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MATERIALS AND METHODS

Species Coverage and Definition of Long-lived Species

A total of 36 mammals representing 14 orders were examined: Cetartiodactyla (*B. mysticetus*, *Tursiops truncates*, *Orcinus orca*, *Lipotes vexillifer*, *Balaenoptera acutorostrata*, *Physeter catodon*, *Neophocaena asiaeorientalis*, *Vicugna pacos*, *Bos Taurus*, *Ovis aries*), Perissodactyla (*Equus caballus*), Carnivora (*Canis lupus familiaris*, *Felis catus*), Chiroptera (*M. brandtii*, *Myotis lucifugus*, *Pteropus vampyrus*), Eulipotyphla (*Sorex araneus*, *Erinaceus europaeus*), Primates (*H. sapiens*, *M. nemestrina*, *Carlito syrichta*, *P. abelii*, *C. jacchus*, *M. murinus*), Rodentia (*H. glaber*, *Rattus norvegicus*, *Mus musculus*, *Cavia porcellus*), Lagomorpha (*Oryctolagus cuniculus*, *Ochotona princeps*), Proboscidea (*L. Africana*) , Hyracoidea (*Procavia capensis*), Afrosoricida (*Echinops telfairi*), Cingulata (*Dasypus novemcinctus*), Pilosa (*Choloepus hoffmanni*), and Didelphimorphia (*Monodelphis domestica*) (Table S1).

We used the scientific method of evaluating longevity quotient (LQ)—i.e., the ratio of the observed maximum lifespan (MLS) to the predicted maximum lifespan[1-2]—to determine whether species are long-lived for their body size. We first obtained the maximum lifespan and body mass (BM) records for all mammals (n = 987) from the AnAge online database.[3] Each species' longevity quotient was calculated to follow the allometric equation for mammals:[2]

$$\mathrm{LQ} = \frac{\mathrm{MLS}}{6.32 \times \mathrm{BM}^{0.139}}$$

Then, we split the dataset into two groups based on longevity quotient: long-lived group contained the species with a longevity quotient greater than 1 SD (standard deviation) from the mean of all mammals, and the control group contained all other species.

Sequence Retrieval and Alignments

Aging-related gene list of human was first retrieved from the GenAge[3] database. The protein-coding sequence (CDS) for each human aging-related gene was then downloaded from the NCBI database. The CDS of other mammalian species was downloaded from NCBI, the OrthoMAM v10 database,[4] and the Bowhead Whale Genome Resource (http://www.bowhead-whale.org/).[5] Additionally, the low quality or unannotated CDS in the database was further verified using BLASTn searches. For each gene, the longest transcript was kept in our analysis. Thus, 115 one-to-one orthologous genes among 36 species were selected for subsequent analysis (Table S2). Next, we performed multiple sequence alignments for each orthologous gene using PRANK with default settings, which uses phylogenetic information to distinguish alignment gaps caused by insertions or deletions and produces good alignments for evolutionary inferences.[6-7] Finally, potentially unreliable regions of multiple alignments were removed using the Gblocks v0.91 program with default settings (“-t = c”).[8]

Molecular Evolution Analyses

The measure of natural selection acting on the genes was determined by estimating the ratio of nonsynonymous (d_N) / synonymous (d_S) substitution rates (d_N/d_S) implemented in the CodeML program of the PAML software package v4.9.[9] Briefly,

$d_N/d_S < 1$, $d_N/d_S = 1$, and $d_N/d_S > 1$ indicate negative selection, neutral evolution, and positive selection, respectively. A well-accepted species tree of 36 species in our study from the TimeTree database (http://www.timetree.org/) was used as the input tree for all analyses.[10]

To investigate whether aging-related genes have undergone significant differences in selection pressures between long-lived species and the control group, the branch-site model was used to test the selection of each extant lineage in this study.[11] Each long-lived species was used as a foreground branch in every run, and all control group species were set as the background branch. Compared with the null hypothesis model of neutral evolution ($d_N/d_S = 1$), foreground branches in the modified model A that have a class of sites with the ratio $d_N/d_S > 1$ for positive selection. All positively selected sites in the branch-site model were identified using a Bayes Empirical Bayes (BEB) analysis with posterior probabilities $\geqslant 0.80$.[12] In addition, the clade model C and its null model M2a_rel (nearly neutral) were used to detect evidence of divergent selective pressures acting across the combined branch of all extant long-lived lineage as the foreground compared with the remaining species in the tree as the background.[13] The clade model C assumes variation in d_N/d_S among sites, allowing a fraction of sites evolving under divergent selective pressures. The model assumes three classes of sites, representing evolutionarily conserved codons, neutral codons, and codons under divergent selection pressures between the foreground and background clades. We set each model with three initial d_N/d_S values (0.5, 1, and 1.5) to obtain the robust average d_N/d_S, and compared this result with that of model M2a_ref. Only genes with an unchangeable likelihood value for the three initial d_N/d_S values were considered. The likelihood ratio test (LRT) with χ^2 distribution was used to determine which models were statistically different from the null model. The *P*-values were adjusted for multiple testing using the false discovery rate (FDR) procedure and adjusted *P*-values < 0.05 were considered significant for branch-site model analysis.[14]

Convergent Evolution Detection

Here, we used two methods to detect the molecular basis of convergent evolution in long-lived species. First, ancestral amino acid sequences were reconstructed for 115 one-to-one orthologous genes among 36 species using the CodeML program in PAML 4.9.[9] Then, convergent amino acid substitutions in independent pairs of long-lived lineage were detected by Zhang and Kumar's method.[15] Considering noise resulting from the random amino acid substitutions of convergence, the JTT-f_{genes} model of amino acid substitution were used to estimate the expected number of molecular convergences in each protein alignment.[16] A Poisson test was finally performed to verify whether the observed number of convergent sites in each gene was significantly more than the expected number caused by random substitution.

Second, we determined unique amino acid substitutions based on sequence alignments using FasParser2,[17] since convergent phenotypic characteristics can also arise from unique substitutions that independently evolved in different species.[18] If the same amino acid changes were identified in at least five long-lived species and none were found in the control group, then these amino acid changes were considered to be long-lived group specific amino acid substitutions.

Association Analysis between Gene Evolution and Phenotypes

Finally, we wished to assess the relationship between the rate of gene evolution and aging-associated life-history traits.[19] To test whether maximum lifespan covaries with body mass and longevity quotient, we first carried out a nonphylogenetic regression using the *lm* function in R 3.5.1. Moreover, we used Pagel's λ model to test for phylogenetic signals in mammalian life-history traits. Pagel's λ describes the proportion of variance that can be attributed to Brownian motion along a phylogeny. A value of λ equal or close to 1 suggests that the character is evolving stochastically, whereas $\lambda < 1$ indicates a departure from neutral drift. Estimates of λ for all life-history traits were computed using the *phytools* package in R 3.5.1.[20]

To explore the potential relationships between the evolutionary rate (d_N / d_S) of aging-related genes and life-history phenotypes, the root-to-tip d_N / d_S that considers the evolutionary history of a locus were calculated for each gene using the free-ratio model from PAML v4.9.[9] For this analysis, a d_S value of approximately 0 along a branch always yields a very high d_N/d_S value. Hence, genes with $d_S < 0.0001$ were discarded in our analysis. Finally, phylogenetic generalized least squares regression was performed in the *caper* package in R 3.5.1[21] to evaluate the associations between Log_{10}-transformed root-to-tip d_N/d_S and life-history traits (longevity quotient without log-transform).[22]

To assess the robustness of the results, we applied a two-step verification procedure as previously described.[23] First, the regression was performed by excluding the species with the largest residue error (e.g., a potential outlier) to report the regression slope *P*-value ("*P* value.robust"). Second, the regression was repeated by excluding each species, one at a time, to report the maximum (i.e., least significant) *P*-value ("*P* value.max"), and ensure that the overall relationship did not depend on any single species. Both *P* value.robust < 0.01 and *P* value.max < 0.1 were chosen as the cut-offs.

