Supplementary methods and results

Sex differences in telomere length

Once we had determined the best function describing the relationship between average telomere length and age, we tested for a difference between the sexes by including a two-level factor for sex in our model. The inclusion of sex did not increase the explanatory power of our best model (ΔAIC=-0.26; LRT: $\chi^2(1)=2.29$, p=0.133), indicating that there was little evidence for a sex difference in average telomere length. To test whether the ageing patterns differed between the sexes, we also tested for interactions between sex and the selected age terms. Model fit was not improved by the inclusion of an interaction between sex and age class (ΔAIC=0.54; LRT: $\chi^2(2)=3.460$, p=0.177) or sex and the linear age term (ΔAIC=1.60; LRT: $\chi^2(2)=2.400$, p=0.301), indicating that ageing patterns did not differ between the sexes. The best age function was the same when the model selection procedure was repeated on male and female datasets separately.

In a previous study, we used a much smaller, largely cross-sectional dataset collected over two years to examine sex differences in telomere length (1). We found an interaction between sex and the linear effect of age in years (LRT: $\chi^2(1)=5.67$, p=0.02). Males, but not females, showed a linear decline in average telomere length with age (β=-0.019 ± 0.008 SE). When we tested the same interaction between sex and a linear effect of age in years in our much larger, longitudinal dataset, the interaction was again statistically significant (LRT: $\chi^2(1)=6.34$, p=0.012). In this model, both sexes showed a statistically significant decline in average telomere length with age, but the decline was again significantly steeper in males (age effect in females: β=-0.016 ± 0.002 SE; age effect in males compared to females: β=-0.013 ± 0.005 SE). However, this model does not account for the non-linear decline in average telomere length with age that is apparent in the new dataset (Figure 1). When this non-linearity was accounted for with the inclusion of a two-level factor for age class (lambs vs adults), the interaction was no longer detectable (see above). We therefore concluded that there was little evidence for a consistent sex difference in average telomere length once the effect of age had been appropriately accounted for. However, we retained sex as a two-level fixed factor when estimating the heritability of telomere length to be conservative.

Separate multivariate models of adults and lambs

To check the consistency of our results, we re-ran the multivariate phenotypic and genetic models of telomere length, body weight and overwinter survival separately on adults (aged ≥ 1 year) and lambs (aged 4 months). For adults, we used the same model structure as outlined in the main text, except we omitted the two-level fixed factor for age class. For lambs, we included fixed effects for sex (two-level factor), twin status (0=no twin; 1=twin) and maternal age (linear and quadratic effects) in the models of weight and survival. In the lamb phenotypic model, we estimated the covariance between telomere length, body weight and overwinter survival at the among-mother, among-year and residual levels (we were unable to estimate the covariance at the among-individual level since we had only one observation per individual). In the genetic model, we estimated the covariance at the genetic, among-mother, among-year and residual levels (the among-mother level represents the maternal effect covariance, that captures similarity among offspring from the same mother that is not explained by genetic effects).

The results from the adult model were largely consistent with the overall dataset (Figure S2; Tables S7 & S9). There was a positive correlation between telomere length and overwinter survival at the among-individual level, which was underpinned by a genetic correlation. The estimates for the among-individual and genetic correlations between telomere length and body weight were negative, but the credible intervals overlapped zero. The credible intervals for the permanent environment, among-year and residual correlations between telomere length and weight and survival broadly overlapped zero. There was a positive association between August weight and overwinter survival at all hierarchical levels.

For lambs, the estimate for the correlation between telomere length and survival probability was positive at the among-mother level, though the credible intervals overlapped zero (Figure S3; Tables S8 & S10). This suggests that the lambs of mothers with longer telomeres also tended to have a higher probability of surviving their first winter. As expected from the overall dataset, this was underpinned by a genetic correlation. The genetic correlation between telomere length and August weight was negative, indicating that lambs with genes to grow large tended to have relatively short telomeres and suggesting a potential trade-off between growth and telomere attrition (though the credible intervals overlapped zero). The credible intervals for the maternal effect, among-year and residual correlations between telomere length and weight and survival broadly overlapped zero. There was a positive association between August weight and first winter survival at the among-mother, among-year and residual levels. The among-mother association was underpinned by a positive maternal effect correlation, rather than a genetic correlation.

Supplementary references:

1. R. L. Watson *et al.*, Sex differences in leucocyte telomere length in a free-living mammal. *Molecular ecology* **26**, 3230-3240 (2017).

Figure S1. Relative telomere length (RTL) varied over the lifespan in Soay sheep. The grey points show the full distribution of the raw data (n=3641 observations of 1586 individuals, with one outlier not shown and n=3 observations from individuals aged > 13 grouped with age 13 for clarity). The black lines show predictions from the best model (Table S2), grey shading represents 95% credible intervals around those predictions.

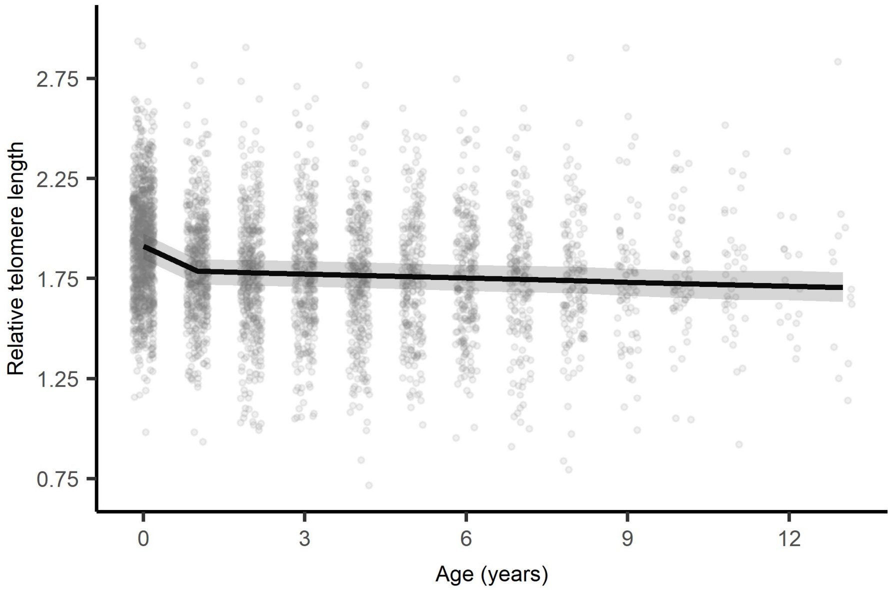

Figure S2. The correlation between relative telomere length (RTL), August body weight and overwinter survival probability at different hierarchical levels in adult Soay sheep (aged ≥ 1 year; n=2468 observations of 879 individuals). Correlations were estimated as the mode of the posterior distribution with 95% higher probability density intervals from multivariate Bayesian mixed-effects models. Panel A shows estimates for the among-individual (teal), among-year (black) and residual correlations (grey) from a phenotypic model (Table S7). Panel B shows estimates for the genetic (teal circles), permanent environment (teal triangles), annual (black) and residual correlations (grey) from a quantitative genetic animal model (Table S9).

