Supplementary Information for

Correlated evolution of social organization and lifespan in mammals

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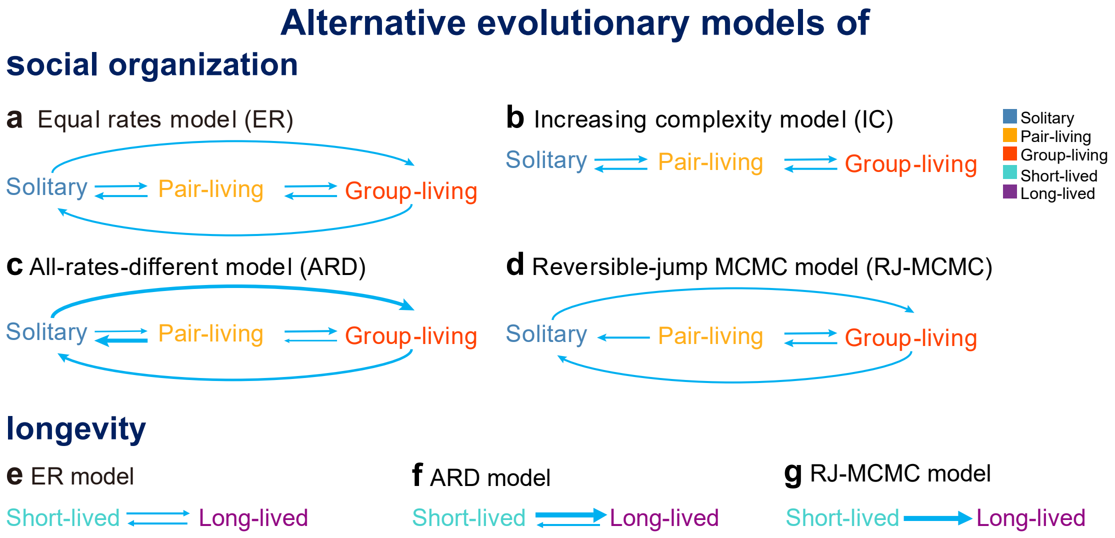
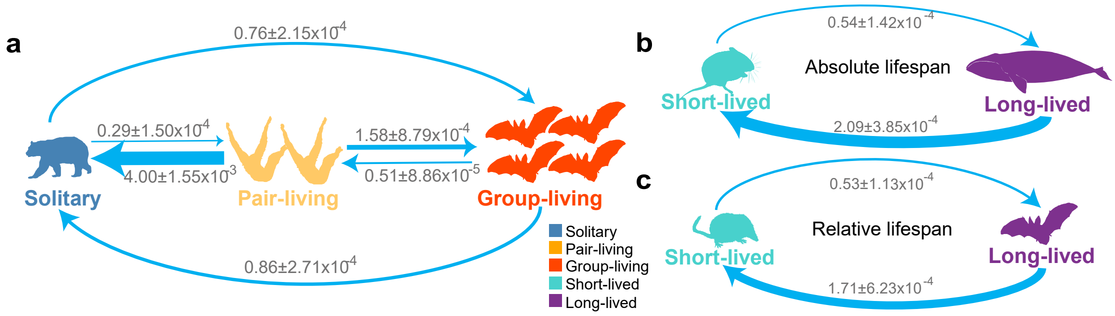
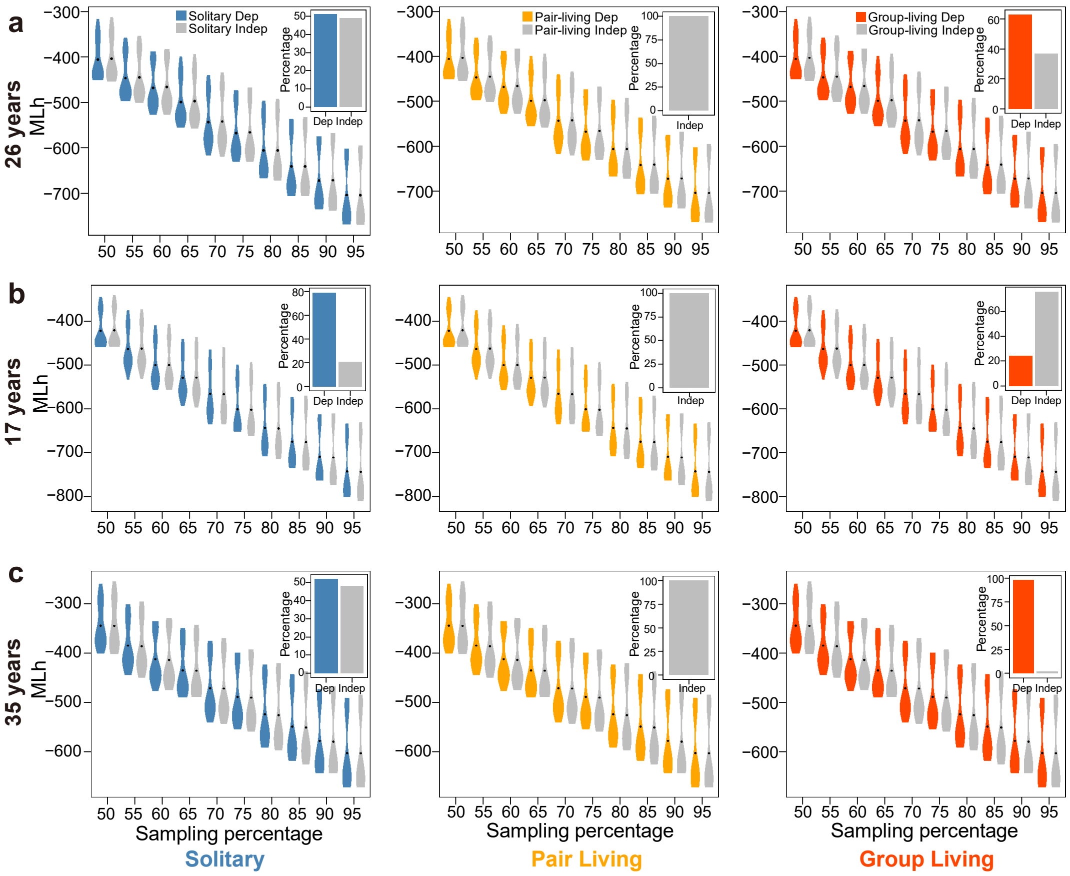
Supplementary Figures



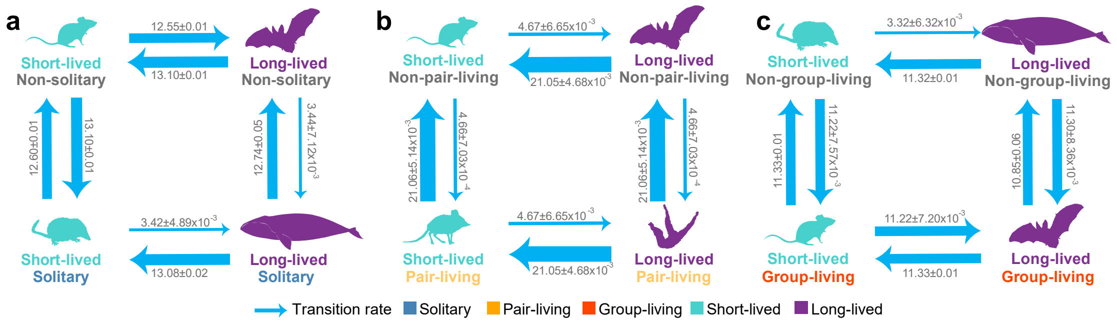
Supplementary Figure 1 Alternative evolutionary models of traits. a-d, social organization and **e-g**, longevity. The ER model (equal rates model): all transition rates are the same. The IC model (increasing complexity model): the model which allows transitions between solitary and pair-living, pair-living and group-living, but not between solitary and group-living. The ARD model (all-rates-different model): all transition rates are different. The RJ-MCMC model (Reversible-jump MCMC model): the model with the highest posterior support that is derived from the data by the reversible-jump procedure in Bayes Traits. Social organization and longevity are colored as follows: solitary = blue; pair-living = orange; group-living = red; short-lived state = cyan; long-lived state = purple. Source data are provided as a Source Data file.



