilis*			NC_014042		
GenBank	N.A.	*Hylobates lar*			NC_002082		
GenBank	N.A.	*Hylobates moloch*			HQ622782		
GenBank	N.A.	*Hylobates pileatus*			NC_014045		
GenBank	N.A.	*Nomascus gabriellae*			NC_018753		
GenBank	N.A.	*Nomascus leucogenys*			NC_021957		
GenBank	N.A.	*Nomascus siki*			NC_014051		
GenBank	N.A.	*Symphalangus syndactylus*			NC_014047		
GenBank	N.A.	*Gorilla beringei graueri*			KF914213		
GenBank	N.A.	*Gorilla gorilla*			NC_001645		
GenBank	N.A.	*Homo sapiens*			NC_012920		

GenBank	N.A.	*Pan paniscus*			NC_001644		
GenBank	N.A.	*Pan troglodytes*			NC_001643		
GenBank	N.A.	*Pongo abelii*			NC_002083		
GenBank	N.A.	*Pongo pygmaeus*			NC_001646		

Table S3. Factor loadings, eigenvalues, and percentage of variance explained for PC1 and PC2 from principal component analysis. Abbreviations of each variable are given in the Materials and Methods.

Variables	Log10-transformed	
	PC1	PC2
SL	0.89	-0.04
BL	0.87	0.09
NO	0.83	-0.17
CIL	0.80	0.10
GI	0.79	-0.36
GIL	0.78	0.02
NEI	0.78	-0.25
NB	0.75	-0.10
PBC	0.72	0.29
NI	0.70	-0.35
PL	0.68	0.33
BH	0.67	0.04
JB	0.62	0.02
SB	0.60	-0.03
VB	0.57	-0.11
PBM3	0.54	0.20
OB	0.42	-0.10
M2-M2	0.10	0.80
M3-M3	0.29	0.79
FH	0.33	0.52
JH	0.36	0.12
OL	0.37	-0.35
CH	0.24	-0.20
Eigenvalues	9.27	2.35
Total variance explained (%)	40.30	10.23

cranial lengths (glabella to inion [GI]; nasion to inion [NI]; nasal ends to inion [NEI]), skull length (SL), cranial breadth (vault [VB]; between supramastoids [SB]), cranial height (CH), nasion to opisthion (NO), nasion to basion (NB), palate length (PL), palate breadth (opposite upper M3 [PBM3] and canines [PBC]), breadth between upper M3 (M3-M3), breadth between upper M2 (M2-M2), basal length (BL), orbit length (OL), orbit breadth (OB), face height (FH), biorbital breadth (BH), jaw lengths (gonion-incision [GIL]; condyle-incision [CIL]), jaw breadth (JB), and jaw height (JH)

Table S4. Primers used in this study.

Gene	Primer name	pair code	Sequences 5' to 3'	Source
CYTB	L14724-HK7	GD7	GGGGACCATCGTTGTATTTCAACT	Modified from L14724 (Irwin et al. 1991)
	LM-H427		TCAGGAAATTTGTGATAACTGTGGC	Current Study
D-Loop	GDL-L1	GDL	CGAAAACAAAATACTCAAATGAACCT	Current Study
	GDL-H2		GGTGATCCATCGTGATGTCTTATT	Current Study
Complete Mitogenome (NGS) [a]	MtG_12s_480_F	TF1	GCTAGGAAACAAACTGGGATTAGATACC	Chen et al. in prep
	MtG_cox3_R		AGCTGCGGCTTCAAAKCCRAARTGRTG	Chen et al. in prep
	MtG_cox3_F	TR1	ATGGCACACCAAGCACAYGCHTWYCAYATAGT	Chen et al. in prep
	MtG_12s_600_R		GGACACCGCCAAGTCCTTTGGGTTTTAA	Chen et al. in prep
Complete Mitogenome (Sanger) [b]	00080-F	MT1	GYTTGGTCCTRGCCTTTC	Current Study
	01050-R		AGTACRCTTACCATGTTAC	Current Study
	00930-F	MT2	ACACACCGCCCGTCAC	Current Study
	02200-R		CAGGTCAATTTCACTGGT	Current Study
	02020-F	MT3	CATCACCTCTAGCATTAC	Current Study
	03240-R		ATTAGGGCGTAGTTWGAG	Current Study
	02770-F	MT4	AAGATGGCAGAGCCCG	Current Study
	04000-R		CAACATTTTCGGGGTATG	Current Study
	03820-F	MT5	CTGACRAAAGAGTTACTTTG	Current Study
	05210-R		GGGCTTAGCTTAATTAAAG	Current Study
	05090-F	MT6	CCAAGAGCCTTCAAAGC	Current Study
	06380-R		CYGTRAATATRTGGTGGGC	Current Study
	05900-F	MT7	TWCTCYCACCCAGGAGC	Current Study
	07080-R		GGGGYTGGCTTGAAACC	Current Study
	07030-F	MT8	AAAGGAAGGAATCGAACC	Current Study
	07990-R		GTCTTTAACTTAAAAGGTTAA	Current Study
	07830-F	MT9	AAAATCTTYGAAATAGGRCC	Current Study
	09090-R		TGGTGGCCTTGGTATGT	Current Study
	08470-F	MT10	CYACCCARCTWTCCATAAA	Current Study
	09650-R		CCTCATCAGTAGATGGAG	Current Study
	05970-F	MT11	TTCGGCTTYGAAGCYGC	Current Study
	10620-R		GTGGTTAAGGGGTCGG	Current Study
	10100-F	MT12	AAAYAAATGATTTCGACTCAT	Current Study
	11360-R		AAGCTTCAGGGGGTTTG	Current Study
	11280-F	MT13	AATCMCTYATCGCATACTC	Current Study