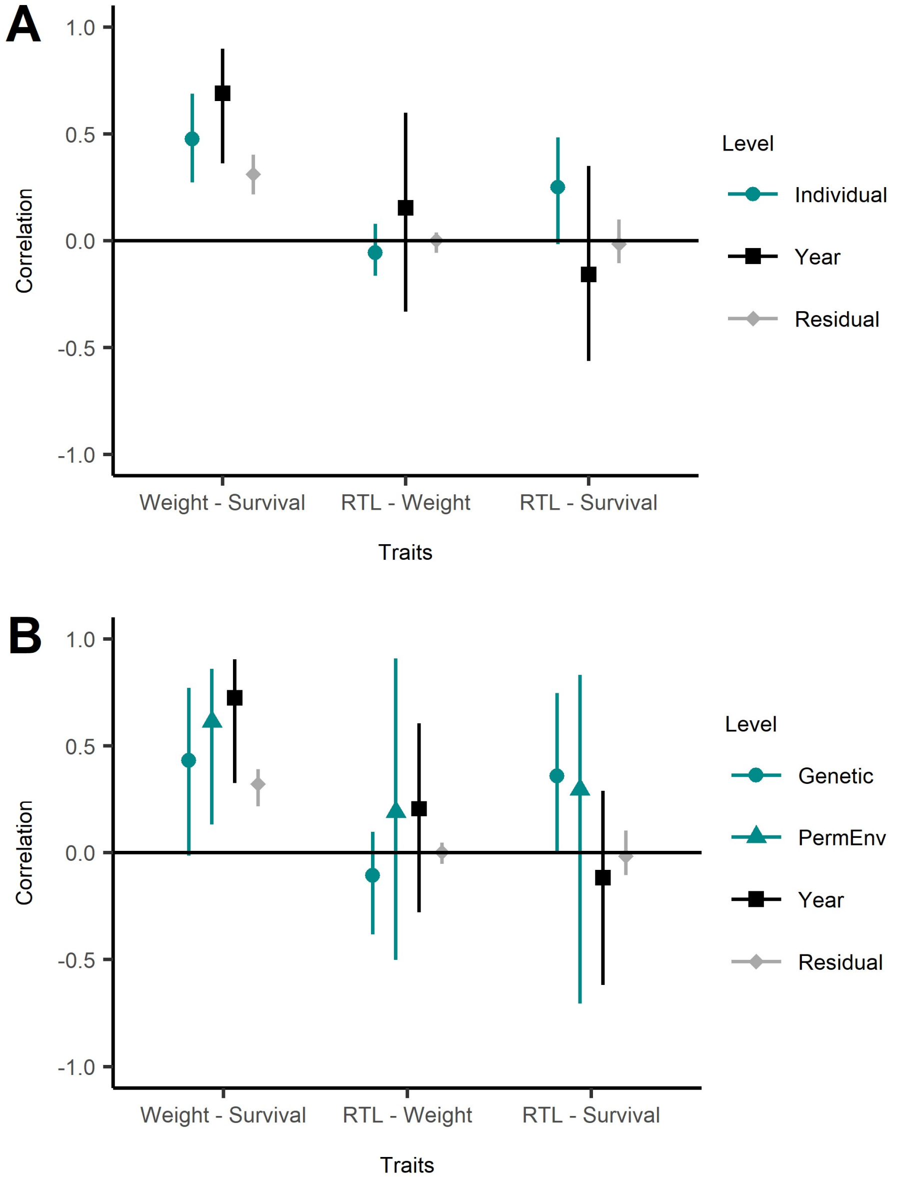

Figure S3. The correlation between relative telomere length (RTL), August body weight and overwinter survival probability at different hierarchical levels in Soay sheep lambs (aged 4 months; n=1056 lambs from 459 mothers). Correlations were estimated as the mode of the posterior distribution with 95% higher probability density intervals from multivariate Bayesian mixed-effects models. Panel A shows estimates for the among-mother (teal), among-year (black) and residual correlations (grey) from a phenotypic model (Table S8). Panel B shows estimates for the genetic (teal circles), maternal effect (teal triangles), annual (black) and residual correlations (grey) from a quantitative genetic animal model (Table S10).

