

## Supplementary Material

Supplementary Table 1: Association of age, gender and technical batch with telomere length

	age			gender			batch		
	beta	se	p-value	beta	se	p-value	beta	se	p-value
ERF	-0.0086	0.0004	$1.56 \times 10^{-102}$	0.0634	0.0123	$2.54 \times 10^{-7}$	-0.0030	0.0003	$1.52 \times 10^{-23}$
GRAPHIC	-0.0068	0.0002	$2.23 \times 10^{-253}$	0.0463	0.0093	$6.41 \times 10^{-7}$	0.0010	0.0005	0.046
LLS	-0.0084	0.0008	$8.64 \times 10^{-26}$	0.0517	0.0100	$2.34 \times 10^{-7}$	-0.0013	0.0004	0.001
NTR	-0.0128	0.0005	$1.53 \times 10^{-144}$	0.0826	0.0141	$4.68 \times 10^{-9}$	-0.0017	0.0002	$1.90 \times 10^{-17}$
QIMR	-0.0166	0.0007	$2.57 \times 10^{-124}$	0.0753	0.0236	0.001	0.0032	0.0007	$4.84 \times 10^{-6}$
TwinsUK	-0.0148	0.0007	$3.21 \times 10^{-99}$	0.0065	0.0345	0.851	0.0029	0.0002	$1.21 \times 10^{-47}$
Meta-analysis	-0.0086	0.0002	0*	0.0566	0.0053	$9.12 \times 10^{-27}$	NA	NA	NA

\*Limits of statistical software reached

Supplementary Table 2: Heritability models including a genetic dominance variance component or a sibling-shared environment component respectively

	Dominance variance			Sibling-shared environment		
	h2	Confidence interval	p-value	h2	Confidence interval	p-value
ERF	NA	NA	NA	0.60	0.53-0.68	$8.60 \times 10^{-68}$
GRAPHIC	NA	NA	NA	0.74	0.67-0.82	$2.07 \times 10^{-103}$
LLS	NA	NA	NA	NA	NA	NA
NTR	0.64	0.53-0.75	$2.15 \times 10^{-123}$	0.62	0.56-0.67	$1.75 \times 10^{-125}$
QIMR	0.71	0.62-0.81	$4.88 \times 10^{-63}$	0.62	0.55-0.69	$1.02 \times 10^{-69}$
TwinsUK	0.82	0.68-0.97	$9.82 \times 10^{-208}$	0.72	0.67-0.76	0*
Meta-analysis	0.71	0.62-0.81	$1.39 \times 10^{-51}$	0.66	0.60-0.72	$1.10 \times 10^{-112}$

\*Limits of statistical software reached