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Supplemental Information

The Genomic Footprints of the Fall and Recovery of the Crested Ibis

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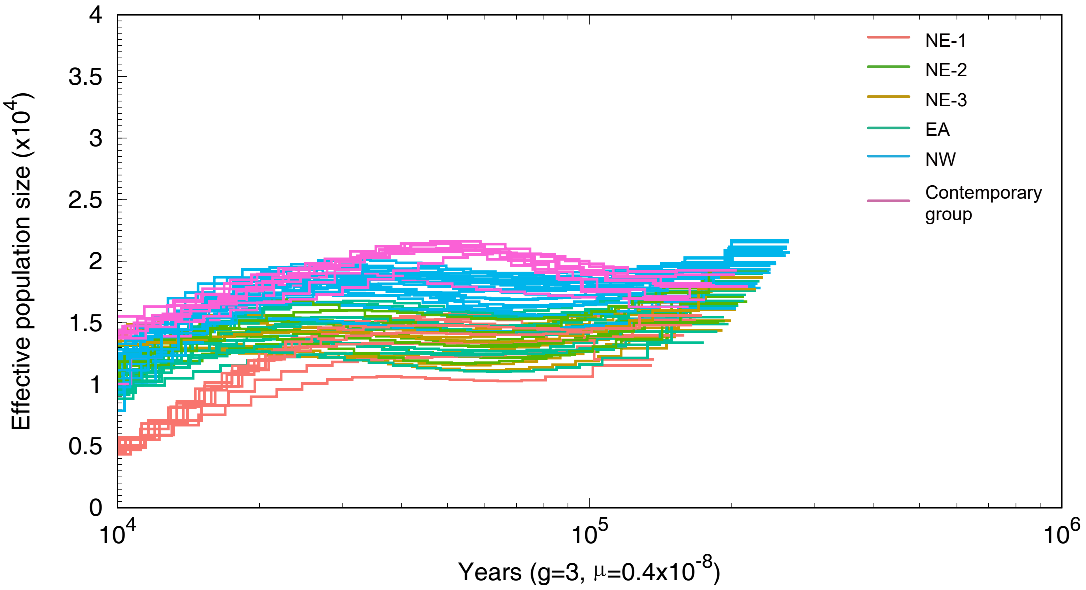

Figure S1. Demographic history estimation based on the pairwise sequentially Markovian coalescent (PSMC) model, Related to Figure 2. Population sizes inferred from the three Northeast (NE) sub groups, as well as the East (EA), Northwest (NW), and Contemporary group (MC). g, generation time; μ, mutation rate.