Pathway Enrichment and Protein-protein Interaction Analysis

We performed a pathway enrichment analysis to explore the biological mechanisms underlying the associations between the candidate genes and longevity pathways. The functional enrichment analyses in Gene Ontology (GO) terms for Biological Process (BP), the Kyoto Encyclopedia of Genes and Genomes (KEGG), Disease Ontology (DO), and Reactome pathway were performed in the R package *clusterProfiler*.[24] DO provides a consistent description of genes in disease perspectives and Reactome is a manually curated resource that describes chemical reactions and biological processes and pathways. For each pathway, the hypergeometric test was used to detect any overrepresentation of our set of genes among all genes in the pathway. FDR was controlled using the Benjamini–Hochberg procedure in R 3.5.1.[25] A protein-protein interaction network analysis was performed using STRING v11.[26]

Supplementary Figure

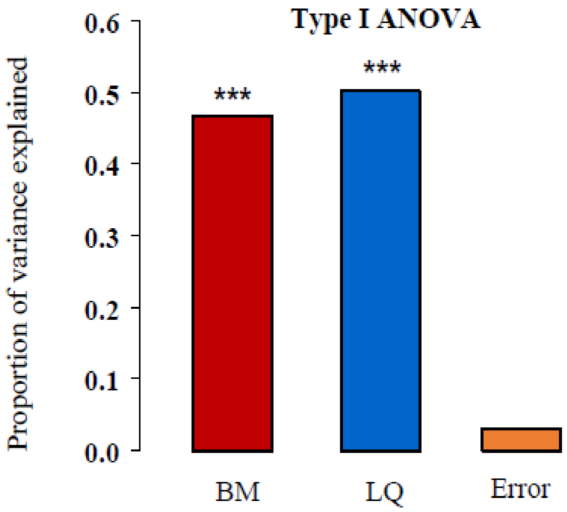

Figure S1. Bar plot showing the variance in maximum lifespan (MLS) explained by each life-history trait (body mass (BM) or longevity quotient (LQ)) as studied in a multivariate model, ***P value < 0.001.

Supplementary Tables

Table S1 Datasets of 36 mammals in the present study.

Order	Species	MLS/year	BM/g	LQ
Cetartiodactyla	*Balaena mysticetus*	211	100,000,000	2.58
	Tursiops truncatus	51.6	200,000	1.50
	Orcinus orca	90	3,987,500	1.72
	Lipotes vexillifer	24	83,500	0.79
	Balaenoptera acutorostrata	50	7,500,000	0.88
	Physeter catodon	77	28,500,000	1.12
	Neophocaena asiaeorientalis	33	32,500	1.23
	Vicugna pacos	25.8	62,000	0.88
	Bos taurus	20	750,000	0.48
	Ovis aries	22.8	80,000	0.75
Perissodactyla	*Equus caballus*	57	300,000	1.56
Carnivora	*Canis lupus familiaris*	24	40,000	0.87
	Felis catus	30	3,900	1.50
Chiroptera	*Myotis brandtii*	41	7	4.95
	Myotis lucifugus	34	10	3.91
	Pteropus vampyrus	20.9	872	1.29
Eulipotyphla	*Sorex araneus*	3.2	9	0.37
	Erinaceus europaeus	11.7	750	0.74
Primates	*Homo sapiens*	122.5	62,035	4.18
	Macaca nemestrina	37.6	7,913	1.71
	Carlito syrichta	16	119.2	1.30
	Pongo abelii	59	64,475	2.00
	Callithrix jacchus	22.8	255.2	1.67
	Microcebus murinus	18.2	64.8	1.61
Rodentia	*Heterocephalus glaber*	31	35	2.99
	Rattus norvegicus	3.8	300	0.27
	Mus musculus	4	20.5	0.42
	Cavia porcellus	12	728	0.76
Lagomorpha	*Oryctolagus cuniculus*	9	1,800	0.50
	Ochotona princeps	7	100	0.58
Afrotheria	*Loxodonta africana*	65	4,800,000	1.21
	Procavia capensis	14.8	3,600	0.75
	Echinops telfairi	19	180	1.46
Cingulata	*Dasypus novemcinctus*	22.3	5,500	1.07
Pilosa	*Choloepus hoffmanni*	41	6,250	1.93
Didelphimorphia	*Monodelphis domestica*	5.1	105	0.42

Table S2 List of 115 aging-related genes used in in the present study.

Gene	**Entrez ID**	**Gene Name**	**Gene Function/GeneCards**
ABL1	25	ABL proto-oncogene 1, non-receptor tyrosine kinase	Cancer
AGTR1	185	angiotensin II receptor, type 1	Metabolism
APOE	348	apolipoprotein E	Metabolism
APP	351	amyloid beta precursor protein	Transcription regulation
APTX	54840	aprataxin	DNA damage repair
ARNTL	406	aryl hydrocarbon receptor nuclear translocator-like	Transcription regulation
ATF2	1386	activating transcription factor 2	Transcription regulation
ATM	472	ATM serine/threonine kinase	Cancer
ATP5O	539	ATP synthase peripheral stalk subunit OSCP	Metabolism
ATR	545	ATR serine/threonine kinase	Cancer
BAX	581	BCL2-associated X protein	Apoptosis
BCL2	596	B-cell CLL/lymphoma 2	Apoptosis
BLM	641	Bloom syndrome, RecQ helicase-like	DNA damage repair
BMI1	648	BMI1 proto-oncogene, polycomb ring finger	DNA damage repair
BRCA1	672	breast cancer 1, early onset	Cancer
BSCL2	26580	Berardinelli-Seip congenital lipodystrophy 2	Immune system
BUB3	9184	BUB3 mitotic checkpoint protein	Cell cycle
C1QA	712	complement component 1, q subcomponent, A chain	Cell cycle
CCNA2	890	cyclin A2	Cell cycle
CDC42	998	cell division cycle 42	Cell cycle
CDK1	983	cyclin-dependent kinase 1	Cell cycle

