

Telomere Length and Parkinson's Disease Traits: A Mendelian Randomization Study

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Abstract

Parkinson's disease (PD) is a neurodegenerative condition influenced by aging, but the biological pathways linking age to PD remain unclear. Telomere length (TL), a marker of cellular aging, has been inconsistently linked to PD in observational studies. To assess potential causal relationships, we conducted two-sample Mendelian randomization (MR), a genetic approach that uses naturally occurring genetic variation to study causality. We used genetic instruments from a large genome-wide association study of TL (472,147 participants) and tested their associations with PD-related traits: disease risk, age at onset, binary motor subtype (tremor-dominant vs. postural instability/gait difficulty), and a continuous motor subtype score. We also assessed reverse causality to test whether PD traits may causally influence TL, using instruments derived from genome-wide association studies for each outcome. No causal relationships were detected in either direction (all $p > 0.05$). These findings suggest that leukocyte TL is not a causal factor for PD risk or related clinical traits. Future research should investigate TL in brain-specific tissues and explore other aging biomarkers in relation to PD.

Keywords

Parkinson's Disease, Telomere Length, Aging, Mendelian Randomization

1. Introduction

Aging is the leading risk factor for Parkinson's Disease (PD), the second most common age-related neurodegenerative disease in the United States after Alzheimer's Disease [1]. It remains unclear which age-related changes in cell function specifically contribute to risk of PD; the underlying mechanisms of neurodegen-

eration and biological aging are closely related, and neuronal cell death is influenced by a wide range of interacting genetic, environmental, and behavioral factors [2]. Measuring the effects of aging and the specific biological pathways impacted by aging that in turn contribute to the risk of PD is challenging [3]. There is also a need to understand the role of aging in other PD-related phenotypes like onset age and severity, as their underlying biological mechanisms are not well understood.

Telomeres are comprised of repeat sequences of DNA that cap the ends of chromosomes in the cell nucleus. Their presence helps to maintain the structural integrity of the ends of chromosomes during cell replication. Telomeres shorten with each mitotic cell replication cycle, and with exposure to oxidative stress [4]. As such, telomere length (TL) is considered a biomarker of cellular aging. TL chronologically varies over time, between individuals, and across cell types. TL is also organism-specific. The rate of TL attrition varies by age, by organ, and with respect to behavioral and environmental factors. Risk of PD has demonstrated varying associations with TL [5]. However, the directionality of this relationship is inconsistent across existing observational studies, which may be affected by issues of confounding, reverse causality, and measurement error [4] [5].

Mendelian randomization (MR) is a robust framework for causal analysis that utilizes genetic data for the construction of instrumental variables. Under the foundational assumptions of 1) instrument strength, 2) independence of the instrument and the outcome, and 3) exclusion—that the instrument is only associated with the outcome via its association with the exposure—it is possible to mitigate the effects of unmeasured confounding, and identify directionality of effect between the exposure and the outcome of the study. Prior investigations have demonstrated a null relationship between leukocyte TL and PD risk using an MR approach [6]. However, an updated genome-wide association study (GWAS) for leukocyte TL provides the opportunity to create stronger genetic instruments that capture a broader amount of variation in the exposure phenotype. Stronger genetic instruments in MR-based approaches may expose subtle relationships between exposures and outcomes that were not detectable in analyses with other genetic instruments. In addition, exploring multiple outcomes or characteristics of a single disease using MR approaches may reveal underlying genetic architecture of these complex phenotypes. Here, we conduct bidirectional MR analysis to investigate the effects of leukocyte TL as a measure of cellular aging on PD risk and other PD-related phenotypes.

2. Methods

2.1. Samples

Summary statistics for TL were obtained from the UK Biobank's 2021 GWAS of leukocyte TL (**Table 1**) [7]. The four PD-related outcomes of interest included PD risk [8], age at onset (AAO) [9], binary motor subtype (BMS; categorized as either the tremor-dominant (TD) or the postural instability/gait difficulty (PIGD) sub-

type), and continuous motor subtype (CMS; a ratio of TD and PIGD scores from the Unified Parkinson's Disease Rating Scale (UPDRS)) [10]. Summary statistics for all four PD-related outcomes were obtained from the International Parkinson Disease Genomics Consortium (IPDGC) (Table 1).

Table 1. Description of summary statistics utilized for genetic instruments in 2-sample Mendelian randomization.

	Phenotype	Sample Size	Authors	nSNPs (trait) ^a	h ² (trait)	h ² (instrument)
Exposure	Telomere Length	472,147 cases	Codd <i>et al.</i> 2021	197	0.08	0.05
	Risk	37,700 cases 1,400,000 controls	Nalls <i>et al.</i> 2019	90	0.27	0.16
Outcomes	Age at Onset	17,415 cases	Blauwendraat <i>et al.</i> 2016	2	0.11	NA
	Binary Disease Subtype	3,212 cases	Alfradique-Dunham <i>et al.</i> 2021	31	NA	NA
	Continuous Disease Subtype	3,212 cases	Alfradique-Dunham <i>et al.</i> 2021	7	NA	NA

a. nSNP: number of SNPs contained in the genetic instrument after clumping; h²: narrow-sense heritability.