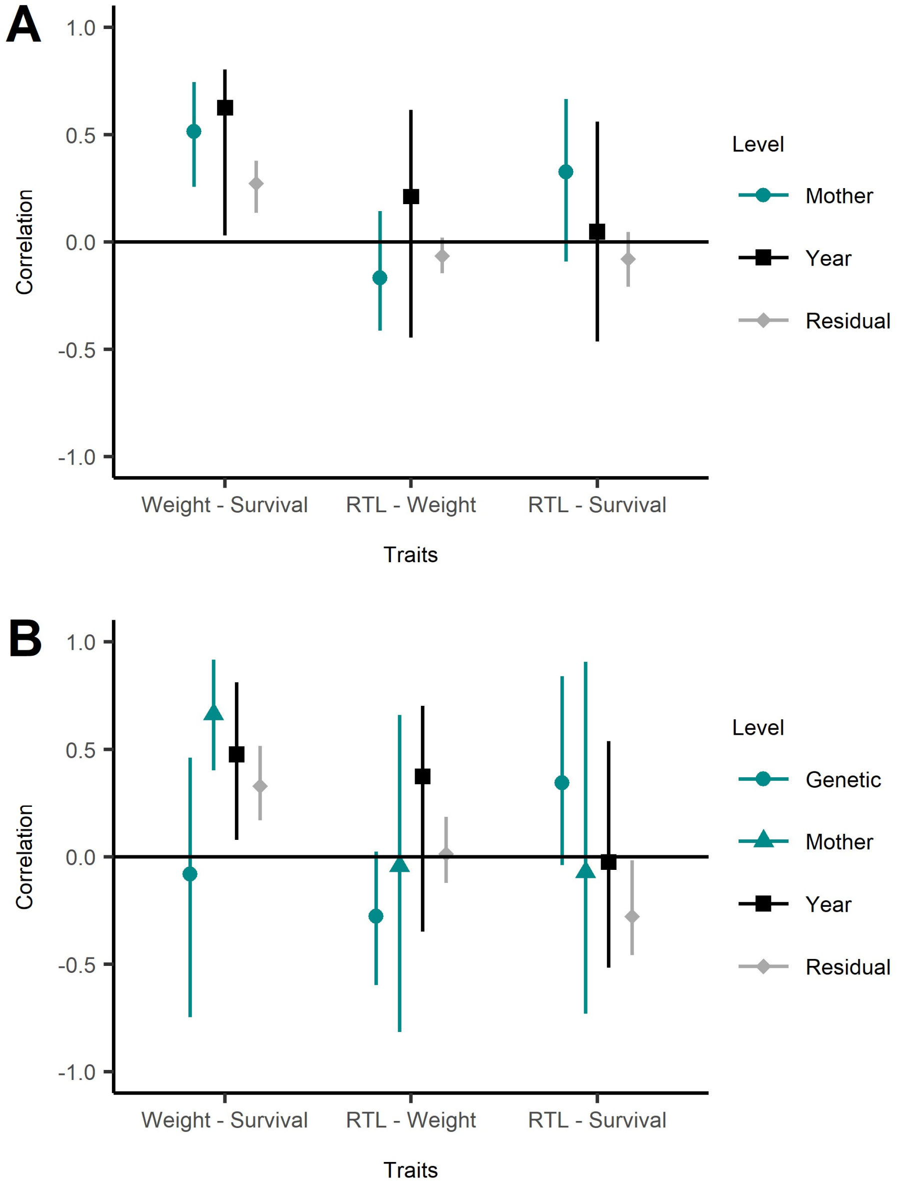

Figure S4. Quality control steps in DNA extraction and telomere length measurement in the white blood cell fraction of blood samples collected from Soay sheep in August 1998 – 2016.

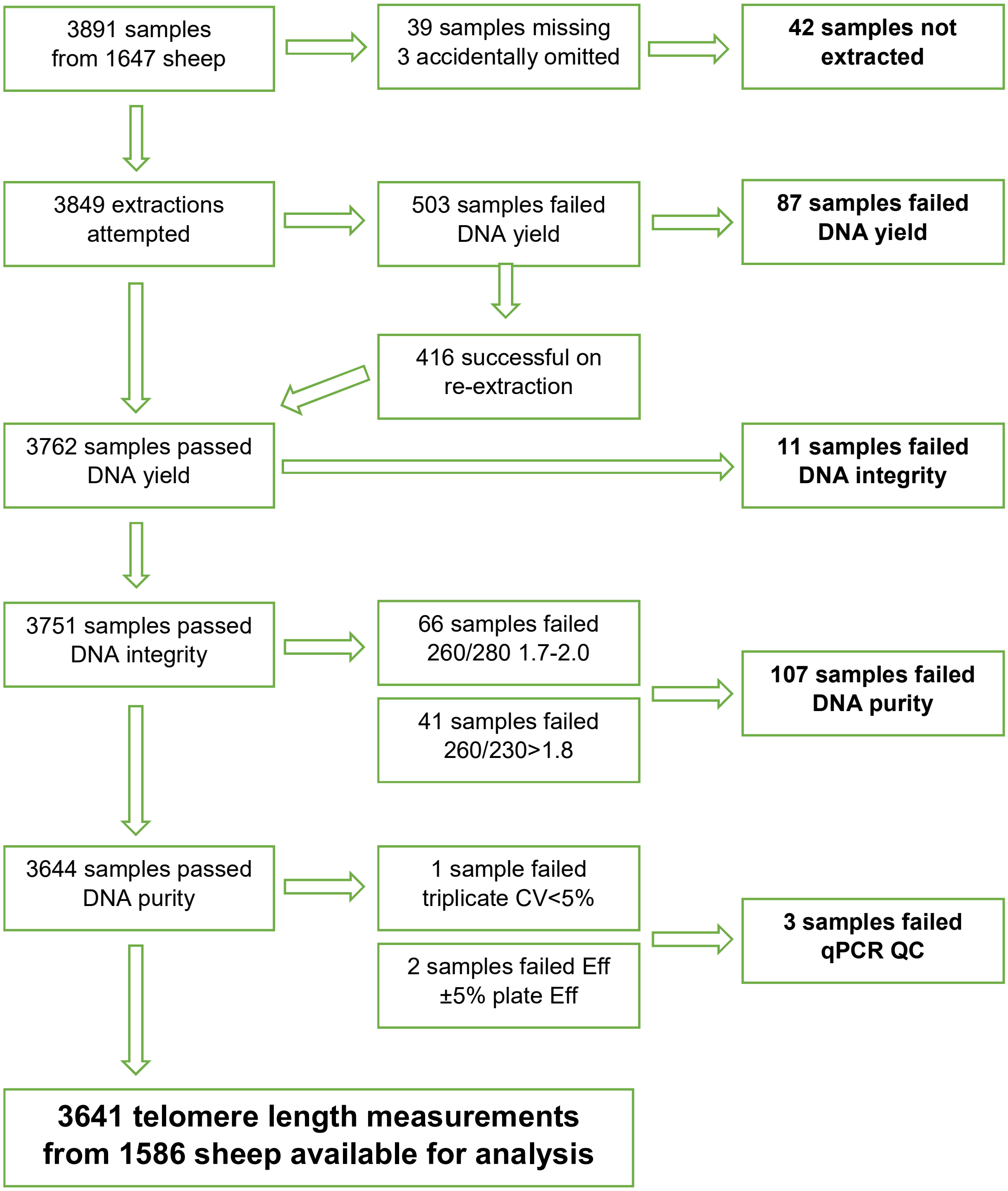

Figure S5. The distribution of relative telomere lengths measured in Soay sheep (n=3641 observations of 1586 individuals), overall (A), in lambs ~4 months (B) and in adults (≥ 1 year). There was one outlier in the adult dataset; exclusion of this outlier did not qualitatively change any of the results.