CDK7	1022	cyclin-dependent kinase 7	Cell cycle
CDKN1A	1026	cyclin-dependent kinase inhibitor 1A	Cell cycle
CDKN2B	1030	cyclin-dependent kinase inhibitor 2B	Cell cycle
CHEK2	11200	checkpoint kinase 2	Cell cycle
CISD2	493856	CDGSH iron sulfur domain 2	Apoptosis
CLOCK	9575	clock circadian regulator	Transcription regulation
CNR1	1268	cannabinoid receptor 1 (brain)	Cell Surface Receptors
COQ7	10229	coenzyme Q7 homolog, ubiquinone (yeast)	Metabolism
CREB1	1385	cAMP responsive element binding protein 1	Transcription regulation
CREBBP	1387	CREB binding protein	Transcription regulation
CSNK1E	1454	casein kinase 1, epsilon	DNA damage repair
CTGF	1490	connective tissue growth factor	Growth regulation
CTNNB1	1499	catenin (cadherin-associated protein), beta 1	Signal transduction
DBN1	1627	drebrin 1	Signal transduction
DGAT1	8694	diacylglycerol O-acyltransferase 1	Metabolism
E2F1	1869	E2F transcription factor 1	Apoptosis
EFEMP1	2202	EGF containing fibulin-like extracellular matrix protein 1	Growth regulation
EGFR	1956	epidermal growth factor receptor	Cancer
EGR1	1958	early growth response 1	Growth regulation
EIF5A2	56648	eukaryotic translation initiation factor 5A2	Transcription regulation
EMD	2010	emerin	Growth regulation
EPOR	2057	Erythropoietin receptor	Growth regulation
EPS8	2059	epidermal growth factor receptor pathway substrate 8	Growth regulation
ERBB2	2064	erb-b2 receptor tyrosine kinase 2	Cancer

ERCC1	2067	excision repair cross-complementation group 1	DNA damage repair
ERCC2	2068	excision repair cross-complementation group 2	DNA damage repair
ERCC3	2071	excision repair cross-complementation group 3	DNA damage repair
ERCC5	2073	excision repair cross-complementation group 5	DNA damage repair
ERCC6	2074	excision repair cross-complementation group 6	DNA damage repair
ERCC8	1161	excision repair cross-complementation group 8	DNA damage repair
ESR1	2099	estrogen receptor 1	Growth regulation
FGF23	8074	fibroblast growth factor 23	Growth regulation
FGFR1	2260	fibroblast growth factor receptor 1	Growth regulation
FOS	2353	FBJ murine osteosarcoma viral oncogene homolog	Transcription regulation
FOXM1	2305	forkhead box M1	Cell cycle
FOXO1	2308	forkhead box O1	Transcription regulation
FOXO3	2309	forkhead box O3	Transcription regulation
FOXO4	4303	forkhead box O4	Transcription regulation
GCLC	2729	glutamate-cysteine ligase, catalytic subunit	Growth regulation
GCLM	2730	glutamate-cysteine ligase, modifier subunit	Growth regulation
GHR	2690	growth hormone receptor	Growth regulation
GHRH	2691	growth hormone releasing hormone	Growth regulation
GRB2	2885	growth factor receptor-bound protein 2	Signal transduction
GRN	2896	granulin	Growth regulation
GSK3B	2932	glycogen synthase kinase 3 beta	Metabolism
GSS	2937	glutathione synthetase	Metabolism
GSTA4	2941	glutathione S-transferase alpha 4	Metabolism
GTF2H2	2966	general transcription factor IIH, polypeptide 2	DNA damage repair

H2AFX	3014	H2A histone family, member X	DNA damage repair
HBP1	26959	HMG-box transcription factor 1	Transcription regulation
HDAC3	8841	histone deacetylase 3	Transcription regulation
HELLS	3070	helicase, lymphoid-specific	DNA damage repair
HESX1	8820	HESX homeobox 1	Transcription regulation
HIF1A	3091	hypoxia inducible factor 1, alpha subunit	Metabolism
HMGB1	3146	high mobility group box 1	DNA damage repair
HMGB2	3148	high mobility group box 2	DNA damage repair
HRAS	3265	Harvey rat sarcoma viral oncogene homolog	Cancer
IGF1	3479	insulin-like growth facto 1	Growth regulation
IGF1R	3480	insulin-like growth factor 1 receptor	Growth regulation
IL2	3558	interleukin 2	Immune system
IL2RG	3561	interleukin 2 receptor, gamma	Immune system
IL7R	3575	interleukin 7 receptor	Immune system
INSR	3643	insulin receptor	Growth regulation
IRS1	3667	insulin receptor substrate 1	Signal transduction
LMNA	4000	lamin A/C	Growth regulation
NCOR1	9611	nuclear receptor corepressor 1	Transcription regulation
NGF	4803	nerve growth factor	Signal transduction
NGFR	4804	nerve growth factor receptor	Signal transduction
NRG1	3084	neuregulin 1	Growth regulation
PDGFB	5155	platelet-derived growth factor beta polypeptide	Growth regulation
PDGFRB	5159	platelet-derived growth factor receptor, beta polypeptide	Growth regulation
PEX5	5830	peroxisomal biogenesis factor 5	Metabolism

PIK3CB	5291	phosphatidylinositol-4,5-bisphosphate 3-kinase, catalytic subunit beta	Signal transduction
PIN1	5300	peptidylprolyl cis/trans isomerase, NIMA-interacting 1	Cell cycle
PLAU	5328	plasminogen activator, urokinase	Signal transduction
PLCG2	5336	phospholipase C, gamma 2	Signal transduction
POU1F1	5449	POU class 1 homeobox 1	Transcription regulation
PPARA	5465	peroxisome proliferator-activated receptor alpha	Metabolism
PRKCD	5580	protein kinase C, delta	Apoptosis
PTEN	5728	phosphatase and tensin homolog	Cell cycle
PTPN1	5770	protein tyrosine phosphatase, non-receptor type 1	Signal transduction
PTPN11	5781	protein tyrosine phosphatase, non-receptor type 11	Signal transduction
RET	5979	ret proto-oncogene	Cell cycle
RPA1	6117	replication protein A1	DNA damage repair
SHC1	6464	SHC transforming protein 1	Growth regulation
SST	6750	somatostatin	Growth regulation
STAT3	6774	signal transducer and activator of transcription 3	Transcription regulation
STAT5A	6776	signal transducer and activator of transcription 5A	Transcription regulation
STAT5B	6777	signal transducer and activator of transcription 5B	Transcription regulation
TCF3	6929	transcription factor 3	Transcription regulation
TP53	7157	tumor protein p53	Cancer
TXN	7295	thioredoxin	Cancer
VCP	7415	valosin containing protein	DNA damage repair
WRN	7486	Werner syndrome, RecQ helicase-like	DNA damage repair

Table S3 List of positively selected genes identified in long-lived species.