2.2. Mendelian Randomization

2-sample Mendelian randomization (2SMR) was used to investigate the relationship between TL and each PD-related outcome, using the R package TwoSampleMR. The TL genetic instrument was constructed using GWAS independent significant signals ($p < 5.0 \times 10^{-8}$) from Codd *et al.* 2021, clumped for linkage disequilibrium (LD) at a threshold of $r^2 < 0.05$. Summary statistics for each SNP in the TL instrument were extracted from the four outcome datasets where available. F-statistics were calculated for each genetic instrumental variable (Supplementary Tables A1(a)-(d)). Associations between exposure and outcome were calculated via inverse-variance weighted meta-analysis, weighted median, simple model, weighted mode, and MR-PRESSO approaches. The MR-Egger intercept test and MR-PRESSO global test were used to detect the presence of directional horizontal pleiotropy.

To investigate the possibility of reverse causality, bidirectional MR was employed to investigate the effects of each PD-related phenotype on TL. Instruments for PD Risk and AAO were constructed using significant independent signals from their respective GWAS. Notably, for the BMS and CMS disease outcomes, no individual SNPs cleared a genome-wide significance p-value threshold of 5.0×10^{-8} ; genetic instruments for these exposures were instead constructed from SNPs with a suggestive association p-value threshold of 1.0×10^{-5} . For all instruments, LD clumping was performed at a threshold of $r^2 < 0.05$. F-statistics were calculated for each genetic instrumental variable (Supplementary Tables A2-A5).

2.3. Ethics Statement

This study was approved by the Case Western Reserve ethics board as non-human subjects research. All data are aggregate summary statistics, with patient consent

obtained from the original genome-wide association analyses.

3. Results

In 2SMR analysis, TL did not appear to have a significant association with any of the four PD-related outcomes ($p > 0.05$) (Table 2). Results of the Egger intercept test and MR-PRESSO test did not indicate the presence of horizontal pleiotropy ($p > 0.05$ for all models).

MR analysis in the reverse direction did not reveal significant causal effects of any of the four PD-related phenotypes on TL (Table 2). Similarly, there were null results for the Egger intercept test and MR-PRESSO for all models, demonstrating a lack of horizontal pleiotropy. Of note, the Egger intercept test could not be performed for the investigation of the effects of PD AAO on TL; only two genetic variants were incorporated into the genetic instrument, which is not sufficient to perform an Egger intercept test.

Table 2. Results for bidirectional Mendelian randomization between Telomere Length and PD traits.

Exposure	Outcome	nSNP ^a	BETA	SE	p	Egger Test p-value	MR-PRESSO p (Global)
Telomere Length	PD Risk	118	0.148	0.086	0.086	0.568	0.109
	PD AAO	108	0.746	0.528	0.158	0.590	0.213
	PD Binary Disease Subtype	118	0.355	0.262	0.175	0.187	0.244
	PD Continuous Disease Subtype	118	-0.109	0.096	0.259	0.162	0.485
PD Risk	Telomere Length	84	0.002	0.005	0.732	0.926	0.941
PD AAO		2	-0.002	0.004	0.566	-	-
PD Binary Disease Subtype		29	-0.003	0.003	0.387	0.874	0.297
PD Continuous Disease Subtype		6	-0.006	0.005	0.217	0.371	0.206

a. nSNP: number of SNPs contained in the genetic instrument after clumping for LD, extracting from the outcome dataset, and data harmonization.

4. Discussion

In this study, we applied bidirectional Mendelian randomization (MR) to examine the potential causal relationship between telomere length (TL)—a marker of cellular aging—and multiple Parkinson’s disease (PD)-related phenotypes, including disease risk, age at onset (AAO), and two motor subtypes: binary motor subtype (BMS) and continuous motor subtype (CMS). Despite using a large and updated genome-wide association study (GWAS) for TL to create a strong genetic instrument, our findings were null across all outcomes and directions, and MR-Egger intercepts did not suggest directional pleiotropy. These results are consistent with earlier MR studies investigating TL and PD risk, that used a different set of genetic instruments [6]. Our work expands on prior work by being the first to evaluate

PD AAO and motor subtypes via MR.

Our findings offer several key implications. First, while previous observational studies have reported conflicting associations between TL and PD risk [5] [11] [12]—ranging from inverse to positive relationships—our MR results suggest that TL, as genetically determined in leukocytes, is unlikely to be a causal driver of PD onset or symptomology. Moreover, the directionality of the beta estimate for CMS hints at a possible trend toward more severe postural instability/gait difficulty (PIGD) motor symptoms in individuals with longer telomeres, though this result was not statistically significant. Future studies with larger sample sizes or more granular phenotype definitions may help clarify whether such trends reflect meaningful biological relationships.