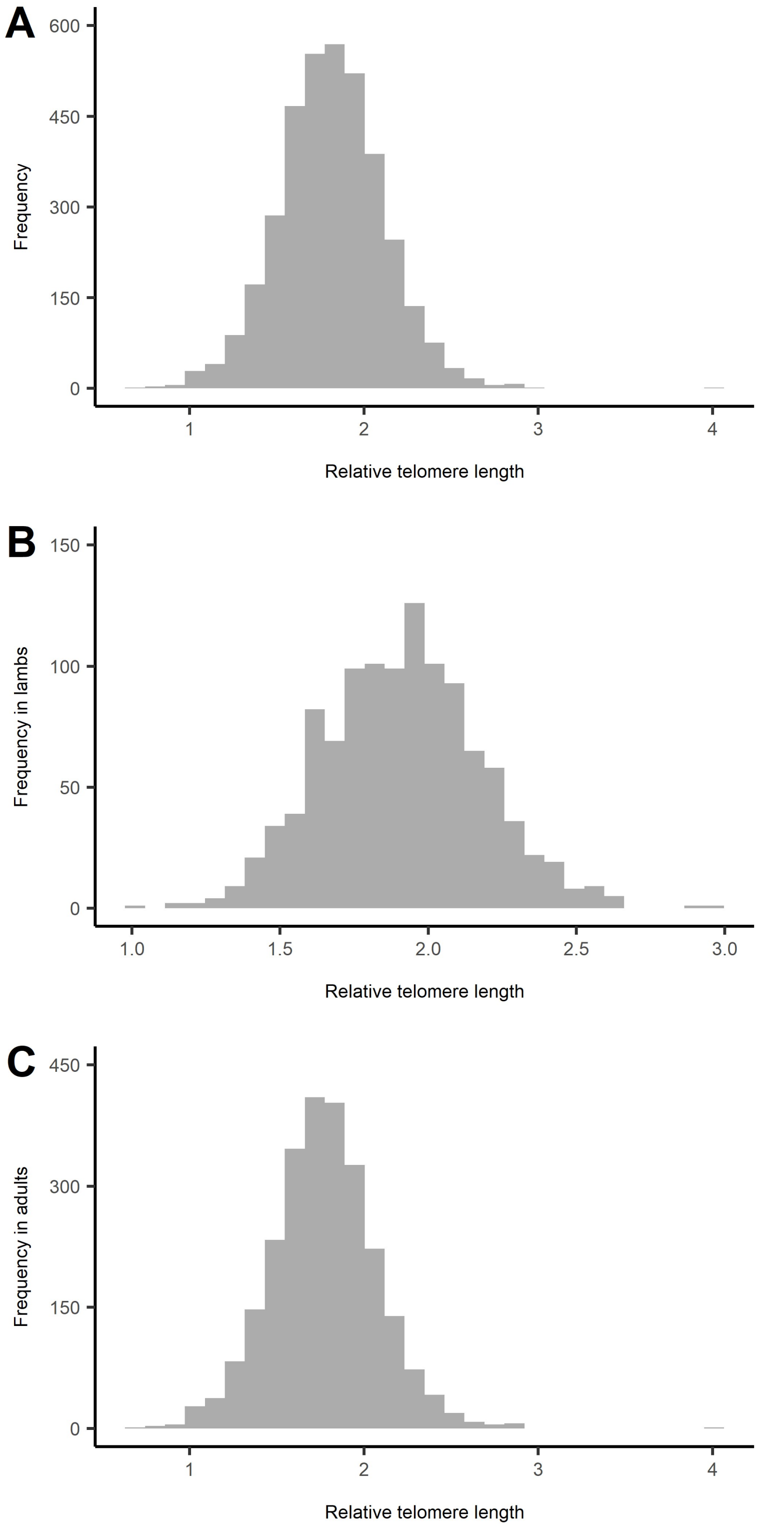

Table S1. Model selection to determine the best function describing the relationship between telomere length and age in Soay sheep. All models included individual, year, qPCR plate and qPCR row as random intercept terms. AgeClass represents a two-level factor indicating whether the sample was taken from a lamb (4 months old) or adult (1 year and older). AgeClass4 represents a four-level factor indicating whether the sample was taken from a lamb (4 months old), a yearling (16 months old), an older adult (2-6 years old) or a geriatric (>6 years old). Linear, quadratic and cubic polynomial functions of age were tested, in addition to threshold functions with a range of different break-points. K indicates the number of parameters estimated for each model, AIC is the Akaike Information Criterion value, and ΔAIC is the difference in AIC value compared to the best model (highlighted in bold). Models were run in *glmmTMB* using maximum likelihood estimation.

Fixed effects	k	AIC	ΔAIC
AgeClass + Age	**8**	**813.39**	**0.00**
AgeClass4	9	813.56	0.17
AgeClass + Age threshold (2 years)	9	814.16	0.77
AgeClass + Age threshold (4 years)	9	814.23	0.84
AgeClass + Age + Age^2	9	814.43	1.04
AgeClass + Age threshold (9 years)	9	814.46	1.08
AgeClass + Age threshold (8 years)	9	814.51	1.13
AgeClass + Age threshold (3 years)	9	814.53	1.14
AgeClass + Age threshold (10 years)	9	814.78	1.39
AgeClass + Age threshold (7 years)	9	814.97	1.58
AgeClass + Age threshold (5 years)	9	814.98	1.59
AgeClass + Age threshold (11 years)	9	815.14	1.75
AgeClass + Age threshold (6 years)	9	815.22	1.83
AgeClass + Age + Age^2 + Age^3	10	816.42	3.03
AgeClass	7	822.20	8.81
Age	7	901.64	88.25
NULL	6	1009.89	196.51

Table S2. Fixed and random effect estimates from the best model of relative telomere length in Soay sheep (from Table S1). Estimates are given as the mode of the posterior distribution with 95% Highest Posterior Density intervals.

		Posterior mode	Lower 95% CI	Upper 95% CI		
	Variance component					
n=3641	ID	0.019	0.015	0.022		
1586 inds	Sample year	0.003	0.001	0.008		
	qPCR plate	0.004	0.002	0.006		
	qPCR row	0.003	0.001	0.017		
	Residual	0.055	0.052	0.059		
	Fixed effect				**pMCMC**	
	Intercept	1.919	1.845	1.973	<0.001	***
	Age class (adult)	-0.118	-0.143	-0.095	<0.001	***
	Age (years)	-0.007	-0.011	-0.003	0.001	***

Table S3. Fixed effects and variance components from a quantitative genetic animal model of relative telomere length in Soay sheep. Estimates are given as the mode of the posterior distribution with 95% credible intervals. The proportion of variance explained by each component was calculated over the entire posterior distribution.