	12360-R		GTTGATRTTTGGGTCTGAG	Current Study
	11990-F	MT14	GTGCAACTCCAAATAAAAG	Current Study
	13240-R		AGGGCTCAGGCGTTGG	Current Study
	13000-F	MT15	TCTGCACCCAYGCCTTC	Current Study
	14200-R		GTATGATGGTTGTTTTTGG	Current Study
	13950-F	MT16	GCACCCGCACCAATAG	Current Study
	14860-R		GGCCTCAYGGGAGGAC	Current Study
	14670-F	MT17	CGAGAYGTAAACTACGGC	Current Study
	15700-R		AGTTAAGTRCTTTTTCTCTG	Current Study
	15110-F	MT18	CAAAATCRCCTTYCACCC	Current Study
	16380-R		TGTCTTATTTAAGGGGAAC	Current Study
	16310-F	MT19	CTGTATCCGGCATCTGG	Current Study
	00340-R		CGCGGTGGCTGGCAC	Current Study

[a]: primers used to amplified the complete mitochondrial genomes of two individuals of hoolock gibbons, which were accomplished by Sanger sequencing

[b]: primers used to amplified the complete mitochondrial genomes of the rest hoolock gibbons, which were accomplished by the NGS.

Tabel S5. Partition scheme and evolutionary models used in phylogenetic analyses using the complete mitochondrial genome and partil CYT B + D-loop

Dataset	Partition	Model	Subset Partitions
Complete mitogenome	P1	GTR+G	12S, 16s
	P2	GTR+G	ATP6_1st, ATP8_1st, ATP8_2nd, CYTB_1st, ND1_1st, ND2_1st, ND3_1st, ND4L_1st, ND4_1st, ND5_1st
	P3	GTR+G	ATP6_2nd, COX3_2nd, CYTB_2nd, ND1_2nd, ND2_2nd, ND3_2nd, ND4L_2nd, ND4_2nd, ND5_2nd
	P4	TrN+G	CYTB_3rd, ND1_3rd, ND2_3rd, ND3_3rd, ND4L_3rd, ND4_3rd, ND5_3rd
	P5	TrNef+G	COX1_1st, COX2_1st, COX3_1st
	P6	HKY+G	COX1_2nd, COX2_2nd
	P7	TrN+G	ATP6_3rd, ATP8_3rd, COX1_3rd, COX2_3rd, COX3_3rd
Partial CYTB + D-loop	P1	K80	CYTB_1st
	P2	HKY	CYTB_2nd
	P3	HKY+G	CYTB_3rd
	P4	HKY+G	D-loop

