Supplementary Information for:

The Genetics of Tiger Pelage Color Variations

Xiao Xu et al.

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Supplementary Discussion

Melanin content in tiger hairs

The melanin content in the zigzag hairs from the background non-striped region of a golden tiger was compared to that of a wild-type orange tiger via spectrophotometric measurement. A significant decrease in eumelanin in the golden tiger's hairs (Figure S1B) was consistent with its observed reduced degree of black pigmentation (Figure 1B). Intriguingly, pheomelanin in the golden tiger's hairs also showed a slight reduction (Figure S1B) despite its prolonged central agouti band, suggesting a likely lower density of pheomelanosomes in the golden tiger's fur, as evident in the overall lighter color of its agouti band (Figures 1A, S1A). It seems surprising yet reasonable that golden tigers with a prolonged pheomelanin band exhibit an overall decrease in pheomelanin content. ASIP expression switches pigment synthesis from eumelanin to pheomelanin by inhibiting MC1R signaling [1, 2]. However, with an increased level of ASIP expression or the extended presence of ASIP, MC1R signaling would be further decreased [2], leading to a reduction in MC1R-associated TYR activity and hence a lower level of pheomelanogenesis. Therefore, the golden tiger blonde color was most likely caused by a lower density of pheomelanosomes as well as a prolonged agouti band in hairs.

Implications for tiger genomic diversity and conservation

In humans, *CORIN* is primarily expressed in cardiac myocytes and regulates blood pressure by converting atrial natriuretic peptide precursor (pro-ANP) into its mature form (ANP) [3, 4]. Mutations in *CORIN* have been associated with human hypertension and heart failure [5-7], symptoms that have not historically been recorded in golden and snow white tigers, although this could simply be due to a lack of studies. Alternatively, the p.H587Y mutation might not affect the efficiency of CORIN in activating natriuretic peptide in tigers, but further studies are needed in this regard. It is also noteworthy that golden and snow white tigers tend to grow larger than their wild-type counterparts in the same captive environment (Dong GX, personal communications). Intriguingly, CORIN has been proposed to regulate body weight by degrading agouti-related protein (AGRP) [8]. AGRP is expressed in the hypothalamus and antagonizes melanocortin receptor 4 (MC4R), which regulates feeding and metabolism [9, 10]. Although CORIN is not expressed in the brain [3], it may be able to reach the hypothalamus through blood circulation [11]. The potential association between CORIN and body mass increases in animals merits further examination.

The *SLC45A2*-associated white tiger morph is a viable, naturally occurring genetic polymorphism that has persisted for centuries in Bengal tigers [12]. Throughout history, white tigers were sighted sporadically across the Indian subcontinent, many of which were captured or shot as mature adults, which provides evidence that they are 'normal' and able to survive and reproduce [13]. The reasons for the extinction of wild white tigers are undoubtedly the same as those that drove the widespread decline of wild tigers in general, rather than the genetic abnormalities. Indeed, although some mutations in *SLC45A2* have been linked to a class of human

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oculocutaneous albinism, various natural polymorphisms in *SLC45A2* occur in people, horses, quail and chickens without causing physiological defects other than hypopigmentation [14, 15]. The physiological effects of the *CORIN* variant on golden and snow white tigers remain unclear, considering the protein's critical involvement in multiple cellular and developmental pathways and the fact that confirmed records in the wild are much less common than in the white tiger.

Well-managed captive populations of wild animals can assist in education, research and fundraising, and have been justified as a genetic reservoir for wild animals and insurance against extinction [16]. However, deliberate inbreeding to maintain recessive traits in captivity have led to many undesirable traits associated with captive white, golden and snow white tigers. Most are probably due to improper husbandry, inbreeding depression and general maladies experienced by captive animals [17].

Materials and Methods

Ethical Statement

Biological samples used in the study were recruited in full compliance with the Convention on International Trade in Endangered Species (CITES) and other relevant permissions issued to S. J. Luo at the School of Life Sciences, Peking University, by the State Forestry Administration of China. All biological samples were collected during veterinary examinations for health and physical conditions, and animals were handled following the general animal welfare code of practice.

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Biological samples

Fifty-one blood samples from 11 wild-type orange, 9 golden, 18 white and 13 snow white tigers were collected from Chimelong Safari Park, Guangzhou, China. Six blood samples from two white and four orange tigers were collected from Shanghai Zoo, Shanghai, China. Forty-three hair samples from 17 orange, 7 golden, 10 white and 9 snow white tigers were collected during grooming from Tiger Preserve, Myrtle Beach, USA. In addition, 96 DNA samples from unrelated animals, including 90 orange and 6 white tigers, were obtained from the DNA collection of the Laboratory of Genomics Diversity, NCI-Frederick, MD. Information regarding all samples is detailed in Table S1.

To obtain cDNA of the identified gene, one skin biopsy sample from a stillborn kitten was collected from Yongkang Veterinary Clinic, Beijing, and stored at -80°C.

Genomic DNA was extracted from blood or hair samples using the DNeasy Blood and Tissue Kit (QIAGEN) and following the manufacturer's instructions. Total RNA was extracted from the cat skin sample with TRIzol (Invitrogen), and cDNAs were subsequently obtained through RT-PCR with the Superscript[®] III First-Strand Synthesis System (Invitrogen).

Visual examination of tiger hair morphology

To examine the morphology of the tiger hairs, clusters of full-length hairs were hand plucked from individuals representing all four tiger color morphs at Chimelong Safari Park, Guangzhou, China. At least four clusters of hairs from the torso flank were taken from the anesthetized animal. Except for the stripeless snow tiger, hairs from both stripes and outside the stripes (background fur) were collected. Individual hairs were isolated from each hair cluster and were observed and photographed using a Leica M125 microscope system with 8x zoom lens under the incident light conditions. The length of each hair section (black tip, sub-apical yellow band and black base) was manually measured on the 8x zoomed screen. In total, 89 and 87 zigzag hairs from the background fur of one orange tiger and one golden tiger, respectively, were measured.

Spectrophotometric determination of eumelanin and pheomelanin

Spectrophotometric assays were conducted to quantitatively measure eumelanin [18] and pheomelanin [19] in different color morphs of tigers. Four specimens of plucked hairs, from stripes and background of a golden tiger and an orange tiger, respectively, were prepared and measured. In addition, plucked hairs from the background fur of a white tiger were used as blank control in both eumelanin and pheomelanin assays. The five hair samples each weighed 7 mg and were homogenized with a glass homogenizer in ddH₂O to a final concentration of 20 mg/mL at 350 μ L and then aliquoted for subsequent assays of eumelanin (absorbance at 350 nm, A₃₅₀) and pheomelanin (absorbance at 400 nm, A₄₀₀) with a BioTek Eon spectrophotometer as described previously. The final result of eumelanin or pheomelanin was normalized to the initial hair quantity, subtracted from the white

tiger hair's reading of eumelanin or pheomelanin, and averaged across three replications.

Candidate gene sequencing

Four pigmentation genes (*MC1R*, *ASIP*, *TYR* and *TYRP1*) known to be involved in the coat color genetics of domestic cats were selected as candidate genes for the tiger *WB* locus [20, 21]. Coding regions of the four genes were amplified and sequenced (Table S2) in unrelated individuals, including golden (n=1), snow white (n=1) and orange (n=6) tigers, following PCR and Sanger sequencing procedures as previously described [15]. No variation associated with *WB* was identified.

Gene mapping via genome-wide association study (GWAS)

Nineteen individuals, including golden (n=1), snow white (n=8) and white (n=10) tigers, were assembled for mapping the *wideband* (*WB* locus) gene. Golden and snow white tigers homozygous at the *WB* locus (*wb/wb*, n=9) were carefully selected from Chimelong Safari Park to represent the GWAS case group. The control group was represented by white tigers that were heterozygous at the *WB* locus (*WB/wb*, n=10). These individuals were selected from the same extended family with the *wb/wb* tigers according to zoo breeding records to ensure a similar genetic background with the case group.

Whole-genome sequencing (WGS) was completed in three *wb/wb* tigers (one golden and two snow white) in our previous study [15]. Restriction-site-associated

DNA (RAD) sequencing was applied to the other 16 individuals. Restriction site *Pst*I was selected for RAD sequencing to ensure a 1/20 kb genome-wide SNP density. A genomic paired-end library for RAD-seq was constructed following protocols described previously [15] and sequenced on an Illumina HiSeq 2000 sequencer. Each RAD library was sequenced to an approximate 11-fold depth with an average of 4.39 Gb of data (Table S3). The RAD-seq and WGS were performed at the Biodynamic Optical Imaging Center (BIOPIC) at Peking University.

Procedures for genome sequencing data processing, including adapter trimming, read alignment and SNPs calling, were performed following the workflow described previously [15]. SNPs with data from at least 17 of the 19 individuals were selected for GWAS analysis. The eight snow white tiger and one golden tiger were set as the case group, and the 10 white tigers were set as the control group. GWAS analysis was performed in PLINK 1.07 [22], and the significance of the genotype-phenotype association was calculated by Fisher's exact test under the recessive model. SNPs with a strong association (p<0.0001) were further examined for the genotypes of the 19 tigers. SNPs with a genotype that failed to match the recessive inheritance pattern of the golden trait were considered as false positive signals and discarded. Scaffolds with positive association signals were classified as candidate scaffolds.

