Supplemental Tables and Figures: Wright et al.

Coefficient	Estimate	Std.Error	p value
Intercept	78.17	0.88	2.0E-16***
Caucasus	1.90	2.07	>0.05
Native American	-3.28	1.59	0.040
Great Britain	2.73	0.89	0.002*
Ireland	0.79	0.89	>0.05
Europe East	1.92	0.91	0.034
Scandinavia	3.91	0.91	1.6E-05***
Italy/Greece	3.50	0.96	2.6E-04**
Europe West	3.21	0.89	3.2E-04*
Iberian Peninsula	2.97	1.11	0.008
European Jewish	2.74	0.93	0.003*
Finland/NW Russia	2.33	1.21	>0.05
Sub-Saharan Africa	-0.38	0.93	>0.05
Near East	1.89	2.22	>0.05
Latino	1.21	0.91	>0.05

r:	0.047
F-statistic:	24.57
df:	146153
p value:	<2.2E-16

S Table 1: Correlation of Maternal Lifespan with Estimate of Ancestral Admixture. Multivariate linear regression analysis of ancestral admixture assignments of and paternal lifespan. Coefficient estimates and SE are in years. Ethnic group included in analysis if there were at least 1000 individuals with > 5% ancestral admixture assignment. Threshold for significance after Bonferroni correction for 14 ancestral admixture assignments was $p < 3.57x10^{-3}$ *. **$p < 1x10^{-4}$; ***$p < 1x10^{-5}$.

Coefficient	Estimate	Std.Error	p value
Intercept	74.57	0.70	2.0E-16***
Caucasus	-1.11	1.80	>0.05
Native American	0.11	1.35	>0.05
Great Britain	-0.42	0.71	>0.05
Ireland	-3.30	0.72	4.7E-06***
Europe East	-1.05	0.73	>0.05
Scandinavia	1.58	0.74	0.032
Italy/Greece	1.68	0.78	0.032
Europe West	0.72	0.72	>0.05
Iberian Peninsula	0.38	0.93	>0.05
European Jewish	1.06	0.75	>0.05
Finland/NW Russia	-1.19	1.04	>0.05
Sub-Saharan Africa	-1.05	0.75	>0.05
Near East	0.12	1.97	>0.05
Latino	1.18	0.79	>0.05

r :	0.056
F-statistic:	42.17
df:	186129
p value:	<2.2E-16

S Table 2: Correlation of Paternal Lifespan with Estimate of Ancestral Admixture. Description of results as in S Table 1.

Trait	Cohort	N samples	N variants, GWAS	Lambda	Bonf. p value	LDSC: N variants	LDSC: intercept	LDSC: mean chi-sq
Lifespan	Maternal 1886-1918	133203	540852	1.030	9.24E-08	385494	1.01 (0.01)	1.033
Lifespan	Maternal 1886-1940	270548	541493	1.113	9.23E-08	390429	1.01 (0.01)	1.097
Lifespan	Paternal 1886-1918	167179	541017	1.084	9.24E-08	385494	1.00 (0.01)	1.085
Lifespan	Paternal 1886-1940	309383	541614	1.182	9.23E-08	390429	0.991 (0.01)	1.161
Age	Male+Female	482068	536775	1.374	9.31E-08	390622	1.04 (0.02)	1.286

S Table 3: Summary statistics for GWA mapping analyses. Lambda is the median genomic variance inflation factor. LD Score regression (LDSC) summary statistics: intercept and mean chi-sq values.

Lifespan	Cohort	Locus	RSID	beta_snp	beta_snp_se	p_val _snp	beta_chip	beta_chip_se	p_val chip
Father	1918	ANRIL	rs1333042	0.324	0.045	4.011E-13	0.043	0.063	0.495
Father	1918	WAPL	rs10887623	-0.418	0.075	2.261E-08	0.040	0.063	0.529
Father	1940	ANRIL	rs1333042	0.248	0.032	6.999E-15	0.011	0.045	0.806
Father	1940	LPA	rs9457925	-0.828	0.119	4.142E-12	0.011	0.045	0.812
Father	1940	SRRM3	rs17685	0.194	0.036	5.414E-08	0.011	0.045	0.804
Father	1940	CHRNA3/5	rs931794	-0.198	0.033	3.194E-09	0.012	0.045	0.788
Mother	1918	APOE	rs4420638	-0.320	0.066	4.825E-06	-0.061	0.070	0.387
Mother	1940	APOE	rs4420638	-0.241	0.044	5.941E-08	-0.081	0.048	0.091

S. Table 4: The effect of the focal SNP and chip version covariate in GWA mapping models for candidate lifespan variants.

Trait	Locus	RSID	Chr	Assoc. Model	Effect (years)	SE (years)	P
Paternal Lifespan	ANRIL	rs1333042	9	Primary	0.64834	0.08936	4.01E-13
				Primary + Med. Ls./Cohort	0.64820	0.08934	4.02E-13
	WAPL	rs10887623	10	Primary	-0.83683	0.14970	2.26E-08
				Primary + Med. Ls./Cohort	-0.83580	0.14966	2.34E-08
Maternal Lifespan	APOE	rs4420638	19	Primary	-0.60198	0.13165	4.83E-06
				Primary + Med. Ls./Cohort	-0.63940	0.13220	1.33E-06

S. Table 5: – Candidate variants for GWA mapping of maternal and paternal lifespan in 1886-1918 birth cohort. We ran two versions of the association mapping model: 1) primary model, which includes the PCs 1-10 and chip version as covariates and 2) primary model with an additional covariate for the median lifespan per birth cohort within the years: 1886-1918.