Branch	**Gene**	**Model**	**LnL**	**2ΔlnL**	**p.adjust**	**Parameters**	**Positive Sites（pp > 0.8）**
Heterocephalus glaber	*IL7R*	ModelA	-5355.063			$\omega_0 = 0.136$ $\omega_1 = 1.0$ $\omega_2 = 55.56$	184 0.990**;
		ModelA Null	-5358.884	7.642	0.006	$\omega_0 = 0.136$ $\omega_1 = 1.0$ $\omega_2 = 1.0$	
	DGAT1	ModelA	-7826.170			$\omega_0 = 0.037$ $\omega_1 = 1.0$ $\omega_2 = 206.344$	271 0.995**;
		ModelA Null	-7831.196	10.051	0.002	$\omega_0 = 0.038$ $\omega_1 = 1.0$ $\omega_2 = 1.0$	
	NGF	ModelA	-4700.352			$\omega_0 = 0.057$ $\omega_1 = 1.0$ $\omega_2 = 19.701$	120 0.986*;
		ModelA Null	-4702.660	4.615	0.032	$\omega_0 = 0.057$ $\omega_1 = 1.0$ $\omega_2 = 1.0$	
	SHC1	ModelA	-8468.794			$\omega_0 = 0.021$ $\omega_1 = 1.0$ $\omega_2 = 23.46$	51 0.972*;
		ModelA Null	-8471.238	4.888	0.027	$\omega_0 = 0.021$ $\omega_1 = 1.0$ $\omega_2 = 1.0$	
	STAT5A	ModelA	-11545.632			$\omega_0 = 0.022$ $\omega_1 = 1.0$ $\omega_2 = 435.158$	519 0.901; 603 0.985*;
		ModelA Null	-11548.466	5.669	0.017	$\omega_0 = 0.022$ $\omega_1 = 1.0$ $\omega_2 = 1.0$	
Balaena mysticetus	*GSK3B*	ModelA	-4458.212			$\omega_0 = 0.01$ $\omega_1 = 1.0$ $\omega_2 = 999.0$	57 0.840; 118 0.841;
		ModelA Null	-4460.432	4.440	0.035	$\omega_0 = 0.01$ $\omega_1 = 1.0$ $\omega_2 = 1.0$	
Homo sapiens	*EMD*	ModelA	-1585.090			$\omega_0 = 0.066$ $\omega_1 = 1.0$ $\omega_2 = 325.92$	6 0.996**;
		ModelA Null	-1588.927	7.674	0.006	$\omega_0 = 0.065$ $\omega_1 = 1.0$ $\omega_2 = 1.0$	
Pongo abelii	*PPARA*	ModelA	-9645.415			$\omega_0 = 0.023$ $\omega_1 = 1.0$ $\omega_2 = 8.497$	220 0.978*; 222 0.992**; 223 0.838; 291 0.989*;
		ModelA Null	-9649.334	7.838	0.005	$\omega_0 = 0.023$ $\omega_1 = 1.0$ $\omega_2 = 1.0$	
	EGR1	ModelA	-8655.636			$\omega_0 = 0.032$ $\omega_1 = 1.0$ $\omega_2 = 10.739$	83 0.994**; 95 0.996**; 313 0.967*; 415 0.562; 417 0.987*;
		ModelA Null	-8660.138	9.005	0.003	$\omega_0 = 0.031$ $\omega_1 = 1.0$ $\omega_2 = 1.0$	
	GSS	ModelA	-7345.481			$\omega_0 = 0.064$ $\omega_1 = 1.0$ $\omega_2 = 999.0$	
		ModelA Null	-7347.529	4.097	0.043	$\omega_0 = 0.063$ $\omega_1 = 1.0$ $\omega_2 = 1.0$	

	GHR	ModelA	-9180.019			$\omega_0 = 0.092$ $\omega_1 = 1.0$ $\omega_2 = 11.079$	59 0.867; 118 0.823; 124 0.830; 156 R 0.927; 160 0.826; 205 1.000**;
		ModelA Null	-9184.384	8.729	0.003	$\omega_0 = 0.092$ $\omega_1 = 1.0$ $\omega_2 = 1.0$	
	STAT5B	ModelA	-11534.536			$\omega_0 = 0.015$ $\omega_1 = 1.0$ $\omega_2 = 12.221$	625 0.962*; 627 0.988*;
		ModelA Null	-11538.173	7.274	0.007	$\omega_0 = 0.015$ $\omega_1 = 1.0$ $\omega_2 = 1.0$	
Microcebus murinus	*HELLS*	ModelA	-12118.730			$\omega_0 = 0.046$ $\omega_1 = 1.0$ $\omega_2 = 73.435$	267 0.956*; 271 0.916;
		ModelA Null	-12123.525	9.590	0.002	$\omega_0 = 0.045$ $\omega_1 = 1.0$ $\omega_2 = 1.0$	
	ATF2	ModelA	-6527.743			$\omega_0 = 0.025$ $\omega_1 = 1.0$ $\omega_2 = 44.668$	295 0.839;
		ModelA Null	-6530.159	4.832	0.028	$\omega_0 = 0.025$ $\omega_1 = 1.0$ $\omega_2 = 1.0$	
Callithrix jacchus	*PLAU*	ModelA	-8085.969			$\omega_0 = 0.055$ $\omega_1 = 1.0$ $\omega_2 = 10.305$	12 0.987*; 30 0.992**;
		ModelA Null	-8087.895	3.852	0.050	$\omega_0 = 0.054$ $\omega_1 = 1.0$ $\omega_2 = 1.0$	
	NCOR1	ModelA	-33035.937			$\omega_0 = 0.044$ $\omega_1 = 1.0$ $\omega_2 = 909.062$	1377 0.991**; 1533 0.995**; 1536 M 0.992**; 1547 0.993**; 1548 0.992**;
		ModelA Null	-33055.111	38.347	0.000	$\omega_0 = 0.043$ $\omega_1 = 1.0$ $\omega_2 = 1.0$	
	ATM	ModelA	-47199.353			$\omega_0 = 0.091$ $\omega_1 = 1.0$ $\omega_2 = 28.599$	164 0.962*;
		ModelA Null	-47203.736	8.766	0.003	$\omega_0 = 0.091$ $\omega_1 = 1.0$ $\omega_2 = 1.0$	
	ERCC6	ModelA	-18105.947			$\omega_0 = 0.046$ $\omega_1 = 1.0$ $\omega_2 = 9.473$	220 0.982*; 787 0.951*;
		ModelA Null	-18107.924	3.953	0.047	$\omega_0 = 0.046$ $\omega_1 = 1.0$ $\omega_2 = 1.0$	
	CREBBP	ModelA	-32203.266			$\omega_0 = 0.029$ $\omega_1 = 1.0$ $\omega_2 = 999.0$	1220 0.992*; 1221 0.972*; 1222 0.953*;
		ModelA Null	-32213.183	19.834	0.000	$\omega_0 = 0.029$ $\omega_1 = 1.0$ $\omega_2 = 1.0$	
Macaca nemestrina	*ERBB2*	ModelA	-22231.960			$\omega_0 = 0.04$ $\omega_1 = 1.0$ $\omega_2 = 147.608$	536 0.984*; 538 0.983*;
		ModelA Null	-22242.961	22.002	0.000	$\omega_0 = 0.04$ $\omega_1 = 1.0$ $\omega_2 = 1.0$	
Choloepus hoffmanni	*VCP*	ModelA	-11067.049			$\omega_0 = 0.001$ $\omega_1 = 1.0$ $\omega_2 = 8.211$	630 0.975*;