Another key consideration is that telomere length was measured in leukocytes, which are often used as proxies for systemic aging due to their accessibility. However, TL varies by tissue type [13], and the correlations between leukocyte TL and telomere dynamics in neurons or glial cells are only modest. The lack of association observed here may reflect a disconnect between systemic TL and disease-relevant cellular aging in brain tissue. Studies have suggested that TL in substantia nigra neurons may be preserved even in PD [14], while stress responses or telomerase activity in glial populations might differ from those in circulating leukocytes. Thus, as GWAS of brain- or muscle-specific TL becomes available, future MR studies could better capture tissue-specific relevance to PD pathology. Nonetheless, null findings in MR may reflect biological complexity, including tissue- or cell-type-specific compensatory mechanisms. For example, increased telomerase activity in neural stem cells, or stress-adaptive responses, may modulate aging effects in the brain differently than in peripheral tissues. These subtleties, coupled with the lifelong accumulation of oxidative and inflammatory insults, underscore the complexity of teasing apart causal versus correlative signals in neurodegenerative disease.

Our findings contrast with several observational studies reporting associations between shorter TL and PD risk. These discrepancies could stem from key limitations in observational designs, including residual confounding, measurement error, and reverse causation. For instance, observational studies may fail to account for shared environmental exposures (e.g., smoking, inflammation) that influence both TL and neurodegeneration. Additionally, survival bias could distort associations if individuals with shorter TL and more severe PD are underrepresented in aging cohorts due to earlier mortality. Mendelian randomization helps address some of these issues but may miss effects driven by non-genetic or later-life processes. Together, these methodological differences may explain the inconsistent findings across studies.

There are strengths and limitations to acknowledge. Mendelian randomization is a robust framework for causal analysis, capable of circumventing issues of reverse causality and unmeasured confounding when exploring the relationship between exposures and outcomes. A key limitation was the comparatively small

sample size of the GWAS cohorts for PD AAO, BMS, and CMS. Smaller sample sizes can lead to weaker GWAS associations, which can hinder the ability of 2SMR to detect exposure-outcome associations. Another concern is the modest heritability explained by the instruments, which is a consistent concern across chronic phenotypes whose genetic architecture is yet to be fully discerned. A final limitation is that we were unable to evaluate horizontal pleiotropy for the AAO analyses.

5. Conclusion

Using two-sample MR and robust genetic instruments, we found no evidence that leukocyte TL causally influences the risk of PD or related clinical features such as AAO or motor subtype. Nor do these PD traits influence leukocyte TL. Our findings highlight several key areas for further investigation. Future MR studies should explore TL in brain or muscle tissues once such data become available. In addition, other biomarkers of cellular aging may offer deeper insight into the biological links between aging and PD. These include epigenetic clocks, mitochondrial DNA copy numbers, cellular senescence markers, oxidative stress biomarkers, and pro-inflammatory cytokines. Integration of transcriptomic or epigenetic data could reveal novel intermediate mechanisms that explain how cellular aging intersects with PD neurodegeneration. Genetic instruments for these biomarkers are emerging and offer exciting opportunities for future research aimed at understanding aging-related vulnerability to PD. Also, to overcome current limitations, future MR studies would benefit from improved genetic instruments for PD-related phenotypes such as age at onset and motor subtype, as well as larger sample sizes that enhance statistical power.

Conflicts of Interest

The authors declare no conflicts of interest regarding the publication of this paper.

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Supplementary Tables

Table A1. (a) Variants used in the genetic instrument for Telomere Length used for PD Risk MR; (b) Variants used in the genetic instrument for Telomere Length used for PD AAO MR; (c) Variants used in the genetic instrument for Telomere Length used for PD Binary Disease Subtype MR; (d) Variants used in the genetic instrument for Telomere Length used for PD Continuous Disease Subtype MR.

(a)