Cohort	Analysis	Locus	RSID	Chr	Effect Allele	Effect Allele	Odds Ratio / Beta (Yrs.)	SE	P_{UC}	P_{GC}	
Male	Case/Control	APOE	rs4420638	19	G	0.18	0.82	0.02	1.03E-25	2.67E-24	***
Female	Case/Control	MAP2K6	rs817555	17	A	0.45	0.93	0.01	2.39E-08	9.84E-08	*
Female	Case/Control	APOE	rs4420638	19	G	0.18	0.77	0.02	4.70E-49	6.86E-45	***
Male+Female	Case/Control	APOE	rs4420638	19	G	0.18	0.79	0.01	1.34E-71	1.02E-62	***
Male+Female	Quantitative	APOE	rs769449	19	A	0.12	-0.74	0.04	5.48E-74	2.35E-54	***

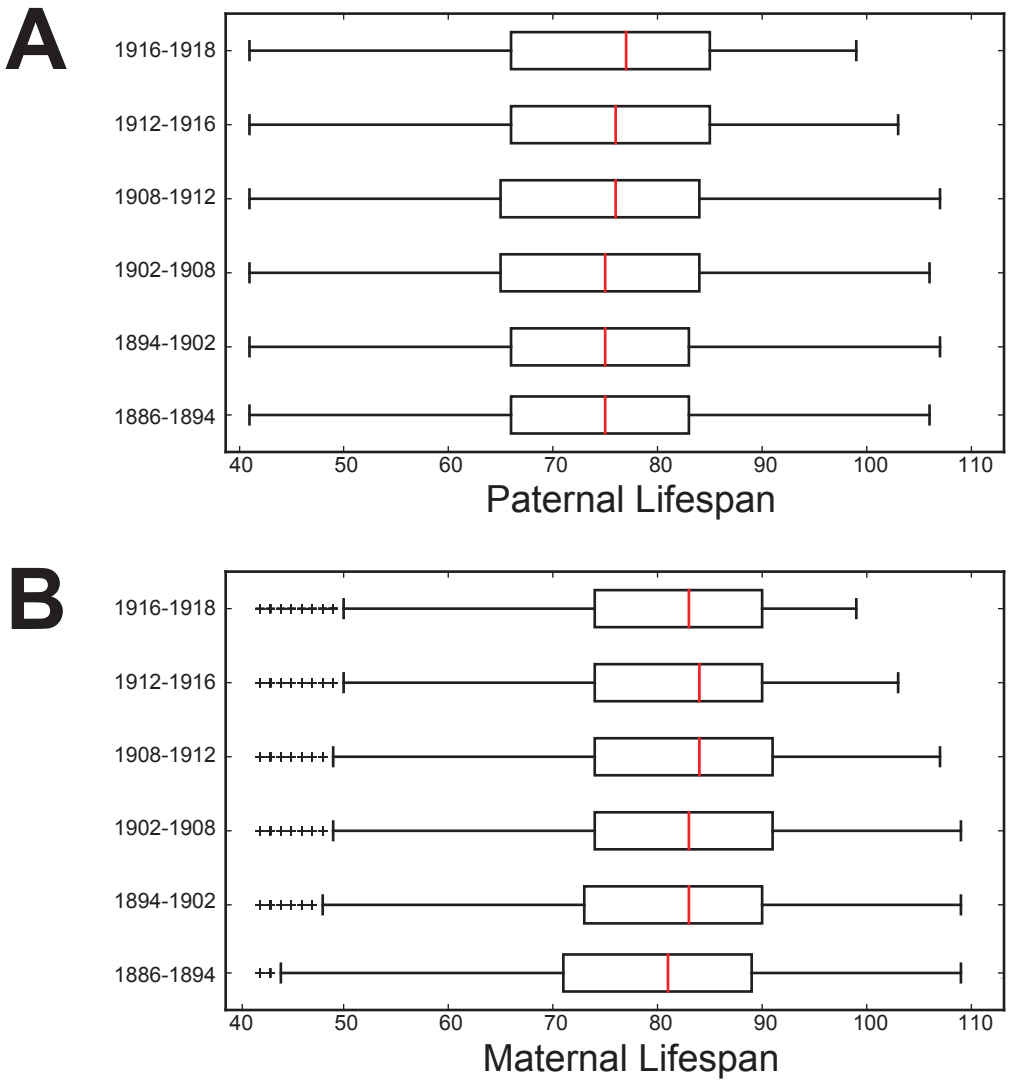
S. Table 6: Candidate loci associated with current age in both case/control and quantitative trait GWA analyses. The additive effect of each locus for case/control analyses is given as an odds ratio and as an effect on years of current age for the quantitative analysis. The statistical significance of the association at each candidate variant is given as an uncorrected (P_{UC}) value and genomic control corrected (P_{GC}) value. Significance of P_{GC} after Bonferroni multiple test correction: *** $P_{Bonf} < 0.001$; * $P_{Bonf} < 0.05$; - $P_{Bonf} > 0.05$.

