Supplementary information, Data S1 Methods

The sixth Chinese Census Data (year 2010) was downloaded from the National Bureau of Statistics of the People's Republic of China (http://www.stats.gov.cn/tjsj/pcsj/rkpc/6rp/indexch.htm). Genes associated with aging in humans were downloaded from GenAge Database of Ageing-Related Genes (http://genomics.senescence.info/genes/, 2015-12-18). Human genes involved in metabolism were downloaded from Virtual Metabolic Human database (https://vmh.uni.lu/#home). Human genes involved in the hypoxia response pathway were retrieved from a previous study [1].

Genome wide single-nucleotide polymorphisms (SNPs) data genotyped by the Affymetrix Genome-Wide Human SNP 6.0 Array, from 31 unrelated Tibetans were from a previous study [2], and genotype data of Han people were downloaded from HapMap (phase II, http://hapmap.ncbi.nlm.nih.gov/). Genome wide SNPs from 327 whole genome sequence data from sheep, goats, cattle, dogs, pigs and horses, which included 134 genomes from the Tibetan Plateau and 193 genomes from domestic populations from lowland areas, called by a stringent pipeline implemented in the GATK program, were from our unpublished paper. Differentiation of each SNP was calculated using F_{ST}[3], XP-EHH (cross population extended haplotype homozygosity)[4], and ΔDAF (the difference of the derived allele frequencies). Transcriptome data on aging was from 7,074 human peripheral blood samples obtained from a previous study [5]. Detailed information about the samples, expression data analysis can be found in the original publication [5]. Lung tissue transcriptomes from four Tibetan pigs and four Min pigs from the lowlands were profiled by RNA-sequencing. Reads were aligned against the reference genome of *Sus scrofa* (Sscrfa 10.2) using TopHat v2.0.4 with default parameters[6] using the gene annotation available at Ensembl v77. Transcripts were first assembled using the reference annotation based transcript assembly method using Cufflinks[7]. Novel transcripts were subsequently extracted from the output of the assemblers using a custom Perl script. The reference annotation was then merged with the novel transcripts to generate a new reference annotation file. To quantify gene expression, the FPKM (Fragments Per Kilobase of transcript per Million mapped reads) values were calculated using Cuffmerge without RABT. One-to-one orthologous genes between human and dog, pig, horse, cattle, and sheep were downloaded from Ensembl (http://www.ensembl.org/) by BioMart. The one-to-one orthologous genes between human and goat were retrieved by reciprocal best hit BLASTP search. Protein-protein interaction data in human was downloaded from BioGRID (http://thebiogrid.org/, BIOGRID-ALL-3.3.124.tab) and InWeb [8] (http://www.broadinstitute.org/~rossin/InWeb3_HC_NonRed.txt). The interaction between aging associated genes and hypoxia response genes were counted. For 1000 random simulation, 154 genes and 305 other genes were randomly chosen and the interactions were counted for each simulation.

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aging-associated genes	**hypoxia response genes**
A2M	ABAT
ABL1	ACE
ADCY5	ACSL6
AGPAT2	ACTN4
AGTR1	ADA
AIFM1	ADAM17
AKT1	ADIPOQ
APEX1	ADM
APOC3	ALAS2
APOE	ALDOC
APP	ANG
APTX	ANGPT2
AR	ANGPT4
ARHGAP1	ANGPTL4
ARNTL	APOLD1

ATF2	AQP1
ATM	ARNT
ATP5O	ARNT2
ATR	ASCL2
BAK1	ATP1B1
BAX	BCL2
BCL2	BIRC2
BDNF	BMP2
BLM	BNIP3
BMI1	CA9
BRCA1	CAPN2
BRCA2	CASP1
BSCL2	CAV1
BUB1B	CCL2
BUB3	CCNB1
C1QA	CD38
CACNA1A	CHRNA4
CAT	CHRNA7
CCNA2	CHRNB2
CDC42	CITED2
CDK1	CLDN3
CDK7	CREBBP
CDKN1A	CRYAA
CDKN2A	CRYAB
CDKN2B	CST3
CEBPA	CXCR4
CEBPB	CYP1A1
CETP	DDIT4
CHEK2	DPP4
CISD2	E2F1
CLOCK	ECE1
CLU	EDN1
CNR1	EDNRA
COQ7	EGLN1
CREB1	EGLN2
CREBBP	EGLN3
CSNK1E	ENG
CTF1	EP300
CTGF	EPAS1
CTNNB1	EPO
DBN1	ERCC3
DDIT3	FLT1
DGAT1	GATA6
DLL3	GPR182