		Posterior mode	**Lower 95%CI**	**Upper 95%CI**		
	Var component				**Proportion**	
n=3632	Additive genetic	0.018	0.014	0.022	0.204	
1582 inds	Permanent env	<0.001	<0.001	0.001	<0.001	
	Maternal effect	<0.001	<0.001	0.003	<0.001	
	Sample year	0.003	0.001	0.008	0.031	
	qPCR plate	0.004	0.002	0.006	0.043	
	qPCR row	0.003	0.001	0.017	0.038	
	Residual	0.054	0.051	0.057	0.630	
	Fixed effect				**pMCMC**	
	Intercept	1.883	1.814	1.955	<0.001	***
	Age class (adult)	-0.110	-0.136	-0.092	<0.001	***
	Sex (males)	0.021	-0.001	0.044	0.069	
	Age (years)	-0.007	-0.011	-0.002	<0.001	***

Table S4a. Variance-covariance matrices from a bivariate model of telomere length in lambs and adults. Variances are shown on the diagonal (in italics), covariances below the diagonal (bottom left) and correlations above the diagonal (top right). Covariances and correlations were deemed to be significant when the credible intervals did not overlap zero (shown in bold). Other fixed and random effects shown in Table S4b. Estimates are given as the mode of the posterior distribution with 95% Highest Posterior Density intervals.

Genetic	Lamb	Adult
Lamb	*0.020* *(0.015–0.028)*	**0.916** **(0.806–0.996)**
Adult	**0.018** **(0.015–0.023)**	*0.019* *(0.015–0.025)*

Year	Lamb	Adult
Lamb	*0.003* *(0.001–0.007)*	**0.770** **(0.313–0.974)**
Adult	**0.002** **(<0.001–0.005)**	*0.003* *(0.001–0.008)*

Residual	Lamb	Adult
Lamb	*0.038* *(0.034–0.046)*	0.036 (-0.196–0.218)
Adult	0.002 (-0.009–0.011)	*0.060* *(0.056–0.064)*

Table S4b. Additional fixed and random effect estimates from a bivariate model of telomere length in lambs and adults. The covariance between lamb and adult telomere length was estimated at the genetic, year and residual levels (see Table S4a). Estimates are given as the mode of the posterior distribution with 95% Highest Posterior Density intervals.

		Posterior mode	**Lower 95% CI**	**Upper 95% CI**		
	Shared random effects					
	qPCR Plate	0.004	0.002	0.005		
	qPCR Row	0.003	0.001	0.017		
Lambs	**Lamb specific random effects**					
	Maternal effect	<0.001	<0.001	0.003		
	Lamb fixed effects				**pMCMC**	
	Intercept	1.899	1.819	1.975	<0.001	***
	Sex (female)	-0.001	-0.035	0.022	0.804	
Adults	**Adult specific random effects**					
	Permanent environment	<0.001	<0.001	0.004		
	Adult fixed effects				**pMCMC**	
	Intercept	1.787	1.701	1.865	<0.001	***
	Sex (female)	-0.033	-0.063	-0.002	0.034	*
	Age	-0.006	-0.011	-0.002	0.006	**

Table S5a. Variance-covariance matrices from a multivariate phenotypic model of telomere length (RTL), August weight and overwinter survival in Soay sheep. Variances are shown on the diagonal (in italics), covariances below the diagonal (bottom left) and correlations above the diagonal (top right). Covariances and correlations were deemed to be significant when the credible intervals did not overlap zero (shown in bold). Other fixed and random effects shown in Table S5b. Estimates are given as the mode of the posterior distribution with 95% Highest Posterior Density intervals.

Individual	RTL	Weight	Survival
RTL	*0.208* *(0.172–0.249)*	-0.067 (-0.188–0.031)	**0.209** **(0.033–0.447)**
Weight	-0.009 (-0.024–-0.004)	*0.078* *(0.069–0.088)*	**0.531** **(0.391–0.713)**
Survival	**0.062** **(0.009–0.130)**	**0.080** **(0.061–0.124)**	*0.360* *(0.170–0.629)*

Year	RTL	Weight	Survival
RTL	*0.035* *(0.020–0.101)*	0.154 (-0.333–0.571)	0.018 (-0.475–0.439)
Weight	0.002 (-0.011–0.016)	*0.009* *(0.005–0.022)*	**0.673** **(0.400–0.897)**
Survival	0.006 (-0.145–0.133)	**0.061** **(0.024–0.157)**	*1.154* *(0.512–2.161)*

Residual	RTL	Weight	Survival
RTL	*0.629* *(0.594–0.665)*	-0.005 (-0.052–0.033)	-0.051 (-0.125–0.048)
Weight	-0.003 (-0.010–0.007)	*0.057* *(0.054–0.061)*	**0.283** **(0.214–0.366)**
Survival	-0.044 (-0.100–0.038)	**0.068** **(0.051–0.089)**	*1.000* *fixed*

Table S5b. Additional fixed and random effect estimates from a multivariate phenotypic model of telomere length (RTL), August weight and overwinter survival in Soay sheep. The covariance between the three traits was estimated at the individual, year and residual levels (see Table S5a). Estimates are given as the mode of the posterior distribution with 95% Highest Posterior Density intervals.

	Posterior mode	**Lower 95% CI**	**Upper 95% CI**	**pMCMC**	
RTL random effects					
qPCR plate	0.039	0.026	0.066		
qPCR row	0.039	0.013	0.187		
RTL fixed effects					
Intercept	-0.206	-0.414	0.031	0.086	.
Age class (lamb)	0.511	0.444	0.581	<0.001	***
Weight random effects					
Mum ID	0.015	0.010	0.024		
Birth year	<0.001	<0.001	0.005		
Weight fixed effects					
Intercept	-0.151	-0.204	-0.071	0.002	**
Age class (lamb)	-0.240	-0.306	-0.183	<0.001	***
Sex (male)	1.526	1.411	1.633	<0.001	***
Age	52.841	50.173	54.806	<0.001	***
Age^2	-29.376	-31.583	-28.129	<0.001	***
Age^3	12.390	10.915	13.766	<0.001	***
Sex (male): Age class (lamb)	-0.658	-0.779	-0.514	<0.001	***
Sex (male): Age	98.442	86.529	106.188	<0.001	***
Sex (male): Age^2	-30.272	-36.095	-18.414	<0.001	***
Sex (male): Age^3	39.649	34.194	52.332	<0.001	***
Survival random effects					
Mum ID	0.092	0.000	0.199		
Birth year	0.221	0.038	0.492		
Survival fixed effects					
Intercept	1.798	1.397	2.613	<0.001	***
Age class (lamb)	-1.956	-2.339	-1.677	<0.001	***
Sex (male)	-0.619	-0.903	-0.427	<0.001	***
Age	-49.746	-63.550	-33.535	<0.001	***
Age^2	-25.744	-40.348	-20.835	<0.001	***
Sex (male): Age class (lamb)	-0.615	-0.901	-0.291	<0.001	***