						p1_h2_obs		p1_h2_int		p2_h2_obs		p2_h2_int			
p1	p2	rg	rg_se	p_value	p1_h2_obs	se	p1_h2_int	se	p2_h2_obs	se	p2_h2_int	se	gcov_int	gcov_int_se
ukbb_paternal	ukbb_maternal	0.9017	0.0604	2.15E-50	0.092	0.0066	1.0394	0.0123	0.0514	0.0054	1.0693	0.0113	0.0804	0.0084
ukbb_paternal	anc_paternal	0.975	0.0575	1.72E-64	0.0926	0.0068	1.0381	0.0124	0.0804	0.0064	0.992	0.0111	-0.0275	0.0081
ukbb_maternal	anc_paternal	0.8779	0.0755	3.16E-31	0.0514	0.0054	1.0693	0.0114	0.0804	0.0064	0.992	0.0111	-0.0174	0.0076
ukbb_paternal	anc_maternal	0.8919	0.08	7.40E-29	0.0922	0.0068	1.0387	0.0124	0.045	0.0072	1.0163	0.0114	-0.0113	0.0075
ukbb_maternal	anc_maternal	1.0166	0.1126	1.76E-19	0.0514	0.0054	1.0694	0.0112	0.045	0.0072	1.0163	0.0114	-0.0152	0.0084
anc_paternal	anc_maternal	0.8769	0.087	7.07E-24	0.0808	0.006	0.9911	0.0107	0.0462	0.0072	1.0129	0.011	0.0837	0.0067

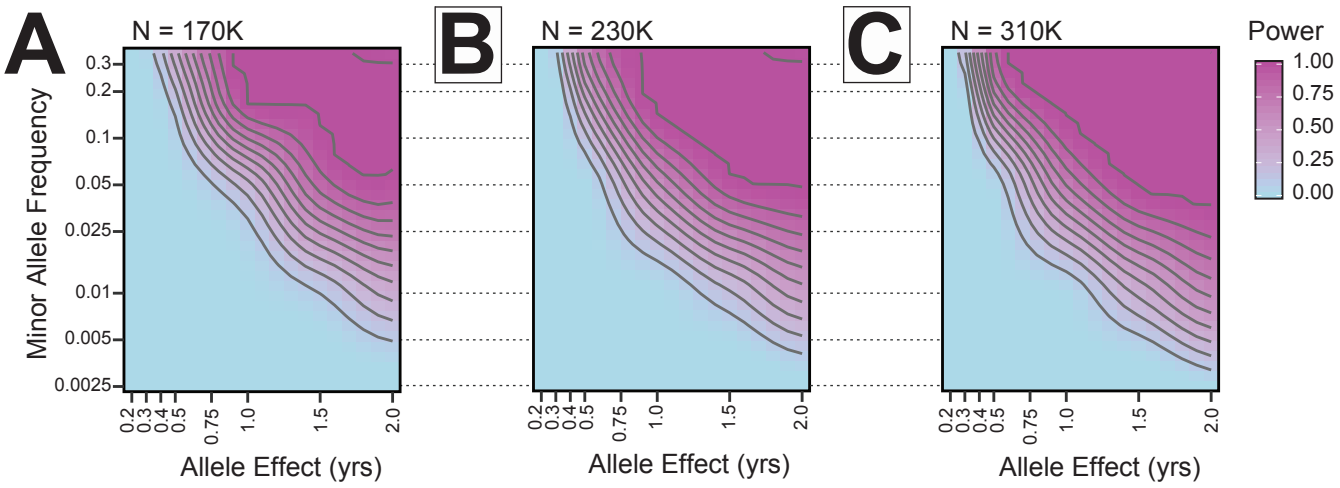
S. Table 7: Genetic correlation analysis between *AncestryDNA* parental lifespan GWA and UKB attained age GWA. Genetic correlation: rg. P value significance of genetic correlation: p_value. Heritability: h2_obs. Intercept for heritability estimate: h2_int. Genetic covariance intercept: gcov_int.

S. Table 8 (separate file): A representative list of SNPs from *AncestryDNA* age and parental lifespan GWA studies with genomic control adjusted p-values less than $3.0x10^{-3}$. This table includes: the rsid name, chromosome position in hg19, effect allele, number of samples included in the association analysis, the z score transformed beta effect size, standard error estimate for beta, the raw p-value and the p-value after genomic control. Note, the effect sizes for lifespan traits have not been re-scaled (doubled) to reflect allelic dosage in parental generation.