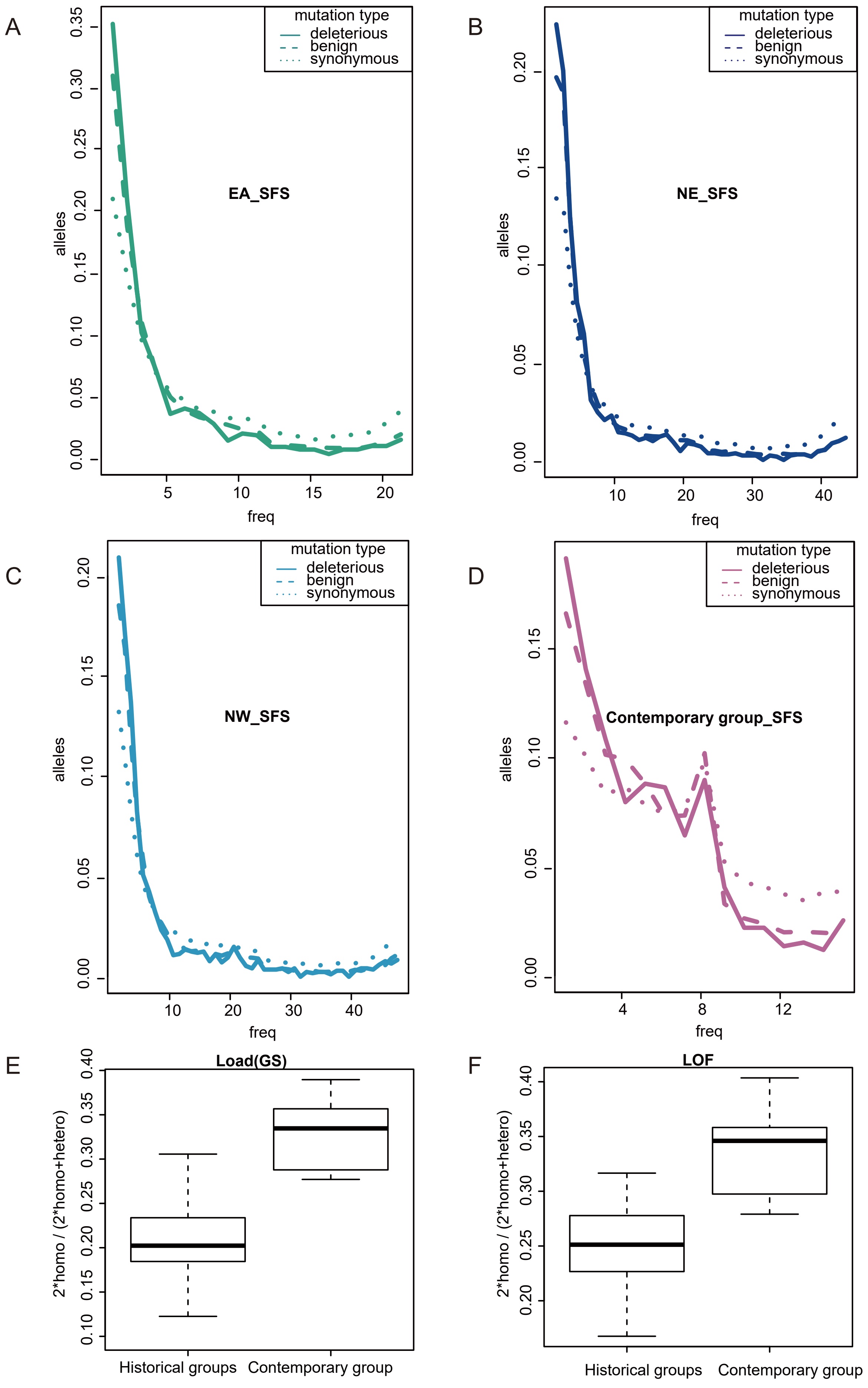
A
mutation type
deleterious
benign
synonymous
EA_SFS
alleles
0.00
0.05
0.10
0.15
0.20
0.25
0.30
0.35
5
10
15
20
freq
B
mutation type
deleterious
benign
synonymous
NE_SFS
alleles
0.00
0.05
0.10
0.15
0.20
10
20
30
40
freq
C
mutation type
deleterious
benign
synonymous
NW_SFS
alleles
0.00
0.05
0.10
0.15
0.20
10
20
30
40
freq
D
mutation type
deleterious
benign
synonymous
Contemporary group_SFS
alleles
0.00
0.05
0.10
0.15
4
8
12
freq
E
Load(GS)
2*homo / (2*homo+hetero)
0.10
0.15
0.20
0.25
0.30
0.35
0.40
Historical groups
Contemporary group
F
LOF
2*homo / (2*homo+hetero)
0.20
0.25
0.30
0.35
0.40
Historical groups
Contemporary group

Figure S2. Patterns of deleterious mutations across populations, Related to Figure 3.

(A)-(D) Site-Frequency-Spectrum for each category: deleterious, benign and synonymous, for each group. All sequenced samples were used for this analysis. The analyses were applied to four groups as follows: East (EA, A), Northeast (NE, B), Northwest (NW, C), and Contemporary groups (D). Comparison of the ratio of homo- to homo- and heterozygous sites. (E) Deleterious missense mutations based on Grantham Scores. (F) Loss of function mutations based on the SnpEff algorithm.