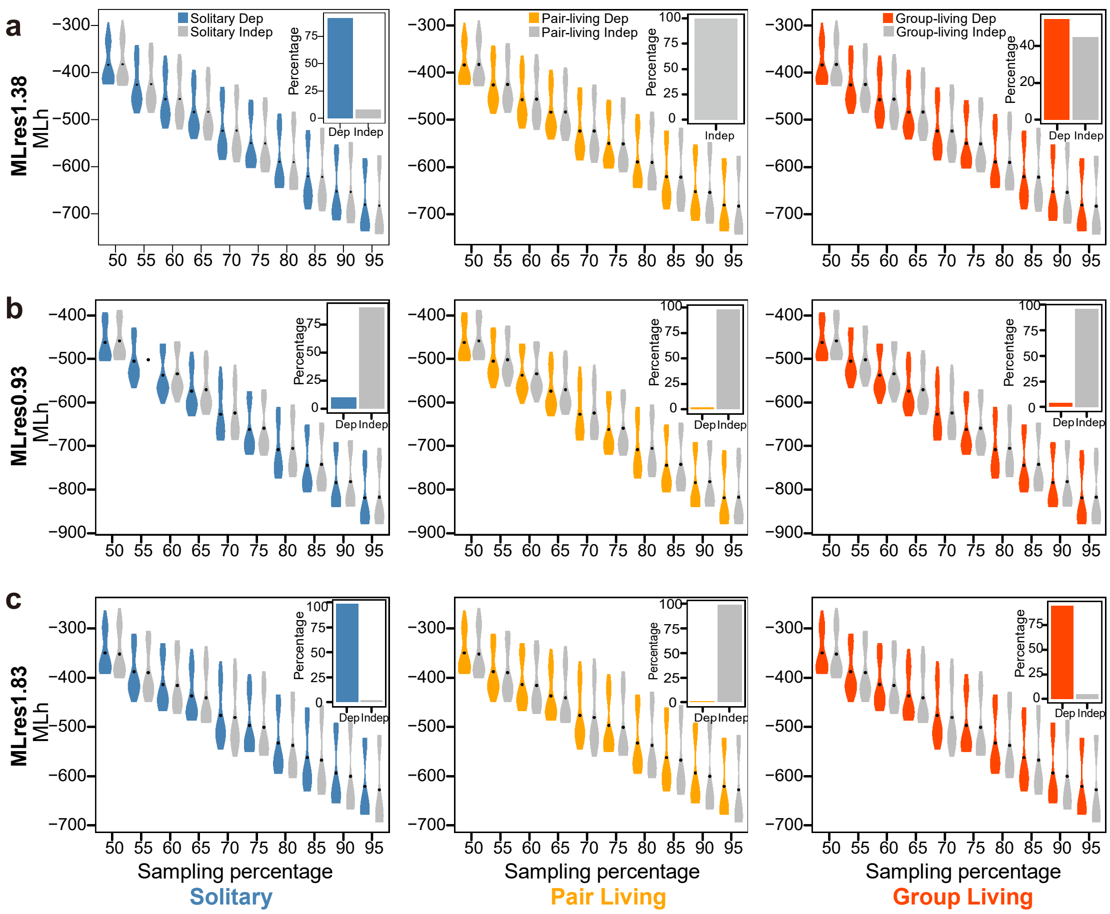
Supplementary Figure 2 The evolutionary pathway of social organization and longevity. a The highest posterior support model for the evolution of social organization. Arrows depict the likelihood of a transition between states and their thickness corresponds to the magnitude of the various rates. Numbers indicate the transition rate (mean ± SD) across ten independent runs. **b** Best supported evolutionary model for absolute longevity. Species with a longevity > 26 years were classified as long-lived species. **c** Best supported evolutionary model for relative longevity. Relative long-lived species were species whose residual of longevity was larger than 1.38 (third quartile value). The residual of longevity for each species was calculated using the body mass adjusted residuals with the equation form the AnAge. The number of species used in these analyses was $n = 974$. Social organization and longevity are colored as follows: solitary = blue; pair-living = orange; group-living = red; short-lived state = cyan; long-lived state = purple. Silhouette images of animals are from PhyloPic database (http://phylopic.org/). Source data are provided as a Source Data file.



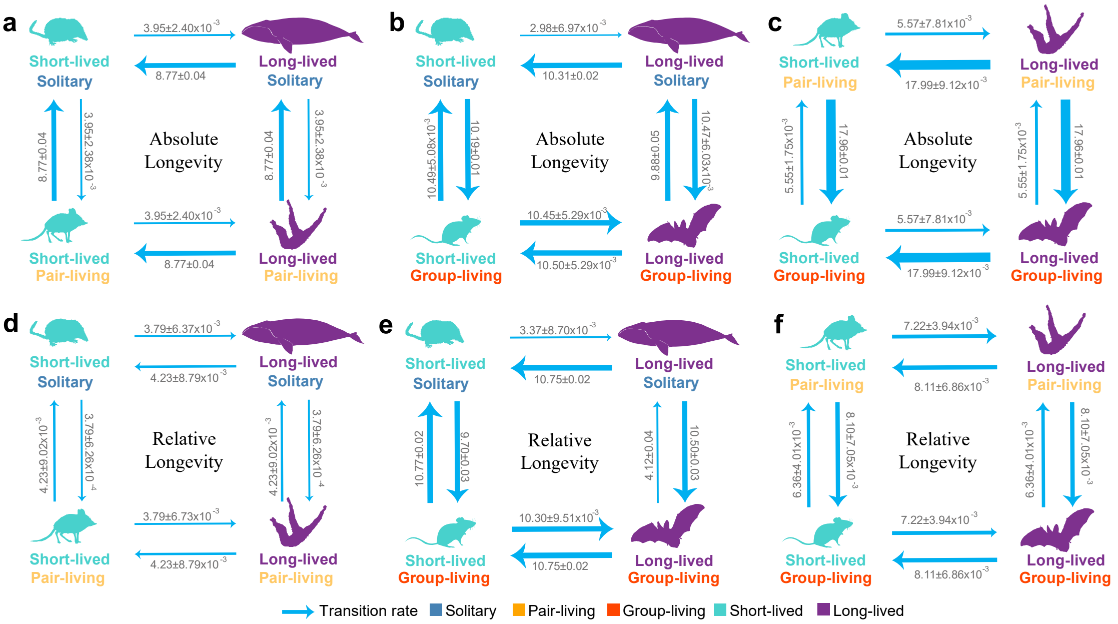
Supplementary Figure 3 The effect of taxonomic sampling on the correlated models of social organization and absolute longevity. Species sampling include 95%, 90%, 85%, 80%, 75%, 70%, 65%, 60%, 55% and 50% of 974 species. A species was classified as long-lived if its maximum lifespan is > 26 years (**a**), > 17 years (**b**) or > 35 years (**c**). In the upper right corner of each plot, bar plots display the supporting proportions of the dependent and independent models. Colors code for social organization: blue = solitary, orange = pair-living and red = group-living. Dep: dependent model; Indep: independent model. Source data are provided as a Source Data file.



