Supplementary Table 1: LBC1936 descriptive data on complete cases split by number of waves attended. mean (SD) or n (%)

Wave	n visits	n	Age (yrs)	Sex (F)	Telomere Length (bp)	Hannum Age (yrs)
1	1	624	69.8 (0.8)	315 (50)	4200 (579)	66.5 (6.3)
	2	46	69.1 (0.6)	18 (39)	4240 (614)	64.7 (9.6)
	3	219	69.0 (0.6)	112 (51)	4176 (491)	64.6 (6.3)
2	2	46	72.1 (0.5)	18 (39)	4224 (1192)	67.4 (6.8)
	3	219	72.0 (0.5)	112 (51)	3909 (681)	69.1 (6.5)
3	3	219	75.8 (0.5)	112 (51)	3663 (678)	71.4 (6.2)

6 individuals had one visit at wave 2; 4 individuals had one visit at wave 3; 21 individuals had 2 visits, one of which was at wave 3.

Supplementary Table 2: LBC1921 descriptive data on complete cases split by number of waves attended. mean (SD) or n (%)

Wave	n visits	n	Age (yrs)	Sex (F)	Telomere Length (bp)	Hannum Age (yrs)
1	1	299	79.1 (0.6)	188 (63)	4064 (385)	74.3 (7.3)
	2	61	79.2 (0.6)	33 (54)	4110 (457)	72.6 (5.5)
	3	50	79.2 (0.6)	26 (52)	4231 (335)	74.2 (6.3)
3	2	61	86.7 (0.4)	33 (54)	4205 (571)	77.9 (5.1)
	3	50	86.7 (0.4)	26 (52)	4240 (353)	78.4 (6.6)
4	3	50	90.1 (0.1)	26 (52)	3194 (659)	80.2 (6.4)

10 individuals had one visit at wave 3; 18 individuals had one visit at wave 4; 14 individuals had two visits, one of which was at wave 4.

Supplementary Table 3: Survival model output for age- and sex-adjusted methylation age and telomere length.

LBC1936 (n = 920, n_{events} = 135)

Covariate	Hazard Ratio	95% CI	P-Value
Telomere Length	0.92	[0.78, 1.09]	0.34
Hannum age	1.18	[1.01, 1.39]	0.036

LBC1921 (n = 414, n_{events} = 280)

Covariate	Hazard Ratio	95% CI	P-Value
Telomere Length	0.86	[0.76, 0.97]	0.017
Hannum age	1.25	[1.11, 1.41]	$3x10^{-4}$

LBC1921 + LBC1936 ($n_{telo/Hannum}$ = 1,484/1,366, n_{events} = 437/427)

Covariate	Hazard Ratio	95% CI	P-Value
Telomere Length	0.88	[0.79, 0.99]	0.027
Hannum age	1.25	[1.12, 1.39]	$4x10^{-4}$

Effect sizes for telomere length and Hannum age are estimated in independent models and are reported per standard deviation.

Supplementary Table 4: Regression output for the age prediction models. The linear model takes a random sample of the population at each wave, such that each individual can only be included at a single wave. The linear mixed model includes a random intercept for participant ID to account for the clustering. The top half of the table shows the univariate results, the bottom half shows the multivariate results. All models adjust for sex.

Univariate Output		LBC1921		LBC1936		LBC1921 + LBC1936	
		Std. Beta	SE	Std. Beta	SE	Std. Beta	SE
Linear model (random subset)	Telomere	-0.37	0.06	-0.26	0.03	-0.15	0.03
	Hannum age	0.33	0.06	0.28	0.04	0.58	0.03
Linear mixed model	Telomere	-0.33	0.03	-0.25	0.02	-0.28	0.01
	Hannum age	0.31	0.03	0.29	0.02	0.59	0.02

Multivariate Output		LBC1921		LBC1936		LBC1921 + LBC1936	
		Std. Beta	SE	Std. Beta	SE	Std. Beta	SE
Linear model (random subset)	Telomere	-0.31	0.07	-0.25	0.04	-0.14	0.04
	Hannum age	0.30	0.06	0.26	0.04	0.55	0.03
Linear mixed model	Telomere	-0.33	0.03	-0.21	0.02	-0.21	0.02
	Hannum age	0.29	0.03	0.27	0.02	0.55	0.02

Figure 1: Spaghetti plots for change in Hannum age and telomere length over time in LBC1936 and LBC1921.