Table S6. Classification results for DFAs

a. Classification results using 23 morphometric variables

Classification Results[b,c]

		species	Predicted Group Membership			Total
			H. hoolock	*H. leuconedys*	*H. tianxing*	
Original	Count	*H. hoolock*	38	0	0	38
		H. leuconedys	2	29	0	31
		H. tianxing	1	2	5	8
	%	*H. hoolock*	100.0	.0	.0	100.0
		H. leuconedys	6.5	93.5	.0	100.0
		H. tianxing	12.5	25.0	62.5	100.0
Cross-validated[a]	Count	*H. hoolock*	28	5	5	38
		H. leuconedys	8	17	6	31
		H. tianxing	4	4	0	8
	%	*H. hoolock*	73.7	13.2	13.2	100.0
		H. leuconedys	25.8	54.8	19.4	100.0
		H. tianxing	50.0	50.0	.0	100.0

a. Cross validation is done only for those cases in the analysis. In cross validation, each case is classified by the functions derived from all cases other than that case.

b. 93.5% of original grouped cases correctly classified.

c. 58.4% of cross-validated grouped cases correctly classified.

b. Classification results using the outlines of Upper M2

Classification Results[b,c]

		species	Predicted Group Membership			Total
			H. hoolock	*H. leuconedys*	*H. tianxing*	
Original	Count	*H. hoolock*	17	1	0	18
		H. leuconedys	3	14	0	17
		H. tianxing	0	1	5	6
	%	*H. hoolock*	94.4	5.6	.0	100.0
		H. leuconedys	17.6	82.4	.0	100.0
		H. tianxing	.0	16.7	83.3	100.0
Cross-validated[a]	Count	*H. hoolock*	13	5	0	18
		H. leuconedys	5	11	1	17
		H. tianxing	0	3	3	6
	%	*H. hoolock*	72.2	27.8	.0	100.0
		H. leuconedys	29.4	64.7	5.9	100.0
		H. tianxing	.0	50.0	50.0	100.0

a. Cross validation is done only for those cases in the analysis. In cross validation, each case is classified by the functions derived from all cases other than that case.

b. 87.8% of original grouped cases correctly classified.

c. 65.9% of cross-validated grouped cases correctly classified.

c. Classification results using the outlines of lower M2

Classification Results[b,c]

		species	Predicted Group Membership			Total
			H. hoolock	*H. leuconedys*	*H. tianxing*	
Original	Count	*H. hoolock*	13	3	1	17
		H. leuconedys	1	18	0	19
		H. tianxing	0	0	6	6
	%	*H. hoolock*	76.5	17.6	5.9	100.0
		H. leuconedys	5.3	94.7	.0	100.0
		H. tianxing	.0	.0	100.0	100.0
Cross-validated[a]	Count	*H. hoolock*	9	6	2	17
		H. leuconedys	6	12	1	19
		H. tianxing	3	1	2	6
	%	*H. hoolock*	52.9	35.3	11.8	100.0
		H. leuconedys	31.6	63.2	5.3	100.0
		H. tianxing	50.0	16.7	33.3	100.0

a. Cross validation is done only for those cases in the analysis. In cross validation, each case is classified by the functions derived from all cases other than that case.

b. 88.1% of original grouped cases correctly classified.

c. 54.8% of cross-validated grouped cases correctly classified.

Table S7. Summary of reads and mapping rates for each sample for the mitogenome sequencing.

Sample	type	# reads	mean length	# mapping	% mapping	Mean coverage ± SD	% missing
KIZ 90218106	tissue	14776	279	14136	95.67%	248.1 ± 126.7	0.00
BSJO	feces	64141	214	17332	27.02%	225.5 ± 106.7	0.00
DANDAN	feces	52324	192	12128	23.18%	189.2 ± 61.2	0.00
DH3	feces	34406	213.5	13735	39.92%	180.0 ± 87	0.00
DH2	feces	65185	192.2	15785	24.22%	177.1 ± 86.3	0.00
BSF	feces	41064	236	12041	29.32%	169.2 ± 77.4	0.00
NANA	feces	109463	210	9464	8.65%	108.4 ± 95.2	0.00
A2	feces	61945	218.1	5389	8.70%	74.9 ± 80.4	5.50
YANYAN	feces	40289	193	5593	13.88%	68.9 ± 77.3	12.10
A1	feces	21336	215	4112	19.27%	55.3 ± 44.5	0.40
BAIMEI (BA)	feces	65077	183	3366	5.17%	34.6 ± 37.9	16.60
DANGDANG	feces	48219	263	2413	5.00%	35.2 ± 21.2	0.00