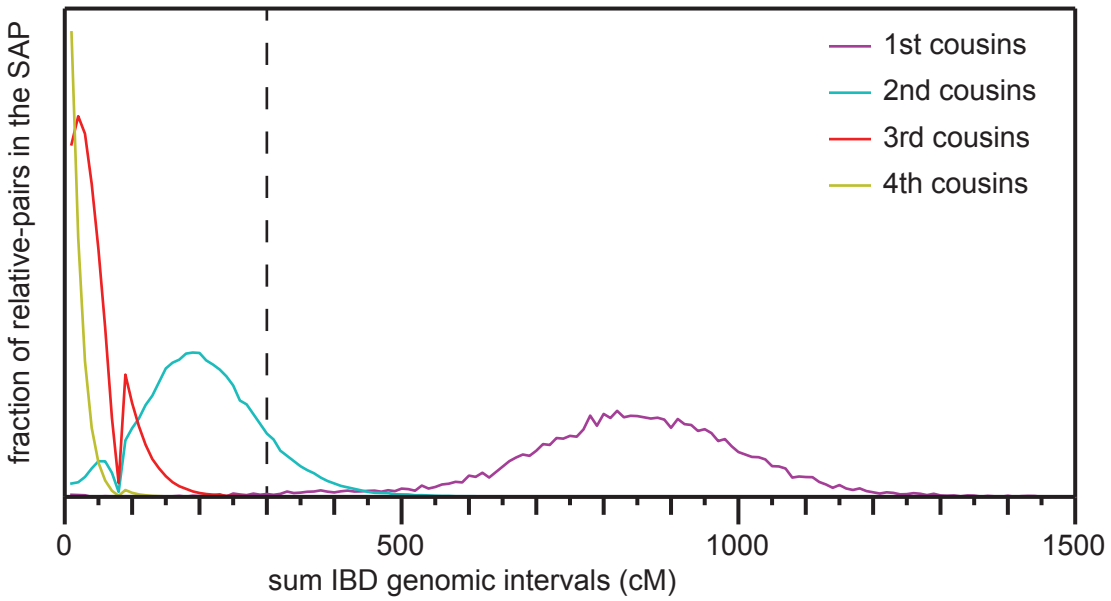
S. Table 9 (separate file): A representative list of SNPs from the meta-analysis between the *AncestryDNA* and UKB parental lifespan GWA studies with p-values less than $2.5x10^{-3}$. This table includes: the rsid name, chromosome position in hg19, effect allele, meta-analysis p-value, meta-analysis sample size, the study-specific p-value, z score transformed beta effect size, and standard error estimate for beta for both the AncestryDNA and UKB studies. Some of the SNPs included in the meta-analysis were imputed in the AncestryDNA dataset, these are denoted with im:<position>. Note, genomic control has not been applied to the p-value for the AncestryDNA analysis and the beta effect size for lifespan traits have not been re-scaled (doubled) to reflect allelic dosage in parental generation.



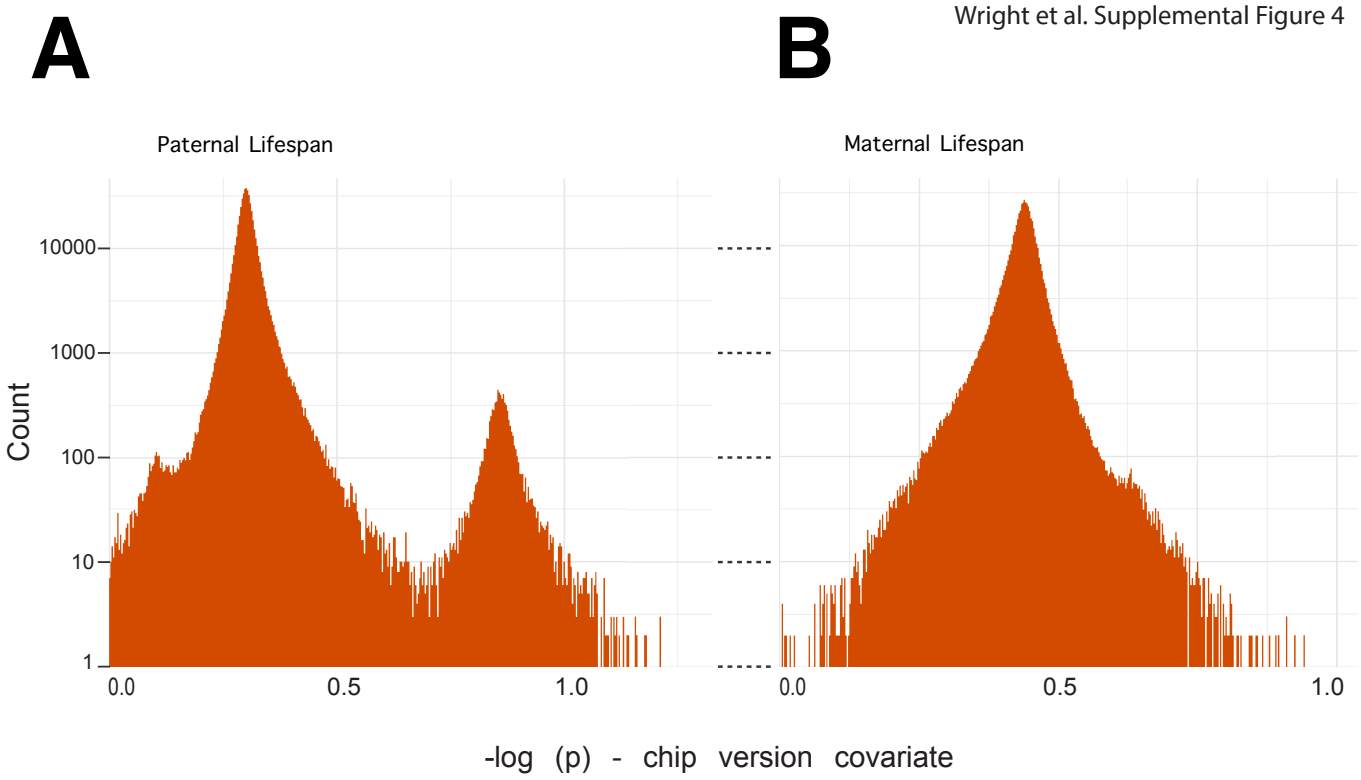
S. Figure 1 – Box plots show the change in paternal (A) and maternal (B) lifespan in birth cohorts ranging from 1886 to 1918. Boxes show the inner and outer quartile range, with the median lifespan depicted as a red line. Whiskers span the 2.5%-97.5% range and outliers are noted with a '+' symbol.



