Supplementary information for *Royal Society Open Science* article:

Smoking does not accelerate leukocyte telomere attrition: a meta-analysis of 18 longitudinal cohorts

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Supplementary Information: Table S1. Summary of LTL data used in the meta-analysis.

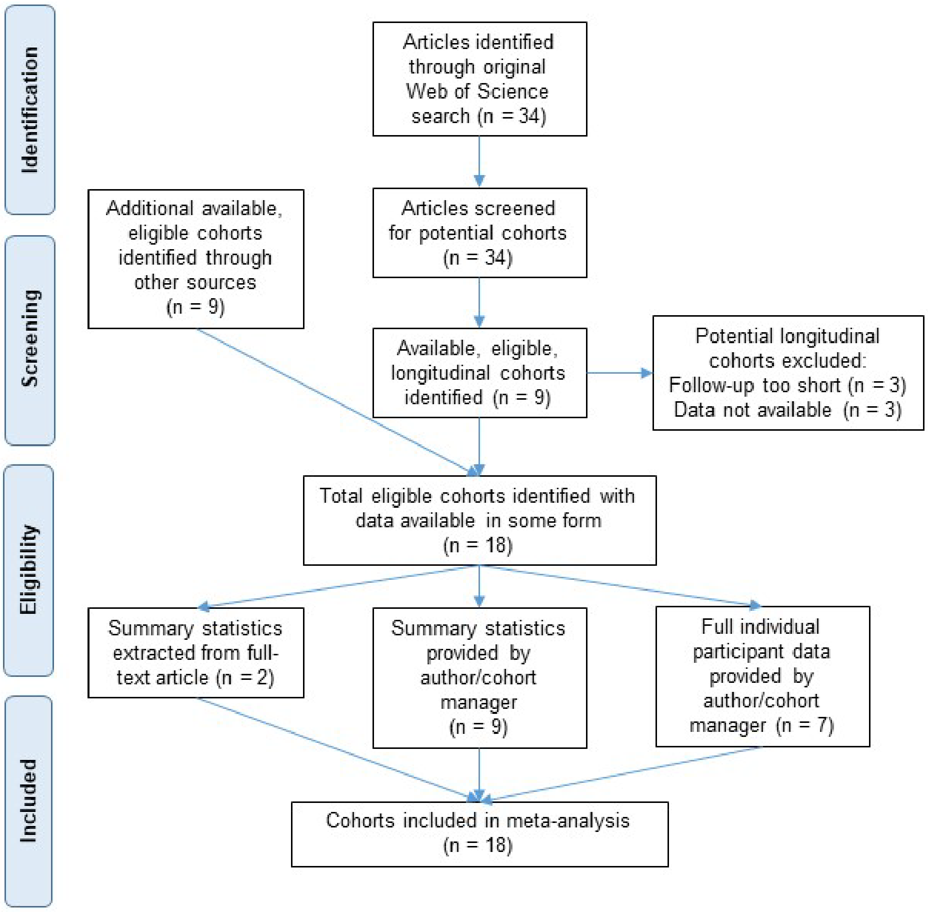
Cohort[1]	LTL measurement		Baseline TL				Follow-up TL				Telomere attrition (/year)				Pearson correlation between baseline and follow-up LTL	
	Method[2]	**Units[3]**	**Smokers**		**Non-smokers**		**Smokers**		**Non-smokers**		**Smokers**		**Non-smokers**		**r**	**p-value**
			Mean	**sd**	**Mean**	**sd**	**Mean**	**sd**	**Mean**	**sd**	**Mean**	**sd**	**Mean**	**sd**		
ADE	TRF	bp	6290.00	721.25	6378.57	465.85	6155.00	855.60	6128.57	490.83	16.44	15.56	30.02	24.20	0.92	<0.0001*
BHS	TRF	bp	7392.00	777.00	7481.00	777.00	7150.00	772.00	7270.00	772.00	42.00	46.00	40.00	46.00	0.95	<0.0001*
BRUNECK	qPCR	T/S	1.64	0.83	1.68	0.84	1.15	0.61	1.18	0.55	0.05	0.06	0.05	0.06	0.64	<0.0001*
CCHS	qPCR	bp	4318.00	1047.00	4434.00	1062.00	4042.00	1010.00	4116.00	1031.00	28.00	120.00	33.00	122.00	0.39	<0.0001*
CCS	qPCR	bp	4302.39	1591.62	4506.89	1867.65	3438.83	1472.86	3080.53	938.18	112.76	288.71	183.06	261.03	0.03	0.5990
DMHDS	qPCR	T/S	1.17	0.37	1.20	0.41	1.02	0.31	1.05	0.31	0.01	0.02	0.01	0.03	0.66	<0.0001*
ERA	TRF	bp	5860.00	0.00	6428.84	620.03	5710.00	0.00	6198.26	601.17	16.04	0.00	24.34	15.52	0.97	<0.0001*
ESTHER	qPCR	bp	5940.00	384.49	6020.00	315.18	5190.00	522.04	5810.00	616.72	1.30	84.35	14.50	99.80	NA	NA
HAS	qPCR	bp	5490.26	1464.64	5417.45	1443.86	3637.15	1539.88	4048.20	1446.62	204.74	265.92	149.04	236.01	-0.16	0.0919
HSS	qPCR	bp	5546.32	543.21	5483.28	527.85	5325.56	406.29	5277.76	344.28	46.12	119.89	42.05	102.77	0.40	<0.0001*
JLRCS	TRF	bp	7253.00	650.00	7361.00	673.00	6907.00	590.00	7053.00	644.00	26.50	14.00	23.50	13.60	0.96	<0.0001*
LBC1921	qPCR	bp	3912.37	301.05	4096.44	457.96	3290.00	770.88	3542.61	791.46	49.64	33.08	64.34	138.97	0.35	0.0017*
LBC1936	qPCR	bp	4073.34	579.07	4207.34	571.33	3680.81	648.08	3805.03	708.36	86.94	119.95	66.38	112.14	0.54	<0.0001*
MONICA	qPCR	T/S	0.75	0.16	0.74	0.16	0.65	0.19	0.67	0.20	0.01	0.02	0.01	0.02	0.37	<0.0001*
NESDA	qPCR	bp	5407.29	623.56	5511.60	614.67	5370.51	403.03	5440.66	446.86	6.13	96.55	11.82	95.26	0.45	<0.0001*
NSHD	qPCR	bp	5610.81	2017.47	5792.41	1827.71	4241.11	1236.59	4297.16	1345.08	148.61	235.88	160.14	234.61	0.12	0.0102*
PREVEND	qPCR	T/S	1.05	0.32	1.09	0.32	1.00	0.36	1.07	0.35	0.01	0.07	0.00	0.07	0.13	<0.0001*
SATSA	qPCR	T/S	0.73	0.19	0.73	0.22	0.72	0.15	0.74	0.17	0.00	0.03	0.00	0.03	0.39	<0.0001*