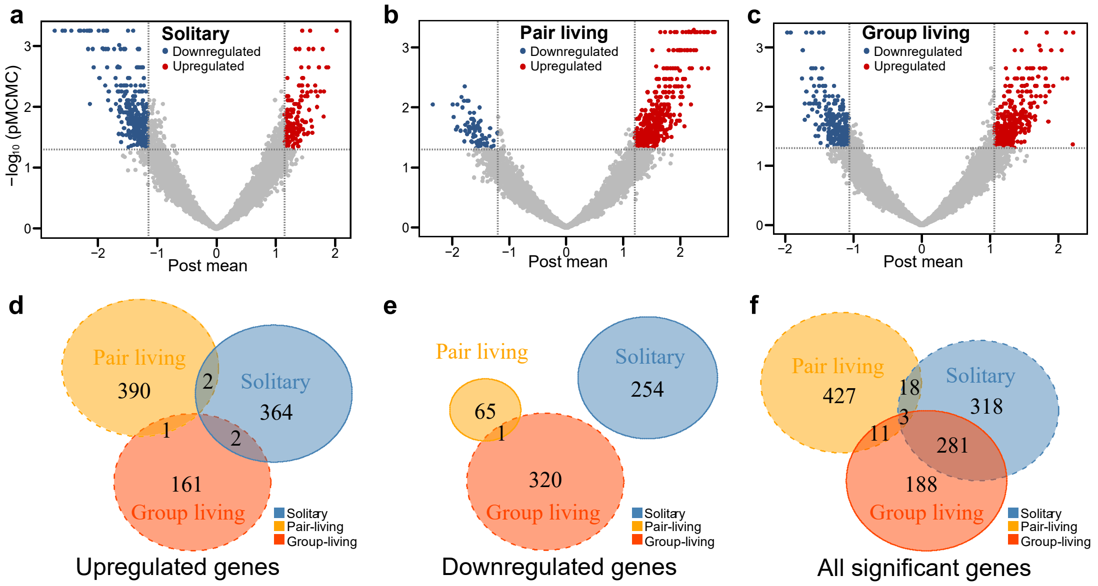
Supplementary Figure 4 Correlated evolution analysis for social organization and relative longevity. Evolutionary models for relative longevity and solitary (**a**); pair-living (**b**); and group-living (**c**). The transition rates from a short-lived to a long-lived state were unequal in **a-c**, showing dependent evolution. Arrows depict the likelihood of transition between states and their thickness corresponds to the magnitude of the various rates. Numbers indicate the transition rate (mean ± SD) across ten independent runs. The number of species used in these analyses was *n* = 974. Social organization and longevity are colored as follows: solitary: blue; pair-living: orange; group-living: red; short-lived state: cyan; long-lived state: purple. Silhouette images of animals are from PhyloPic database (http://phylopic.org/). Source data are provided as a Source Data file.



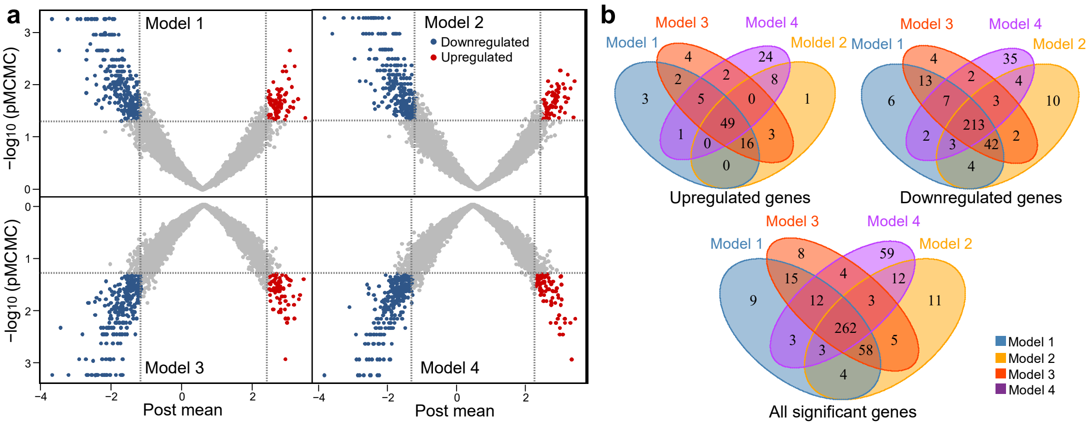
Supplementary Figure 5 The effect of taxonomic sampling on the correlated models of social organization and relative longevity. Species sampling include 95%, 90%, 85%, 80%, 75%, 70%, 65%, 60%, 55% and 50% of 974 species. A species was classified as long-lived if the residual of its maximum lifespan is > 1.38 (**a**), > 0.93 (**b**) or > 1.83 (**c**). In the upper right corner of each plot, bar plots display the supporting proportions of the dependent and independent models. Colors code for social organization and longevity: blue = solitary, orange = pair-living and red = group-living. Dep: dependent model; Indep: independent model. Source data are provided as a Source Data file.



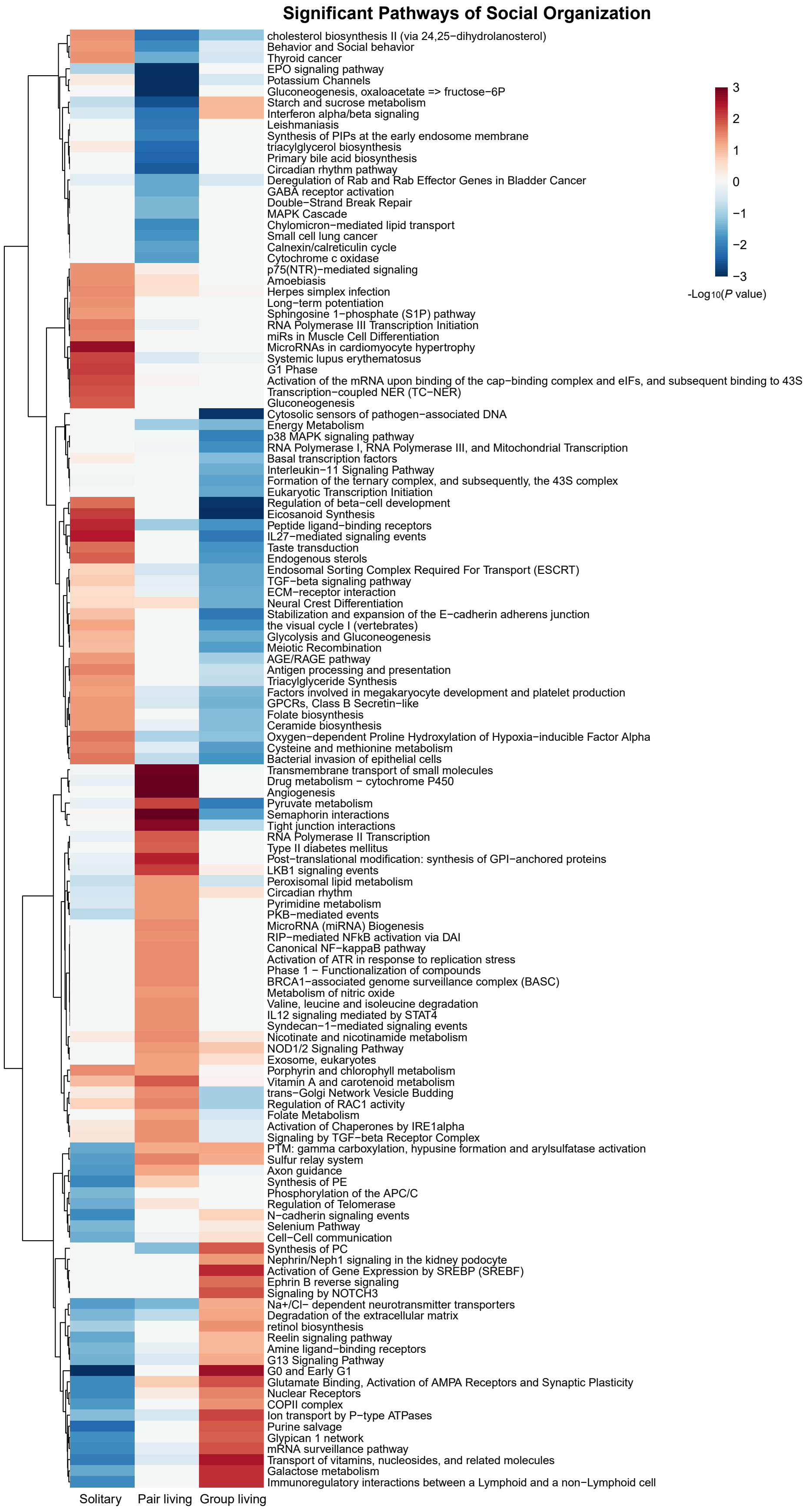
Supplementary Figure 6 Correlated evolution analyses for social organization and longevity using uni-state sub-datasets. Different sub-datasets were used in three different types of models: solitary-pair-living and absolute/relative longevity (species: $n_{\text{uni-state}} = 556$); solitary-group-living and absolute/relative longevity (species: $n_{\text{uni-state}} = 859$); and pair-living-group-living and absolute/relative longevity (species: $n_{\text{uni-state}} = 433$). Evolutionary models for absolute longevity (> 26 years, **a**, **b**, and **c**) and relative longevity (residuals > 1.38, **d**, **e**, and **f**). The transition rates from a short-lived to a long-lived state were equal in **a**, **c**, **d**, **f** showing independent evolution, but were unequal in **b**, **e** showing correlated evolution. Arrows depict the likelihood of transition between states, and their thickness corresponds to the magnitude of the various rates. Numbers indicate the transition rate (mean ± SD) across ten independent runs. Colors code for social organization: blue = solitary, orange = pair-living, red = group-living, cyan = short-lived state, and purple = long-lived state. Silhouette images of animals are from PhyloPic database (http://phylopic.org/). Source data are provided as a Source Data file.