rsID	CHR	BP	A1	A2	EAFF	BETA	SE	pval	R ²	F-Statistic
rs138895564	5	1.30E+06	C	T	0.990903	-0.835	0.010969	1.10E-59	0.012578	50.95611
rs183553155	16	7.40E+07	G	A	0.989437	-0.931	0.010204	3.10E-12	0.018136	73.88732
rs115451758	5	1.30E+06	G	A	0.989626	1.088	0.009949	6.70E-17	0.024289	99.58028
rs139795227	1	9.30E+07	A	C	0.985979	-0.942	0.008673	6.70E-12	0.024522	100.561
rs146546514	3	1.70E+08	C	A	0.983095	-0.923	0.008418	2.30E-22	0.028324	116.6052
rs144204502	17	7.60E+07	C	T	0.987438	1.106	0.008929	3.40E-28	0.030362	125.257
rs33987166	5	1.30E+06	T	C	0.975189	-0.907	0.006633	8.00E-50	0.039778	165.7125
rs78491606	3	7.30E+07	A	C	0.981567	1.079	0.007398	1.90E-24	0.042127	175.9286
rs79717857	5	1.30E+06	C	A	0.973921	-0.950	0.006633	3.80E-15	0.045872	192.3205
rs154979	6	3.30E+07	C	A	0.971166	-0.957	0.006122	1.70E-13	0.051287	216.2527
rs138061125	7	1.60E+08	G	A	0.969815	-0.958	0.005867	2.60E-13	0.053723	227.1058
rs182059586	16	1.50E+07	T	C	0.97489	1.059	0.006633	4.90E-17	0.054871	232.2397
rs141379009	11	1.10E+08	T	G	0.974488	1.096	0.006378	8.70E-48	0.059767	254.2795
rs35640778	20	6.20E+07	G	A	0.979243	1.232	0.007143	9.60E-195	0.061748	263.2608
rs115251750	5	1.30E+06	G	A	0.964935	-0.965	0.005357	4.50E-11	0.06297	268.822
rs61748181	5	1.30E+06	C	T	0.971072	1.061	0.005867	2.80E-23	0.063219	269.9568
rs80324517	6	204031	G	A	0.951741	-0.961	0.004592	1.80E-17	0.084798	370.6399
rs9952504	18	657458	A	G	0.958066	1.054	0.005357	2.40E-24	0.089336	392.4231
rs76219171	16	5.00E+07	G	A	0.941567	-0.965	0.004082	7.80E-17	0.102393	456.3202
rs3093888	14	2.10E+07	G	A	0.94869	1.029	0.004592	1.50E-10	0.103168	460.1719
rs55765053	20	6.20E+07	C	T	0.933938	-0.978	0.004082	3.6E-08	0.118084	535.6108
rs17185038	1	2.80E+07	C	G	0.93539	1.026	0.004082	2.10E-10	0.127323	583.6303
rs11769630	7	5.00E+07	T	A	0.927773	1.026	0.003827	4.30E-11	0.141174	657.5597
rs111811424	18	674579	C	T	0.913521	-0.962	0.003571	1.40E-27	0.146145	684.6772
rs11579626	1	1.50E+08	A	C	0.915118	-0.973	0.003827	1.30E-13	0.147187	690.4035
rs34003787	16	7.30E+07	C	T	0.912293	1.024	0.003571	1.90E-11	0.167898	807.1491
rs72801474	5	1.30E+08	G	A	0.911707	1.021	0.003571	3.90E-09	0.1679	807.1652
rs76666449	12	1.20E+08	T	C	0.899375	-0.970	0.003316	8.20E-19	0.170459	821.9904
rs73581419	14	2.20E+07	C	T	0.893395	-0.977	0.003061	1.30E-12	0.181917	889.5328
rs5030755	17	1.80E+06	A	G	0.886658	-0.970	0.003316	6.20E-22	0.189286	933.9801

rs2259797	20	6.20E+07	T	C	0.907332	1.084	0.003571	1.30E-116	0.197734	985.937
rs3761121	20	6.20E+07	T	C	0.878032	-0.980	0.003061	7.30E-11	0.205785	1036.483
rs4919611	10	1.00E+08	C	A	0.112898	1.026	0.003316	5.10E-16	0.210995	1069.743
rs79824385	18	4.20E+07	T	A	0.870276	-0.969	0.003061	7.90E-27	0.211793	1074.876
rs7012816	8	7.10E+07	G	A	0.870003	-0.982	0.002806	3E-09	0.218197	1116.447
rs12615793	2	5.40E+07	G	A	0.859605	-0.956	0.002806	1.80E-55	0.220594	1132.182
rs28711261	16	6.80E+07	A	G	0.867449	-0.983	0.003061	1.6E-08	0.222275	1143.275
rs11866592	16	7.50E+07	G	A	0.85802	-0.966	0.002806	1.30E-33	0.227172	1175.863
rs12613375	2	5.90E+07	C	T	0.862288	-0.982	0.002806	9.10E-10	0.229097	1188.791
rs4724	17	7.80E+06	G	A	0.883402	1.057	0.003061	9.80E-69	0.22996	1194.605
rs9990898	4	1.60E+08	T	C	0.857338	-0.970	0.002806	3.00E-26	0.230374	1197.398
rs762679	8	4.90E+07	T	A	0.143499	-0.969	0.003061	1.40E-27	0.231036	1201.878
rs1291143	20	3.60E+07	A	C	0.150974	-0.952	0.002806	1.80E-69	0.23243	1211.323
rs12572897	10	9.60E+07	G	A	0.869908	1.033	0.003061	3.60E-27	0.241295	1272.218
rs11557154	9	3.40E+07	C	T	0.86997	1.035	0.002806	1.10E-30	0.242164	1278.264
rs1985369	7	1.60E+08	A	G	0.131822	1.031	0.003061	3.60E-25	0.24353	1287.796
rs1609812	11	5.20E+06	G	A	0.160214	-0.954	0.002806	3.90E-65	0.244949	1297.731
rs12369950	12	2.50E+07	T	C	0.859325	1.018	0.003061	8.00E-10	0.250633	1337.921
rs6030416	20	3.60E+07	T	G	0.135696	1.035	0.003061	1.50E-30	0.25107	1341.036
rs429358	19	4.50E+07	T	C	0.846031	-0.983	0.002806	3.80E-10	0.251816	1346.359
rs1957937	14	9.60E+07	A	T	0.83982	-0.979	0.002551	1.90E-14	0.257979	1390.765
rs932002	1	2.30E+08	C	T	0.849157	1.041	0.002806	7.30E-47	0.277515	1536.539
rs1332941	13	4.20E+07	A	G	0.179534	-0.974	0.002806	5.90E-21	0.279675	1553.143
rs9419958	10	1.10E+08	T	C	0.13861	1.084	0.003061	2.60E-167	0.280789	1561.743
rs12941945	17	4.10E+07	A	G	0.832437	1.026	0.002551	3.00E-22	0.293862	1664.711
rs41269079	1	4.50E+07	T	A	0.811009	-0.985	0.002551	1.70E-09	0.297487	1693.945
rs61818036	1	1.50E+08	G	A	0.176391	1.019	0.002551	2.10E-12	0.301808	1729.185
rs3768321	1	4.00E+07	G	T	0.810305	1.016	0.002551	1.10E-09	0.317418	1860.214
rs8088824	18	4.20E+07	C	T	0.236812	-0.974	0.002296	8.10E-28	0.343148	2089.779
rs4743037	9	1.10E+08	C	T	0.769126	-0.985	0.002296	5.10E-10	0.344646	2103.7
rs1907702	12	8.90E+07	G	A	0.233229	-0.985	0.002551	5.90E-10	0.347096	2126.599
rs2056726	7	1.00E+08	G	A	0.785624	1.023	0.002551	7.90E-21	0.352694	2179.59
rs1727302	12	1.20E+08	G	A	0.259019	-0.980	0.002296	8.40E-18	0.368805	2337.325
rs1023767	8	9.60E+07	G	A	0.762405	1.018	0.002296	5.00E-15	0.375567	2405.956
rs7705526	5	1.30E+06	C	A	0.673422	-0.925	0.002296	2.40E-282	0.376317	2413.662
rs2303262	16	8.20E+07	C	T	0.222887	1.048	0.002551	2.90E-85	0.38056	2457.586