Candidate scaffolds were mapped to the cat genome (*Felis_catus 6.2*) [23] to determine conserved syntenies. Haplotypes of the 19 individuals across the candidate scaffolds were inferred using PHASE 2.1 [24] and combined based on the scaffold synteny. The haplotype block shared by the nine individuals from the case group was

designated as the putative region for the WB locus.

Identification of the feline wideband gene

Tiger coding exons within the candidate region were obtained from the tiger reference genome annotation and subsequently refined by aligning with the available human, mouse and dog CDS. In addition to the genome data of the three *wb/wb* tigers, the WGS data of 30 orange tigers (unrelated to any golden tiger lineages) from another independent study were also analyzed together. SNPs/indels from non-coding regions were first excluded, and those not fixed in the three *wb/wb* tigers were also excluded. To eliminate common variations within tiger populations, SNPs/indels presented in any of the 31 orange tigers were further excluded. SNPs/indels causing amino acid changes from the remaining SNPs/indels within the candidate region were selected and considered the putative mutation(s).

The potential impact of non-synonymous substitutions in coding regions was evaluated by multivariate analysis of protein polymorphism (MAPP) [25], which considers both evolutionary constraints and the physicochemical properties of amino acid residues; a MAPP score greater than 10 suggests a likely impact of such changes on protein function.

The putative mutation was then validated in an extended sample set of 197 unrelated tigers, including 123 orange, 16 golden, 36 white and 22 snow white tigers. Primers (Table S2) to amplify the candidate *golden* gene were designed based on the tiger reference genome with Primer3 (http://bioinfo.ut.ee/primer3-0.4.0/primer3/). PCR and sequencing procedures followed protocols previously described. In addition, the *SLC45A2* p.A477V variant was also examined in the same set of tiger samples.

Functional validation of the CORIN p.H587Y mutation

Because sequences of *CORIN* from either cat or tiger were unavailable, we obtained the full cDNA of cat *CORIN* by RT-PCR with a cat skin sample. Sequences of tiger *CORIN* and *ASIP* cDNA were then assembled by aligning cat *CORIN* and cat *ASIP* (NM_001009190) to the tiger reference genome [7]. The cDNAs of tiger *CORIN* and tiger *ASIP* were synthesized accordingly and ligated to the expression vector p3XFIAG-CMV-14, with three tandem FLAG epitopes fused to the C-terminal end. The tiger *CORIN* p.H587Y mutant was obtained by site-directed mutagenesis.

Plasmids containing *CORIN*, the *CORIN* p.H587Y mutation and *ASIP* were transfected into human HEK 293 cells, and *CORIN* and the *CORIN* p.H587Y mutation were co-transfected with *ASIP*. The culture medium was replaced after 18 hours with fresh medium, and the culture supernatants were harvested after another 12 hours. To detect CORIN's effect on the secreted ASIP, the medium of ASIP-expressing cells was mixed with CORIN-variant-expressing cells and cultured for another 3 and 6 hours. HEK 293 cells were lysed in a buffer containing 50 mM Tris-HCl (pH 8.0), 150 mM NaCl, 1% Triton X-100. The expression of tiger CORIN, CORIN p.H587Y, and ASIP from the cell lysates and medium were detected by Western blotting using anti-FIAG antibody.

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Supplementary Tables and Figures

Table S1. Tiger samples used in the study.

Table S2. Primers for PCR amplification and Sanger sequencing.

Table S3. Summary of RAD-seq and WGS in 19 tigers for GWAS.

Table S4. Genes located within the 9.2 Mb region associated with the WB locus.

Figure S1. (A) Photographic and schematic illustration of tiger zigzag hairs. (B)
Spectrophotometric measurement of eumelanin and pheomelanin in agouti zigzag
hairs from orange and golden tigers. The value was calculated from three replicates
using non-pigmented hairs from a white tiger's background fur as the baseline blank.
(C) Association of the "wideband" trait on tiger genome scaffolds 1457 and 97. The
scaffold orientation is indicated by arrows, and the *wideband*-linked genomic region
is specified.

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ble S1. Tiger samples used in the study.