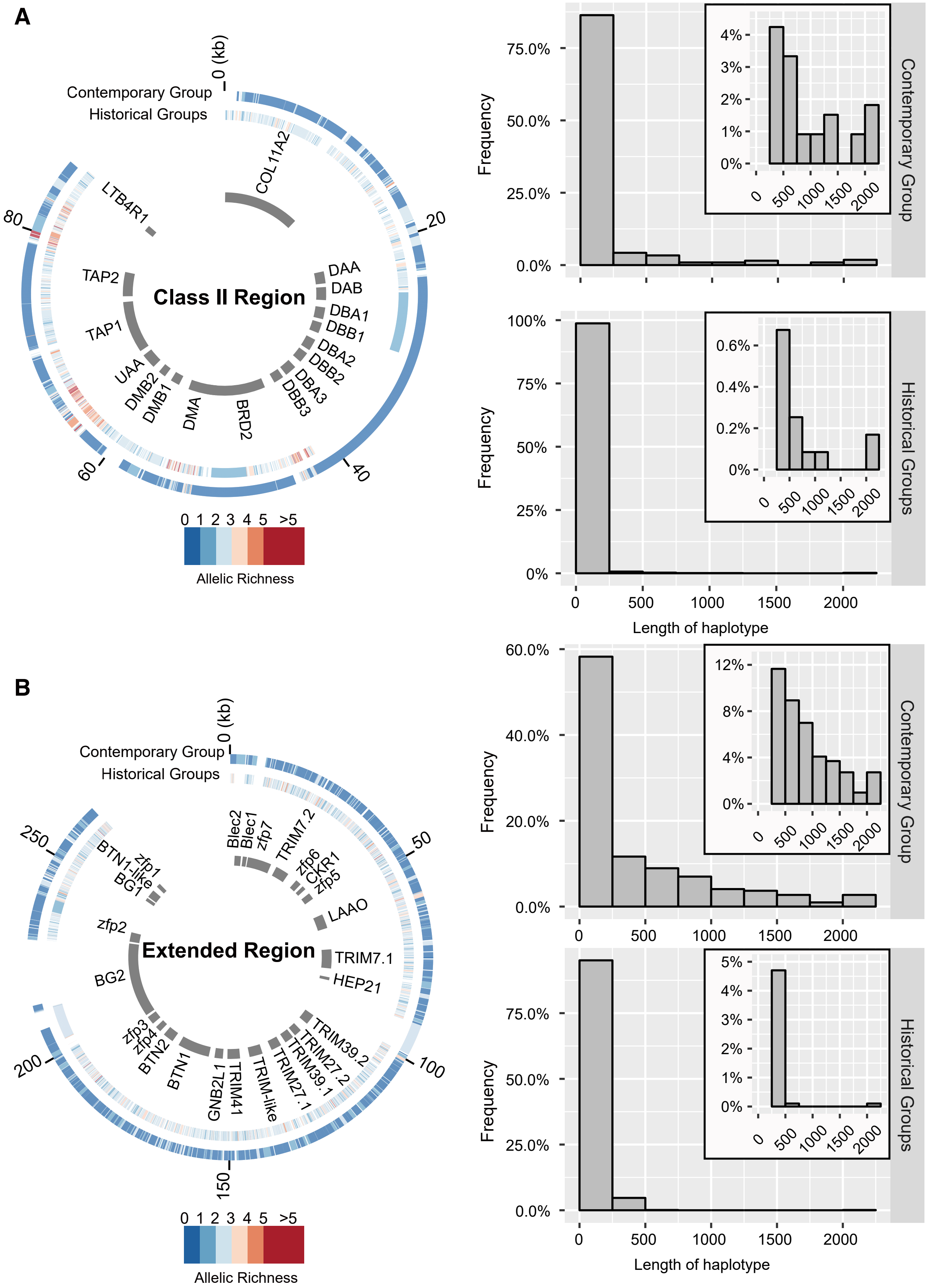
A
0 (kb)
Contemporary Group
Historical Groups
COL11A2
LTB4R1
80
20
TAP2
Class II Region
DAA
DAB
DBA1
DBB1
DBA2
DBB2
DBA3
DBB3
TAP1
UAA
DMB2
DMB1
DMA
BRD2
60
40
0 1 2 3 4 5 >5
Allelic Richness
Frequency
75.0%
50.0%
25.0%
0.0%
4%
3%
2%
1%
0%
0
500
1000
1500
2000
Contemporary Group
Frequency
100%
75%
50%
25%
0%
0.6%
0.4%
0.2%
0%
0
500
1000
1500
2000
Historical Groups
0
500
1000
1500
2000
Length of haplotype
B
0 (kb)
Contemporary Group
Historical Groups
250
50
Blec2
Blec1
zfp7
TRIM7.2
zfp6
CKR1
zfp5
BTN1-like
zfp1
BG1
LAAO
zfp2
Extended Region
TRIM7.1
HEP21
BG2
zfp3
zfp4
BTN2
BTN1
GNB2L1
TRIM41
TRIM-like
TRIM27.1
TRIM39.1
TRIM27.2
TRIM39.2
200
100
150
0 1 2 3 4 5 >5
Allelic Richness
Frequency
60.0%
40.0%
20.0%
0.0%
12%
8%
4%
0%
0
500
1000
1500
2000
0
500
1000
1500
2000
Contemporary Group
Frequency
75.0%
50.0%
25.0%
0.0%
5%
4%
3%
2%
1%
0%
0
500
1000
1500
2000
Historical Groups
0
500
1000
1500
2000
Length of haplotype

Figure S3. Haplotype structures and length distribution of Class II and Extended Regions in the historical and contemporary groups, Related to Figure 4.