rs2069536	17	7.40E+07	A	G	0.249795	1.015	0.002296	1.80E-10	0.386209	2517.027
rs13230646	7	2.40E+07	T	C	0.751055	1.017	0.002296	8.90E-14	0.386875	2524.11
rs13129697	4	9.90E+06	T	G	0.720832	-0.983	0.002296	1.50E-14	0.389013	2546.931
rs8105767	19	2.20E+07	A	G	0.70533	-0.968	0.002041	2.50E-50	0.38913	2548.19
rs75664430	17	8.10E+06	C	G	0.751972	1.024	0.002296	3.60E-24	0.391362	2572.202
rs7218033	17	1.70E+06	C	T	0.746597	1.023	0.002296	1.00E-22	0.396192	2624.776
rs35671754	2	2.20E+08	G	T	0.704253	-0.988	0.002296	1.4E-08	0.406683	2741.921
rs4758644	12	1.20E+08	A	C	0.269222	1.017	0.002296	2.70E-13	0.407091	2746.566
rs3891167	18	658423	A	G	0.746565	1.044	0.002296	1.20E-70	0.412395	2807.462
rs11190184	10	1.00E+08	G	C	0.71576	1.017	0.002296	1.10E-14	0.420968	2908.248
rs939916	11	202253	G	A	0.330033	-0.976	0.002041	6.60E-29	0.421497	2914.573
rs35601737	19	1.30E+07	C	G	0.704101	1.014	0.002041	1.90E-10	0.428518	2999.519
rs13062095	3	1.00E+08	T	C	0.672157	-0.986	0.002041	9.70E-11	0.428555	2999.975
rs17677991	15	4.20E+07	C	G	0.657877	-0.978	0.002041	4.40E-26	0.430773	3027.247
rs10840270	11	9.60E+06	C	G	0.344316	-0.986	0.002296	1.30E-11	0.439058	3131.043
rs2293607	3	1.70E+08	T	C	0.757553	1.099	0.002296	<1.0E-314	0.44331	3185.512
rs111527438	17	2.90E+07	T	C	0.648749	-0.987	0.002296	3.10E-09	0.444051	3195.091
rs7790856	7	1.20E+08	C	T	0.710861	1.045	0.002296	1.80E-87	0.448889	3258.263
rs66731853	1	2.10E+07	G	A	0.682696	1.018	0.002041	1.50E-16	0.449125	3261.373
rs6565924	18	7.50E+07	A	G	0.638554	-0.987	0.002041	2.90E-10	0.449759	3269.729
rs869785	3	2.40E+07	T	C	0.327529	1.015	0.002041	4.40E-12	0.453923	3325.171
rs11556924	7	1.30E+08	C	T	0.624146	-0.987	0.002041	6.80E-10	0.457134	3368.503
rs2276182	18	5.20E+07	C	G	0.596773	-0.977	0.002041	2.80E-30	0.459633	3402.579
rs2811491	3	1.30E+08	C	A	0.39223	-0.985	0.002041	8.90E-14	0.462681	3444.565
rs4530278	19	3.40E+07	G	T	0.40185	-0.986	0.002041	1.50E-11	0.467459	3511.372
rs10845387	12	1.20E+07	G	A	0.647334	1.014	0.002041	1.50E-11	0.46955	3540.984
rs1980240	15	5.70E+07	A	C	0.594757	-0.987	0.002041	2.20E-10	0.469671	3542.693
rs11646283	16	9.10E+06	T	C	0.589297	-0.985	0.002041	5.30E-14	0.469746	3543.768
rs6669563	1	3.20E+07	G	A	0.562232	-0.982	0.002041	2.10E-19	0.474848	3617.063
rs762810	14	6.60E+07	C	A	0.647514	1.020	0.002041	4.30E-22	0.475109	3620.837
rs5742915	15	7.40E+07	T	C	0.554171	-0.981	0.002041	1.60E-21	0.475706	3629.527
rs56178008	2	2.90E+07	T	A	0.562503	-0.986	0.002041	9.70E-13	0.478597	3671.822
rs4498805	1	1.10E+08	G	T	0.453368	-0.985	0.002041	5.70E-14	0.481002	3707.382
rs8114049	20	6.20E+07	C	T	0.330913	1.043	0.002041	1.40E-85	0.481623	3716.611
rs10774625	12	1.10E+08	A	G	0.476428	-0.984	0.002041	1.70E-15	0.483177	3739.816