E2F1
EEF1A1
EEF1E1
EEF2
EFEMP1
EGF
EGFR
EGR1
EIF5A2
ELN
EMD
EP300
EPOR
EPS8
ERBB2
ERCC1
ERCC2
ERCC3
ERCC4
ERCC5
ERCC6
ERCC8
ESR1
FAS
FEN1
FGF21
FGF23
FGFR1
FLT1
FOS
FOXM1
FOXO1
FOXO3
FOXO4
GCLC
GCLM
GH1
GHR
GHRH
GHRHR
GPX1
GPX4
GRB2
GRN
HIF1A
HIF3A
HMOX1
HMOX2
HSD11B2
HSP90B1
HYOU1
IL18
ITGA2
ITPR1
ITPR2
JAG2
KCNA5
KCNK3
KCNMA1
LCT
LONP1
MB
MMP14
MMP2
MT-CYB
MT-ND4
MT-ND5
MT3
NARFL
NF1
NOS1
NOS3
NPPC
P2RX3
PAM
PDE5A
PDGFA
PDGFB
PDIA2
PDLIM1
PGF
PLAT
PLAU
PLD2
PLOD1
PLOD2
PML
PPARA

GSK3A
GSK3B
GSR
GSS
GSTA4
GSTP1
GTF2H2
H2AFX
HBP1
HDAC1
HDAC2
HDAC3
HELLS
HESX1
HIC1
HIF1A
HMGB1
HMGB2
HOXB7
HOXC4
HRAS
HSF1
HSP90AA1
HSPA1A
HSPA1B
HSPA8
HSPA9
HSPD1
HTRA2
HTT
IGF1
IGF1R
IGF2
IGFBP2
IGFBP3
IKBKB
IL2
IL2RG
IL6
IL7
IL7R
INS
INSR
IRS1
PRKAA1
PRKCQ
PSEN2
PTK2B
PYGM
RHOA
RYR1
RYR2
SCAP
SCFD1
SCNN1B
SCNN1G
SDC2
SERPINA1
SFRP1
SHH
SLC11A2
SLC2A8
SLC8A1
SMAD3
SMAD4
SMAD9
SOCS3
SOD2
SOD3
STAT5B
TFRC
TGFB1
TGFB2
TGFB3
TGFBR1
TH
THBS1
TLR2
TLR4
TRH
TXN2
UBE2B
UBQLN1
UCN3
UCP2
UCP3
USF1
VCAM1

IRS2
JAK2
JUN
JUND
KCNA3
KL
LEP
LEPR
LMNA
LMNB1
LRP2
MAP3K5
MAPK14
MAPK3
MAPK8
MAPK9
MAPT
MAX
MDM2
MED1
MIF
MLH1
MSRA
MT1E
MT-CO1
MTOR
MXD1
MXI1
MYC
NBN
NCOR1
NCOR2
NFE2L1
NFE2L2
NFKB1
NFKB2
NFKBIA
NGF
NGFR
NOG
NR3C1
NRG1
NUDT1
PAPPA
VEGFA
VHL
VLDLR
XRCC1

PARP1 PCK1 PCMT1 PCNA PDGFB PDGFRA PDGFRB PDPK1 PEX5 PIK3CA PIK3CB PIK3R1 PIN1 PLAU PLCG2 PMCH PML POLA1 POLB POLD1 POLG PON1 POU1F1 PPARA PPARG PPARGC1A PPM1D PPP1CA PRDX1 PRKCA PRKCD PRKDC PROP1 PSEN1 PTEN PTGS2 PTK2 PTK2B PTPN1 PTPN11 PYCR1 RAD51 RAD52 RAE1	

RB1 RECQL4 RELA RET RGN RICTOR RPA1 S100B SDHC SERPINE1 SHC1 SIN3A SIRT1 SIRT3 SIRT6 SIRT7 SLC13A1 SNCG SOCS2 SOD1 SOD2 SP1 SPRTN SQSTM1 SST SSTR3 STAT3 STAT5A STAT5B STK11 STUB1 SUMO1 SUN1 TAF1 TBP TCF3 TERC TERF1 TERF2 TERT TFAP2A TFDP1 TGFB1 TNF	

TOP1 TOP2A TOP2B TOP3B TP53 TP53BP1 TP63 TP73 TPP2 TRAP1 TRPV1 TXN UBB UBE2I UCHL1 UCP1 UCP2 UCP3 VCP VEGFA WRN XPA XRCC5 XRCC6 YWHAZ ZMPSTE24	