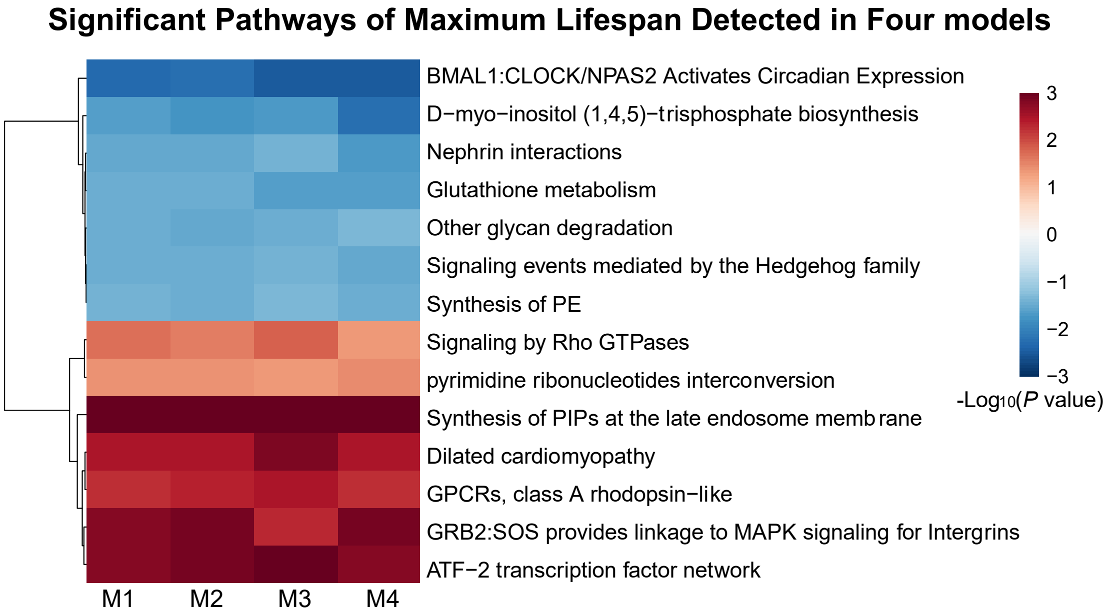
Supplementary Figure 7 Significant genes whose expression was associated with social organization. a Solitary, **b** Pair-living and **c** Group-living. Genes are colored: blue = downregulate genes; red = upregulated genes; gray = non-significant genes. They were generated from MCMCglmm analysis. Genes whose pMCMC < 0.05 and |posterior mean| > cut score (see Methods) were identified as significant genes. A gene with a positive or negative posterior mean had an up- or down-regulated expression, respectively. The number of overlapping genes between solitary, pair-living and group-living are displayed for upregulated genes (**d**) downregulated genes (**e**) and upregulated and downregulated genes (**f**). Blue = solitary, orange = pair-living, and red = group-living. Source data are provided as a Source Data file.



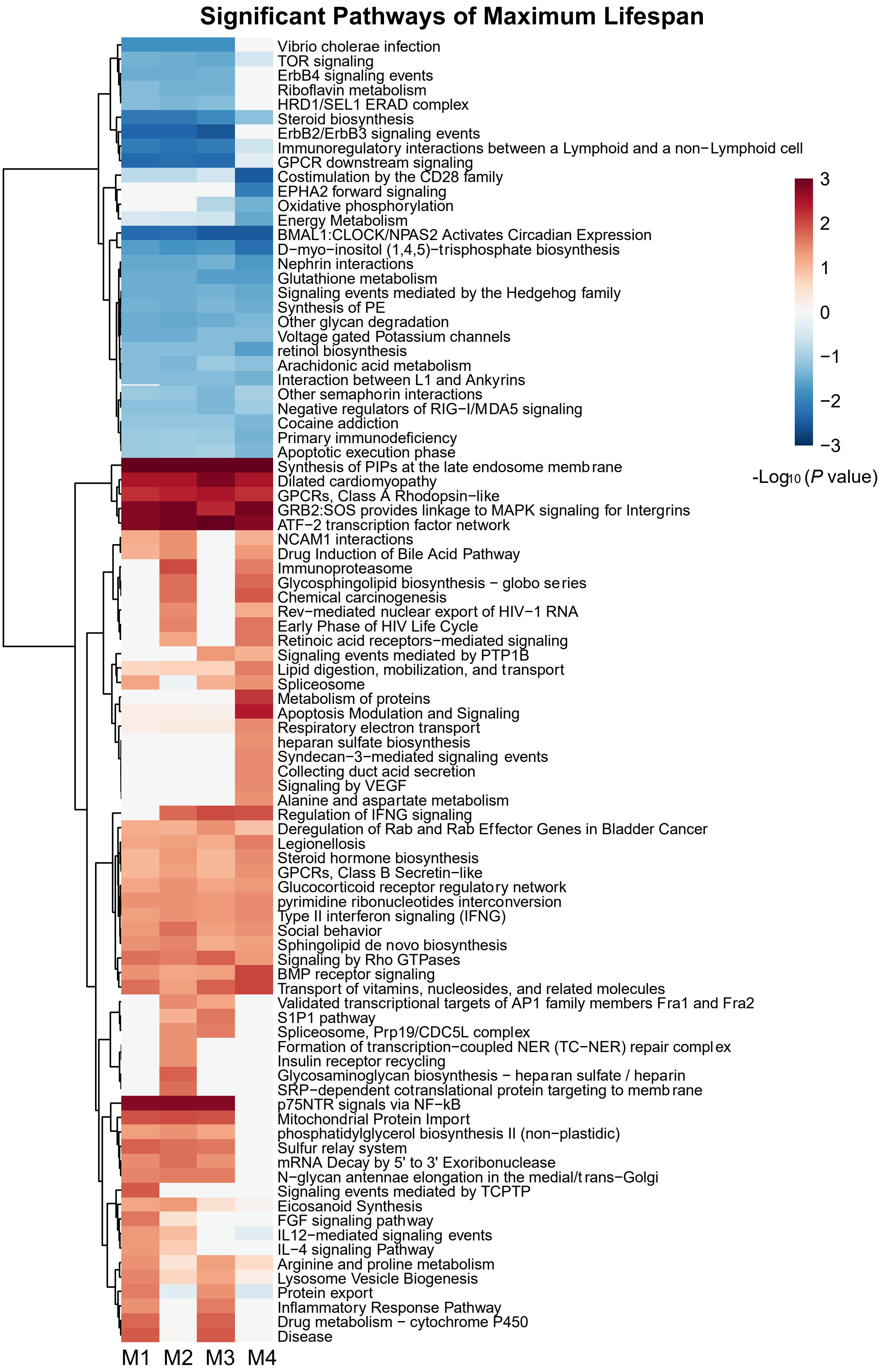
Supplementary Figure 8 Significant genes whose expression was associated with longevity. a Model 1-4. Downregulated genes = blue, upregulated genes = red and non-significant genes = gray. They were generated from MCMCglmm analysis. Genes whose pMCMC < 0.05 and |posterior mean| > cut score (see Methods) were identified as significant genes. A gene with a positive or negative posterior mean had an up- or down-regulated expression, respectively. **b** The number of overlapping upregulated-, downregulated- or all significant- genes in four models. Model 1 = blue, model 2 = yellow, model 3 = red and model 4 = purple. Source data are provided as a Source Data file.