[1]Full details of each cohort are provided in Table 1; [2]Measurement methods for LTL: TRF = terminal restriction fragment and qPCR = quantitative polymerase chain reaction; [3]Units of LTL measurement: bp = base pairs and T/S = T/S ratios.

Supplementary Information: Table S2. Results from the leave-one-out sensitivity analysis of model 6.

Cohort omitted	Summary SMD		Heterogeneity statistics				
	Estimate* [95% CI]	p-value	Q_{16}	p-value	τ^2	I^2 (%)	H^2
ADE	-0.02 [-0.07, 0.04]	0.5116	24.06	0.0881	0.00	37.93	1.61
BHS	-0.02 [-0.08, 0.05]	0.6091	24.56	0.078	0.01	41.03	1.70
BRUNECK	-0.02 [-0.08, 0.04]	0.5257	24.64	0.0764	0.00	40.44	1.68
CCHS	-0.03 [-0.09, 0.03]	0.3793	21.65	0.155	0.00	32.98	1.49
CCS	-0.03 [-0.08, 0.03]	0.2978	19.97	0.2215	0.00	30.71	1.44
DMHDS	-0.02 [-0.08, 0.04]	0.5217	24.61	0.077	0.01	40.93	1.69
ERA	-0.02 [-0.07, 0.04]	0.5214	24.39	0.0814	0.00	37.93	1.61
ESTHER	-0.03 [-0.08, 0.03]	0.3552	22.49	0.1282	0.00	34.74	1.53
HAS	-0.02 [-0.07, 0.04]	0.5973	23.93	0.091	0.00	38.05	1.61
HSS	-0.02 [-0.08, 0.04]	0.5721	24.64	0.0764	0.00	40.12	1.67
JLRCS	-0.01 [-0.06, 0.05]	0.8152	20.47	0.1996	0.00	29.70	1.42
LBC1921	-0.02 [-0.07, 0.04]	0.5256	24.64	0.0765	0.00	38.03	1.61
LBC1936	-0.01 [-0.07, 0.05]	0.6828	23.16	0.1096	0.00	36.99	1.59
MONICA	0.00 [-0.05, 0.05]	0.9947	18.39	0.3017	0.00	13.68	1.16
NESDA	-0.03 [-0.09, 0.03]	0.3918	23.27	0.1068	0.00	36.71	1.58
NSHD	-0.02 [-0.08, 0.04]	0.4743	24.33	0.0825	0.00	39.61	1.66
PREVEND	-0.01 [-0.08, 0.05]	0.6692	23.98	0.09	0.01	38.68	1.63
SATSA	-0.02 [-0.07, 0.04]	0.6088	24.25	0.0841	0.00	38.80	1.63