Table S6a. Variance-covariance matrices from a multivariate animal model of telomere length (RTL), August weight and overwinter survival in Soay sheep. Variances are shown on the diagonal (in italics), covariances below the diagonal (bottom left) and correlations above the diagonal (top right). Covariances and correlations were deemed to be significant when the credible intervals did not overlap zero (shown in bold). Other fixed and random effects shown in Table 6b. Estimates are given as the mode of the posterior distribution with 95% Highest Posterior Density intervals.

Genetic	RTL	Weight	Survival
RTL	*0.217*	**-0.230**	0.251
	(0.175–0.257)	**(-0.428– -0.008)**	(-0.049–0.560)
Weight	-0.017	*0.032*	**0.514**
	(-0.035–0.001)	*(0.022–0.050)*	**(0.063–0.704)**
Survival	0.042	**0.036**	*0.201*
	(-0.002–0.118)	**(0.002–0.075)**	*(0.054–0.418)*

PermEnv	RTL	Weight	Survival
RTL	*<0.001*	0.369	0.499
	(<0.001–0.021)	(-0.598–0.942)	(-0.516–0.973)
Weight	<0.001	*0.053*	**0.602**
	(-0.005–0.020)	*(0.043–0.066)*	**(0.362–0.919)**
Survival	<0.001	**0.065**	*0.184*
	(-0.011–0.045)	**(0.029–0.109)**	*(0.032–0.472)*

Year	RTL	Weight	Survival
RTL	*0.047*	0.286	0.084
	(0.017–0.106)	(-0.312–0.574)	(-0.434–0.445)
Weight	0.004	*0.011*	**0.689**
	(-0.010–0.018)	*(0.005–0.024)*	**(0.373–0.891)**
Survival	0.016	**0.071**	*0.929*
	(-0.156–0.127)	**(0.022–0.171)**	*(0.517–2.271)*

Residual	RTL	Weight	Survival
RTL	*0.611*	-0.005	-0.040
	(0.579–0.646)	(-0.044–0.036)	(-0.126–0.038)
Weight	-0.001	*0.059*	**0.303**
	(-0.008–0.007)	*(0.055–0.063)*	**(0.212–0.355)**
Survival	-0.044	**0.073**	*1.000*
	(-0.098–0.029)	**(0.052–0.088)**	*fixed*

Table S6b. Additional fixed and random effect estimates from a multivariate animal model of telomere length, August weight and overwinter survival in Soay sheep. The covariance between the three traits was estimated at the genetic, maternal, year and residual levels (see Table 6a). Estimates are given as the mode of the posterior distribution with 95% Highest Posterior Density intervals.

	Posterior mode	Lower 95% CI	Upper 95% CI	pMCMC	
RTL random effects					
qPCR plate	0.045	0.026	0.065		
qPCR row	0.041	0.015	0.193		
RTL fixed effects					
Intercept	-0.221	-0.462	0.011	0.042	*
Age class (lamb)	0.494	0.425	0.557	<0.001	***
Weight random effects					
Mum ID	0.009	0.002	0.015		
Birth year	<0.001	<0.001	0.006		
Weight fixed effects					
Intercept	-0.133	-0.215	-0.065	<0.001	***
Age class (lamb)	-0.247	-0.302	-0.187	<0.001	***
Sex (male)	1.518	1.434	1.648	<0.001	***
Age	53.487	50.726	55.641	<0.001	***
Age^2	-29.845	-31.298	-27.777	<0.001	***
Age^3	11.782	10.682	13.521	<0.001	***
Sex (male): Age class (lamb)	-0.659	-0.791	-0.535	<0.001	***
Sex (male): Age	98.353	87.480	106.064	<0.001	***
Sex (male): Age^2	-27.232	-35.244	-17.532	<0.001	***
Sex (male): Age^3	42.394	34.133	51.630	<0.001	***
Survival random effects					
Mum ID	0.001	<0.001	0.141		
Birth year	0.236	0.040	0.454		
Survival fixed effects					
Intercept	1.856	1.220	2.368	<0.001	***
Age class (lamb)	-2.033	-2.346	-1.684	<0.001	***
Sex (male)	-0.621	-0.895	-0.436	<0.001	***
Age	-44.832	-59.699	-30.202	<0.001	***
Age^2	-29.573	-38.785	-19.788	<0.001	***
Sex (male): Age class (lamb)	-0.561	-0.925	-0.289	0.002	**

Table S7a. Variance-covariance matrices from a multivariate phenotypic model of telomere length, August weight and overwinter survival in adult Soay sheep (age ≥ 1 year). Variances are shown on the diagonal (in italics), covariances below the diagonal (bottom left) and correlations above the diagonal (top right). Covariances and correlations were deemed to be significant when the credible intervals did not overlap zero (shown in bold). Other fixed and random effects shown in Table S7b. Estimates are given as the mode of the posterior distribution with 95% Highest Posterior Density intervals.

Individual	RTL	Weight	Survival
RTL	*0.219* *(0.181–0.271)*	-0.058 (-0.164–0.079)	0.250 (-0.017–0.485)
Weight	-0.010 (-0.031–0.015)	*0.155* *(0.130–0.178)*	**0.475** **(0.275–0.689)**
Survival	0.067 (>-0.001–0.138)	**0.121** **(0.059–0.165)**	*0.345* *(0.068–0.665)*

Year	RTL	Weight	Survival
RTL	*0.038* *(0.020–0.111)*	0.153 (-0.331–0.600)	-0.158 (-0.562–0.352)
Weight	0.004 (-0.018–0.025)	*0.013* *(0.009–0.037)*	**0.691** **(0.363–0.898)**
Survival	-0.034 (-0.163–0.119)	**0.073** **(0.029–0.119)**	*0.900* *(0.466–1.912)*

Residual	RTL	Weight	Survival
RTL	*0.647* *(0.605–0.691)*	0.002 (-0.057–0.037)	-0.016 (-0.105–0.099)
Weight	<0.001 (-0.013–0.009)	*0.085* *(0.079–0.092)*	**0.312** **(0.215–0.404)**
Survival	-0.013 (-0.085–0.080)	**0.096** **(0.059–0.116)**	*1.000* *fixed*

Table S7b. Additional fixed and random effect estimates from a multivariate phenotypic model of telomere length, August weight and overwinter survival in adult Soay sheep (aged ≥ 1 year). The covariance between the three traits was estimated at the individual, year and residual levels (see Table S7a). Estimates are given as the mode of the posterior distribution with 95% Highest Posterior Density intervals.