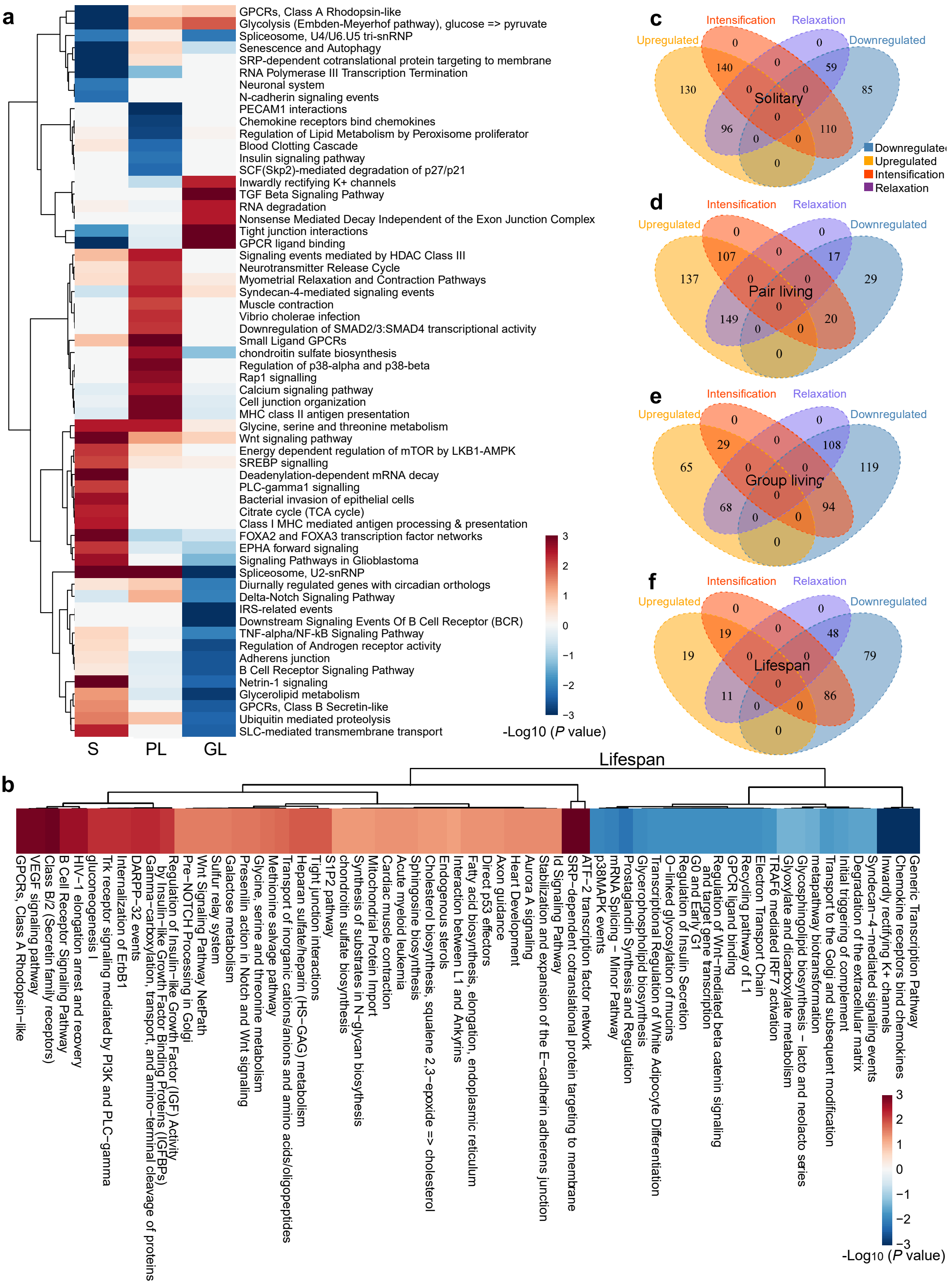
Supplementary Figure 9 Significant pathways of gene expression related to social organization. Polysel method was conducted to detect significant pathways. Post mean of each of 13,402 orthologous genes from MCMCglmm analysis was used to calculate SUMSTAT score. The pathway is shown if its *P* value is less than 0.05 or the absolute of the log10 of *P* value is greater than 1.30. Source data are provided as a Source Data file.



Supplementary Figure 10 Longevity-related pathways of gene expression were identified in four models. M1-M4: model 1 to model 4. Polysel method was conducted to detect significant pathways. Post mean of each of 13,402 orthologous genes from MCMCglmm analysis was used to calculate SUMSTAT score. The pathway is shown if its *P* value is less than 0.05 or the absolute of the log10 of *P* value is greater than 1.30. Source data are provided as a Source Data file.



Supplementary Figure 11 Longevity-related pathways of gene expression were detected in each of four models. M1-M4: model 1 to model 4. Polysel method was conducted to detect significant pathways. Post mean of each of 13,402 orthologous genes from MCMCglmm analysis was used to calculate SUMSTAT score. The pathway is shown if its *P* value is less than 0.05 or the absolute of the log10 of *P* value is greater than 1.30. Source data are provided as a Source Data file.



Supplementary Figure 12 Genes and pathways under selection in social organization and longevity. a Pathways under significant intensified or relaxed selection in social organization. S: solitary, PL: pair-living, GL: group-living. Polysel method was conducted to detect significant pathways. The *K* value of each of 13402 orthologous genes from RELAX was used to calculate SUMSTAT score. The pathway is shown if its *P* value is less than 0.01 or the absolute of the log10 of *P* value is greater than two. **b** The pathways under selection in the long-lived state. Polysel with *K* value was used and the pathway is displayed if its *P* value is less than

0.05 or the absolute of the log10 of *P* value is greater than 1.3. The genes who changed expression significantly and also experienced selection in solitary (**c**), pair-living (**d**) and group-living (**e**) and longevity (**f**). Downregulated genes = blue, upregulated genes = yellow, intensification genes = red and relaxation genes = purple. Source data are provided as a Source Data file.

Supplementary Tables

Supplementary Table 1 Summary of category traits of 974 mammalian species.

Trait	Number of species (proportion)			
Social organization	Solitary	Pair-living	Group-living	
	497 (51.03%)	115 (11.81%)	412 (42.30%)	
Activity	Nocturnal	Diurnal	Others	
	319 (33.69%)	320 (33.79%)	308 (32.52%)	
Lifestyle	Terrestrial	Arboreal and Semiarboreal	Aerial	Others
	583 (59.85%)	127 (26.08%)	63 (6.47%)	74 (7.60%)
Fossoriality	Subterranean	Nonfossorial		
	21 (2.16%)	953 (97.84%)		

Supplementary Table 2 Top ten evolutionary models of social organizations in mammals. The data of 974 species with social polymorphism was used to conduct ten independent interactions. The top ten models account for 93.31%, 92.92%, 93.28%, 92.87%, 93.67%, 93.22%, 93.28%, 93.25%, 92.51% and 93.50% of the posterior sample for ten runs, respectively. The results of the first three interactions were shown here. Rate coefficient q_{ij} describes the transition rates between state i and j, where the subscripts i and j correspond to two states of three social organizations (0: solitary; 1: pair-living; 2: group-living). Z refers to the rate value of zero while 0s and 1s denote different non-zero transition rates. Frequency = visits to model in posterior sample of 500,000 observations. PDF = probability density; CDF = cumulative density.