		ModelA Null	-11069.586	5.074	0.024	$\omega_0 = 0.001$ $\omega_1 = 1.0$ $\omega_2 = 1.0$	
	PDGFRB	ModelA	-19634.792			$\omega_0 = 0.041$ $\omega_1 = 1.0$ $\omega_2 = 3.404$	157 0.993**; 200 0.993**; 202 0.995**; 203 0.992**; 223 0.996**; 227 0.889; 230 0.977*; 235 0.991**; 320 0.985*; 348 0.838; 411 0.962*;
		ModelA Null	-19638.735	7.886	0.005	$\omega_0 = 0.041$ $\omega_1 = 1.0$ $\omega_2 = 1.0$	
	FOXO4	ModelA	-6679.140			$\omega_0 = 0.073$ $\omega_1 = 1.0$ $\omega_2 = 37.485$	37 0.848; 164 0.849; 169 0.835; 227 0.811; 330 0.826;
		ModelA Null	-6681.398	4.517	0.034	$\omega_0 = 0.072$ $\omega_1 = 1.0$ $\omega_2 = 1.0$	
	IGF1	ModelA	-1755.382			$\omega_0 = 0.032$ $\omega_1 = 1.0$ $\omega_2 = 25.79$	81 0.995**;
		ModelA Null	-1757.452	4.140	0.042	$\omega_0 = 0.031$ $\omega_1 = 1.0$ $\omega_2 = 1.0$	
	PTPN1	ModelA	-4097.124			$\omega_0 = 0.022$ $\omega_1 = 1.0$ $\omega_2 = 11.213$	148 0.999**; 150 0.989*;
		ModelA Null	-4100.872	7.496	0.006	$\omega_0 = 0.022$ $\omega_1 = 1.0$ $\omega_2 = 1.0$	
	APOE	ModelA	-4064.174			$\omega_0 = 0.097$ $\omega_1 = 1.0$ $\omega_2 = 11.505$	22 0.934; 100 0.974*; 145 0.969*;
		ModelA Null	-4067.841	7.335	0.007	$\omega_0 = 0.097$ $\omega_1 = 1.0$ $\omega_2 = 1.0$	
Myotis lucifugus	*CTGF*	ModelA	-4684.116			$\omega_0 = 0.028$ $\omega_1 = 1.0$ $\omega_2 = 52.795$	253 0.987*;
		ModelA Null	-4686.771	5.310	0.021	$\omega_0 = 0.028$ $\omega_1 = 1.0$ $\omega_2 = 1.0$	
	BCL2	ModelA	-2485.926			$\omega_0 = 0.03$ $\omega_1 = 1.0$ $\omega_2 = 999.0$	60 0.990*;
		ModelA Null	-2489.412	6.971	0.008	$\omega_0 = 0.028$ $\omega_1 = 1.0$ $\omega_2 = 1.0$	
	GHRH	ModelA	-1064.223			$\omega_0 = 0.112$ $\omega_1 = 1.0$ $\omega_2 = 25.548$	30 0.960*; 37 0.865;
		ModelA Null	-1066.620	4.793	0.029	$\omega_0 = 0.111$ $\omega_1 = 1.0$ $\omega_2 = 1.0$	
	PDGFRB	ModelA	-19994.262			$\omega_0 = 0.041$ $\omega_1 = 1.0$ $\omega_2 = 890.292$	534 0.976*; 536 0.830; 537 0.984*;
		ModelA Null	-20003.164	17.804	0.000	$\omega_0 = 0.042$ $\omega_1 = 1.0$ $\omega_2 = 1.0$	
	PLCG2	ModelA	-20036.080			$\omega_0 = 0.024$ $\omega_1 = 1.0$ $\omega_2 = 398.617$	665 0.962*;
		ModelA Null	-20040.208	8.256	0.004	$\omega_0 = 0.024$ $\omega_1 = 1.0$ $\omega_2 = 1.0$	

	DBN1	ModelA	-6652.028			$\omega_0 = 0.023$ $\omega_1 = 1.0$ $\omega_2 = 998.998$	244 0.991**;
		ModelA Null	-6655.057	6.058	0.014	$\omega_0 = 0.022$ $\omega_1 = 1.0$ $\omega_2 = 1.0$	
	ERCC3	ModelA	-12103.038			$\omega_0 = 0.011$ $\omega_1 = 1.0$ $\omega_2 = 6.5$	623 0.978*; 626 0.959*;
		ModelA Null	-12105.404	4.731	0.030	$\omega_0 = 0.011$ $\omega_1 = 1.0$ $\omega_2 = 1.0$	
	ABL1	ModelA	-15096.886			$\omega_0 = 0.02$ $\omega_1 = 1.0$ $\omega_2 = 769.282$	518 0.951*;
		ModelA Null	-15099.527	5.283	0.022	$\omega_0 = 0.02$ $\omega_1 = 1.0$ $\omega_2 = 1.0$	
Myotis brandtii	*CTGF*	ModelA	-4627.497			$\omega_0 = 0.029$ $\omega_1 = 1.0$ $\omega_2 = 23.054$	248 0.986*;
		ModelA Null	-4629.796	4.598	0.032	$\omega_0 = 0.029$ $\omega_1 = 1.0$ $\omega_2 = 1.0$	
	EGFR	ModelA	-20310.597			$\omega_0 = 0.039$ $\omega_1 = 1.0$ $\omega_2 = 8.506$	145 0.824; 274 0.973*; 309 0.956*; 371 0.971*;
		ModelA Null	-20313.278	5.363	0.021	$\omega_0 = 0.038$ $\omega_1 = 1.0$ $\omega_2 = 1.0$	
	DBN1	ModelA	-6674.313			$\omega_0 = 0.02$ $\omega_1 = 1.0$ $\omega_2 = 998.999$	247 0.991**; 251 0.569;
		ModelA Null	-6676.998	5.370	0.020	$\omega_0 = 0.02$ $\omega_1 = 1.0$ $\omega_2 = 1.0$	
	ABL1	ModelA	-15365.754			$\omega_0 = 0.02$ $\omega_1 = 1.0$ $\omega_2 = 999.0$	514 0.952*;
		ModelA Null	-15368.346	5.184	0.023	$\omega_0 = 0.02$ $\omega_1 = 1.0$ $\omega_2 = 1.0$	

Table S4 List of 16 unique positively selected genes identified in long-lived species none in the Control group.

Branch	**Gene**	**Model**	**LnL**	**2ΔlnL**	**p.adjust**	**Parameters**	**Positive Sites（pp > 0.8）**
Heterocephalus glaber	*SHC1*	ModelA	-8468.794			$\omega_0 = 0.021$ $\omega_1 = 1.0$ $\omega_2 = 23.46$	51 0.972*;
		ModelA Null	-8471.238	4.888	0.027	$\omega_0 = 0.021$ $\omega_1 = 1.0$ $\omega_2 = 1.0$	
Homo sapiens	*EMD*	ModelA	-1585.090			$\omega_0 = 0.066$ $\omega_1 = 1.0$ $\omega_2 = 325.92$	6 0.996**;
		ModelA Null	-1588.927	7.674	0.006	$\omega_0 = 0.065$ $\omega_1 = 1.0$ $\omega_2 = 1.0$	
Pongo abelii	*PPARA*	ModelA	-9645.415			$\omega_0 = 0.023$ $\omega_1 = 1.0$ $\omega_2 = 8.497$	220 0.978*; 222 0.992**; 223 0.838; 291 0.989*;
		ModelA Null	-9649.334	7.838	0.005	$\omega_0 = 0.023$ $\omega_1 = 1.0$ $\omega_2 = 1.0$	
	EGR1	ModelA	-8655.636			$\omega_0 = 0.032$ $\omega_1 = 1.0$ $\omega_2 = 10.739$	83 0.994**; 95 0.996**; 313 0.967*; 415 0.562; 417 0.987*;
		ModelA Null	-8660.138	9.005	0.003	$\omega_0 = 0.031$ $\omega_1 = 1.0$ $\omega_2 = 1.0$	
	STAT5B	ModelA	-11534.536			$\omega_0 = 0.015$ $\omega_1 = 1.0$ $\omega_2 = 12.221$	625 0.962*; 627 0.988*;
		ModelA Null	-11538.173	7.274	0.007	$\omega_0 = 0.015$ $\omega_1 = 1.0$ $\omega_2 = 1.0$	
Microcebus murinus	*HELLS*	ModelA	-12118.730			$\omega_0 = 0.046$ $\omega_1 = 1.0$ $\omega_2 = 73.435$	267 0.956*; 271 0.916;
		ModelA Null	-12123.525	9.590	0.002	$\omega_0 = 0.045$ $\omega_1 = 1.0$ $\omega_2 = 1.0$	
Callithrix jacchus	*NCOR1*	ModelA	-33035.937			$\omega_0 = 0.044$ $\omega_1 = 1.0$ $\omega_2 = 909.062$	1377 0.991**; 1533 0.995**; 1536 M 0.992**; 1547 0.993**; 1548 0.992**;
		ModelA Null	-33055.111	38.347	0.000	$\omega_0 = 0.043$ $\omega_1 = 1.0$ $\omega_2 = 1.0$	
Macaca nemestrina	*ERBB2*	ModelA	-22231.960			$\omega_0 = 0.04$ $\omega_1 = 1.0$ $\omega_2 = 147.608$	536 0.984*; 538 0.983*;
		ModelA Null	-22242.961	22.002	0.000	$\omega_0 = 0.04$ $\omega_1 = 1.0$ $\omega_2 = 1.0$	
Choloepus hoffmanni	*VCP*	ModelA	-11067.049			$\omega_0 = 0.001$ $\omega_1 = 1.0$ $\omega_2 = 8.211$	630 0.975*;
		ModelA Null	-11069.586	5.074	0.024	$\omega_0 = 0.001$ $\omega_1 = 1.0$ $\omega_2 = 1.0$	