	Posterior mode	Lower 95% CI	Upper 95% CI	pMCMC	
RTL random effects					
qPCR plate	0.046	0.027	0.076		
qPCR row	0.030	0.010	0.147		
RTL fixed effects					
Intercept	-0.038	-0.246	0.217	0.762	
Weight random effects					
Mum ID	0.043	0.023	0.064		
Birth year	<0.001	<0.001	0.005		
Weight fixed effects					
Intercept	1.537	1.440	1.655	<0.001	***
Sex (female)	-1.887	-1.979	-1.803	<0.001	***
Age	29.701	27.378	30.997	<0.001	***
Age^2	-21.722	-22.770	-20.252	<0.001	***
Age^3	10.923	10.007	12.493	<0.001	***
Sex (male): Age	58.770	50.603	70.354	<0.001	***
Sex (male): Age^2	-2.629	-13.900	12.330	0.840	
Sex (male): Age^3	38.328	30.799	47.288	<0.001	***
Survival random effects					
Mum ID	0.001	<0.001	0.195		
Birth year	0.077	0.014	0.249		
Survival fixed effects					
Intercept	0.612	0.076	1.189	0.036	*
Sex (female)	1.213	0.984	1.595	<0.001	***
Age	-46.557	-59.024	-35.522	<0.001	***
Age^2	-21.016	-27.432	-11.245	<0.001	***
Sex (male): Age	-35.333	-69.240	-5.893	0.032	*
Sex (male): Age^2	-40.402	-67.255	-8.578	0.008	**

Table S8a. Variance-covariance matrices from a multivariate phenotypic model of telomere length, August weight and overwinter survival in Soay sheep lambs (~4 months old). Variances are shown on the diagonal (in italics), covariances below the diagonal (bottom left) and correlations above the diagonal (top right). Covariances and correlations were deemed to be significant when the credible intervals did not overlap zero (shown in bold). Other fixed and random effects shown in Table S8b. Estimates are given as the mode of the posterior distribution with 95% Highest Posterior Density intervals.

Mother	RTL	Weight	Survival
RTL	*0.113* *(0.055–0.188)*	-0.168 (-0.413–0.142)	0.327 (-0.091–0.655)
Weight	-0.026 (-0.058–0.020)	*0.179* *(0.121–0.225)*	**0.515** **(0.257–0.744)**
Survival	0.073 (-0.016–0.149)	**0.142** **(0.046–0.216)**	*0.399* *(0.132–0.681)*

Year	RTL	Weight	Survival
RTL	*0.045* *(0.009–0.119)*	0.211 (-0.445–0.615)	0.047 (-0.464–0.562)
Weight	0.005 (-0.044–0.066)	*0.113* *(0.046–0.264)*	**0.626** **(0.029–0.803)**
Survival	0.012 (-0.214–0.265)	**0.189** **(-0.036–0.691)**	*2.314* *(0.946–5.891)*

Residual	RTL	Weight	Survival
RTL	*0.782* *(0.687–0.858)*	-0.065 (-0.146–0.019)	-0.080 (-0.208–0.045)
Weight	-0.036 (-0.082–0.011)	*0.402* *(0.360–0.445)*	**0.283** **(0.134–0.379)**
Survival	-0.037 (-0.185–0.037)	**0.196** **(0.085–0.247)**	*1.000* *fixed*

Table S8b. Additional fixed and random effect estimates from a multivariate phenotypic model of telomere length, August weight and overwinter survival Soay sheep lambs (~4 months old). The covariance between the three traits was estimated at the maternal, year and residual levels (see Table S8a). Estimates are given as the mode of the posterior distribution with 95% Highest Posterior Density intervals.

	Posterior mode	**Lower 95% CI**	**Upper 95% CI**		
RTL random effects					
qPCR plate	0.026	<0.001	0.063		
qPCR row	0.065	0.022	0.314		
RTL fixed effects				**pMCMC**	
Intercept	-0.068	-0.296	0.219	0.836	
Weight fixed effects					
Intercept	0.509	0.368	0.762	<0.001	***
Sex (female)	-0.561	-0.631	-0.463	<0.001	***
Twin (1)	-1.275	-1.368	-1.097	<0.001	***
Mum Age	8.019	5.050	10.522	<0.001	***
MumAge^2	-23.236	-25.039	-20.001	<0.001	***
Survival fixed effects					
Intercept	-0.402	-1.212	0.493	0.424	
Sex (female)	0.612	0.413	0.866	<0.001	***
Twin (1)	-0.577	-0.900	-0.254	<0.001	***
Mum Age	1.940	-4.446	9.658	0.460	
MumAge^2	-12.985	-20.845	-6.610	<0.001	***

Table S9a. Variance-covariance matrices from a multivariate animal model of telomere length (RTL), August weight and overwinter survival in adult Soay sheep (aged ≥ 1 year). Variances are shown on the diagonal (in italics), covariances below the diagonal (bottom left) and correlations above the diagonal (top right). Covariances and correlations were deemed to be significant when the credible intervals did not overlap zero (shown in bold). Other fixed and random effects shown in Table S9b. Estimates are given as the mode of the posterior distribution with 95% Highest Posterior Density intervals.