Run 1

Model	Rate coefficients						Frequency	PDF	CDF
	q01	q02	q10	q12	q20	q21			
1	Z	1	0	1	1	1	158956	0.32	0.32
2	0	1	1	0	1	0	65003	0.13	0.45
3	1	0	0	1	0	1	49490	0.10	0.55
4	0	1	1	1	1	0	46001	0.09	0.64
5	1	0	0	0	0	1	41375	0.08	0.72
6	Z	0	1	0	0	0	38283	0.08	0.80
7	1	1	0	1	1	1	27705	0.05	0.85
8	0	0	1	1	0	0	17787	0.04	0.89
9	0	1	1	Z	1	0	11703	0.02	0.91
10	1	1	0	0	1	1	10265	0.02	0.93

Run 2

Model	Rate coefficients						Frequency	PDF	CDF
	q01	q02	q10	q12	q20	q21			
1	Z	1	0	1	1	1	173691	0.35	0.35
2	0	1	1	0	1	0	55788	0.11	0.46
3	1	0	0	1	0	1	48895	0.10	0.56
4	0	1	1	1	1	0	38729	0.07	0.63
5	1	0	0	0	0	1	37936	0.08	0.71
6	Z	0	1	0	0	0	37234	0.07	0.78
7	1	1	0	1	1	1	31060	0.06	0.84
8	0	0	1	1	0	0	20857	0.05	0.89
9	1	1	0	0	1	1	10388	0.02	0.91
10	0	1	1	Z	1	0	10015	0.02	0.93

Run 3

Model	Rate coefficients						Frequency	PDF	CDF
	q01	q02	q10	q12	q20	q21			
1	Z	1	0	1	1	1	160048	0.32	0.32
2	0	1	1	0	1	0	57631	0.12	0.44
3	1	0	0	1	0	1	54117	0.10	0.54
4	1	0	0	0	0	1	44305	0.09	0.63
5	0	1	1	1	1	0	41199	0.08	0.71
6	Z	0	1	0	0	0	39550	0.08	0.79
7	1	1	0	1	1	1	27985	0.06	0.85
8	0	0	1	1	0	0	20036	0.04	0.89
9	1	1	0	0	1	1	11183	0.02	0.91
10	0	1	1	Z	1	0	10352	0.02	0.93

Supplementary Table 3 Top five evolutionary models of longevity in mammals. The number of species used in these analyses was *n* = 974. Three of ten independent interactions were shown. Rate coefficient q01 describes the transition rates for the short-lived state to the long-lived state, while q10 represents the transition rates for the long-lived state to the short-lived state (0: short-lived; 1: long-lived). Z refers to the rate value of zero while 0s and 1s denote different non-zero transition rates. Frequency = visits to model in posterior sample of 500,000 observations. PDF = probability density; CDF = cumulative density.

Run 1

Absolute lifespan

Model	Rate coefficients		Frequency	PDF	CDF
	q01	q02			
1	0	1	421873	0.84	0.84
2	1	0	78116	>0.15	>0.99
3	0	0	11	<0.01	1.00

Relative lifespan

Model	Rate coefficients		Frequency	PDF	CDF
	q01	q02			
1	1	0	256682	0.51	0.51
2	0	1	240716	0.48	0.99
3	0	0	2602	0.01	1.00

Run 2

Absolute lifespan

Model	Rate coefficients		Frequency	PDF	CDF
	q01	q02			
1	0	1	371588	0.73176	0.74
2	1	0	128405	>0.25	>0.99
3	0	0	7	<0.01	1.00

Relative lifespan

Model	Rate coefficients		Frequency	PDF	CDF
	q01	q02			
1	1	0	250760	0.50	0.50
2	0	1	246521	0.49	0.99
3	0	0	2719	0.01	1.00

Run 3

Absolute lifespan

Model	Rate coefficients		Frequency	PDF	CDF
	q01	q02			
1	0	1	306174	0.61	0.61
2	1	0	193819	0.38	>0.99
3	0	0	7	<0.01	1.00

Relative lifespan

Model	Rate coefficients		Frequency	PDF	CDF
	q01	q02			
1	1	0	254041	0.51	0.51
2	0	1	243330	0.48	>0.99
3	0	0	2629	<0.01	1.00

Supplementary Table 4 Comparative phylogenetic analyses of longevity among different types of social organization. pMCMC values were calculated using MCMCglmm models. They were fitted with longevity as the response variable and social organization, adult body mass, activity, lifestyle, and fossoriality as predictor variables. Both multi-states (species: *n* = 947) and uni-state (species: *n* = 897) of social organization were considered in the MCMCglmm models. The significant factors are highlighted in bold. The reference categories were solitary for social organization, diurnal for activity, terrestrial for lifestyle, and non-fossorial for fossoriality.

Factors using multi-states	post.mean	95%CI	eff.samp	pMCMC	
(Intercept)	0.64	[0.28, 0.98]	1800	**<0.0006**	***
PairLiving	0.10	[0.05, 0.14]	1800	**0.0011**	**
GroupLiving	0.06	[0.03, 0.10]	1957	**<0.0006**	***
Solitary & PairLiving	0.03	[-0.09, 0.14]	1800	0.6578	
PairLiving & GroupLiving	0.06	[0.01, 0.10]	1800	**0.0322**	*
Activity_Nocturnal	0.04	[-0.01, 0.07]	1800	0.0822	
Activity_Others	0.05	[0.02, 0.08]	1800	**0.0011**	**
Lifestyle_Aerial	0.16	[-0.17, 0.48]	1548	0.3244	
Lifestyle_Arboreal	0.02	[-0.04, 0.08]	1957	0.5133	
Lifestyle_Semiarboreal	0.03	[-0.02, 0.08]	1800	0.2878	
Lifestyle_Freshwater	-0.10	[-0.30, 0.11]	1800	0.3367	
Lifestyle_Marine	-0.06	[-0.22, 0.10]	1551	0.5033	
Lifestyle_Terrestrial & Marine	-0.01	[-0.10, 0.09]	1800	0.8467	
Fossoriality_Subterranean	0.10	[-0.01, 0.21]	1800	0.0667	
log$_{10}$(AdultBodyMass)	0.15	[0.12, 0.17]	1800	**<0.0006**	***
Species Number	947				

Factors using uni-state	post.mean	95%CI	eff.samp	pMCMC	
(Intercept)	0.64	[0.29, 1.03]	1663	**0.0011**	**
PairLiving	0.10	[0.06, 0.15]	1979	**<0.0006**	***
GroupLiving	0.06	[0.03, 0.09]	1800	**0.0011**	**
Activity_Nocturnal	0.03	[-0.01, 0.07]	1842	0.1167	
Activity_Others	0.05	[0.02, 0.08]	2357	**0.0056**	**
Lifestyle_Aerial	0.16	[-0.17, 0.47]	1800	0.3267	
Lifestyle_Arboreal	0.02	[-0.04, 0.08]	1800	0.5722	
Lifestyle_Semiarboreal	0.03	[-0.02, 0.08]	1800	0.2467	
Lifestyle_Freshwater	-0.10	[-0.31, 0.11]	1800	0.3511	
Lifestyle_Marine	-0.06	[-0.22, 0.09]	1800	0.4544	
Lifestyle_Terrestrial & Marine	-0.01	[-0.10, 0.10]	1800	0.8511	
Fossoriality_Subterranean	0.09	[-0.04, 0.21]	1800	0.1389	
log$_{10}$(AdultBodyMass)	0.15	[0.12, 0.17]	1800	**<0.0006**	***
Species Number	897				

Supplementary Table 5 Top ten models of correlated evolution of solitary and longevity in mammals. The data of 974 species with social polymorphism was used to conduct ten independent interactions. The top ten models account for 99.59%, 99.61%, 99.58%, 99.62%, 99.53%, 99.54%, 99.59%, 99.61%, 99.65% and 99.57% of the posterior sample for ten runs, respectively. The results of three interactions were shown here. Rate coefficient q_{ij} describes the transition rates between state: 1 = short-lived/non-solitary; 2 = long-lived/non-solitary, 3 = short-lived/solitary, 4 = long-lived/solitary. That is, for example, q_{12} describes the transition rate from the short-lived state to the long-lived state in non-solitary. Z refers to the rate value of zero while 0s and 1s denote different non-zero transition rates. Frequency = visits to model in posterior sample of 500,000 observations. PDF = probability density; CDF = cumulative density.