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Brahman Golden TT CC Tiger Preserve Myrele Beach, USA, Andre B. capitve F. individual for validation Matar Golden TT CT Tiger Preserve Myrele Beach, USA, Andre B. capitve F. individual for validation Padha Golden TT CT Tiger Preserve Myrele Beach, USA, Andre B. capitve M. individual for validation Raga Golden TT CC Tiger Preserve Myrele Beach, USA, Andre B. capitve M. individual for validation Rama Golden TT CC Tiger Preserve Myrele Beach, USA, Andre B. capitve M. individual for validation RAMOM TT Chimelong Sariar Park, China, Dong GX. capitve F. RAD-seq for white GZXD045 Snow TT TT Chimelong Sariar Park, China, Dong GX. capitve M. RAD-seq for white GZXD035 Snow TT TT Chimelong Sariar Park, China, Dong GX. capitve M. RAD-seq for white GZXD035 Snow TT TT Chimelong Sariar Park, China, Dong GX. capitve M. RAD-seq for white GZXD035 Snow TT TT Chimelong Sariar Park, China, Dong GX. capitve M. <t< td=""><td>GZXJ039</td><td>Golden</td><td>TT</td><td>СТ</td><td>Chimelong Safari Park, China, Dong GX</td><td>captive</td><td>F</td><td>WGS for wideband & white</td></t<>	GZXJ039	Golden	TT	СТ	Chimelong Safari Park, China, Dong GX	captive	F	WGS for wideband & white
Knpa Mata Golden TT CT Tiger Preserve Myrile Beach, USA, Antle B. capive F. individual for validation Mukari Golden TT CT Tiger Preserve Myrile Beach, USA, Antle B. capive F. individual for validation Raga Golden TT CC Tiger Preserve Myrile Beach, USA, Antle B. capive F. Mukari Golden TT CC Tiger Preserve Myrile Beach, USA, Antle B. capive F. RAD-seq for white GZX1006 Snow TT TT Chimalong Shafir Park, China, Dong GX. capive F. RAD-seq for white GZX1005 Snow TT TT Chimalong Shafir Park, China, Dong GX. capive F. RAD-seq for white GZX1035 Snow TT TT Chimalong Shafir Park, China, Dong GX. capive M. WGS for widehand & white GZX1035 Snow TT TT Chimalong Shafir Park, China, Dong GX. capive M. RAD-seq for white GZX1045 Snow TT TT Chimalong Shafir Park, China, Dong GX. capive F. RAD-seq for white GZX1045 Snow TT TT Chimalong Shafir Park, China, Dong GX. capive M. RAD-seq for white	Brahman	Golden	TT	CC	Tiger Preserve Myrtle Beach, USA, Antle B	captive	М	individual for validation
Matha Golden TT CT Tiger Preserve Myrtle Beach, USA, Ante B Captive M individual for validation Rag Golden TT CT Tiger Preserve Myrtle Beach, USA, Ante B captive M individual for validation Rag Golden TT CT Tiger Preserve Myrtle Beach, USA, Ante B captive M individual for validation GZXJ006 Snow TT TT Chimelong Safari Park, China, Dong GX captive F RAD-seq for white GZXJ005 Snow TT TT Chimelong Safari Park, China, Dong GX captive F RAD-seq for white GZXJ005 Snow TT TT Chimelong Safari Park, China, Dong GX captive F RAD-seq for white GZXJ005 Snow TT TT Chimelong Safari Park, China, Dong GX captive M RAD-seq for white GZXJ005 Snow TT TT Chimelong Safari Park, China, Dong GX captive M RAD-seq for white GZXJ004 Snow TT TT Chimelong Safari Park, China, Dong GX captive M RAD-seq for white GZXJ045 Snow TT TT Chimelong Safari Pa	Krupa	Golden	TT	ĊŤ	Tiger Preserve Myrtle Beach, USA, Antle B	captive	F	individual for validation
Muktari Golden TT CT Tiger Preserve Myrite Beach, USA, Antle B exprive M Individual for validation Raga Golden TT CC Tiger Preserve Myrite Beach, USA, Antle B captive M Individual for validation GZZJ004 Snow TT TT Chimelong Safari Park, China, Dong GX captive F RAD-seq for white GZZJ030 Snow TT TT Chimelong Safari Park, China, Dong GX captive F RAD-seq for white GZZJ031 Snow TT TT Chimelong Safari Park, China, Dong GX captive M WGIS Soft or widzhond & white GZZJ033 Snow TT TT Chimelong Safari Park, China, Dong GX captive M WGIS Soft or widzhond & white GZZJ034 Snow TT TT Chimelong Safari Park, China, Dong GX captive R RAD-seq for white GZZJ045 Snow TT TT Chimelong Safari Park, China, Dong GX captive R RAD-seq for white Captive R	Mata	Golden	TT	ĊT	Tiger Preserve Myrtle Beach, USA, Antle B	captive	F	individual for validation
Padia Colden TT CT Tiger Preserve Myrtle Beach, USA, Antle B captive F individual for validation Rapa Golden TT CC Tiger Preserve Myrtle Beach, USA, Antle B captive M individual for validation GZX1004 Snow TT TT Chimelong Safari Park, China, Dong GX captive F RAD-seq for white GZX1005 Snow TT TT Chimelong Safari Park, China, Dong GX captive F RAD-seq for white GZX1005 Snow TT TT Chimelong Safari Park, China, Dong GX captive F RAD-seq for white GZX1005 Snow TT TT Chimelong Safari Park, China, Dong GX captive F RAD-seq for white GZX1035 Snow TT TT Chimelong Safari Park, China, Dong GX captive F RAD-seq for white GZX1045 Snow TT TT Chimelong Safari Park, China, Dong GX captive F RAD-seq for white GZX1045 Snow TT TT	Muktari	Golden	TT	СТ	Tiger Preserve Myrtle Beach USA Antle B	captive	M	individual for validation
Raga Golden TT CC Tiger Preserve Myrtle Beach, USA, Antle B captive M individual for validation GZX004 Snow TT TT Chimelong Safari Park, China, Dong GX captive F RAD-seq for white GZX004 Snow TT TT Chimelong Safari Park, China, Dong GX captive F RAD-seq for white GZX013 Snow TT TT Chimelong Safari Park, China, Dong GX captive F RAD-seq for white GZX0145 Snow TT TT Chimelong Safari Park, China, Dong GX captive M WGB for wideband white GZX0105 Snow TT TT Chimelong Safari Park, China, Dong GX captive R AD-seq for white GZX0104 Snow TT TT Chimelong Safari Park, China, Dong GX captive R AD-seq for white GZX0104 Snow TT TT Chimelong Safari Park, China, Dong GX captive R AD-seq for white GZX0103 Snow TT TT Chimelong Safari Park, China, Dong GX ca	Padha	Golden	TT	CT	Tiger Preserve Myrtle Beach USA Antle B	captive	F	individual for validation
Rama Golden T CC Tiger Preserve Myrtle Beach, USA. Antle B captive M individual for validation GZX0004 Snow TT TT Chinnelong Safari Park, China, Dong GX captive F RAD-seq for white GZX003 Snow TT TT Chinnelong Safari Park, China, Dong GX captive F RAD-seq for white GZX032 Snow TT TT Chinnelong Safari Park, China, Dong GX captive M WGS for wideband ewideband GZX034 Snow TT TT Chinnelong Safari Park, China, Dong GX captive R RAD-seq for wideband GZX043 Snow TT TT Chinnelong Safari Park, China, Dong GX captive R RAD-seq for wideband GZX043 Snow TT TT Chinnelong Safari Park, China, Dong GX captive RAD-seq for wideband GZX043 Snow TT TT Chinnelong Safari Park, China, Dong GX captive RAD-seq for wideband GZX043 Snow TT TT Chinnelong Safari Park,	Raga	Golden	TT	CC	Tiger Preserve Myrtle Beach USA Antle B	captive	M	individual for validation
Caration Ti Ti Ti Chimelong Safari Park, China, Dong GX, captive F RAD-seq for white GZX0005 Snow TT TT Chimelong Safari Park, China, Dong GX, captive F RAD-seq for white GZX0313 Snow TT TT Chimelong Safari Park, China, Dong GX, captive F RAD-seq for white GZX032 Snow TT TT Chimelong Safari Park, China, Dong GX, captive F RAD-seq for white GZX033 Snow TT TT Chimelong Safari Park, China, Dong GX, captive F RAD-seq for white GZX033 Snow TT TT Chimelong Safari Park, China, Dong GX, captive F RAD-seq for white GZX034 Snow TT TT Chimelong Safari Park, China, Dong GX, captive F RAD-seq for white GZX034 Snow TT TT Chimelong Safari Park, China, Dong GX, captive F RAD-seq for white GZX034 Snow TT TT Chimelong Safari Park, China, Dong GX, captive F RAD-seq for white GZX048 Snow TT TT Chimelong Safari Park, China, Dong GX, captive F RAD-seq for white GZX048 Snow TT TT Chimelong Safari Park, China, Dong GX, captive F RAD-seq for white GZX048 Snow TT TT Chimelong Safari Park, China, Dong GX, captive F RAD-seq for white GZX047 Snow TT TT TT Triger Preserve Myrtle Beach, USA, Antle B captive F Individual for validation of the state Safari Park, China, Dong GX, captive F RAD-seq for white Mathematical Safari Park, China, Dong GX, captive F Individual for validation Rashas Snow TT TT Triger Preserve Myrtle Beach, USA, Antle B captive F Individual for validation Sranawati Snow TT TT Triger Preserve Myrtle Beach, USA, Antle B captive F Individual for validation Srinbad Snow TT TT Triger Preserve Myrtle Beach, USA, Antle B captive F Individual for validation Srinbad Snow TT TT Triger Preserve Myrtle Beach, USA, Antle B captive F Individual for validation Srinbad Snow TT TT Triger Preserve Myrtle Beach, USA, Antle B captive F Individual for validation Srinbad Snow TT TT Triger Preserve Myrtle Beach, USA, Antle B captive F Individual for validation Srinbad Snow TT TT Triger Preserve Myrtle Beach, USA, Antle B captive F Individual for validation Srinbad Snow TT TT Triger Preserve Myrtle Beach, USA, Antle B captive F Individual for va	Rama	Golden	TT	CC	Tiger Preserve Myrtle Beach, USA, Antle B	captive	M	individual for validation
GZX1004 Snow TT TT Chimelong Safari Park, China, Dong GX captive F RAD-seq for white GZX1003 Snow TT TT Chimelong Safari Park, China, Dong GX captive F RAD-seq for white GZX1034 Snow TT TT Chimelong Safari Park, China, Dong GX captive F RAD-seq for white GZX1035 Snow TT TT Chimelong Safari Park, China, Dong GX captive W WGS for wideband & white GZX1035 Snow TT TT Chimelong Safari Park, China, Dong GX captive F RAD-seq for wideband GZX1045 Snow TT TT Chimelong Safari Park, China, Dong GX captive F RAD-seq for wideband GZX1045 Snow TT TT Chimelong Safari Park, China, Dong GX captive F RAD-seq for wideband GZX1045 Snow TT TT Chimelong Safari Park, China, Dong GX captive F RAD-seq for wideband GZX1045 Snow TT TT TG Freeserve Myric Beach, USA, Antle B captive F RAD-seq for wideband GZX1045 Snow TT TT Tig reserve Myric Beach, USA, Antle B	Kailla	Golden	11	ce	riger rieserve wrytte beach, 05/4,74itte b	captive	IVI	individual for validation
CZZ1006 Snow TT TT Chinelong Safair Park, China, Dong GX captive F RAD-seq for white CZX1031 Snow TT TT Chinelong Safair Park, China, Dong GX captive F RAD-seq for white CZX1033 Snow TT TT Chinelong Safair Park, China, Dong GX captive WGS for widebond & white CZX1033 Snow TT TT Chinelong Safair Park, China, Dong GX captive F RAD-seq for widebond GZX1034 Snow TT TT Chinelong Safair Park, China, Dong GX captive RAD-seq for widebond GZX1044 Snow TT TT Chinelong Safair Park, China, Dong GX captive RAD-seq for widebond GZX1045 Snow TT TT TT Chinelong Safair Park, China, Dong GX captive RAD-seq for widebond GZX1045 Snow TT TT TT Tig Preserve Myrtle Beach, USA, Antle B captive F RAD-seq for widebond Supsit Snow TT TT Tig Preserve Myrtle Beach, USA, Antle B captive F RAD-seq for widebond widebond <t< td=""><td>GZX1004</td><td>Snow</td><td>ТТ</td><td>ТТ</td><td>Chimelong Safari Park China Dong GX</td><td>captive</td><td>F</td><td>RAD-sea for white</td></t<>	GZX1004	Snow	ТТ	ТТ	Chimelong Safari Park China Dong GX	captive	F	RAD-sea for white
CZZJ031 Snow TT TT Chimelong Safai Park, Chima, Dong GX captive F RAD-seq for white GZZJ033 Snow TT TT Chimelong Safai Park, Chima, Dong GX captive W WGS for wideband & white GZZJ035 Snow TT TT Chimelong Safai Park, Chima, Dong GX captive W WGS for wideband Schard Ander Schard	GZX1006	Snow	TT	TT	Chimelong Safari Park, China, Dong GX	captive	F	RAD-seq for white
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CZZ103 Snow TT TT Chimelong Safai Park, Chima, Dong GX captive M WGS for widehoud & white CZZ1035 Snow TT TT Chimelong Safai Park, Chima, Dong GX captive M RAD-seq for widehoud GZX1035 Snow TT TT Chimelong Safai Park, Chima, Dong GX captive M RAD-seq for widehoud GZX1037 Snow TT TT Chimelong Safai Park, Chima, Dong GX captive M RAD-seq for widehoud GZX1047 Snow TT TT Chimelong Safai Park, Chima, Dong GX captive M RAD-seq for widehoud GZX1045 Snow TT TT Chimelong Safai Park, Chima, Dong GX captive M RAD-seq for widehoud GZX1047 Snow TT TT Tig Preserve Myrte Reach, USA, Andte B captive M individual for validation Iayta Snow TT TT Tig Preserve Myrte Reach, USA, Andte B captive M individual for validation Iayta Snow TT TT Tig Preserve Myrte Reach, USA, Andte B captive M individual for validation Snow TT TT Tig Preserve Myrte Reach, USA, Andte B captive M individual for validation Snawari Snow TT TT Ti	GZX1032	Snow	TT	TT	Chimelong Safari Park, China, Dong GX	captive	F	RAD see for white