	FOXO4	ModelA	-6679.140			$\omega_0 = 0.073$ $\omega_1 = 1.0$ $\omega_2 = 37.485$	37 0.848; 164 0.849; 169 0.835; 227 0.811; 330 0.826;
		ModelA Null	-6681.398	4.517	0.034	$\omega_0 = 0.072$ $\omega_1 = 1.0$ $\omega_2 = 1.0$	
	IGF1	ModelA	-1755.382			$\omega_0 = 0.032$ $\omega_1 = 1.0$ $\omega_2 = 25.79$	81 0.995**;
		ModelA Null	-1757.452	4.140	0.042	$\omega_0 = 0.031$ $\omega_1 = 1.0$ $\omega_2 = 1.0$	
Myotis lucifugus	*CTGF*	ModelA	-4684.116			$\omega_0 = 0.028$ $\omega_1 = 1.0$ $\omega_2 = 52.795$	253 0.987*;
		ModelA Null	-4686.771	5.310	0.021	$\omega_0 = 0.028$ $\omega_1 = 1.0$ $\omega_2 = 1.0$	
	BCL2	ModelA	-2485.926			$\omega_0 = 0.03$ $\omega_1 = 1.0$ $\omega_2 = 999.0$	60 0.990*;
		ModelA Null	-2489.412	6.971	0.008	$\omega_0 = 0.028$ $\omega_1 = 1.0$ $\omega_2 = 1.0$	
	GHRH	ModelA	-1064.223			$\omega_0 = 0.112$ $\omega_1 = 1.0$ $\omega_2 = 25.548$	30 0.960*; 37 0.865;
		ModelA Null	-1066.620	4.793	0.029	$\omega_0 = 0.111$ $\omega_1 = 1.0$ $\omega_2 = 1.0$	
	ERCC3	ModelA	-12103.038			$\omega_0 = 0.011$ $\omega_1 = 1.0$ $\omega_2 = 6.5$	623 0.978*; 626 0.959*;
		ModelA Null	-12105.404	4.731	0.030	$\omega_0 = 0.011$ $\omega_1 = 1.0$ $\omega_2 = 1.0$	
	DBN1	ModelA	-6652.028			$\omega_0 = 0.023$ $\omega_1 = 1.0$ $\omega_2 = 998.998$	244 0.991**;
		ModelA Null	-6655.057	6.058	0.014	$\omega_0 = 0.022$ $\omega_1 = 1.0$ $\omega_2 = 1.0$	
Myotis brandtii	*CTGF*	ModelA	-4627.497			$\omega_0 = 0.029$ $\omega_1 = 1.0$ $\omega_2 = 23.054$	248 0.986*;
		ModelA Null	-4629.796	4.598	0.032	$\omega_0 = 0.029$ $\omega_1 = 1.0$ $\omega_2 = 1.0$	
	DBN1	ModelA	-6674.313			$\omega_0 = 0.02$ $\omega_1 = 1.0$ $\omega_2 = 998.999$	247 0.991**; 251 0.569;
		ModelA Null	-6676.998	5.370	0.020	$\omega_0 = 0.02$ $\omega_1 = 1.0$ $\omega_2 = 1.0$	

Table S5 List of positively selected genes identified in the Control group (lifespan with non-increased).

Branch	**Gene**	**ModelA LnL**	**ModelA Null LnL**	**2ΔLnL**	**P.adj**	**ω**	**Positive Sites (pp > 0.8)**
Monodelphis domestica	*C1QA*	-5538.881	-5545.187	12.610	0.000	999.000	73 0.867;
	CDKN2B	-1863.771	-1865.890	4.237	0.040	999.000	
	E2F1	-2392.934	-2395.489	5.111	0.024	172.285	13 0.958*; 120 0.996**;
	EPOR	-6314.556	-6317.221	5.331	0.021	999.000	
	GRN	-10086.825	-10089.485	5.320	0.021	6.174	82 0.997**; 218 0.937; 237 0.921; 361 0.928;
	PDGFRB	-19240.541	-19242.569	4.055	0.044	999.000	
	TCF3	-5075.225	-5079.541	8.633	0.003	999.000	37 0.900;
	WRN	-20595.302	-20597.668	4.732	0.030	3.803	122 0.815; 140 0.916; 179 0.880; 221 0.944; 754 0.930; 830 0.800;
Erinaceus europaeus	*ATP5O*	-5154.135	-5158.448	8.626	0.003	998.999	108 0.955*;
	EGFR	-19923.857	-19927.105	6.498	0.011	222.335	108 0.879; 362 0.992**;
	ERCC2	-9250.400	-9252.840	4.881	0.027	76.206	115 0.971*;
	IL7R	-5444.146	-5448.084	7.878	0.005	998.996	130 0.959*;
	IRS1	-17165.290	-17168.343	6.106	0.013	71.541	813 0.980*;
	PLCG2	-19713.551	-19716.032	4.962	0.026	193.319	529 0.848;973 0.958*;
	PRKCD	-10447.433	-10449.841	4.814	0.028	289.954	126 0.956*;
	WRN	-20593.655	-20597.108	6.905	0.009	48.257	46 0.977*;
Sorex araneus	*ATM*	-46023.593	-46025.930	4.675	0.031	71.039	1292 0.918;
	CSNK1E	-3547.007	-3550.472	6.929	0.008	131.183	196 S 0.999**;
	DGAT1	-7318.911	-7321.407	4.992	0.025	10.190	144 0.974*; 155 0.979*;
	EGFR	-19918.687	-19921.351	5.328	0.021	6.760	51 0.815; 61 0.969*; 273 0.979*; 311 0.974*;

