**Supplemental materials and methods**

***Assay of the PS heme-containing protein***

The relative molecular weights of the heme-containing globin in the PS of plateau zokors were measured by sepharose gel chromatography. Sephadex G-100 (Sigma, USA) was used as a chromatographic packing gel, and blue dextran 2000 (Nanjing Built Biotechnology Co., Ltd.) was used as an indicator molecule. The freeze-dried PS powders (10 mg) of plateau zokors were weighted and mixed with blue dextran 2000 (0.5 mg) and N-acetyl tyrosine ethyl ester saturated solution (0.5 mL) in turn, and then the samples were loaded into the column and eluted using a phosphate buffer of pH 7.4 at a flow rate of 0.4 mL/min. The volume of eluent that was required to make the blue dextran 2000 and red hemoglobin migrate out of the column was regarded as the elution volume of the two kinds of molecules. According to the principles of sepharose gel chromatography, the elution volume of a protein is directly and positively related to the logarithm of its molecular weight. The relative molecular weights of the heme-containing proteins in the PS of plateau zokors were calculated using the following formula: LogMr/Vr = Log2000000/Ve, where Mr is the relative molecular weight of the hemoglobin, Vr is the elution volume of the hemoglobin, and Ve is the elution volume of the blue dextran 2000 molecule.

***Identification of the PS heme-containing protein encoding gene***

*Construction of tree species from mtDNA data*

Complete mitochondrial DNA (mtDNA) sequences for 11 mammalian species were downloaded from the National Center for Biotechnology Information (NCBI) ([www.ncbi.nlm.nih.gov](http://www.ncbi.nlm.nih.gov)) (Table 2). The mtDNA phylogenetic trees were reconstructed using MrBayes 3.2.6 (1). Bayesian inference (BI) with Markov-chain Monte Carlo (MCMC) (2) sampling was performed using MrBayes 3.2.6 run for one million generations. We made two simultaneous runs, sampling trees every 1,000 generations, with three heated and one cold chain to encourage swapping among the MCMC chains and to avoid the analysis remaining in local rather than global optima. jModelTest (3) was used to select the optimal models based on the Akaike Information Criterion (AIC) (4). The convergence of sampled parameters and potential autocorrelation (effective sampling size/ESS for all parameters>200) was investigated in Tracer 1.6 ([http://tree.bio.ed.ac.uk/software/ tracer/](http://tree.bio.ed.ac.uk/software/%20tracer/)). Additionally, the average SD of split frequencies between both runs was checked (<0.01). The Bayesian posterior probabilities were obtained from the 50% majority rule consensus of the post-burn-in trees sampled at stationarity, after removing the first 25% of trees as a “burn-in” stage.

*Phylogenetic relationships of β-globin genes of plateau zokor*

The alignments of the *β*-globin genes by DNA sequencing and genomic annotating were conducted using MAFFT 7.0 (5). Phylogenetic relationships among the *β-*globin genes and the β*-*like globins were inferred using a maximum-likelihood tree-building method. Maximum-likelihood tree searches were conducted using IQ-tree implemented in Phylosuite 1.2.2 (6, 7), and the ModelFinder program was used to estimate the parameters of a TPM3+F+G4 model of nucleotide substitution (8). Measures of bootstrap support were based on 1,000 pseudo-replicates (9). The identity of the *β-*globin genes sequences and β-globin amino acid sequences by DNA sequencing, genomic annotating and detected by MS of plateau zokor were investigated by pairwise analyses of sequence similarity using NDAMAN 9.0, respectively.

*The relationships of the γ and γ-like gene of 11 species*

Sequence alignments were carried out using the program ClustalX 1.81. The relationships of the *γ* gene(*HBG*) and *γ*-like (*HBGlike*) of 11 species described above were analysed by conducting Bayesian inference tree; the method was same as that used for the mtDNA tree. Phylogeny reconstructions were based on the coding sequence, 1 kb of the upstream flanking sequence, 1 kb of the downstream flanking sequence, and intron 2. For analyses based on the 11-mammalian species sequence alignment, we used the HKY+F+G4 model (upstream flanking sequence, intron 2 and downstream flanking sequence) and a TPM3+F+G4 model (exon 1, exon2 and exon3). The homology of the β-globin amino acid sequences of plateau zokor was investigated by pairwise analyses of sequence similarity using NDAMAN 9.0. To root the Bayesian inference tree, the corresponding major aldult *β* globin sequence (*HBB*) of humanwas used as the outgroups.

*Molecular clock*

The coding sequences of the *HBGlike* of plateau zokor and the *HBG* of the11-mammalian species were aligned using MAFFT 7.0. Maximum-likelihood tree of these genes was conducted using the same method described above. To determine the approximate ages of the *γ*-like gene, we estimated the time of divergence between the *γ*-like and *γ* genes using MEGA 7.0 (10). As a calibration point, we used a range of Euarchontoglires-Laurasiatheria divergence times spanning about 85 Mya (11). To root the maximum-likelihood tree, the major aldult *β* globin gene (*HBB*) of humanwas used as the outgroup.