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022003 Show TT TT Chimelong Safari Park, China, Dong GX captive MRAD-seq for wideband 0220037 Snow TT TT Chimelong Safari Park, China, Dong GX captive F RAD-seq for wideband 0220037 Snow TT TT Chimelong Safari Park, China, Dong GX captive F RAD-seq for wideband 0220037 Snow TT TT Chimelong Safari Park, China, Dong GX captive MRAD-seq for wideband 0220037 Snow TT TT Chimelong Safari Park, China, Dong GX captive MRAD-seq for wideband 0220037 Snow TT TT Chimelong Safari Park, China, Dong GX captive MRAD-seq for wideband 0220037 Snow TT TT Tiger Preserve Myrile Beach, USA, Antle B captive Maividual for validation Namkar Snow TT TT Tiger Preserve Myrile Beach, USA, Antle B captive Minividual for validation Sinhakar Snow TT TT Tiger Preserve Myrile Beach, USA, Antle B captive Minividual for validation Sinhakar Snow TT TT Tiger Preserve Myrile Beach, USA, Antle B captive Minividual for validation	GZX1025	Snow	11 TT		Chimelong Safari Park, China, Dong CX	captive	M	WGS for wideband & white
D2-D039 July 11 11 Chimelong Safari Park, China, Dong GX captive F RAD-seq for widehand GZX1033 Snow TT TT Chimelong Safari Park, China, Dong GX captive F RAD-seq for widehand GZX1043 Snow TT TT Chimelong Safari Park, China, Dong GX captive F RAD-seq for widehand GZX1043 Snow TT TT Chimelong Safari Park, China, Dong GX captive F RAD-seq for widehand GZX1045 Snow TT TT Trimelong Safari Park, China, Dong GX captive F individual for validation Amar Snow TT TT Triger Preserve Myrtle Beach, USA, Antle B captive F individual for validation Anars Snow TT TT Triger Preserve Myrtle Beach, USA, Antle B captive F individual for validation Snarasvati Snow TT TT Triger Preserve Myrtle Beach, USA, Antle B captive F individual for validation Sinhad Snow TT TT Triger Preserve Myrtle Beach, USA, Antle B captive F	0ZAJ033	Show	11 TT		China Lana Cafari Darla China, Dong CX	captive	IVI M	PAD and for wideband & while
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GZX1045 Snow 11 11 Chimelong Safari Park, China, Dong GX captive RAD-seq for wideband GZX1047 Snow TT TT Chimelong Safari Park, China, Dong GX captive RAD-seq for wideband GZX1047 Snow TT TT Chimelong Safari Park, China, Dong GX captive RAD-seq for wideband GZX1048 Snow TT TT Chimelong Safari Park, China, Dong GX captive RAD-seq for wideband Joyti Snow TT TT Tiger Preserve Myrtle Beach, USA, Antle B captive individual for validation Joyti Snow TT TT Tiger Preserve Myrtle Beach, USA, Antle B captive individual for validation Sinabad Snow TT TT Tiger Preserve Myrtle Beach, USA, Antle B captive individual for validation Sinabad Snow TT TT Tiger Preserve Myrtle Beach, USA, Antle B captive individual for validation GZX0001 White CT TT Tiger Preserve Myrtle Beach, USA, Antle B captive individual for validation GZX0002 White CT TT Tig	GZXJ037	Snow			Chimelong Safari Park, China, Dong GX	captive	F	RAD-seq for <i>wiaebana</i>
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GZXJ048 Snow T1 TT Chimelong Safar Park, China, Dong GX captive R AD-seq for wideband Amar Snow TT TT Chimelong Safar Park, China, Dong GX captive R AD-seq for wideband Joyti Snow TT TT Tiger Preserve Myrtle Beach, USA, Antle B captive F individual for validation Raksha Snow TT TT Tiger Preserve Myrtle Beach, USA, Antle B captive F individual for validation Saraswati Snow TT TT Tiger Preserve Myrtle Beach, USA, Antle B captive F individual for validation Saraswati Snow TT TT Tiger Preserve Myrtle Beach, USA, Antle B captive F individual for validation Simbad Snow TT TT Tiger Preserve Myrtle Beach, USA, Antle B captive F individual for validation Simbad Snow TT TT Tiger Preserve Myrtle Beach, USA, Antle B captive F individual for validation Simbad Snow TT TT Tiger Preserve Myrtle Beach, USA, Antle B captive F individual for validation Sundri Snow TT TT Tiger Preserve Myrtle Beach, USA, Antle B captive F individual for validation GZX1000 White CT TT Chimelong Safari Park, China, Dong GX captive F individual for validation GZX1000 White CC TT Chimelong Safari Park, China, Dong GX captive F individual for validation GZX1000 White CC TT Chimelong Safari Park, China, Dong GX captive M RAD-seq for wideband GZX1000 White CC TT Chimelong Safari Park, China, Dong GX captive M individual for validation GZX1010 White CC TT Chimelong Safari Park, China, Dong GX captive M individual for validation GZX1010 White CC TT Chimelong Safari Park, China, Dong GX captive M individual for validation GZX1010 White CC TT Chimelong Safari Park, China, Dong GX captive M individual for validation GZX1010 White CC TT Chimelong Safari Park, China, Dong GX captive F RAD-seq for wideband GZX1014 White CT TT Chimelong Safari Park, China, Dong GX captive F RAD-seq for wideband GZX1014 White CT TT Chimelong Safari Park, China, Dong GX captive F RAD-seq for wideband GZX1014 White CT TT Chimelong Safari Park, China, Dong GX captive F RAD-seq for wideband GZX1014 White CT TT Chimelong Safari Park, China, Dong GX captive F RAD-seq for wideband GZX101	GZXJ047	Snow	TT	TT	Chimelong Safari Park, China, Dong GX	captive	M	RAD-seq for wideband
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Animal Color (C>1) Owner & Contact Status Sex Note GZZ006 Mile CC T Stanging Zoo, China, Zheng JQ captive F individual for validatio GZX016 Orange CC CC Chinnelong Safari Park, China, Dong GX captive F individual for validatio GZX017 Orange CC CC Chinnelong Safari Park, China, Dong GX captive F individual for validatio GZX0103 Orange CC CC Chinnelong Safari Park, China, Dong GX captive mindividual for validatio GZX0120 Orange CC CC Chinnelong Safari Park, China, Dong GX captive mindividual for validatio GZX0120 Orange CC CC Chinnelong Safari Park, China, Dong GX captive mindividual for validatio GZX0120 Orange CC CC Chinnelong Safari Park, China, Dong GX captive mindividual for validatio GZX0120 Orange CC CC Chinnelong Safari Park, China, Dong GX captive mindividual for validatio GZX0125 Orange CC CC Cri	Animal SHZO06 GZXJ015 GZXJ016 GZXJ017	Color White	$\frac{(C>T)}{CC}$	(C>T)	Owner & Contact	Status	Sex	Note
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YaamOrangeCTCTTiget Tresteve Myrile Beach, USA, Antle BcaptiveMIndividual for validatioYaamOrangeCTCTTiger Preserve Myrile Beach, USA, Antle BcaptiveFindividual for validatioPTIP103OrangeCCCCPeking University, China, Luo SJwildunkindividual for validatioPTIP105OrangeCCCCPeking University, China, Luo SJwildunk'individual for validatioPTIP108OrangeCCCCPeking University, China, Luo SJunk'Mindividual for validatioPTIP118OrangeCCCCPeking University, China, Luo SJwildFindividual for validatioPTIP122OrangeCCCCPeking University, China, Luo SJwildFindividual for validatioPTIP124OrangeCCCCPeking University, China, Luo SJwildFindividual for validatioPTIP124OrangeCCCCPeking University, China, Luo SJwildMindividual for validatioPTIP124OrangeCCCCPeking University, China, Luo SJwildMindividual for validatioPTIP134OrangeCCCCPeking University, China, Luo SJwildFindividual for validatioPTIP152OrangeCCCCPeking University, China, Luo SJwildFindividual for validatioPTIP153OrangeCCCCPeking University, China, Luo SJwild<	Veda	Orange	CT	CT	Tiger Preserve Myrtle Beach, USA, Antle B	captive	Г М	individual for validation
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TameTheoremT	Vana	Orange	CT	CT	Tiger Preserve Myrtle Beach USA Antle B	captive	Г F	individual for validation
PTIP105OrangeCCPeking University, China, Luo SJwildunk individual for validatioPTIP108OrangeCCCCPeking University, China, Luo SJunk individual for validatioPTIP109OrangeCCCCPeking University, China, Luo SJunk'Mindividual for validatioPTIP118OrangeCCCCPeking University, China, Luo SJwildFindividual for validatioPTIP122OrangeCCCCPeking University, China, Luo SJwildFindividual for validatioPTIP123OrangeCCCCPeking University, China, Luo SJwildFindividual for validatioPTIP124OrangeCCCCPeking University, China, Luo SJwildFindividual for validatioPTIP124OrangeCCCCPeking University, China, Luo SJwildMindividual for validatioPTIP124OrangeCCCCPeking University, China, Luo SJwildMindividual for validatioPTIP134OrangeCCCCPeking University, China, Luo SJwildFindividual for validatioPTIP151OrangeCCCCPeking University, China, Luo SJwildFindividual for validatioPTIP153OrangeCCCCPeking University, China, Luo SJwildFindividual for validatioPTIP154OrangeCCCCPeking University, China, Luo SJwildFindividual for validatio <td< td=""><td>PTIP103</td><td>Orange</td><td>CC</td><td>CC</td><td>Peking University China Luo SI</td><td>wild</td><td>unk</td><td>individual for validation</td></td<>	PTIP103	Orange	CC	CC	Peking University China Luo SI	wild	unk	individual for validation
PTIP108OrangeCCCCPeking University, China, Luo SJcaptiveFindividual for validatioPTIP109OrangeCCCCPeking University, China, Luo SJunk'Mindividual for validatioPTIP120OrangeCCCCPeking University, China, Luo SJwildFindividual for validatioPTIP123OrangeCCCCPeking University, China, Luo SJwildFindividual for validatioPTIP124OrangeCCCCPeking University, China, Luo SJwildFindividual for validatioPTIP124OrangeCCCCPeking University, China, Luo SJwildFindividual for validatioPTIP124OrangeCCCCPeking University, China, Luo SJwildMindividual for validatioPTIP124OrangeCCCCPeking University, China, Luo SJwildMindividual for validatioPTIP134OrangeCCCCPeking University, China, Luo SJwildFindividual for validatioPTIP151OrangeCCCCPeking University, China, Luo SJwildFindividual for validatioPTIP152OrangeCCCCCCPeking University, China, Luo SJwildFindividual for validatioPTIP152OrangeCCCCCCPeking University, China, Luo SJwildFindividual for validatioPTIP153OrangeCCCCCCPeking University, China, Luo SJ<	PTIP105	Orange	CC	CC	Peking University, China Luo SI	wild	unk	individual for validation
PTIP109OrangeCCCCPeking University, China, Luo SJunkMindividual for validatioPTIP118OrangeCCCCPeking University, China, Luo SJwildFindividual for validatioPTIP122OrangeCCCCPeking University, China, Luo SJwildFindividual for validatioPTIP123OrangeCCCCPeking University, China, Luo SJwildFindividual for validatioPTIP124OrangeCCCCPeking University, China, Luo SJwildMindividual for validatioPTIP126OrangeCCCCPeking University, China, Luo SJwildMindividual for validatioPTIP126OrangeCCCCPeking University, China, Luo SJwildMindividual for validatioPTIP134OrangeCCCCPeking University, China, Luo SJwildFindividual for validatioPTIP151OrangeCCCCPeking University, China, Luo SJwildMindividual for validatioPTIP157OrangeCCCCPeking University, China, Luo SJwildMindividual for validatioPTIP160OrangeCCCCPeking University, China, Luo SJwildMindividual for validatioPTIP157OrangeCCCCPeking University, China, Luo SJwildMindividual for validatioPTIP160OrangeCCCCCCPeking University, China, Luo SJwildM <td>PTIP108</td> <td>Orange</td> <td>CC</td> <td>ČČ</td> <td>Peking University, China, Luo SI</td> <td>captive</td> <td>F</td> <td>individual for validation</td>	PTIP108	Orange	CC	ČČ	Peking University, China, Luo SI	captive	F	individual for validation