Run 1 for absolute longevity (> 26 years)

Model	Rate coefficients								Frequency	PDF	CDF
	q12	q13	q21	q24	q31	q34	q42	q43			
1	1	1	1	1	1	0	1	1	430730	0.86	0.86
2	0	0	0	0	0	1	0	0	39873	0.08	0.94
3	1	1	1	1	1	0	1	0	12875	0.03	0.97
4	1	1	1	0	1	0	1	1	4647	0.01	0.98
5	0	0	0	1	0	1	0	0	4336	0.01	0.99
6	0	0	0	0	0	1	0	1	3487	<0.007	
7	0	0	0	1	0	1	0	1	1089	<0.003	
8	1	1	1	0	1	0	1	0	457	<0.001	
9	2	1	1	2	2	0	1	2	283	<0.001	
10	1	2	2	1	1	0	2	1	282	<0.001	

Run 1 for relative longevity (residuals > 1.38)

Model	Rate coefficients								Frequency	PDF	CDF
	q12	q13	q21	q24	q31	q34	q42	q43			
1	1	1	1	0	1	0	1	1	246299	0.49	0.49
2	0	0	0	1	0	1	0	0	222148	0.45	0.94
3	1	0	0	1	1	1	0	0	5989	0.01	0.95
4	1	1	1	0	1	0	0	1	4149	<0.01	>0.95
5	0	0	0	1	0	1	1	0	3558	<0.01	0.96
6	0	1	1	0	0	0	1	1	3264	<0.01	0.97
7	1	0	0	1	1	1	1	0	1897	<0.01	>0.97
8	1	0	0	1	0	1	0	0	1233	<0.01	<0.98
9	1	1	1	1	1	0	1	1	1160	<0.01	<0.98
10	0	1	1	0	0	0	0	1	1072	<0.01	>0.98

Run 2 for absolute longevity (> 26 years)

Model	Rate coefficients								Frequency	PDF	CDF
	q12	q13	q21	q24	q31	q34	q42	q43			
1	1	1	1	1	1	0	1	1	429406	0.86	0.86
2	0	0	0	0	0	1	0	0	41023	0.08	0.94
3	1	1	1	1	1	0	1	0	16821	0.03	0.97
4	0	0	0	0	0	1	0	1	5979	0.01	0.98
5	0	0	0	1	0	1	0	0	2364	0.01	0.99
6	1	1	1	0	1	0	1	1	1752	<0.004	
7	1	2	2	1	1	0	2	1	268	<0.001	
8	2	1	1	2	2	0	1	2	265	<0.001	
9	1	1	1	1	1	0	1	Z	260	<0.001	
10	2	1	1	2	2	0	1	1	134	<0.001	

Run 2 for relative longevity (residuals > 1.38)

Model	Rate coefficients								Frequency	PDF	CDF
	q12	q13	q21	q24	q31	q34	q42	q43			
1	1	1	1	0	1	0	1	1	235471	0.47	0.47
2	0	0	0	1	0	1	0	0	229460	0.46	0.93
3	1	0	0	1	1	1	0	0	6901	0.01	0.94
4	1	1	1	0	1	0	0	1	4796	0.01	0.95
5	0	0	0	1	0	1	1	0	4268	0.01	0.96
6	0	1	1	0	0	0	1	1	3776	0.01	0.97
7	1	0	0	1	0	1	0	0	1834	<0.01	<0.98
8	1	0	0	1	1	1	1	0	1829	<0.01	<0.98
9	0	1	1	0	0	0	0	1	1668	<0.01	>0.98
10	0	0	0	0	0	1	0	0	1321	<0.01	<0.99

Run 3 for absolute longevity (> 26 years)

Model	Rate coefficients								Frequency	PDF	CDF
	q12	q13	q21	q24	q31	q34	q42	q43			
1	1	1	1	1	1	0	1	1	429152	0.86	0.86
2	0	0	0	0	0	1	0	0	40364	0.08	0.94
3	1	1	1	1	1	0	1	0	15949	0.03	0.97
4	0	0	0	0	0	1	0	1	5551	0.01	0.98
5	1	1	1	0	1	0	1	1	3289	0.01	0.99
6	0	0	0	1	0	1	0	0	2069	<0.005	
7	0	0	0	1	0	1	0	1	439	<0.001	
8	1	1	1	0	1	0	1	0	313	<0.001	
9	1	2	2	1	1	0	2	1	295	<0.001	
10	2	1	1	2	2	0	1	2	258	<0.001	

Run 3 for relative longevity (residuals > 1.38)

Model	Rate coefficients								Frequency	PDF	CDF
	q12	q13	q21	q24	q31	q34	q42	q43			
1	1	1	1	0	1	0	1	1	243882	0.49	0.49
2	0	0	0	1	0	1	0	0	222481	0.44	0.93
3	1	0	0	1	1	1	0	0	5184	0.01	0.94
4	1	1	1	0	1	0	0	1	4949	0.01	0.95
5	0	0	0	1	0	1	1	0	4646	0.01	0.96
6	0	1	1	0	0	0	1	1	3946	0.01	0.97
7	1	0	0	1	1	1	1	0	2533	<0.01	<0.98
8	0	1	1	0	0	0	0	1	1719	<0.01	<0.98
9	0	0	0	0	0	1	0	0	1611	<0.01	>0.98
10	1	0	0	1	0	1	0	0	1423	<0.01	>0.98

Supplementary Table 6 Top ten models of correlated evolution of group-living and longevity in mammals. The data of 974 species with social polymorphism was used to conduct ten independent interactions. The top ten models account for 99.98%, 99.98 %, 99.99%, 99.98%, 99.99%, 99.99%, 99.98%, 99.98%, 99.99% and 99.99% of the posterior sample for ten runs, respectively. The results of the first three interactions were shown here. Rate coefficient q_{ij} describes the transition rates between state: 1 = short-lived/non-group-living; 2 = long-lived/non-group-living, 3 = short-lived/group-living, 4 = long-lived/group-living. That is, for example, q_{12} describes the transition rate from the short-lived state to the long-lived state in non-group-living. Z refers to the rate value of zero while 0s and 1s denote different non-zero transition rates. Frequency = visits to model in posterior sample of 500,000 observations. PDF = probability density; CDF = cumulative density.

Run 1 for absolute longevity (> 26 years)

Model	Rate coefficients								Frequency	PDF	CDF
	q12	q13	q21	q24	q31	q34	q42	q43			
1	0	1	1	1	1	1	1	1	488016	0.97	0.97
2	1	0	0	0	0	0	0	0	11731	0.02	0.99
3	0	1	1	1	1	1	0	1	121	<0.001	
4	0	2	1	1	1	2	2	1	11	<0.001	
5	0	2	2	1	1	2	2	1	9	<0.001	
6	0	1	2	1	2	1	1	2	8	<0.001	
7	0	1	2	2	2	2	2	2	8	<0.001	
8	0	1	2	2	2	1	2	2	7	<0.001	
9	0	2	1	2	1	2	2	1	6	<0.001	
10	0	1	2	2	2	1	1	2	5	<0.001	

Run 1 for relative longevity (residuals > 1.38)

Model	Rate coefficients								Frequency	PDF	CDF
	q12	q13	q21	q24	q31	q34	q42	q43			
1	0	1	1	1	1	1	1	1	406562	0.81	0.81
2	1	0	0	0	0	0	0	0	67726	0.14	0.95
3	1	0	0	0	0	0	1	0	12822	0.02	0.97
4	0	1	1	1	1	1	0	1	7110	0.01	0.98
5	0	0	1	1	1	0	0	1	2665	0.01	0.99
6	1	1	0	0	0	1	1	0	1162	<0.01	>0.99
7	0	0	1	0	1	0	0	1	624	<0.01	
8	1	1	0	1	0	1	1	0	240	<0.001	
9	0	1	1	0	1	1	0	1	152	<0.001	
10	0	0	1	1	1	1	0	1	142	<0.001	

Run 2 for absolute longevity (> 26 years)

Model	Rate coefficients								Frequency	PDF	CDF
	q12	q13	q21	q24	q31	q34	q42	q43			
1	0	1	1	1	1	1	1	1	491265	0.98	0.98
2	1	0	0	0	0	0	0	0	8367	0.01	0.99
3	1	0	0	0	0	0	1	0	146	<0.001	
4	0	1	1	1	1	1	0	1	65	<0.001	
5	1	0	1	0	0	0	0	0	17	<0.001	
6	0	2	1	2	1	2	2	1	14	<0.001	
7	0	1	0	1	1	1	1	1	12	<0.001	
8	0	1	2	1	2	1	1	2	12	<0.001	
9	0	2	1	1	1	2	2	1	8	<0.001	
10	0	1	2	1	2	1	2	2	6	<0.001	

Run 2 for relative longevity (residuals > 1.38)