rs4742448	9	826585	C	G	0.530842	-0.985	0.002041	6.40E-14	0.483377	3742.805
rs1143697	17	7.60E+07	T	C	0.536558	-0.986	0.002041	5.50E-12	0.483595	3746.081
rs4695407	4	4.90E+07	A	G	0.492157	-0.986	0.002041	1.50E-12	0.486075	3783.455
rs2293579	11	4.70E+07	G	A	0.613726	1.013	0.002041	3.30E-10	0.486622	3791.753
rs6590343	11	1.30E+08	A	G	0.483615	-0.988	0.002041	1.50E-09	0.487619	3806.911
rs4731541	7	1.30E+08	C	G	0.375099	1.021	0.002041	1.40E-23	0.488908	3826.613
rs28502153	22	1.70E+07	C	A	0.622042	1.022	0.002041	1.20E-25	0.491363	3864.38
rs6776756	3	1.30E+08	G	A	0.402438	1.017	0.002041	1.10E-17	0.497597	3961.975
rs8102497	19	5.70E+07	G	A	0.568172	1.015	0.002041	1.40E-13	0.505649	4091.665
rs871134	4	7.00E+06	C	T	0.430968	1.018	0.002041	1.70E-19	0.508448	4137.732
rs8053839	16	4.80E+07	G	T	0.458038	1.014	0.002041	1.00E-11	0.510576	4173.124
rs12884911	14	6.50E+07	C	T	0.49667	1.013	0.002041	2.90E-11	0.513148	4216.294
rs9398196	6	1.10E+08	A	G	0.47995	1.014	0.002041	9.50E-13	0.513371	4220.065
rs41272947	3	1.60E+08	G	A	0.458021	1.017	0.002041	5.90E-18	0.513646	4224.712
rs2306646	8	2.20E+07	G	C	0.440525	1.021	0.002041	3.30E-25	0.514069	4231.876
rs10112752	8	7.40E+07	G	A	0.569631	1.029	0.002041	9.50E-46	0.519581	4326.331
rs611646	11	1.10E+08	T	A	0.591315	1.038	0.002041	3.50E-73	0.520446	4341.335

SNP: SNP rsID; **CHR:** Chromosome of SNP; **BP:** Base-pair location of SNP (hg19); **A1:** Effect allele; **A2:** Other allele; **EAF:** Effect allele frequency; **BETA:** SNP effect estimate; **SE:** SE of SNP effect estimate; **pval:** P-value for effect allele on Telomere length.

(b)