PTIP118OrangeCCCCPeking University, China, Luo SJwildFindividual for validatioPTIP122OrangeCCCCPeking University, China, Luo SJwildFindividual for validatioPTIP123OrangeCCCCPeking University, China, Luo SJwildFindividual for validatioPTIP124OrangeCCCCPeking University, China, Luo SJwildFindividual for validatioPTIP126OrangeCCCCPeking University, China, Luo SJwildMindividual for validatioPTIP134OrangeCCCCPeking University, China, Luo SJwildMindividual for validatioPTIP134OrangeCCCCPeking University, China, Luo SJwildFindividual for validatioPTIP151OrangeCCCCPeking University, China, Luo SJwildFindividual for validatioPTIP153OrangeCCCCPeking University, China, Luo SJwildFindividual for validatioPTIP150OrangeCCCCPeking University, China, Luo SJwildFindividual for validatioPTIP150OrangeCCCCPeking University, China, Luo SJwildFindividual for validatioPTIP150OrangeCCCCPeking University, China, Luo SJwildFindividual for validatioPTIP150OrangeCCCCCPeking University, China, Luo SJwildF <td>PTIP109</td> <td>Orange</td> <td>ČČ</td> <td>ČČ</td> <td>Peking University, China, Luo SJ</td> <td>unk</td> <td>M</td> <td>individual for validation</td>	PTIP109	Orange	ČČ	ČČ	Peking University, China, Luo SJ	unk	M	individual for validation
PTIP122OrangeCCCCPeking University, China, Luo SJwildFindividual for validatioPTIP123OrangeCCCCPeking University, China, Luo SJwildFindividual for validatioPTIP124OrangeCCCCPeking University, China, Luo SJwildFindividual for validatioPTIP126OrangeCCCCPeking University, China, Luo SJwildMindividual for validatioPTIP126OrangeCCCCPeking University, China, Luo SJwildMindividual for validatioPTIP146OrangeCCCCPeking University, China, Luo SJwildFindividual for validatioPTIP146OrangeCCCCPeking University, China, Luo SJwildFindividual for validatioPTIP151OrangeCCCCPeking University, China, Luo SJwildFindividual for validatioPTIP152OrangeCCCCPeking University, China, Luo SJwildFindividual for validatioPTIP153OrangeCCCCPeking University, China, Luo SJwildFindividual for validatioPTIP154OrangeCCCCPeking University, China, Luo SJwildFindividual for validatioPTIP154OrangeCCCCPeking University, China, Luo SJwildFindividual for validatioPTIP159OrangeCCCCPeking University, China, Luo SJwildKindiv	PTIP118	Orange	CC	CC	Peking University, China, Luo SJ	wild	F	individual for validation
PTIP123OrangeCCCCPeking University, China, Luo SJwildFindividual for validatioPTIP124OrangeCCCCPeking University, China, Luo SJwildFindividual for validatioPTIP126OrangeCCCCPeking University, China, Luo SJwildMindividual for validatioPTIP127OrangeCCCCPeking University, China, Luo SJwildMindividual for validatioPTIP134OrangeCCCCPeking University, China, Luo SJwildFindividual for validatioPTIP151OrangeCCCCPeking University, China, Luo SJunkMindividual for validatioPTIP152OrangeCCCCPeking University, China, Luo SJwildFindividual for validatioPTIP153OrangeCCCCPeking University, China, Luo SJwildMindividual for validatioPTIP154OrangeCCCCPeking University, China, Luo SJwildMindividual for validatioPTIP154OrangeCCCCPeking University, China, Luo SJwildFindividual for validatioPTIP159OrangeCCCCPeking University, China, Luo SJwildFindividual for validatioPTIP164OrangeCCCCPeking University, China, Luo SJwildMindividual for validatioPTIP159OrangeCCCCPeking University, China, Luo SJunkMindivid	PTIP122	Orange	CC	CC	Peking University, China, Luo SJ	wild	F	individual for validation
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PTIP170OrangeCCCCPeking University, China, Luo SJunkMIndividual for validatioPTIP170OrangeCCCCPeking University, China, Luo SJwildMindividual for validatioPTIP173OrangeCCCCPeking University, China, Luo SJunkMindividual for validatioPTIP174OrangeCCCCPeking University, China, Luo SJunkMindividual for validatioPTIP176OrangeCCCCPeking University, China, Luo SJunkMindividual for validatioPTIP178OrangeCCCCPeking University, China, Luo SJunkMindividual for validatioPTIP179OrangeCCCCPeking University, China, Luo SJunkunkindividual for validatioPTIP184OrangeCCCCPeking University, China, Luo SJunkunkindividual for validatioPTIP186OrangeCCCCPeking University, China, Luo SJunkunkindividual for validatioPTIP217OrangeCCCCPeking University, China, Luo SJunkunkindividual for validatioPTIP218OrangeCCCCPeking University, China, Luo SJcaptiveMindividual for validatioPTIP220OrangeCCCCPeking University, China, Luo SJcaptiveMindividual for validatioPTIP2220OrangeCCCCPeking University, China, Luo SJcaptiveF	PTIP164	Orange		CC	Peking University, China, Luo SJ	unk	M	individual for validation
PTIP173OrangeCCCCPeking University, China, Luo SJwildMindividual for validationPTIP173OrangeCCCCPeking University, China, Luo SJunkMindividual for validationPTIP174OrangeCCCCPeking University, China, Luo SJunkMindividual for validationPTIP176OrangeCCCCPeking University, China, Luo SJunkMindividual for validationPTIP178OrangeCCCCPeking University, China, Luo SJunkMindividual for validationPTIP179OrangeCCCCPeking University, China, Luo SJunkunkindividual for validationPTIP184OrangeCCCCPeking University, China, Luo SJunkunkindividual for validationPTIP186OrangeCCCCPeking University, China, Luo SJunkunkindividual for validationPTIP217OrangeCCCCPeking University, China, Luo SJunkunkindividual for validationPTIP218OrangeCCCCPeking University, China, Luo SJcaptiveMindividual for validationPTIP220OrangeCCCCPeking University, China, Luo SJcaptiveMindividual for validationPTIP222OrangeCCCCPeking University, China, Luo SJcaptiveMindividual for validationPTIP2220OrangeCCCCPeking University, China, Luo SJcaptiv	PTIP170	Orange	CC	CC	Peking University, China, Luo SI	wild	M	individual for validation
PTIP174OrangeCCCCPeking University, China, Luo SJunkIndividual for validationPTIP174OrangeCCCCPeking University, China, Luo SJwildMindividual for validationPTIP176OrangeCCCCPeking University, China, Luo SJunkMindividual for validationPTIP178OrangeCCCCPeking University, China, Luo SJunkMindividual for validationPTIP179OrangeCCCCPeking University, China, Luo SJunkunkindividual for validationPTIP184OrangeCCCCPeking University, China, Luo SJunkunkindividual for validationPTIP185OrangeCCCCPeking University, China, Luo SJunkunkindividual for validationPTIP217OrangeCCCCPeking University, China, Luo SJunkunkindividual for validationPTIP218OrangeCCCCPeking University, China, Luo SJcaptiveMindividual for validationPTIP220OrangeCCCCPeking University, China, Luo SJcaptiveMindividual for validationPTIP220OrangeCCCCPeking University, China, Luo SJcaptiveFindividual for validationPTIP2220OrangeCCCCPeking University, China, Luo SJcaptiveFindividual for validationPTIP2220OrangeCCCCPeking University, China, Luo SJcaptive <td>PTIP173</td> <td>Orange</td> <td>CC</td> <td>CC</td> <td>Peking University, China Luo SI</td> <td>unk</td> <td>M</td> <td>individual for validation</td>	PTIP173	Orange	CC	CC	Peking University, China Luo SI	unk	M	individual for validation
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PTIP179OrangeCCCCPeking University, China, Luo SJwildunkindividual for validationPTIP184OrangeCCCCPeking University, China, Luo SJunkFindividual for validationPTIP185OrangeCCCCPeking University, China, Luo SJunkunkindividual for validationPTIP186OrangeCCCCPeking University, China, Luo SJunkunkindividual for validationPTIP217OrangeCCCCPeking University, China, Luo SJcaptiveMindividual for validationPTIP218OrangeCCCCPeking University, China, Luo SJcaptiveMindividual for validationPTIP220OrangeCCCCPeking University, China, Luo SJcaptiveMindividual for validationPTIP220OrangeCCCCPeking University, China, Luo SJcaptiveFindividual for validation	PTIP178	Orange	ĊĊ	CC	Peking University, China, Luo SJ	unk	unk	individual for validation
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PTIP186OrangeCCCCPeking University, China, Luo SJunkunkindividual for validationPTIP217OrangeCCCCPeking University, China, Luo SJcaptiveMindividual for validationPTIP218OrangeCCCCPeking University, China, Luo SJcaptiveMindividual for validationPTIP220OrangeCCCCPeking University, China, Luo SJcaptiveMindividual for validationPTIP222OrangeCCCCPeking University, China, Luo SJcaptiveFindividual for validationPTIP222OrangeCCCCPeking University, China, Luo SJcaptiveFindividual for validation	PTIP185	Orange	CC	CC	Peking University, China, Luo SJ	unk	unk	individual for validation
PTIP217OrangeCCCCPeking University, China, Luo SJcaptiveMindividual for validationPTIP218OrangeCCCCPeking University, China, Luo SJcaptiveMindividual for validationPTIP220OrangeCCCCPeking University, China, Luo SJcaptiveMindividual for validationPTIP222OrangeCCCCPeking University, China, Luo SJcaptiveFindividual for validationPTIP222OrangeCCCCPeking University, China, Luo SJcaptiveFindividual for validation	PTIP186	Orange	CC	CC	Peking University, China, Luo SJ	unk	unk	individual for validation
PTIP218 Orange CC CC Peking University, China, Luo SJ captive M individual for validation PTIP220 Orange CC CC Peking University, China, Luo SJ captive F individual for validation PTIP222 Orange CC CC Peking University, China, Luo SJ captive F individual for validation PTIP222 Orange CC CC Peking University, China, Luo SJ captive F individual for validation	PTIP217	Orange	CC	CC	Peking University, China, Luo SJ	captive	Μ	individual for validation
PTIP220 Orange CC CC Peking University, China, Luo SJ captive F individual for validation	PTIP218	Orange	CC	CC	Peking University, China, Luo SJ	captive	М	individual for validation
DTID222 Orange CC CC Daline University Chine I of C	PTIP220	Orange	CC	CC	Peking University, China, Luo SJ	captive	F	individual for validation
r in 222 Grange CC CC Pering University, China, Luo SJ captive M individual for validation	PTIP222	Orange	CC	CC	Peking University, China, Luo SJ	captive	М	individual for validation
PTIP226 Orange CC CC Peking University, China, Luo SJ unk M individual for validation	PTIP226	Orange	CC	CC	Peking University, China, Luo SJ	unk	Μ	individual for validation
PTIP24 Orange CC CC Peking University, China, Luo SJ captive F individual for validation	PTIP24	Orange	CC	CC	Peking University, China, Luo SJ	captive	F	individual for validation
PTIP241 Orange CC CC Peking University, China, Luo SJ unk F individual for validation	PTIP241	Orange	CC	CC	Peking University, China, Luo SJ	unk	F	individual for validation
PTIP242 Orange CC CC Peking University, China, Luo SJ unk unk individual for validation	PTIP242	Orange			Peking University, China, Luo SJ	unk	unk	individual for validation
PTIP244 Orange CC CC Peking University, China, Luo SJ Unk M individual for validation	r11P244 DT1D247	Orange			Peking University, Unina, Luo SJ Daking University, China, Luc SJ	unk	IVI E	individual for validation
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PTIP250 Orange CC CC Deking University China Luo SJ Captive M individual for Validation	1 111240 DTID250	Orange			Peking University, China, Luo SJ	wild	IVI F	individual for validation
PTIP253 Orange CC CC Peking University China Luo SJ WIIU F Individual for validation	PTIP252	Orange	CC		Peking University, China Luo SJ	cantive	F	individual for validation
PTIP253 Orange CC CC Peking University China Luo SJ Captive I individual for validation	PTIP254	Orange	CC	CC	Peking University, China Luo SJ	captive	M	individual for validation
PTIP256 Orange CC CC Peking University China Luo SI captive F individual for validation	PTIP256	Orange	CC	CC	Peking University, China Luo SJ	captive	F	individual for validation
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PTIP257OrangeCCCCPeking University, China, Luo SJcaptiveMindividual for validationPTIP258OrangeCCCCPeking University, China, Luo SJcaptiveMindividual for validation	PTIP257 PTIP258	Orunze			, ====, === , === , == , == , == ,	r	-	ioi · andunon