Genetic	RTL	Weight	Survival
RTL	*0.205 (0.153–0.271)*	-0.108 (-0.383–0.096)	**0.360 (0.007–0.748)**
Weight	-0.007 (-0.052–0.012)	*0.083 (0.052–0.125)*	0.431 (-0.015–0.770)
Survival	**0.058 (0.003–0.149)**	0.057 (-0.008–0.115)	*0.160 (0.023–0.431)*

PermEnv	RTL	Weight	Survival
RTL	*<0.001 (<0.001–0.055)*	0.189 (-0.502–0.908)	0.296 (-0.706–0.831)
Weight	<0.001 (-0.014–0.033)	*0.088 (0.061–0.125)*	**0.614 (0.130–0.859)**
Survival	0.001 (-0.044–0.040)	**0.066 (0.011–0.131)**	*0.146 (0.001–0.475)*

Year	RTL	Weight	Survival
RTL	*0.054 (0.021–0.119)*	0.205 (-0.280–0.605)	-0.118 (-0.620–0.209)
Weight	0.006 (-0.014–0.030)	*0.017 (0.009–0.040)*	**0.725 (0.326–0.905)**
Survival	-0.023 (-0.173–0.119)	**0.099 (0.020–0.199)**	*0.815 (0.442–1.939)*

Residual	RTL	Weight	Survival
RTL	*0.655 (0.610–0.696)*	<0.001 (-0.053–0.045)	-0.017 (-0.105–0.103)
Weight	<0.001 (-0.012–0.011)	*0.086 (0.079–0.091)*	**0.323 (0.215–0.392)**
Survival	-0.013 (-0.084–0.084)	**0.090 (0.064–0.118)**	*1.000 fixed*

Table S9b. Additional fixed and random effect estimates from a multivariate animal model of telomere length, August weight and overwinter survival in adult Soay sheep (aged ≥ 1 year). The covariance between the three traits was estimated at the genetic, permanent environment, year and residual levels (see Table S9a). Estimates are given as the mode of the posterior distribution with 95% Highest Posterior Density intervals.

	Posterior mode	Lower 95% CI	Upper 95% CI	pMCMC	
RTL random effects					
qPCR plate	0.049	0.028	0.074		
qPCR row	0.038	0.014	0.176		
RTL fixed effects					
Intercept	-0.165	-0.352	0.148	0.384	
Weight random effects					
Mum ID	0.013	<0.001	0.034		
Birth year	<0.001	<0.001	0.005		
Weight fixed effects					
Intercept	1.547	1.433	1.667	<0.001	***
Sex (female)	-1.912	-1.982	-1.819	<0.001	***
Age	30.862	28.273	32.229	<0.001	***
Age^2	-21.492	-22.851	-20.252	<0.001	***
Age^3	11.035	9.993	12.495	<0.001	***
Sex (male): Age	62.598	50.351	69.917	<0.001	***
Sex (male): Age^2	-3.649	-13.880	11.712	0.906	
Sex (male): Age^3	40.542	31.582	47.779	<0.001	***
Survival random effects					
Mum ID	0.001	<0.001	0.131		
Birth year	0.105	0.010	0.235		
Survival fixed effects					
Intercept	0.514	-0.061	1.064	0.076	.
Sex (female)	1.307	1.004	1.607	<0.001	***
Age	-47.620	-56.697	-33.993	<0.001	***
Age^2	-20.097	-27.739	-11.337	<0.001	***
Sex (male): Age	-43.659	-69.752	-4.599	0.030	*
Sex (male): Age^2	-37.638	-68.473	-6.376	0.016	*

Table S10a. Variance-covariance matrices from a multivariate animal model of telomere length (RTL), August weight and overwinter survival in in Soay sheep lambs (~4 months old). Variances are shown on the diagonal (in italics), covariances below the diagonal (bottom left) and correlations above the diagonal (top right). Covariances and correlations were deemed to be significant when the credible intervals did not overlap zero (shown in bold). Other fixed and random effects shown in Table S10b. Estimates are given as the mode of the posterior distribution with 95% Highest Posterior Density intervals.

Genetic	RTL	Weight	Survival
RTL	*0.465* *(0.294–0.578)*	-0.278 (-0.597–0.023)	0.345 (-0.038–0.839)
Weight	-0.075 (-0.128–0.009)	*0.089* *(0.038–0.170)*	-0.081 (-0.748–0.461)
Survival	0.159 (-0.021–0.314)	-0.004 (-0.118–0.096)	*0.359* *(<0.001–0.772)*

Maternal	RTL	Weight	Survival
RTL	*<0.001* *(<0.001–0.072)*	-0.043 (-0.817–0.661)	-0.071 (-0.733–0.906)
Weight	0.003 (-0.036–0.031)	*0.135* *(0.089–0.193)*	**0.663** **(0.403–0.916)**
Survival	<0.001 (-0.072–0.063)	**0.167** **(0.073–0.251)**	*0.349* *(0.144–0.714)*

Year	RTL	Weight	Survival
RTL	*0.044* *(0.009–0.117)*	0.374 (-0.347–0.702)	-0.025 (-0.516–0.538)
Weight	0.016 (-0.034–0.079)	*0.115* *(0.056–0.271)*	**0.477** **(0.078–0.811)**
Survival	0.014 (-0.287–0.298)	0.325 (-0.005–0.782)	*2.263* *(1.139–6.784)*

Residual	RTL	Weight	Survival
RTL	*0.418* *(0.323–0.534)*	0.013 (-0.121–0.184)	**-0.278** **(-0.457–-0.016)**
Weight	0.005 (-0.044–0.070)	*0.327* *(0.277–0.398)*	**0.331** **(0.170–0.516)**
Survival	**-0.152** **(-0.300–-0.013)**	**0.182** **(0.098–0.309)**	*1.000* *fixed*

Table 10b. Additional fixed and random effect estimates from a multivariate animal model of telomere length (RTL), August weight and overwinter survival in in Soay sheep lambs (~4 months old). The covariance between the three traits was estimated at the genetic, maternal, year and residual levels (see Table S10a). Estimates are given as the mode of the posterior distribution with 95% Highest Posterior Density intervals.

	Posterior mode	**Lower 95% CI**	**Upper 95% CI**		
RTL random effects					
qPCR plate	0.051	0.029	0.079		
qPCR row	0.029	0.012	0.175		
RTL fixed effects				**pMCMC**	
Intercept	-0.203	-0.413	0.195	0.450	
Weight fixed effects					
Intercept	0.571	0.392	0.802	<0.001	***
Sex (female)	-0.553	-0.641	-0.470	<0.001	***
Twin (1)	-1.200	-1.344	-1.089	<0.001	***
Mum Age	7.439	5.186	10.359	<0.001	***
MumAge^2	-22.307	-25.268	-20.153	<0.001	***
Survival fixed effects					
Intercept	-0.625	-1.268	0.516	0.330	
Sex (female)	0.664	0.394	0.921	<0.001	***
Twin (1)	-0.651	-1.031	-0.285	<0.001	***
Mum Age	1.933	-4.252	11.739	0.360	
MumAge^2	-14.537	-23.213	-7.483	0.002	**