1	Supplementary Methods, Tables and Figures for:
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3	Reduced costs of reproduction in females mediate a shift from a male-biased to a
4	female-biased lifespan in humans
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9	Supplementary Methods
10	
11	Data
12	The Utah Population Database (UPDB) is one of the most comprehensive computerised
13	genealogies in the world. Genealogy records are gathered and provided by the Genealogical
14	Society of Utah and span the pioneer settlement era in Utah in the mid-1800s as well as their
15	Utah descendants until the present day <sup>1</sup> . These records include information on fertility and
16	mortality for parents and their children. Before 1890 polygamy was practiced by a minority
17	of the population <sup>2</sup> . Non-paternity rates in Utah are lower than the US average <sup>3</sup> . The Utah
18	population during the period studied here suffered less mortality than most comparable
19	populations, especially at early ages <sup>4</sup> .
20	
21	For this study, we focussed on the time period surrounding the demographic transition and
22	included individuals from the UPDB that were born between 1820 and 1920 (no individual
23	born before 1920 was still alive at the end of data coverage for this study in 2012). We
24	required full information for a number of variables that were entered as fixed and random
25	effects in the models, namely reproductive history, whether the individual was involved in a

26 polygamous marriage (4.7% of females and 1.9% of males), whether the individual was born in Utah (54% of females and 52% of males), birth order in three levels denoting whether an 27 individual was the firstborn son, the firstborn daughter, or laterborn of either sex (to control 28 29 for effects of inherited wealth), and the identity of the birth mother (maternal identity, to account for non-independence of individuals born in the same family). All individuals with 30 full information for these fixed and random effects also had known birth and death dates, 31 32 hence censoring was not employed in survival models. Individuals were divided into four birth cohorts of 25 years each, commencing 1820. This resulted in a total sample size of 33 34 75,667 reproducing females and 64,933 reproducing males.

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Because the dataset is built from descendant genealogies, it likely underrepresents individuals 36 37 that are known to not reproduce. In the present study, 1.7% of married individuals were known to be nulliparous, likely representing a non-random subset of the population because 38 involuntary childlessness may be more common in frail individuals. Because of the difficulty 39 40 to achieve a representative subset of nulliparous individuals and our interest in the cost of increased parity and the effect of changes in parity on lifespan, we therefore focussed on only 41 reproducing individuals in the main analyses. For comparison, we include Kaplan-Meier 42 survivor curves for presumably nulliparous individuals of the two sexes over the studied time 43 44 period in Supplementary Fig. 1. These should be interpreted with knowledge of the lowered 45 accuracy of the data in these individuals, because individuals that were registered as nonreproducers may be so because of a lack of information regarding their reproduction. 46

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## 48 Sexual dimorphism in lifespan

To look at the differences in survival patterns between the two sexes and how this changed
over time, we used the *survival* package in R<sup>5</sup> to plot Kaplan-Meir survival curves for the two

51 sexes in four cohorts of 25 years each, starting at the year 1820. Because the interest was in 52 adult survival and we focussed on only reproducing individuals, individuals that died before reproductive age are not included in the survival analyses. Hence, the first deaths occur at age 53 54 15. We tested if the sexes differed significantly with log rank and Wilcoxon tests in each cohort (Figure 1). We then proceeded with parametric accelerated failure time (AFT) survival 55 models using the *survreg* function in the survival package. AFT models assume that the 56 effects of covariates are multiplicative with respect to survival time. Parametric models 57 require that a distribution is specified for the survival times. We compared the fit of 58 59 exponential, Weibull, log-normal and log-logistic models using two approaches: graphically, by comparing the predicted estimates from the fitted model with the observed Kaplan-Meier 60 estimate of the survivor function, and analytically, by comparing model fits with different 61 distributions specified, using  $\chi^2$ -tests for nested models (exponential, Weibull and log-62 logistic) and using Akaikes information criterion (AIC) for non-nested models. This showed 63 that a Weibull distribution provided the best fit. The Gompertz model was not intended to 64 65 study mortality patterns beyond the age of about 80 years and thus was not considered<sup>6</sup>. Models included as fixed effects polygamy status, birth in or outside of Utah, birth order and 66 birth cohort. Sex was added as a stratified fixed effect to allow different baseline survival 67 shapes for the two sexes. Observations were clustered by maternal identity to account for 68 69 clustering within mothers. The interaction between sex and birth cohort indicates whether the 70 two sexes differ in each cohort. To ensure that these results are not dependant on the arbitrary division of the data into 25 year birth cohorts, we repeated the analyses, first with the data 71 divided into 5 cohorts of 20 years each, and second, with birth year treated as a continuous 72 73 variable. Results were robust to these alternative model specifications (not shown). Mortality during migration to Utah is likely to have had sex-specific effects on survival. The analyses 74 detailed above includes all individuals with known birth and death information, regardless of 75