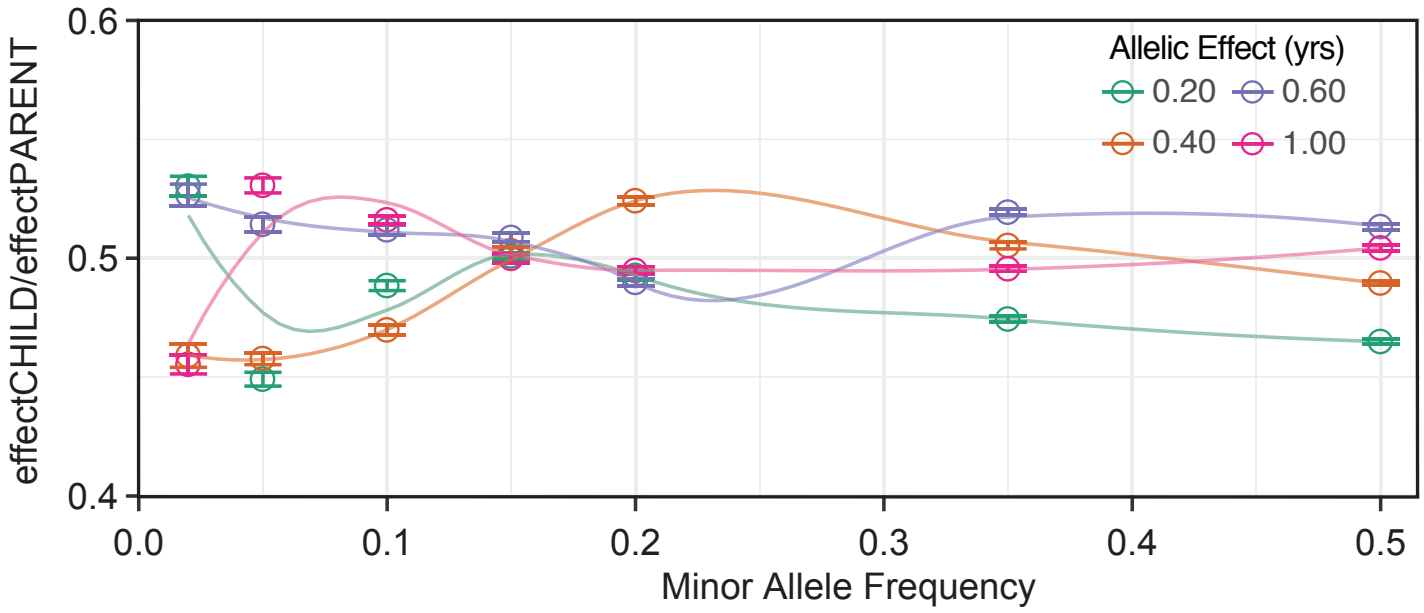
S. Figure 2 – Power calculations for lifespan analysis with mapping population size of:(**A**) 170,000, (**B**) 230,000 and (**C**) 310,000 individuals.



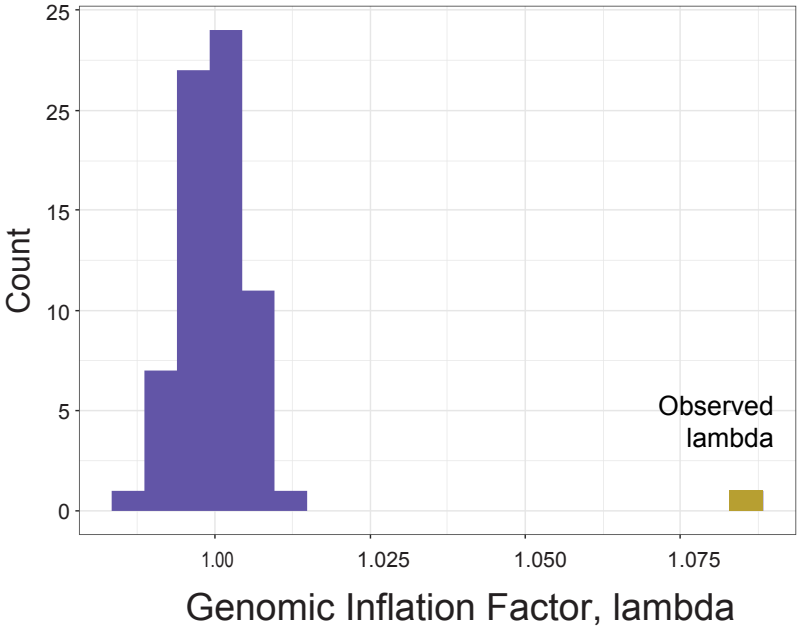
S. Figure 3 – Distribution of genome wide measure of identity-by-decent (IBD) for 1st-4th cousins in the SAP. IBD measurements binned into 10cM intervals. The skew in the distribution at <90 cM IBD caused by 'Timber' filtering of small and widely shared genomic intervals, see methods. Dashed line at 300cM is the threshold to remove close relatives in GWA mapping analyses.



S. Figure 4 – Histogram of p-values for chip version covariate in GWA mapping model of (**A**) paternal lifespan and (**B**) maternal lifespan from 1886-1918 cohort.