	EPS8	-14962.767	-14966.722	7.910	0.005	373.849	530 0.817;
	ERCC6	-17724.447	-17726.886	4.878	0.027	999.000	185 0.975*;
	GRN	-10094.133	-10096.535	4.804	0.028	998.931	280 0.956*;
	GSS	-7146.296	-7153.182	13.772	0.000	26.969	172 0.995**; 177 0.870; 200 0.960*; 249 0.923;
	H2AFX	-2278.693	-2281.319	5.253	0.022	999.000	
	HRAS	-3295.259	-3298.141	5.763	0.016	80.693	170 0.991**;
	IGF1R	-22181.252	-22185.272	8.041	0.005	70.778	65 0.875; 140 0.841; 176 0.860; 285 0.970*; 534 0.914; 570 0.892; 707 0.978*;
	IRS1	-17163.660	-17165.692	4.065	0.044	15.888	545 0.932; 566 0.943; 649 0.900;
	LMNA	-9797.589	-9803.020	10.863	0.001	514.980	456 0.942; 463 0.986*; 587 0.990*;
	WRN	-20583.204	-20587.344	8.280	0.004	8.207	78 0.993**; 392 0.982*; 412 0.985*; 452 0.986*; 787 0.988*; 821 0.982*;
Felis catus	*APOE*	-3957.453	-3960.139	5.373	0.020	998.996	104 0.930;
	PLCG2	-19706.626	-19710.700	8.149	0.004	67.517	259 0.957*; 261 0.930; 443 0.942;
	WRN	-20565.656	-20584.162	37.013	0.000	30.642	108 0.903; 127 0.997**; 128 0.937;130 0.997**; 149 1.000**;154 0.998**; 156 0.999**; 239 0.946;408 0.809; 735 0.943;
Canis lupus familiaris	*APP*	-11003.084	-11006.903	7.639	0.006	136.604	7 0.991**;
	GRN	-10090.512	-10094.067	7.112	0.008	14.168	243 0.992**; 317 0.988*;
	NGF	-4527.964	-4531.354	6.780	0.009	25.363	122 0.874; 134 0.848; 147 0.996**;
Equus caballus	*C1QA*	-5543.481	-5545.757	4.551	0.033	5.377	47 0.925; 74 0.976*; 101 0.897; 103 0.965*;
	H2AFX	-2277.210	-2279.188	3.955	0.047	57.333	7 0.975*; 100 0.873;
	IRS1	-17153.003	-17165.938	25.871	0.000	999.000	845 0.991**; 846 0.978*; 847 0.807;
	PDGFRB	-19242.686	-19253.151	20.929	0.000	999.000	370 0.964*; 395 0.983*;

Vicugna pacos	*ATM*	-46018.456	-46025.051	13.190	0.000	999.000	
	POU1F1	-4055.775	-4058.869	6.188	0.013	56.107	109 0.940; 110 0.995**;
	WRN	-20594.354	-20596.545	4.382	0.036	12.190	41 0.832;
Balaenoptera acutorostrata	*CREBBP*	-31777.346	-31780.419	6.147	0.013	999.000	
	TP53	-6740.036	-6742.380	4.687	0.030	803.289	16 0.934; 256 0.774;
Physeter catodon	*PEX5*	-10500.399	-10502.424	4.051	0.044	34.021	176 0.979*;
	RET	-18990.461	-18993.624	6.326	0.012	999.000	
	WRN	-20587.788	-20593.753	11.930	0.001	57.266	28 0.932;103 0.936; 104 0.954*; 123 0.931; 313 0.932; 361 0.849; 391 0.937; 727 0.937;
Lipotes vexillifer	*CTNNB1*	-11720.807	-11728.532	15.450	0.000	41.950	232 0.998**; 237 0.998**; 241 0.998**;
Neophocaena asiaeorientalis	*EGFR*	-19922.900	-19925.149	4.499	0.034	51.671	449 0.974*;
	HBP1	-7063.837	-7067.297	6.919	0.009	999.000	
	PLCG2	-19713.812	-19717.161	6.698	0.010	100.437	349 0.863;
Tursiops truncatus	*ATF2*	-6389.079	-6398.543	18.928	0.000	999.000	229 0.864; 230 0.861; 231 0.985*; 233 0.862;
	RPA1	-7529.648	-7533.595	7.895	0.005	47.310	18 0.843; 20 0.947; 103 0.949; 165 0.937; 351 0.850;
Bos taurus	*ATF2*	-6397.059	-6403.995	13.872	0.000	999.000	291 0.989*;
	PLCG2	-19707.070	-19711.233	8.326	0.004	215.766	671 0.999**;
	STAT5A	-11169.276	-11173.284	8.017	0.005	999.000	564 0.839; 567 0.979*;
	TP53	-6737.635	-6739.930	4.591	0.032	17.863	217 0.803; 234 0.994**;
Ovis aries	*BLM*	-16541.616	-16543.674	4.115	0.042	19.666	310 0.959*;
	C1QA	-5546.774	-5549.762	5.974	0.015	39.244	167 0.996**;
	EFEMP1	-5816.921	-5823.437	13.034	0.000	999.000	91 0.987*;
	ERCC1	-3386.015	-3390.291	8.551	0.003	999.000	32 0.995**;
	ERCC6	-17723.956	-17726.237	4.563	0.033	27.178	524 0.805; 729 0.981*;

	FGFR1	-11324.135	-11331.225	14.181	0.000	561.209	29 0.984*;
	LMNA	-9755.026	-9775.625	41.199	0.000	200.920	216 0.833; 258 0.989*; 261 0.881; 265 1.000**; 266 0.996**; 268 1.000**; 271 0.989*; 273 0.999**;
	STAT5A	-11160.425	-11165.223	9.596	0.002	31.393	287 0.997**; 530 0.997**;
Pteropus vampyrus	*ERCC5*	-10725.028	-10728.066	6.076	0.014	999.000	102 0.952*;
	GTF2H2	-6238.838	-6242.162	6.649	0.010	34.116	331 0.998**;
	PLAU	-8042.448	-8045.076	5.255	0.022	19.959	111 0.986*;
	TP53	-6738.410	-6740.684	4.549	0.033	9.279	3 0.967*; 236 0.980*;
Oryctolagus cuniculus	*APOE*	-3955.420	-3959.370	7.899	0.005	998.999	30 0.995**;
	APP	-11007.255	-11009.516	4.523	0.033	857.138	64 0.822;
	ERCC1	-3382.099	-3384.199	4.199	0.040	8.279	32 0.997**; 33 0.997**;
Ochotona princeps	*BRCA1*	-6668.587	-6670.550	3.927	0.048	19.169	205 0.932;
	FGFR1	-11291.278	-11299.194	15.833	0.000	22.174	106 0.949; 293 0.996**; 313 0.959*; 315 0.995**; 317 0.996**; 322 1.000**;
	PTPN11	-7799.861	-7802.652	5.582	0.018	8.277	36 0.976*; 37 0.956*;
	TCF3	-5077.244	-5079.570	4.651	0.031	42.495	22 0.930; 30 0.854; 135 0.975*; 151 0.980*;
Cavia porcellus	*ABL1*	-14934.278	-14936.725	4.893	0.027	14.298	594 0.974*;
	BRCA1	-6668.680	-6670.745	4.131	0.042	124.250	90 0.917;
	CLOCK	-10373.627	-10377.753	8.252	0.004	33.836	540 0.978*; 542 0.960*;
	COQ7	-4030.303	-4033.199	5.793	0.016	15.511	30 0.995**; 132 0.931;
	GSK3B	-4550.408	-4562.021	23.227	0.000	396.636	269 0.999**; 270 0.995**;
	IL7R	-5446.285	-5448.529	4.488	0.034	50.989	22 0.912; 145 0.883;
	PTEN	-3919.257	-3921.259	4.004	0.045	999.000	211 0.947;
Rattus norvegicus	*APTX*	-4872.003	-4874.539	5.072	0.024	142.605	63 0.949;