76 whether they were born or died in Utah or elsewhere. Because all individuals in the first 77 cohort were born outside Utah, most of these individuals suffered the hardships of migration, affecting the sexes differently and resulting in an overall more robust cohort surviving to old 78 79 ages. Subsequent cohorts are composed of four categories: individuals that 1) were born elsewhere and migrated to Utah, 2) were born and died in Utah, 3) were born in Utah and 80 died elsewhere and, 4) were born and died outside of Utah. Cohort 2 thus offers the 81 opportunity to compare migrants into Utah with individuals that spent their entire lives in 82 Utah during a time period when migration still imposed hardships (Supplementary Fig. 1a). 83 84 To test for a healthy migrant effect, we used a parametric survival model that adjusted for polygamy status and birth order as fixed effects, and clustered the observations by maternal 85 identity. Because the conditions during migration changed over time, we validated the use of 86 87 cohort 2 for this comparison by comparing migrants in cohort 2 with migrants in cohort 1 (Supplementary Fig. 1b) and looked at the difference in survival between migrants in these 88 two cohorts in a parametric survival model within each sex, with covariates as described 89 90 above.

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## 92 Reproduction-lifespan trade-off

To test for a trade-off between reproduction and lifespan in the two sexes, we investigated the 93 relationship between number of children born and post-reproductive lifespan with two 94 95 approaches. First, we employed the R-package *MCMCglmm*, which uses an iterative Bayesian approach<sup>7</sup> and provides meaningful error estimates for derived variables by direct 96 sampling from the posterior distribution. Individuals were required to live until age 55 or 97 98 older, in order to focus on the effect of reproduction on late life mortality (100% of all women and 96.8% of all men had finished reproduction by this age). This avoids 99 100 confounding deaths caused by childbearing (Figure 1) with post-reproductive mortality.

101 Hence, we subtracted 55 years from the total lifespan to obtain the response variable postreproductive lifespan. Our selection criteria restricted the total sample size to 118,911 102 individuals. Models controlled for a number of fixed effects as described above (polygamy 103 104 status, whether the individual was born in Utah, birth order and birth cohort). Maternal identity was included as a random effect to account for non-independence of observations 105 within families. Number of children born was standardised within sexes prior to the analysis 106 107 (mean of zero; SD of one) and we used post-reproductive lifespan as a Gaussian response variable. The initial model included the interaction between sex and both the linear and the 108 109 quadratic (non-linear) term for number of children born. The 95% Bayesian credibility intervals for the interaction term indicate whether the linear or quadratic slope of the 110 relationship between number of children and post-reproductive lifespan differed significantly 111 112 between the two sexes. The quadratic term was not significant and subsequently excluded from the model. Because the maximum number of children was 64 in males and 21 in 113 females, we investigated whether males with extreme values influenced the result by 114 removing the 282 males with 22 or more children, generally polygamist men. After this 115 equalisation of potential reproductive effort in the two sexes, we re-estimated the above 116 model. This did not influence the results so we present results from the full dataset. To obtain 117 sex-specific estimates for the relationship between reproductive effort and lifespan, we re-118 estimated the model for each sex separately. In the sex-specific models, the quadratic effect 119 120 was significant in both sexes and was thus retained in both models. Because males that continued to reproduce after age 55 might inflate the estimates, the male-specific model was 121 re-estimated excluding the 3.2% of males that continued to reproduce after age 55. This did 122 123 not influence the results so we present results from the full dataset. All models were run with a prior with V = 1 and a degree of belief parameter (nu) of 0.002. Convergence of runs was 124 assessed by visual inspection of output plots. 125

Alternatively, post-reproductive lifespan can be analysed in a survival model framework. To 127 increase comparability with the models on sexual dimorphism in lifespan, and to obtain sex-128 129 specific estimates of acceleration factors for individuals with different levels of reproductive output, we used parametric survival models using the function survreg in the R-package 130 survival. The subset used for analyses was restricted to individuals that survived until age 55 131 132 and their lifespan was used as the response variable. A Weibull distribution provided the best fit to the data in both sexes. Models included fixed effects as above, observations were 133 134 clustered by maternal identity and birth cohort was added as a stratified fixed effect to allow different baseline survival shapes for each birth cohort. To obtain acceleration factors for 135 different levels of reproductive output, we grouped the number of children born into six 136 137 different levels representing low to high reproductive investment: one child, two to four children, five to eight children, nine to 14 children, 15 to 21 children and 22 to 64 children 138 (males only). 139

140

Infant mortality may influence reproductive decisions and thus affect costs of reproduction, 141 potentially in a sex-specific manner. The main cause of infant mortality in historical Utah 142 was infectious diseases<sup>4</sup> and it is thus possible that infant mortality could affect the health and 143 144 survival of mothers and fathers differently. While infant mortality in historical Utah was 145 comparatively low, in the current study, 33% of reproducing women with full known reproductive history from birth cohorts 1 and 2 (that reproduced when fertility rates were 146 high, Figure 1) lost one or more infants during the first year of life, while this dropped to 23% 147 148 for women from cohorts 3 and 4 (that reproduced when fertility rates were lower). To account for the effects of infant mortality, we repeated the analyses of costs of reproduction with 149 150 infant loss included as a two-level covariate (the individual had one or more children that