		CORIN	SLC45A2		Birth		
Animal	Color	(C>T)	(C>T)	Owner & Contact	Status	Sex	Note
PTIP263	Orange	CC	CC	Peking University, China, Luo SJ	wild	М	individual for validation
PTIP264	Orange	CC	CC	Peking University, China, Luo SJ	wild	F	individual for validation
PTIP269	Orange	CC	CC	Peking University, China, Luo SJ	captive	F	individual for validation
PTIP271	Orange	CC	CC	Peking University, China, Luo SJ	wild	М	individual for validation
PTIP272	Orange	CC	CC	Peking University, China, Luo SJ	captive	F	individual for validation
PTIP273	Orange	CC	CC	Peking University, China, Luo SJ	captive	F	individual for validation
PTIP274	Orange	CC	CC	Peking University, China, Luo SJ	captive	F	individual for validation
PTIP276	Orange	CC	CC	Peking University, China, Luo SJ	unk	М	individual for validation
PTIP279	Orange	CC	CC	Peking University, China, Luo SJ	captive	F	individual for validation
PTIP282	Orange	CC	CC	Peking University, China, Luo SJ	captive	F	individual for validation
PTIP283	Orange	CC	CC	Peking University, China, Luo SJ	unk	М	individual for validation
PTIP285	Orange	CC	CC	Peking University, China, Luo SJ	captive	F	individual for validation
PTIP286	Orange	CC	CC	Peking University, China, Luo SJ	captive	F	individual for validation
PTIP288	Orange	CC	CC	Peking University, China, Luo SJ	captive	F	individual for validation
PTIP293	Orange	ČČ	ČČ	Peking University, China, Luo SJ	unk	F	individual for validation
PTIP296	Orange	CC	ĊĊ	Peking University, China, Luo SI	wild	M	individual for validation
PTIP300	Orange	CC	ČČ	Peking University, China, Luo SI	wild	M	individual for validation
PTIP301	Orange	CC	ČČ	Peking University, China, Luo SI	unk	F	individual for validation
PTIP302	Orange	CC	ČČ	Peking University China Luo SI	unk	M	individual for validation
PTIP303	Orange	CC	ČČ	Peking University China Luo SI	captive	M	individual for validation
PTIP305	Orange	CC	CC	Peking University, China Luo SI	unk	F	individual for validation
PTIP306	Orange	CC	CC	Peking University, China, Luo SJ	wild	M	individual for validation
PTIP307	Orange	CC	CC	Peking University, China Luo SJ	wild	M	individual for validation
PTIP309	Orange	CC	CC	Peking University, China Luo SJ	unk	F	individual for validation
PTIP310	Orange	CC	CC	Peking University, China, Luo SJ	wild	F	individual for validation
PTIP311	Orange	CC	CC	Peking University, China, Luo SJ	unk	M	individual for validation
PTIP312	Orange	CC	CC	Peking University, China, Luo SJ	unk	E	individual for validation
PTIP313	Orange	CC	CC	Peking University, China, Luo SJ	unk	M	individual for validation
DTID315	Orange	CC		Peking University, China, Luo SJ	wild	M	individual for validation
DTID316	Orange			Peking University, China, Luo SJ	wnu	unk	individual for validation
DTID220	Orange		CC	Deking University, China, Luo SJ	antivo	M	individual for validation
F 11F 320 DT1D227	Orange		CC	Peking University, China, Luo SJ	unk	wi	individual for validation
F 11F 327	Orange		CC	Petring University, China, Luo SJ	unk	unk	individual for validation
F 11F 330	Orange		CC	Peking University, China, Luo SJ	unk	unk	individual for validation
	Orange		CC	Peking University, China, Luo SJ	unk	unk	individual for validation
F 11F 332	Orange		CC	Petring University, China, Luo SJ	unk	M	individual for validation
PTIP30	Orange			Peking University, China, Luo SJ	unk	M	individual for validation
PTIP56	Orange	CC		Peking University, China, Luo SJ	unk 1	M	individual for validation
PTIP05	Orange			Peking University, China, Luo SJ	unk	M E	
PTIP70	Orange			Peking University, China, Luo SJ	unk	Г	individual for validation
PTIP/2	Orange			Peking University, China, Luo SJ	unk	M	individual for validation
PTIP83	Orange			Peking University, China, Luo SJ	unk	F	individual for validation
PTIP84	Orange			Peking University, China, Luo SJ	unk	F	individual for validation
PTIP88	Orange			Peking University, China, Luo SJ	unk	M	individual for validation
PTIP99	Orange			Peking University, China, Luo SJ	unk	F M	individual for validation
SHZOOI	Orange	CC		Shanghai Zoo, China, Zheng JQ	captive	M	individual for validation
SHZO02	Orange	CC	CC	Shanghai Zoo, China, Zheng JQ	captive	M	individual for validation
SHZO03	Orange	CC	CC	Shanghai Zoo, China, Zheng JQ	captive	M	individual for validation
SHZO04	Orange	CC	CC	Shanghai Zoo, China, Zheng JQ	captive	М	individual for validation