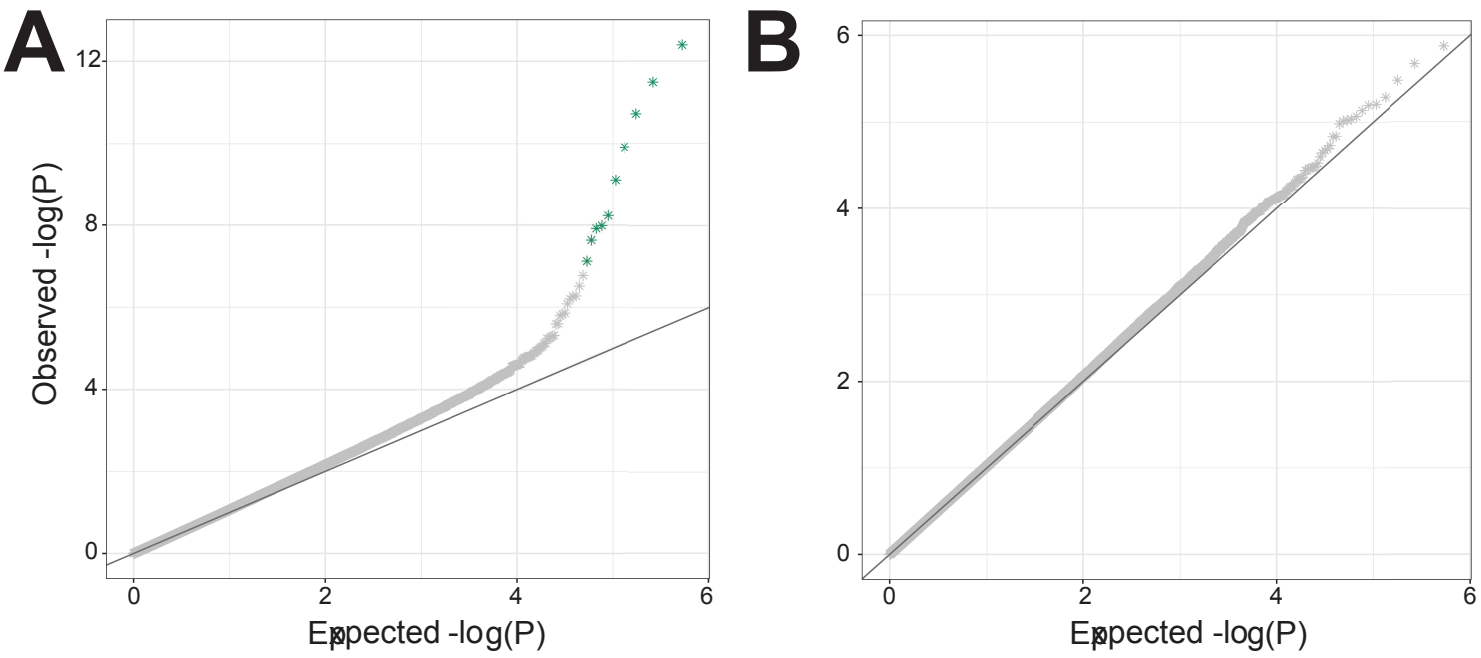


S. Figure 5 – Ratio of mutation effect size estimated using genotype of children versus genotype of parents. Plot means (+/- 95% CI) from 50 replicate simulations per parameter combination.

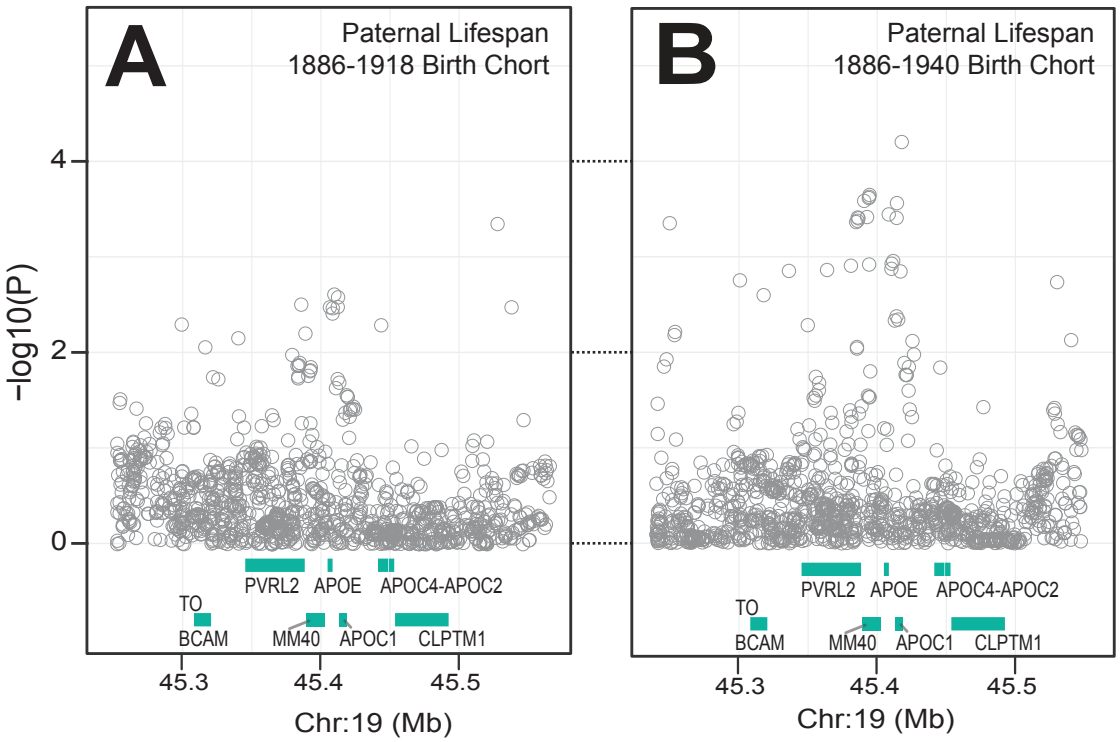


Wright et al. Supplemental Figure 6

S. Figure 6 – Histogram of genomic inflation factors, lambda, from randomly permuted lifespan values from paternal lifespan dataset, 1886-1918 cohort, noted with purple colored bars. The gold colored bar is the observed lambda value for this cohort.