151	died d	uring the first year of life versus all children survived their first year of life). This did
152	not inf	luence the results (not shown) and we thus present models excluding this variable,
153	becaus	e the predictions regarding how infant mortality is expected to influence total fertility
154	and se	x-specific survival patterns are not straightforward.
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156	Refere	ences
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## 172 Supplementary tables and figures

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- **Table S1.** Averages (± SD) and sample sizes of number of children and lifespan in the two
- sexes in four birth cohorts in historical Utah.
- 176

Birth cohort	Average children $\pm$ SD		Average lifespan $\pm$ SD		N	
	females	males	females	males	females	males
1820 to 1844	8.5 ± 3.3	$11.1 \pm 5.7$	$68.3 \pm 17.8$	$70.1 \pm 14.3$	3298	3793
1845 to 1869	$7.8\pm3.3$	8.3 ± 3.8	$69.5\pm17.5$	$70.2 \pm 14.6$	17331	16403
1870 to 1894	$5.8 \pm 3.1$	$5.8 \pm 3.0$	$72.4 \pm 18.1$	$70.8 \pm 15.6$	37156	33919
1895 to 1919	$4.2\pm2.5$	$4.2\pm2.4$	$76.7 \pm 17.5$	$72.6 \pm 15.7$	17882	10818

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## 178 Table S2. Proportion of reproducing women who died the same year in which they gave

birth to their last child, in four birth cohorts in historical Utah. Sample sizes as reported in

- 180 Table S1.
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1820 to 1844	1845 to 1869	1870 to 1894	1895 to 1919
0.0633	0.053	0.037	0.019

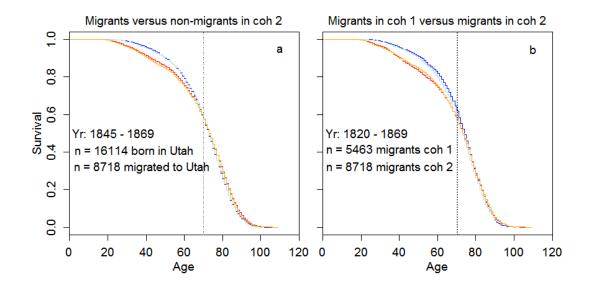
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182

184 **Figure S1.** 

Comparison of sex-specific survival patterns between (a) individuals that migrated into Utah 185 and individuals that spent their entire lives in Utah in birth cohort (coh) 2 and (b) individuals 186 that migrated into Utah in birth cohort 1 compared to migrants in birth cohort 2. Birth cohort 187 2 is composed of four groups of individuals with respect to migratory status: individuals that 188 were born and died in Utah, individuals that were born elsewhere and died in Utah, 189 190 individuals that were born in Utah but died elsewhere and individuals that spent their entire lives outside Utah. In (a), the first two of these groups are compared, separately in the two 191 192 sexes. The early migrants to Utah faced harsher conditions during migration than later migrants. Therefore, figure (b) compares the effects of migration on survival in the early 193 migrants into Utah of cohort 1 with the later migrants of cohort 2, separately in the two sexes. 194 195 Note that migrants into Utah in cohort 2 thus appear in both figures, males in light blue and 196 females in orange. In (a), these migrants are compared to non-migrants within the same cohort (males in blue and females in red), whereas in (b), the migrants in cohort 2 are 197 compared to migrants in cohort 1 (males in blue and females in red). Shown are the birth 198 years (Yr) contained in birth cohort 1 (a) or 1 and 2 (b) and the sample size in each group 199 (N). Dotted vertical lines indicate the average lifespan of (a) non-migrants (black) and 200 migrants (grey) in both sexes pooled and of (b) migrants in cohort 1 (black) and cohort 2 201 (grey). All p-values were > 0.2 from GW and LR tests of the difference between individuals 202 203 within each sex that were born in Utah and individuals that migrated into Utah (a), and likewise (b), all p-values comparing migrants in cohort 1 to migrants in cohort 2 were > 0.25204 in females. Migrant males in cohort 1 tended to live longer than migrant males in cohort 2, 205 GW  $\chi^2 = 9.3$ , p = 0.002, LR  $\chi^2 = 3.7$ , p = 0.053. 206

207



209 **Figure S2.** 

210 Age-specific adult survival for females (red) and males (blue) that presumably did not

- reproduce, divided into four 25-year birth cohorts that cover the demographic transition in
- 212 Utah. Shown in each figure are the birth years contained in that cohort (Yr), the sample size
- 213 (n), the average  $\pm$  SD number of children born to females (CHf), the  $\chi^2$  and p-values
- 214 indicating differences in the survivor function between the two sexes from the Peto and Peto
- 215 modification of the Gehan-Wilcoxon test (GW, this test weights differences in survivorship
- that occur early more heavily than differences at later survival times) and from a log-rank test
- 217 (LR, this test weights differences at later survival times more heavily). Dotted vertical lines
- 218 indicate the average lifespan of each sex in each cohort.