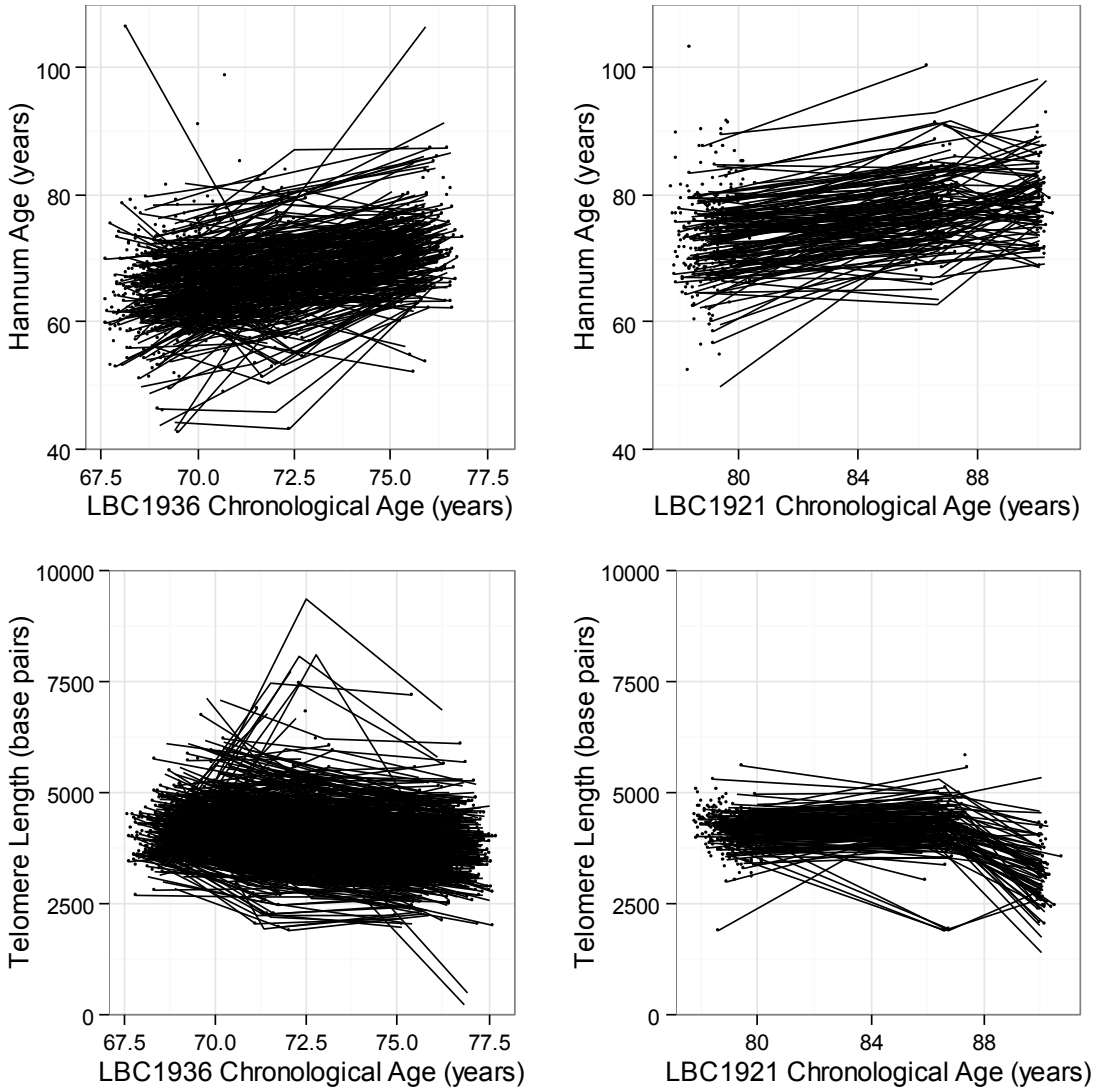
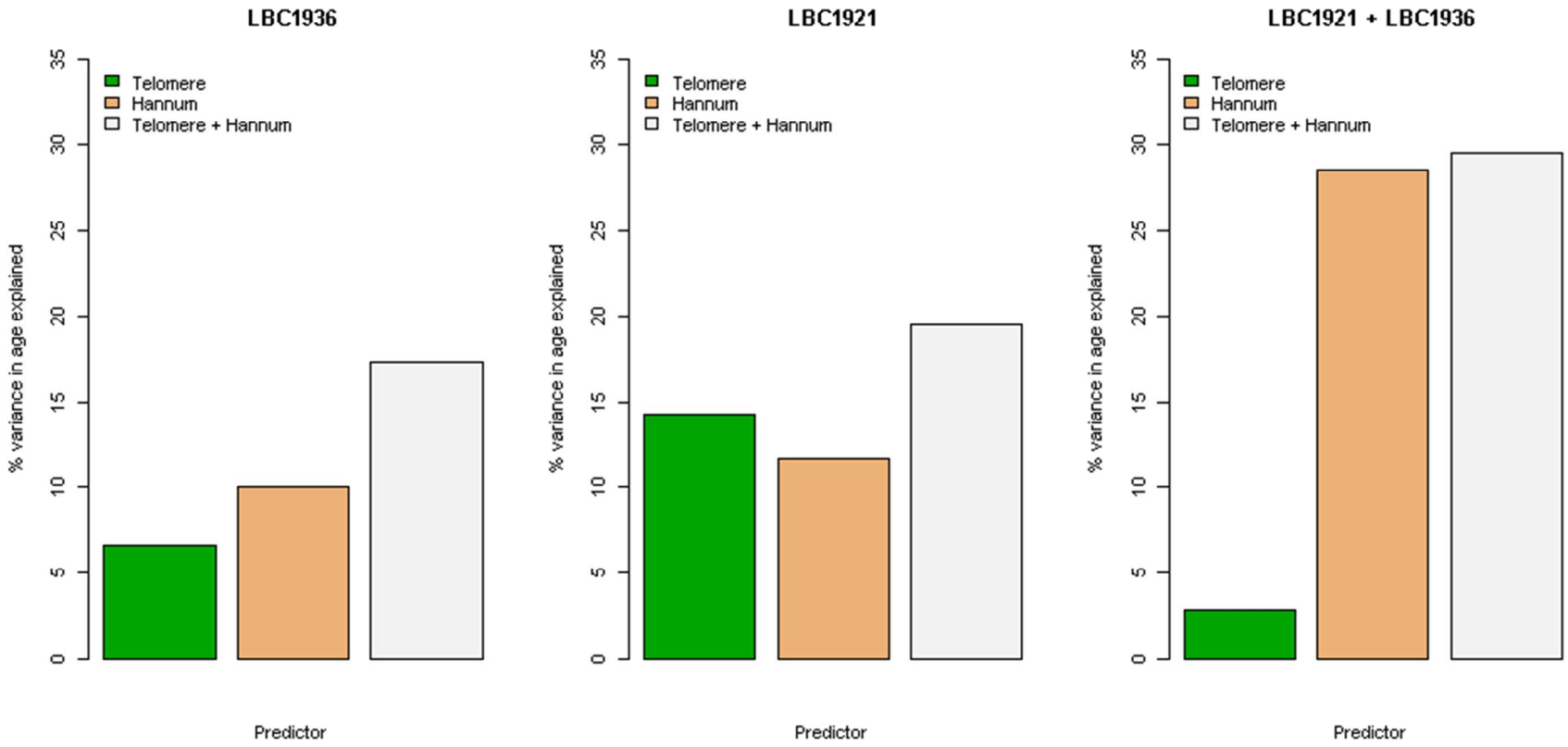
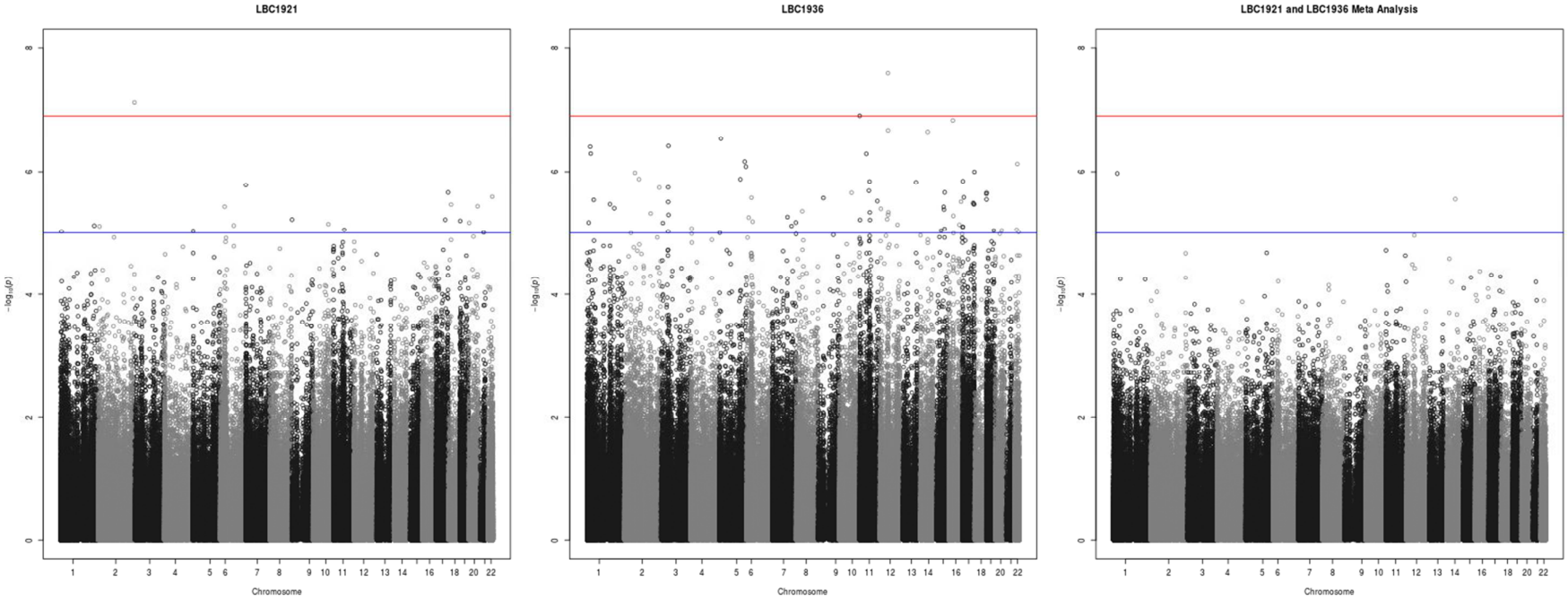


Figure 2: Proportion of variance in age explained by Hannum age and telomere length.



Supplementary Figure 1: EWAS of Telomere Length in LBC1921, LBC1936, and meta analysis.



The red line represents the Bonferroni significant threshold of $P = 1.2 \times 10^{-7}$; the blue line represents the nominal significance threshold of $P = 1 \times 10^{-5}$.