1. unk = unknown

Table S2. Primers for PCR amplification and Sanger sequencing.	

Gene and	Amplicon			
Amplicon	size (bp)	Forward primer (5' to 3')	Reverse primer (5' to 3')	Reference
	100			
MCIR-ex-a	429	CATTGTGCCTGAGCTGACAT	GTCTCCAGCACACTGCTCAC	Xu et al. (2013)
MC1R-ex-b	399	CTGCACTCGCCCATGTATTA	CACCAGCATGGCTACAAAGA	Xu <i>et al</i> . (2013)
MC1R-ex-c	472	TCGCCTACTACGATCACACG	GCCATAGGATATCCCCACCT	Xu <i>et al</i> . (2013)
ASIP-ex1	418	TCATCAGTTCCCCTTTCCTG	GGGAGCACGTTTGACATCTT	Xu et al. (2013)
ASIP-ex2	348	CTCTTCTCCCACACCCTGAG	CCCTTAGCTCTCTGGGCTTC	Xu et al. (2013)
ASIP-ex3	450	AGAGTTCCCAAGGCTGAGGT	AAATGCAAGAAAGCCACACC	Xu et al. (2013)
TYR-ex1-a	366	GCAGGAGAGATGCAGAGGAG	TTGGAGGGTCTGAAATCTGG	Xu et al. (2013)
TYR-ex1-b	386	TGTTCCCACAGCAACAAGAA	TTTGGCAACTTCATGGGATT	Xu et al. (2013)
TYR-ex1-c	371	TCGCTTCTCTGTGCAGTTTG	GATCCGTGAAGACGAGGGTA	Xu et al. (2013)
TYR-ex2	310	CATGATTCAGAAAAACAGAAGAAA	TCTCTAGCCACAACTCCTTTAACA	Xu et al. (2013)
TYR-ex3	356	TTTGCCTCCAACTCCTTACG	TTTCAACTACCAGGGCCAAC	Xu et al. (2013)
TYR-ex4	298	TTGGCATCCTTCCATGTCTT	GGCTTTGGGGGATAGCATTGT	Xu et al. (2013)
TYR-ex5	423	TAGCAGAGCTGGCATTCAAA	AAAATGAGGTCAACCTTGTTGG	Xu et al. (2013)
TYRP1-ex1	399	GGGAAGGGAATCATGTGCTA	CATTCGTTAGCAGGTCATGG	Xu et al. (2013)
TYRP1-ex2	511	TGCCATTTTGCTTTCTCCTT	TGTACATGCAGATCCCCACT	Xu et al. (2013)
TYRP1-ex3	399	GTGGCACATTTTCACGTTTG	CTGTCGGGGACCTGAAAAG	Xu et al. (2013)
TYRP1-ex4	355	CAGGGAGAAAACCAAGCAAA	TGAGGACTTTCAGACAGCACA	Xu et al. (2013)
TYRP1-ex5	249	TTCTGTAAGTGTTCCTATACCCTGT	TGTGACAACTAGATAAAATCAAAGCA	Xu et al. (2013)
TYRP1-ex6	289	AGACATTGGCAACGGTTTTC	CCATACCACCTGAACGGTCT	Xu et al. (2013)
TYRP1-ex7	217	TTAACAAGATGTCTTTGGCATATTT	TTTTGGTAATTTCCACAGAAAAGA	Xu et al. (2013)
TYRP1-ex8	250	TGTTCTCCTTTTGTTTTTCACAG	CAGAGAATTGGTCGTTTGTCA	Xu et al. (2013)
SLC45A2-ex7	288	TGTTCCTGTGTTTCCCTTGC	CCCTTCACTGTGTTGGAGGT	Xu et al. (2013)
Corin-ex13	214	TGCTTCCAGGTTTTCTGTCC	TCCTAGCCAGGCATTAACGTA	this study
Corin-cds	3311	GAGGAGCAAGTCGTCCGTAG	GGAAGCACTCCACAGTCAAA	this study

	Raw bases	Unique mapped	Unique mapped	WGS Seq depth (unique	Unique mapped read pairs	No. PstI	<i>Pst</i> I coverage	<i>Pst</i> I site coverage		
Sample ID	(Gb)	(Gb)	ratio	maps)	(M)	sites ¹	ratio	depth ²	SNP count ³	SNP ratio
RAD-sea										
GZXJ036	7.270	4.142	56.97%	n/a	21.395	671,459	90.80%	14.466	626.233	70.64%
GZXJ037	4.495	2.634	58.60%	n/a	13.597	656,863	88.82%	9.193	468,226	52.81%
GZXJ046	4.634	3.579	77.23%	n/a	18.462	689,209	93.20%	12.482	645,676	72.83%
GZXJ047	5.255	4.065	77.36%	n/a	20.977	685,594	92.71%	14.183	667,337	75.27%
GZXJ048	4.753	3.705	77.95%	n/a	19.113	684,725	92.59%	12.923	631,050	71.18%
GZXJ050	3.537	2.739	77.43%	n/a	14.185	665,320	89.97%	9.591	530,173	59.80%
GZXJ007	3.992	3.078	77.08%	n/a	15.916	686,072	92.77%	10.761	595,826	67.21%
GZXJ008	3.864	2.986	77.28%	n/a	15.428	657,450	88.90%	10.431	581,613	65.60%
GZXJ040	3.866	2.980	77.07%	n/a	15.408	660,228	89.28%	10.418	559,905	63.15%
GZXJ041	3.844	2.992	77.84%	n/a	15.466	678,701	91.78%	10.457	580,632	65.49%
GZXJ042	4.270	3.315	77.62%	n/a	17.108	675,690	91.37%	11.567	610,789	68.89%
GZXJ043	4.833	3.739	77.36%	n/a	19.285	690,705	93.40%	13.039	649,919	73.31%
GZXJ044	4.613	3.553	77.02%	n/a	18.331	670,745	90.70%	12.394	650,634	73.39%
GZXJ045	4.315	3.355	77.76%	n/a	17.298	665,133	89.94%	11.696	631,453	71.22%
GZXJ049	4.659	3.619	77.67%	n/a	18.666	685,771	92.73%	12.621	643,323	72.56%
GZXJ051	2.038	1.624	79.68%	n/a	8.398	617,060	83.44%	5.678	356,051	40.16%
Average	4.390	3.256	75.12%	n/a	16.815	671,295	90.77%	11.369	589,303	66.47%
Total	70.239	52.103	74.18%	n/a	269.034	739,518	100%	181.898	886,564	100%
WGS										
GZXJ034	85.036	74.027	87.05%	30.558						
GZXJ035	78.945	70.798	89.68%	29.608						
GZXJ039	82.319	74.385	90.36%	31.108						
Average	82.100	73.07	89.03%	30.558						

Table S3. Summary of RAD-seq and WGS in 19 tigers for GWAS.