rsID	CHR	BP	A1	A2	EAF	BETA	SE	pval	R ²	F-Statistic
rs66731853	1	2.10E+07	G	A	0.682696	1.018	0.002041	1.50E-16	0.449125281	354.0479
rs17185038	1	2.80E+07	C	G	0.93539	1.026	0.004082	2.10E-10	0.127322268	63.35771
rs6669563	1	3.20E+07	G	A	0.562232	-0.982	0.002041	2.10E-19	0.474848387	392.6609
rs3768321	1	4.00E+07	G	T	0.810305	1.016	0.002551	1.10E-09	0.317418198	201.941
rs41269079	1	4.50E+07	T	A	0.811009	-0.985	0.002551	1.70E-09	0.297486977	183.8912
rs139795227	1	9.30E+07	A	C	0.985979	-0.942	0.008673	6.70E-12	0.024522306	10.9167
rs4498805	1	1.10E+08	G	T	0.453368	-0.985	0.002041	5.70E-14	0.481002215	402.4658
rs11579626	1	1.50E+08	A	C	0.915118	-0.973	0.003827	1.30E-13	0.147187455	74.94879
rs61818036	1	1.50E+08	G	A	0.176391	1.019	0.002551	2.10E-12	0.301807962	187.7168
rs932002	1	2.30E+08	C	T	0.849157	1.041	0.002806	7.30E-47	0.277515158	166.8036
rs56178008	2	2.90E+07	T	A	0.562503	-0.986	0.002041	9.70E-13	0.47859667	398.6055
rs12615793	2	5.40E+07	G	A	0.859605	-0.956	0.002806	1.80E-55	0.220594188	122.9073
rs12613375	2	5.90E+07	C	T	0.862288	-0.982	0.002806	9.10E-10	0.229097063	129.0527
rs35671754	2	2.20E+08	G	T	0.704253	-0.988	0.002296	1.4E-08	0.406682965	297.6573
rs869785	3	2.40E+07	T	C	0.327529	1.015	0.002041	4.40E-12	0.453922959	360.9738

rs78491606	3	7.30E+07	A	C	0.981567	1.079	0.007398	1.90E-24	0.042126825	19.09845
rs13062095	3	1.00E+08	T	C	0.672157	-0.986	0.002041	9.70E-11	0.428554827	325.6711
rs2811491	3	1.30E+08	C	A	0.39223	-0.985	0.002041	8.90E-14	0.462680534	373.935
rs6776756	3	1.30E+08	G	A	0.402438	1.017	0.002041	1.10E-17	0.497597239	430.1039
rs41272947	3	1.60E+08	G	A	0.458021	1.017	0.002041	5.90E-18	0.513645938	458.6261
rs2293607	3	1.70E+08	T	C	0.757553	1.099	0.002296	<1.0E-314	0.44330966	345.8127
rs871134	4	7.00E+06	C	T	0.430968	1.018	0.002041	1.70E-19	0.508447728	449.1837
rs13129697	4	9.90E+06	T	G	0.720832	-0.983	0.002296	1.50E-14	0.389012608	276.4896
rs4695407	4	4.90E+07	A	G	0.492157	-0.986	0.002041	1.50E-12	0.486074555	410.7241
rs9990898	4	1.60E+08	T	C	0.857338	-0.970	0.002806	3.00E-26	0.2303736	129.9871
rs33987166	5	1.30E+06	T	C	0.975189	-0.907	0.006633	8.00E-50	0.039777853	17.98941
rs7705526	5	1.30E+06	C	A	0.673422	-0.925	0.002296	2.40E-282	0.376317385	262.0222
rs79717857	5	1.30E+06	C	A	0.973921	-0.950	0.006633	3.80E-15	0.045871889	20.87793
rs115251750	5	1.30E+06	G	A	0.964935	-0.965	0.005357	4.50E-11	0.062969855	29.18277
rs61748181	5	1.30E+06	C	T	0.971072	1.061	0.005867	2.80E-23	0.063218849	29.30595
rs115451758	5	1.30E+06	G	A	0.989626	1.088	0.009949	6.70E-17	0.024288954	10.81023
rs72801474	5	1.30E+08	G	A	0.911707	1.021	0.003571	3.90E-09	0.167900476	87.6242
rs80324517	6	204031	G	A	0.951741	-0.961	0.004592	1.80E-17	0.084797595	40.23591
rs154979	6	3.30E+07	C	A	0.971166	-0.957	0.006122	1.70E-13	0.051287372	23.47595
rs9398196	6	1.10E+08	A	G	0.47995	1.014	0.002041	9.50E-13	0.513371007	458.1216
rs13230646	7	2.40E+07	T	C	0.751055	1.017	0.002296	8.90E-14	0.386875438	274.0122
rs11769630	7	5.00E+07	T	A	0.927773	1.026	0.003827	4.30E-11	0.141173966	71.38333
rs2056726	7	1.00E+08	G	A	0.785624	1.023	0.002551	7.90E-21	0.352694305	236.6118
rs7790856	7	1.20E+08	C	T	0.710861	1.045	0.002296	1.80E-87	0.44888932	353.7104
rs11556924	7	1.30E+08	C	T	0.624146	-0.987	0.002041	6.80E-10	0.457134193	365.6778
rs4731541	7	1.30E+08	C	G	0.375099	1.021	0.002041	1.40E-23	0.48890839	415.4092
rs1985369	7	1.60E+08	A	G	0.131822	1.031	0.003061	3.60E-25	0.243530257	139.8005
rs2306646	8	2.20E+07	G	C	0.440525	1.021	0.002041	3.30E-25	0.514069229	459.4038
rs762679	8	4.90E+07	T	A	0.143499	-0.969	0.003061	1.40E-27	0.231036441	130.4734
rs7012816	8	7.10E+07	G	A	0.870003	-0.982	0.002806	3E-09	0.218197351	121.1992
rs10112752	8	7.40E+07	G	A	0.569631	1.029	0.002041	9.50E-46	0.519581492	469.6576
rs1023767	8	9.60E+07	G	A	0.762405	1.018	0.002296	5.00E-15	0.375567177	261.1857
rs11557154	9	3.40E+07	C	T	0.86997	1.035	0.002806	1.10E-30	0.242164155	138.7657
rs4743037	9	1.10E+08	C	T	0.769126	-0.985	0.002296	5.10E-10	0.344646348	228.3733
rs12572897	10	9.60E+07	G	A	0.869908	1.033	0.003061	3.60E-27	0.241295242	138.1094