(Left) Haplotype blocks are detected based on the SNP datasets for historical and contemporary groups, respectively. Colored circles show the haplotype structure (each box indicates the start and end SNPs of one haplotype) and the diversity along the regions (color indicates the allelic richness). The allelic richness of historical groups is estimated in the random way (see Method). Gaps in the colored circles are the intervals between two neighboring haplotype blocks. Genomic structures of the regions are drawn as grey bars, with different sizes showing different gene loci of varied sizes. (Right) Length distribution of haplotype blocks. Haplotype blocks with lengths larger than 2000 bp are grouped into the last bar. The plotting area for the bin of 250-2000bp is enlarged in the top right corner. (A) Haplotype blocks and length distribution in the Class II region. (B) Haplotype blocks and length distribution in the Extended region.

Table S1. Effective population sizes (*Ne*) of each group at the sampling time point estimated by NeEstimator, Related to Figure 2.

Four general geographic groups are the East (EA), Northeast (NE), Northwest (NW), and Contemporary groups. Following the insights shown by the NJ tree, the *Ne* of three NE subgroups was calculated respectively.

Group	Number of individuals	Number of SNPs[a]	*Ne*[b]
NE-1	8	1,527,932	72.7(71.2-74.2)
NE-2	8	1,652,489	144.5(139.2-150.2)
NE-3	6	1,687,450	94.7(91.3-98.4)
EA	11	1,339,682	356.2(335.7-379.4)
NW	23[c]	1,522,027	163.2(161.3-165.1)
Contemporary	8	1,124,530	10.7(10.7-10.8)

a: Only SNP loci without missing data were used in this analysis.

b: Data are represented as mean (95% CIs).

c: CHKSEI14060220 is not involved.

Table S2. Summary of estimated inbreeding coefficient (F_{UNI}) and *Ne*, Related to Figure 3.

SNP VCF files for *Pan paniscus*, *Pongo abelii*, *Pongo pygmaeus*, *Pan troglodytes* and *Gorilla gorilla* are from [S1]. SNP VCF file for *Vulpes Vulpes* is from [S2]. SNP VCF files for *Ursus maritimus* and *Ursus arctos* are from [S3]. SNP VCF file for *Anas platyrhynchos* is from [S4]. SNP VCF file for Tibetan fowl from Qinghai is from [S5]. Raw sequence read FASTQ files for *Platyspiza crassirostris* are from [S6]. SNP BAM files for *Ficedula albicollis* are from [S7]. Raw sequence read FASTQ files for *Ailuropoda melanoleuca* are from [S8]. Raw sequence read FASTQ files for *Ectopistes migratorius* are from [S9].

Species	Conservation status[a]	F_{UNI}	*Ne*
Pan paniscus	EN	0.027804	40.5
Pongo abelii	CR	-0.003456	223.8
Pongo pygmaeus	CR	0.001124	100.3
Pan troglodytes	EN	0.112602	5.8
Gorilla gorilla	CR	0.073231	26.6
Vulpes vulpes	LC	-0.075651	370.0
Ursus maritimus	VU	-0.062079	238.7
Ursus arctos	LC	0.093783	7.2
Anas platyrhynchos	LC	0.015845	161.9
Tibetan fowl from Qinghai	LC	0.059132	35.0
Platyspiza crassirostris	LC	0.086422	5.0
Ficedula albicollis	LC	0.001172	272.0
Ailuropoda melanoleuca	VU	0.085511	29.0
Ectopistes migratorius	EX	-0.006270	64.0
Historical groups of *Nipponia nippon*	EX	0.044317	72.7-356.2
Contemporary group of *Nipponia nippon*	EN	0.172716	10.7

a: Five conservation status are listed in the table: Least concern (LC), Vulnerable (VU), Endangered (EN), Critically endangered (CR), and Extinct (EX).

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