**Expression of γ-likesubunit in ATII, culture solution supernatants, LBs and PS**

*Isolation, purification and culture of ATII*

The lung tissues of plateau zokors and SD rats were perfused intensively with solution I (NaCl 137 mM, KCl 2.7 mM, Na2HPO4 8.1 mM, KH2PO4 1.56 mM, Heparin sodium 12,500 U/mL, pH 7.40). During perfusion, the lungs were inflated with air from the tracheal cannula to total lung capacity (4–5 mL) several times to perfuse the lungs completely and remove the blood. The intact lung was moved carefully and washed in PBS three times. Next, the lung was washed with solution II (solution I plus EDTA-2Na 0.2 mM and EGTA 0.2 mM). A total of 12–15 mL of 0.25% trypsin-EDTA (Gibco, USA) injected continually via the trachea for 20 min at 37°C for three times. Then the trachea and large airways were discarded, each lung was minced with sharp scissors to a final size of 1 mm3 in Dulbecco’s Modified Eagles Medium (DMEM) (Gibco, USA) without fetal bovine serum (FBS) (Gibco, USA). Five mL of FBS were added to stop the trypsin reaction, and the minced tissue suspension was moved into a 50 mL centrifuge tube and shaken in a reciprocating water bath (37°C) at 130 cycles/min for 5 min. The lung minces and cell suspension were filtered sequentially through 70 μm and 40 μm filters, and centrifuged at 1,100 rpm for 8 min. The supernatant was discarded, and the pelleted cells were then resuspended in Dulbecco's phosphate-buffered saline (DPBS) (Gibco, USA). A volume of twice as much ACK Lysis Buffer (Solarbio, China) was added, the tube was incubated at room temperature for 10 min, and then centrifuged at 1,100 rpm for 5 min. The cells were incubated in DMEM (with 20% FBS) in a 25 cm2 culture flask at 37°C, 45 min for three times. The unattached cells were incubated in a rat IgG-coated polystyrene bacteriological 100 mm petri dish (0.5 mg/mL rat IgG/dish) at 37°C for 2 h. The unattached cells were collected and centrifuged at 1,100 rpm for 8 min, the supernatant was discarded. Finally, the ATII cells were cultured in DMEM supplemented with 20% FBS in 5% CO2 (in air) at 37°C. The BCIP/NBT basic phosphate kit (Beyotime, China) was used to verified the purity of ATII cell, the results showed that the dark blue granules were observed in the cytoplasm of the ATII cell (Suppl Fig S2).

*Isolation and purification of LBs*

The lung of plateau zokors and SD rats were perfused intensively with a 0.32 M sucrose solution. During LBs isolation, all solutions were at 4°C, saline free, and contained 0.01 M HEPES (pH=7.4). The lungs were excised out of the chest cavity briefly rinsed in 1.0 M sucrose, and the tracheas and large airways were discarded. To increase the LBs yield, the lungs from three animals were combined, minced with sharp scissors, and the tissue was added to a 1.0 M sucrose solution producing a 15% (wt/vol) lung homogenate suspension. Homogenization was carried out using a homogenizer (PRO 200, USA) to promote the release of intracellular contents from the lung tissue. The collected homogenate was filtered through a 4-ply gauze to remove large cellular debris, and then centrifuged at 500 g for 15 min at 2°C. A 1.0 M sucrose tissue homogenate was layered below volumes of 0.32 M sucrose and 0.68 M sucrose before centrifugation at 64,000 g for 2 h at 4°C in a Sorvall LYNX 6 000 Superspeed Centrifuge (Thermo, USA). The interfacial band between the 0.32 and 0.68 M sucrose layers was collected, and concentrated 1.0 M sucrose was added to the collected interfacial materials to produce a sucrose solution of 0.58 M. The LB in the 0.58 M sucrose solution was then layered beneath a 0.32 M sucrose and 0.45 M sucrose layers before being centrifuged again as described above. Purified LBs were then collected at the 0.45-0.58 M sucrose interfacial band. Subsequently, the isolated LB solution was diluted to a 0.2 M sucrose, and LBs were pelleted by centrifugation at 40,000 g for 15 min at 4°C. The isolated LB pellet was resuspended in 50 μl of saline and frozen at −20°C for subsequent analysis.

*Transmission electron microscopy (TEM) examination*

The isolated ATII and LBs samples were resuspended in 0.2% agar, solidified at 4°C, and then fixed in 2.5% glutaraldehyde. The subsequent process was according to Chen *et al*. (2004) (12), including postfixation with 1% osmium tetroxide for 1 h. Then specimens were dehydrated in 30%, 50%, 70%, and 90% acetone for 10 min and dehydrated in 100% acetone for three times. The specimens were embedded in Epon-Araldite resin at 37°C for 12 h and at 60°C for 48 h. Ultra-thin (80 nm) sections were cut (Leica, EM UC7, Heidelberg, Germany) and dyed with 2% uranyl acetate and 1% lead citrate. The specimens were identified using transmission electron microscope (Hitachi, H-7650, Japan) at the Laboratory of Electrical Microscopy, Medical College of Xian Jiaotong University.

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**Supplemental Figures and Legends**



Figure S1. The entire lane with molecular weight marker at the high altitude (3 600 m) and the low altitude (2, 200 m) in lung tissues of plateau zokor. The lane 1 was the molecular weight marker, the lanes from 2 to 9 were the altitude of 3, 600 m (n=8), the lanes from 10 to 17 were the altitude of 2 200 m (n=8).



Figure S2. The identified results by BCIP/NBT basic phosphate kit of the ATII cells in SD rats. objective magnification: 20×, scale bar=100 μm,