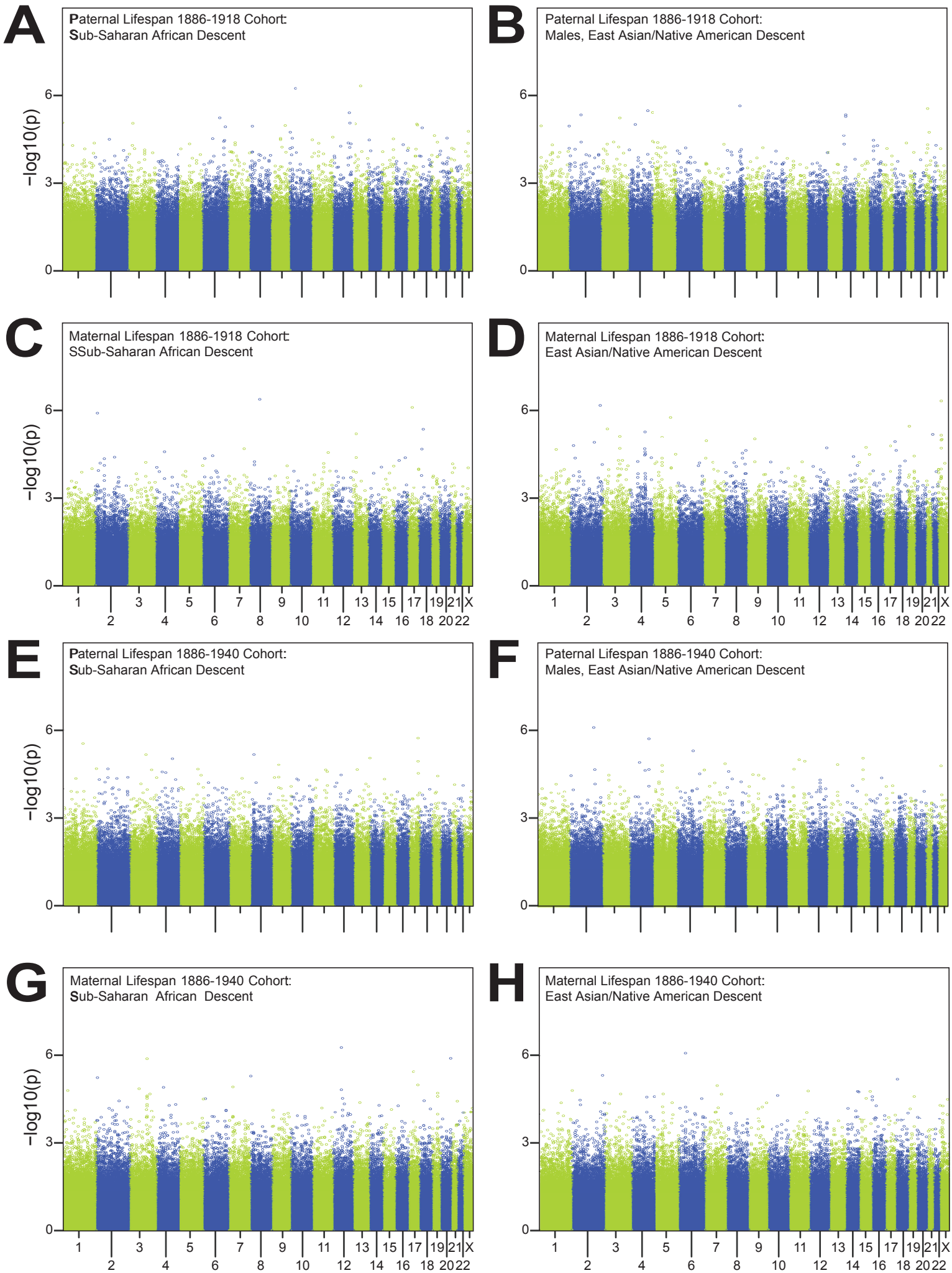
S. Figure 7 – QQ plot of p values for variants associated with lifespan in GWA mapping models with an additional covariate for the median lifespan per birth cohort for (A) fathers and (B) mothers born between 1886 and 1918. These QQ plots are analogous to Figure 3A-B, which depict results from GWA mapping models with chip version and PC1-10 were the only covariates.