1. A *PstI* site was counted only when both upstream and downstream of the site were covered by the P1 reads of RADSeq data. 2. *PstI* site coverage depth was calculated by uniquely mapped read pairs divided by number of PstI sites.

3. A SNP was counted only when data was available from 6 samples and exhibited polymorphism among the samples.

Table S4. Genes located within the 9.2 Mb region associated with the WB locus

Scaffold	start	end	Gene	Description
scaffold1457	1702057	1714742	OCIAD2	OCIA domain containing 2.
scaffold1457	1723169	1748562	OCIAD1	OCIA domain containing 1.
scaffold1457	1758261	1758548	RPS21	Ribosomal protein S21.
scaffold1457	1907736	2054288	FRYL	FRY-like.
scaffold1457	2059201	2061054	ZAR1	Zygote arrest 1, the maternal effect gene is oocyte-specific and encodes a protein that is thought to function in the initiation of embryogenesis.
scaffold1457	2064914	2069943	SLC10A4	Solute carrier family 10, member 4.
scaffold1457	2136797	2174285	SLAIN2	SLAIN motif family, member 2
scaffold1457	2303541	2391690	TEC	The protein encoded by this gene belongs to the Tec family of non-receptor protein-tyrosine kinases containing a pleckstrin homology domain.
scaffold1457	2413405	2455308	TXK	TXK tyrosine kinase.
scaffold1457	2474274	2499970	NIPAL1	NIPA-like domain containing 1
scaffold1457	2531986	2552038	CNGA1	The protein encoded by this gene is involved in phototransduction.
scaffold1457	2567931	2635094	NFXL1	Nuclear transcription factor, X-box binding-like 1.
scaffold1457	2643215	2892269	CORIN	CORIN, a serine protease, regulates blood pressure by converting pro-ANP to active ANP, and modifys pigmentation through agouti pathway.
scaffold1457	2896348	2972767	ATP10D	ATPase, Class V, Type 10D.
scaffold1457	3024887	3032276	COMMD8	COMM domain containing 8.
scaffold1457	3053059	3152623	GABRB1	GABRB1 is a member of the GABA-A receptor gene family of heteromeric pentameric ligand-gated ion channels.
scaffold1457	3457791	3522485	GABRA4	GABRA4 is a member of the GABA-A receptor gene family of heterometric ligand-gated ion channels
scaffold1457	3695631	3695858	COX7B2	Cytochrome c oxidase subunit VIIb2
scaffold1457	3718243	3719410	AMDI	This gene encodes an important intermediate enzyme (adenosylmethionine decarboxylase 1) in polyamine biosynthesis.
scatfold1457	3957480	4080396	GABRA2	GABRA2 is a member of the GABAA receptor gene family of heteromeric pentameric ligand-gated ion channels.
scatfold1457	4180616	4245668	GABRGI	GABRGI is a member of the GABA-A receptor gene family of heteromeric pentameric ligand-gated ion channels.
scatfold1457	5191460	5191870	AHCY	This gene encodes adenosylhomocystemase, which regulates the intracellular S-adenosylhomocysteme (SAH) concentration thought to be important for transmethylation reactions.
scatfold1457	5247021	5247604	PFNI	This gene encodes a member of the profilin family of small actin-binding profeins. The encoded profein plays an important role in actin dynamics by regulating actin polymerization in response to extracellular signals.
scaffold145/	5313895	5340309	GNPDA2	Glucosamine-o-phosphate deaminase 2 is an allosteric enzyme that catalyzes the reversible reaction converting D-glucosamine-o-phosphate into D-fructose-o-phosphate and ammonium.
scaffold145/	5344182	5365639	GUFI	GUPI GIPase nomolog.
scaffold145/	5387429	5411941		Yipi domain family, member 7.
scarrold1457	5499902	59500279	CALMI	Insigence encodes a memoer of the Er-nand calcium-binding protein family.
scarrold145/	5001425	5852257	CDVCD1	Potassium channel tetrametrzation domain containing 8
scarrold9/	5//5555	5901979	GRACKI MDDL 42	In is gene encodes a protein which contains GKX-like domains; these domains play a role in the 5-glutationylation of proteins and may be involved in actin organization in hair cents.
scarfold9/	5267250	5550087	MKPL42	Milocononriai ribosomai protein L42.
scalfold97	5255011	5255451	SUISA2	Air ase, annuopius phonpiu dansporter (AFLI), class 1, type 6A, include 1.
scaffold07	5105008	5108111	TOMILI	Suits a family internor 5. TOMUL belonge to a family of TOM1 (604700) related proteins involved in andocytosis
scaffold97	5127140	5151148	REND4	Town in outpains of a family of Town (out 700)-foliated proteins involved in endocytosis. BEN domain containing 4
scaffold97	5027882	5083207	SLC3049	Solute exercise family 30 (zinc transporter) member 9
scaffold97	4965341	4984434	TMFM33	Transmersen protein 33
scaffold97	4799268	4801620	PHOX28	Principle homeobox 25 functions as a transcription factor involved in the development of several major noradrenergic neuron populations and the determination of neurotransmitter phenotype
scaffold97	4543535	4743582	LIMCHI	I III and calonin homology domains 1
scaffold97	4340395	4353221	UCHL1	The protein encoded by this gene belongs to the pentidase C12 family. This enzyme is a thiol protease that hydrolyzes a pentide bond at the C-terminal glycine of ubiquitin
scaffold97	3921344	4110223	APRR2	The protein encoded by this gene interacts with the cytonlasmic domains of anyloid beta (A) precursor protein and anyloid beta (A4) precursor-like protein 2
scaffold97	3612440	3622668	RBM47	RNA binding molt protein 47.
scaffold97	3543968	3556619	CHRNA9	This gene is a member of the ligand-gated ionic channel family and nicotinic acetylcholine receptor gene superfamily. It encodes a plasma membrane protein that forms homo- or hetero-oligomeric divalent cation channels.
scaffold97	3471842	3472404	RHOH	The protein encoded by this gene is a member of the Ras superfamily of guanosine triphosphate (GTP)-netabolizing enzymes.
scaffold97	3342991	3395241	N4BP2	NEDD4 binding protein 2 can bind to both B-cell leukemia/lymphoma 3 (BCL-3) and neural precursor cell expressed, developmentally downregulated 4, (Nedd4) proteins.
scaffold97	3109775	3237547	PDS5A	The protein encoded by this gene binds to the cohesin complex and associates with chromatin through most of the cell cycle.
scaffold97	2993833	3062282	UBE2K	The protein encoded by this gene belongs to the ubiquitin-conjugating enzyme family. This protein interacts with RING finger proteins, and it can ubiquitinate huntingtin, the gene product for Huntington's disease.
scaffold97	2853674	2894549	SMIM14	Small integral membrane protein 14.
scaffold97	2808961	2825017	UGDH	The protein encoded by this gene converts UDP-glucose to UDP-glucuronate and thereby participates in the biosynthesis of glycosaminoglycans such as hyaluronan, chondroitin sulfate, and heparan sulfate.
scaffold97	2785239	2800594	LIAS	Lipoic acid synthetase, involves in the cell growth.
scaffold97	2780714	2784403	RPL9	Ribosomal protein L9.
scaffold97	2741158	2774128	KLB	Klotho beta is an essential cofactor for FGF21 activity and suggested that the Klotho gene family may have evolved to confer tissue-specific bioactivity on FGF19 (603891) subfamily members.
scaffold97	2643471	2706239	RFC1	This gene encodes the large subunit of replication factor C, a five subunit DNA polymerase accessory protein, which is a DNA-dependent ATPase required for eukaryotic DNA replication and repair.
scaffold97	2534048	2624602	WDR19	This gene encodes a member of the WD repeat protein family. Members of this family are involved in a variety of cellular processes, including cell cycle progression, signal transduction, apoptosis, and gene regulation.
scaffold97	2434396	2499017	KLHL5	Kelch-like family member 5.
scaffold97	2346827	2380860	TMEM156	Transmembrane protein 156.
scaffold97	2255513	2310967	FAM114A1	Family with sequence similarity 114, member A1.
scaffold97	2217896	2220283	TLR6	Toll-like receptor 6 is a member of the Toll-like receptor (TLR) family which plays a fundamental role in pathogen recognition and activation of innate immunity.
scaffold97	2190563	2191732	TLR1	Toll-like receptor 1 is a member of the Toll-like receptor (TLR) family which plays a fundamental role in pathogen recognition and activation of innate immunity.
scaffold97	2163113	2165542	TLR10	Toll-like receptor 10 is a member of the Toll-like receptor (TLR) family which plays a fundamental role in pathogen recognition and activation of innate immunity.
scaffold97	2081886	2098226	KLF3	Kruppel-like factor 3 (basic).
scaffold97	1728297	1728665	RPL41	Ribosomal protein L41.
scaffold97	1429354	1643878	TBC1D1	TBC1D1 is the tounding member of a family of proteins sharing a 180- to 200-amino acid TBC domain presumed to have a role in regulating cell growth and differentiation.