	TP53	-6739.875	-6742.120	4.491	0.034	29.162	65 0.984*;
Mus musculus	*CDK1*	-4086.492	-4088.416	3.847	0.050	20.118	25 0.987*;
	ERCC5	-10720.589	-10724.764	8.351	0.004	998.999	439 0.940; 440 0.972*;
	PLCG2	-19713.235	-19716.547	6.623	0.010	29.784	446 0.951*;
	PTPN1	-3967.679	-3970.183	5.007	0.025	16.519	54 0.992**;
Carlito syrichta	*APP*	-11004.452	-11006.442	3.979	0.046	17.595	29 0.971*;
	ATM	-46020.707	-46022.678	3.942	0.047	6.273	947 0.863;
	ATR	-37799.307	-37801.665	4.716	0.030	26.025	1415 0.852; 1445 0.878; 2092 0.963*;
	BRCA1	-6666.566	-6669.328	5.524	0.019	20.846	46 0.922; 156 0.891; 190 0.870;
	CDKN1A	-2402.539	-2405.375	5.672	0.017	998.997	
	ERCC6	-17722.824	-17725.639	5.629	0.018	214.303	337 0.982*;
	PLCG2	-19712.406	-19714.546	4.282	0.039	63.187	279 0.947; 404 0.960*;
Dasypus novemcinctus	*FGFR1*	-11325.901	-11331.003	10.204	0.001	720.678	25 0.982*;
	PDGFB	-2522.677	-2526.832	8.311	0.004	25.259	91 0.995**; 95 0.996**; 100 0.996**;
	PDGFRB	-19249.314	-19251.419	4.211	0.040	12.923	234 0.952*; 324 0.978*; 342 0.978*;
	RET	-18991.404	-18993.583	4.357	0.037	513.465	15 0.959*;
	TP53	-6739.030	-6742.070	6.079	0.014	9.568	39 0.884; 45 0.831; 158 0.870; 212 0.907;
	TXN	-1842.886	-1846.297	6.822	0.009	998.999	37 0.998**;
Procavia capensis	*CCNA2*	-5425.443	-5430.899	10.912	0.001	999.000	77 0.806; 309 0.994**;
	ERCC8	-3368.939	-3373.330	8.782	0.003	999.000	207 0.996**;
	GRN	-10091.036	-10094.985	7.899	0.005	30.580	238 0.993**;
	GSS	-7142.769	-7149.881	14.223	0.000	18.826	64 0.993**;180 0.999**;
	HRAS	-3292.198	-3295.910	7.423	0.006	516.135	98 0.993**;
	IL7R	-5446.572	-5448.580	4.016	0.045	247.285	16 0.933;
	NGF	-4530.766	-4534.491	7.452	0.006	56.211	20 0.969*;

Loxodonta africana	*H2AFX*	-2275.081	-2277.260	4.359	0.037	152.949	7 0.983*; 100 0.916;
	HDAC3	-5300.482	-5303.360	5.756	0.016	15.752	189 0.995**; 191 0.935;
	INSR	-23208.190	-23219.297	22.214	0.000	999.000	751 0.986*; 752 0.981*; 753 0.983*; 1038 0.906;
Echinops telfairi	*ATR*	-37801.729	-37803.898	4.337	0.037	461.674	1310 0.964*;
	BSCL2	-5499.130	-5502.035	5.810	0.016	324.696	256 0.971*;
	GHR	-9029.318	-9031.404	4.171	0.041	29.614	71 0.881;
	HESX1	-2747.147	-2750.473	6.651	0.010	72.536	35 0.991**;
	LMNA	-9809.656	-9802.213	14.887	0.000	1.949	
	PDGFRB	-19251.301	-19253.511	4.422	0.035	998.998	64 0.961*; 271 0.978*;

Table S6. Lambda (λ) parameter estimates for life-history traits in mammals

Life-History Trait	**λ**	***P* (λ)[a]**
MLS	0.97	<0.001
BM	0.99	<0.001
LQ	0.97	0.004

[a] Significance of difference of the **λ** model.

Table S7. Summary of genes with a root-to-tip d_N/d_S significantly correlated with maximum lifespan (MLS), body mass (BM), longevity quotient (LQ).

formula	**model**	**outlier sample**	**R^2**	**lambda**	**coefficient**	**p value**	**p value.robust**	**R^2.robust**	**p value.max**
BM ~ BMI1	pgls	"Balaena_mysticetus"	0.2845	0.94	4.0224	0.0006	0.0004	0.311	0.0157
BM ~ CTNNB1	pgls	"Myotis_brandtii"	0.2076	1	5.1071	0.0035	0.0035	0.2126	0.0216
BM ~ E2F1	pgls	"Orcinus_orca"	0.1146	0.961	3.2092	0.0246	0.0066	0.1792	0.0203
BM ~ ERBB2	pgls	"Physeter_catodon"	0.1539	1	6.6927	0.0104	0.0043	0.1985	0.034
BM ~ IGF1	pgls	"Balaena_mysticetus"	0.227	0.983	-3.1432	0.0034	0.0045	0.2204	0.016
BM ~ IGF1R	pgls	"Loxodonta_african"	0.3368	0.849	-4.8164	0.0001	0.0001	0.3558	0.0003
BM ~ PDGFB	pgls	"Myotis_brandtii"	0.1799	0.931	7.015	0.0065	0.0028	0.2226	0.0091
LQ ~ CDK1	pgls	"Myotis_brandtii"	0.337	0.439	1.7315	0.0045	0.002	0.2435	0.0075
LQ ~ ERCC3	ols	"Myotis_brandtii"	0.1541	0	1.8044	0.0103	0.0024	0.2236	0.0085
LQ ~ HRAS	pgls	"Homo_sapiens"	0.2071	0.735	0.6264	0.0035	0.0005	0.2959	0.0045
LQ ~ INSR	ols	"Homo_sapiens"	0.2197	0	3.574	0.0023	0.0003	0.3103	0.0035
MLS ~ ARNTL	pgls	"Sorex_araneus"	0.1233	0.886	0.9055	0.022	0.0044	0.2029	0.0202
MLS ~ ATM	pgls	"Balaena_mysticetus"	0.1834	0.894	3.7153	0.0053	0.0025	0.2216	0.0517
MLS ~ BMI1	pgls	"Rattus_norvegicus"	0.2084	0.855	0.7916	0.0034	0.0008	0.2756	0.0034
MLS ~ CDK1	ols	"Mus_musculus"	0.369	0	0.7481	0.0001	0.0001	0.4139	0.0003
MLS ~ CTNNB1	pgls	"Sorex_araneus"	0.143	1	1.0173	0.0144	0.0014	0.2537	0.0079
MLS ~ ERCC3	pgls	"Equus_caballus"	0.1007	0.753	0.5619	0.0333	0	0.4039	0.001
MLS ~ ERCC5	pgls	"Balaena_mysticetus"	0.1829	0.673	1.6322	0.0054	0.0058	0.1851	0.088
MLS ~ NRG1	pgls	"Balaena_mysticetus"	0.1874	0.997	0.6153	0.0049	0.0018	0.2356	0.0589
MLS ~ STAT5A	ols	"Homo_sapiens"	0.4206	0	1.4094	0	0	0.4723	0

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