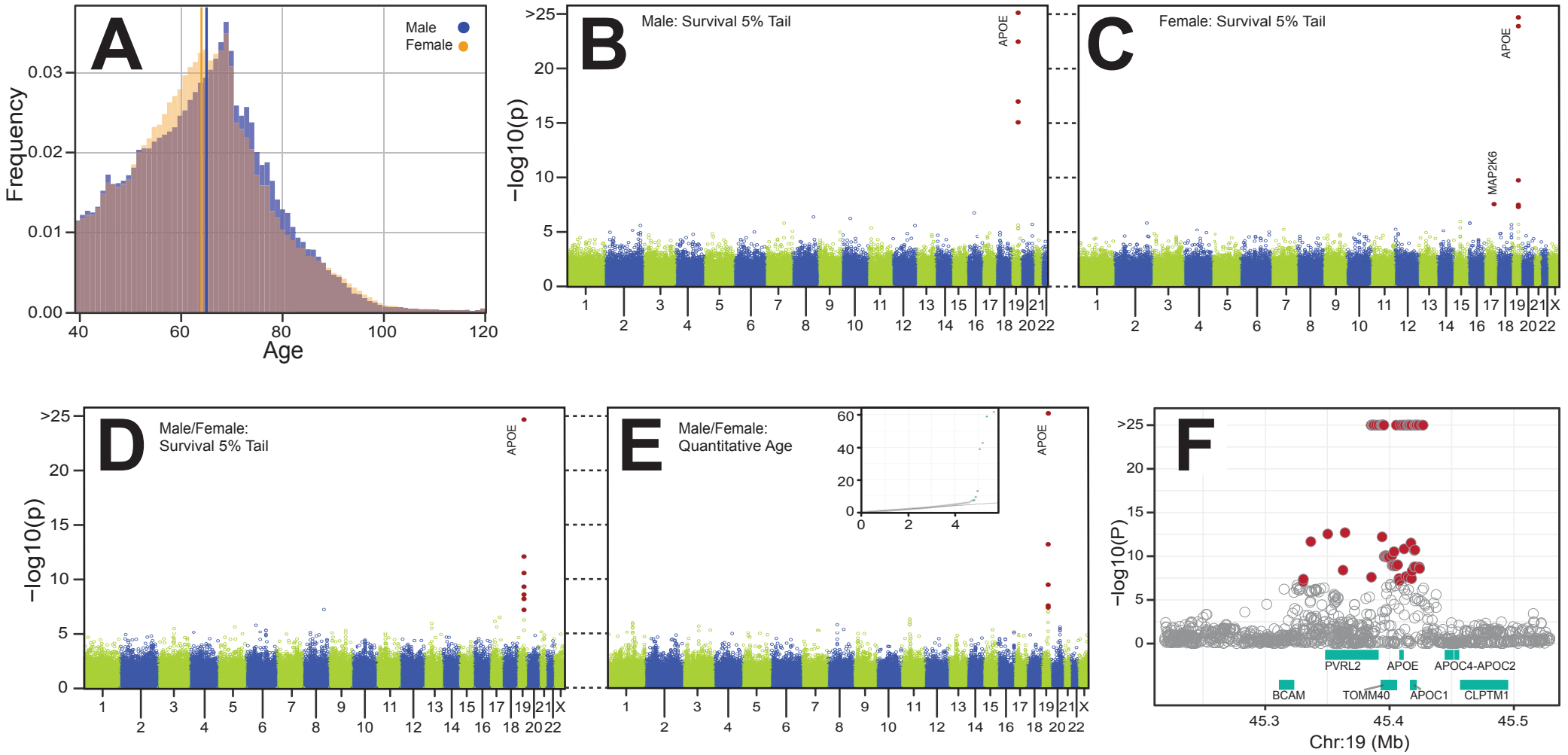


S. Figure 8 –Manhattan plot of association test statistics from analyses of paternal lifespan: (**A**) cohort 1886-1918 and (**B**) cohort 1886-1940. Association analysis using imputed data at APOE locus. Solid red circle are SNPs with Bonferroni corrected p-values less than 0.05. Cyan bars: hg19 gene models.

Next page:

S. Figure 9 – Manhattan plot of GWA analysis of lifespan in 1886-1918 birth cohort: (**A**) paternal; Sub-Saharan Africa, (**B**) paternal; East Asian/Native American, (**C**) maternal; Sub-Saharan Africa, and (**D**) maternal; East Asian/Native American population groups. GWA Analysis of 1886-1940 birth cohorts: (**E**) paternal; Sub-Saharan Africa, (**F**) paternal; East Asian/ Native American, (**G**) maternal; Sub-Saharan Africa, and (**H**) maternal; East Asian/Native American population groups.


A
Paternal Lifespan 1886-1918 Cohort:
Sub-Saharan African Descent
B
Paternal Lifespan 1886-1918 Cohort:
Males, East Asian/Native American Descent
C
Maternal Lifespan 1886-1918 Cohort:
SSub-Saharan African Descent
D
Maternal Lifespan 1886-1918 Cohort:
East Asian/Native American Descent
E
Paternal Lifespan 1886-1940 Cohort:
Sub-Saharan African Descent
F
Paternal Lifespan 1886-1940 Cohort:
Males, East Asian/Native American Descent
G
Maternal Lifespan 1886-1940 Cohort:
Sub-Saharan African Descent
H
Maternal Lifespan 1886-1940 Cohort:
East Asian/Native American Descent
−log10(p)
0
3
6
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 X



S. Figure 10 – (**A**) Distribution of the age of genotyped men and women in 2016. Median values noted with colored vertical lines. paternal individuals are denoted with blue, maternal individuals with orange, and overlapping values are dark orange. Manhattan plots of GWA results for case/control analyses of survival to 5% of age distribution: (**B**) male, (**C**) female, and (**D**) combine male and female. (**E**) Manhattan plot of quantitative trait GWA results for the current age of all individuals, both men and women, between the ages 40-120. (**F**) Association analysis with imputed genotypes at APOE locus. Annotation details are the same as in Figure 3.