Model	Rate coefficients								Frequency	PDF	CDF
	q12	q13	q21	q24	q31	q34	q42	q43			
1	0	1	1	1	1	1	1	1	385618	0.77	0.77
2	1	0	0	0	0	0	0	0	86249	0.17	0.94
3	1	0	0	0	0	0	1	0	11689	0.02	0.96
4	0	1	1	1	1	1	0	1	11075	0.02	0.98
5	0	0	1	1	1	0	0	1	2511	<0.01	>0.99
6	1	1	0	0	0	1	1	0	943	<0.01	
7	0	0	1	0	1	0	0	1	550	<0.01	
8	0	1	0	1	1	1	0	1	328	<0.001	
9	1	1	0	1	0	1	1	0	205	<0.001	
10	1	0	0	1	0	0	1	0	94	<0.001	

Run 3 for absolute longevity (> 26 years)

Model	Rate coefficients								Frequency	PDF	CDF
	q12	q13	q21	q24	q31	q34	q42	q43			
1	0	1	1	1	1	1	1	1	499851	0.99	0.99
2	0	1	2	1	2	1	1	2	18	<0.001	
3	0	2	1	2	1	2	2	1	17	<0.001	
4	0	1	2	2	2	1	1	2	8	<0.001	
5	0	2	1	1	1	2	2	1	7	<0.001	
6	0	2	1	1	1	2	1	1	6	<0.001	
7	0	2	1	2	1	1	2	1	6	<0.001	
8	0	1	1	2	2	1	1	2	5	<0.001	
9	0	1	1	2	2	1	2	2	5	<0.001	
10	0	2	1	2	1	2	1	1	5	<0.001	

Run 3 for relative longevity (residuals > 1.38)

Model	Rate coefficients								Frequency	PDF	CDF
	q12	q13	q21	q24	q31	q34	q42	q43			
1	0	1	1	1	1	1	1	1	401162	0.80	0.80
2	1	0	0	0	0	0	0	0	69870	0.14	0.94
3	1	0	0	0	0	0	1	0	12830	0.03	0.97
4	0	1	1	1	1	1	0	1	10595	0.02	0.99
5	0	0	1	1	1	0	0	1	2273	<0.01	>0.99
6	1	1	0	0	0	1	1	0	953	<0.01	
7	0	1	1	0	1	1	0	1	714	<0.01	
8	0	0	1	0	1	0	0	1	521	<0.01	
9	0	1	0	1	1	1	0	1	228	<0.001	
10	1	1	0	1	0	1	1	0	112	<0.001	

Supplementary Table 7 Likelihoods of dependent and independent models estimated for the correlated evolution of social organization and longevity using a different phylogenetic tree. The number of species used in these analyses was *n* = 974. The phylogenetic tree was from Upham et al., 2019. Absolute long-lived species were categorized using three cut-offs: longevity > 26 years or longevity > 17 years or longevity > 35 years. Relative long-lived species were classified using the body mass adjusted residuals: longevity > 1.38, longevity > 0.93 or longevity > 1.83.

Social states (no/yes)	Longevity states (no/yes)	Mean likelihood of model		Log BF	Correlated evolution
		Dependent	Independent		
Solitary	Absolute long-lived (> 26 years)	-800.83	-801.99	2.32	Yes
Pair living	Absolute long-lived (> 26 years)	-661.14	-654.56	-13.16	No
Group living	Absolute long-lived (> 26 years)	-783.89	-784.15	0.52	No
Solitary	Absolute long-lived (> 17 years)	-822.98	-832.67	19.38	Yes
Pair living	Absolute long-lived (> 17 years)	-697.75	-692.53	-10.44	No
Group living	Absolute long-lived (> 17 years)	-814.53	-816.04	3.02	Yes
Solitary	Absolute long-lived (> 35 years)	-702.69	-702.61	-0.16	No
Pair living	Absolute long-lived (> 35 years)	-540.00	-544.49	8.98	Yes
Group living	Absolute long-lived (> 35 years)	-677.66	-686.79	18.26	Yes
Solitary	Relative long-lived (Residuals > 1.38)	-770.82	-782.61	23.58	Yes
Pair living	Relative long-lived (Residuals > 1.38)	-644.20	-638.00	-12.40	No
Group living	Relative long-lived (Residuals > 1.38)	-759.20	-766.00	13.60	Yes
Solitary	Relative long-lived (Residuals > 0.93)	-924.18	-925.33	2.30	Yes
Pair living	Relative long-lived (Residuals > 0.93)	-798.96	-793.29	-11.34	No
Group living	Relative long-lived (Residuals > 0.93)	-911.33	-913.20	3.74	Yes
Solitary	Relative long-lived (Residuals > 1.83)	-718.98	-735.46	32.96	Yes
Pair living	Relative long-lived (Residuals > 1.83)	-581.79	-575.57	-12.44	No
Group living	Relative long-lived (Residuals > 1.83)	-704.43	-718.62	28.38	Yes

Supplementary Table 8 Likelihoods of dependent and independent models estimated for the correlated evolution of social organization and longevity using uni-state sub-datasets. Different sub-datasets were used in three different types of models: solitary-pair-living models and absolute/relative longevity (species: $n_{\text{uni-state}}$ = 556); solitary-group-living and absolute/relative longevity (species: $n_{\text{uni-state}}$ = 859); and pair-living-group-living and absolute/relative longevity (species: $n_{\text{uni-state}}$ = 433). Absolute long-lived species were categorized using three cut-offs: longevity > 26 years or longevity > 17 years, or longevity > 35 years. Relative long-lived species were classified using the body mass adjusted residuals: longevity > 1.38, longevity > 0.93, or longevity > 1.83.

Social states	Longevity states (no/yes)	Mean likelihood of model		Log BF	Correlated evolution
		Dependent	Independent		
Solitary-Pair living	Absolute long-lived (> 26 years)	-321.69	-319.14	-5.10	No
Solitary-Pair living	Absolute long-lived (> 17 years)	-390.85	-388.36	-4.98	No
Solitary-Pair living	Absolute long-lived (> 35 years)	-257.15	-253.87	-6.56	No
Solitary-Pair living	Relative long-lived (Residuals > 1.38)	-310.37	-307.53	-5.68	No
Solitary-Pair living	Relative long-lived (Residuals > 0.93)	-470.67	-465.67	-10.00	No
Solitary-Pair living	Relative long-lived (Residuals > 1.83)	-247.90	-244.75	-6.30	No
Solitary-Group living	Absolute long-lived (> 26 years)	-659.99	-662.76	5.54	Yes
Solitary-Group living	Absolute long-lived (> 17 years)	-680.46	-684.07	7.22	Yes
Solitary-Group living	Absolute long-lived (> 35 years)	-582.55	-590.02	14.94	Yes
Solitary-Group living	Relative long-lived (Residuals > 1.38)	-630.77	-637.55	13.56	Yes
Solitary-Group living	Relative long-lived (Residuals > 0.93)	-760.14	-758.94	-2.40	No
Solitary-Group living	Relative long-lived (Residuals > 1.83)	-565.70	-577.48	23.56	Yes
Pair living-Group living	Absolute long-lived (> 26 years)	-336.12	-332.15	-7.94	No
Pair living-Group living	Absolute long-lived (> 17 years)	-296.14	-292.67	-6.94	No
Pair living-Group living	Absolute long-lived (> 35 years)	-288.54	-286.74	-3.60	No
Pair living-Group living	Relative long-lived (Residuals > 1.38)	-305.64	-302.86	-5.56	No
Pair living-Group living	Relative long-lived (Residuals > 0.93)	-334.66	-331.36	-6.60	No
Pair living-Group living	Relative long-lived (Residuals > 1.83)	-300.82	-296.67	-8.30	No

Supplementary Table 9 Summary of category traits of 94 mammalian species used in the transcriptomic analyses.

Trait	Number of species (proportion)		
Social organization	Solitary	Pair-living	Group-living
	26 (27.66%)	11 (11.70%)	65 (69.15%)
Activity	Nocturnal	Diurnal	Others
	54 (57.45%)	21 (22.34%)	19 (20.21%)
Diet	Carnivore	Herbivore	Omnivore
	50 (53.19%)	23 (24.47%)	21 (22.34%)
Lifestyle	Non-aerial	Aerial	
	59 (62.77%)	35 (37.23%)	

Supplementary References

References of **Supplementary Data 1** and **Supplementary Data 3 (separate files)**

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