*Negative parameter estimates for the summary standardized mean difference (SMD) correspond to faster attrition in smokers. The cohort with the largest influence is shaded.



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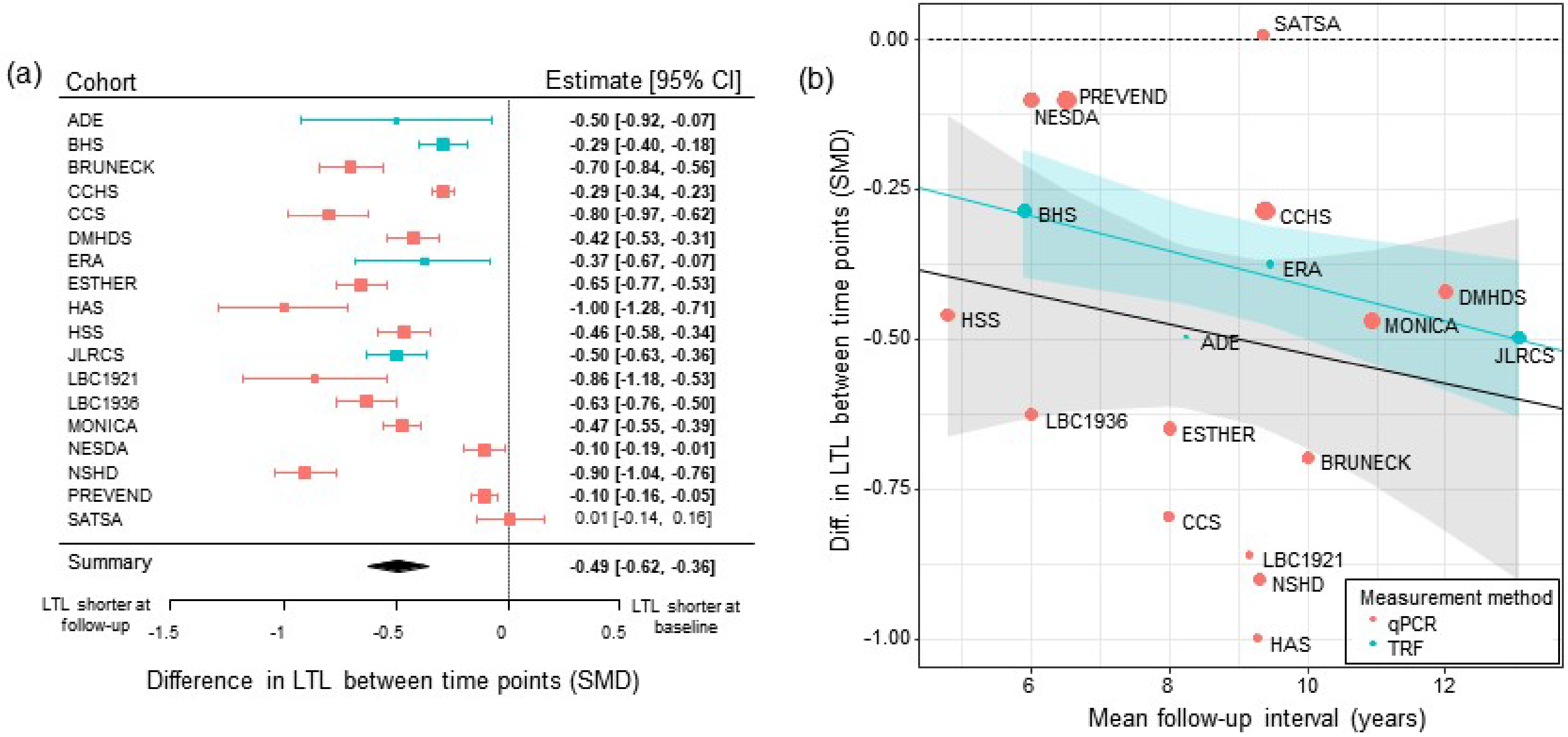

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