rs11190184	10	1.00E+08	G	C	0.71576	1.017	0.002296	1.10E-14	0.420967557	3177.598
rs4919611	10	1.00E+08	C	A	0.112898	1.026	0.003316	5.10E-16	0.210995462	116.1291
rs9419958	10	1.10E+08	T	C	0.13861	1.084	0.003061	2.60E-167	0.280789	169.5396
rs939916	11	202253	G	A	0.330033	-0.976	0.002041	6.60E-29	0.421497147	316.4001
rs1609812	11	5.20E+06	G	A	0.160214	-0.954	0.002806	3.90E-65	0.244948852	140.8791
rs10840270	11	9.60E+06	C	G	0.344316	-0.986	0.002296	1.30E-11	0.439057642	339.8997
rs2293579	11	4.70E+07	G	A	0.613726	1.013	0.002041	3.30E-10	0.486621901	411.625
rs611646	11	1.10E+08	T	A	0.591315	1.038	0.002041	3.50E-73	0.520445648	471.2865
rs141379009	11	1.10E+08	T	G	0.974488	1.096	0.006378	8.70E-48	0.059766962	27.60407
rs6590343	11	1.30E+08	A	G	0.483615	-0.988	0.002041	1.50E-09	0.487618651	413.2705
rs10845387	12	1.20E+07	G	A	0.647334	1.014	0.002041	1.50E-11	0.469550439	384.4019
rs12369950	12	2.50E+07	T	C	0.859325	1.018	0.003061	8.00E-10	0.250633413	145.2419
rs1907702	12	8.90E+07	G	A	0.233229	-0.985	0.002551	5.90E-10	0.347095826	230.8593
rs10774625	12	1.10E+08	A	G	0.476428	-0.984	0.002041	1.70E-15	0.483177011	405.9867
rs76666449	12	1.20E+08	T	C	0.899375	-0.970	0.003316	8.20E-19	0.170458645	89.2336
rs1727302	12	1.20E+08	G	A	0.259019	-0.980	0.002296	8.40E-18	0.368805094	253.7353
rs4758644	12	1.20E+08	A	C	0.269222	1.017	0.002296	2.70E-13	0.407091485	298.1616
rs1332941	13	4.20E+07	A	G	0.179534	-0.974	0.002806	5.90E-21	0.279675214	168.606
rs3093888	14	2.10E+07	G	A	0.94869	1.029	0.004592	1.50E-10	0.103168095	49.95532
rs73581419	14	2.20E+07	C	T	0.893395	-0.977	0.003061	1.30E-12	0.181917107	96.56587
rs12884911	14	6.50E+07	C	T	0.49667	1.013	0.002041	2.90E-11	0.513147712	457.7123
rs762810	14	6.60E+07	C	A	0.647514	1.020	0.002041	4.30E-22	0.475108511	393.0707
rs1957937	14	9.60E+07	A	T	0.83982	-0.979	0.002551	1.90E-14	0.257978866	150.9786
rs17677991	15	4.20E+07	C	G	0.657877	-0.978	0.002041	4.40E-26	0.430772542	328.6318
rs1980240	15	5.70E+07	A	C	0.594757	-0.987	0.002041	2.20E-10	0.469670651	384.5875
rs5742915	15	7.40E+07	T	C	0.554171	-0.981	0.002041	1.60E-21	0.475706314	394.014
rs8053839	16	4.80E+07	G	T	0.458038	1.014	0.002041	1.00E-11	0.510576225	453.0258
rs76219171	16	5.00E+07	G	A	0.941567	-0.965	0.004082	7.80E-17	0.102392985	49.53719
rs28711261	16	6.80E+07	A	G	0.867449	-0.983	0.003061	1.6E-08	0.222275166	124.1116
rs183553155	16	7.40E+07	G	A	0.989437	-0.931	0.010204	3.10E-12	0.018135754	8.021057
rs11866592	16	7.50E+07	G	A	0.85802	-0.966	0.002806	1.30E-33	0.227171562	127.6493
rs2303262	16	8.20E+07	C	T	0.222887	1.048	0.002551	2.90E-85	0.380559519	266.7905
rs7218033	17	1.70E+06	C	T	0.746597	1.023	0.002296	1.00E-22	0.396191847	284.9404
rs5030755	17	1.80E+06	A	G	0.886658	-0.970	0.003316	6.20E-22	0.189286367	101.391
rs4724	17	7.80E+06	G	A	0.883402	1.057	0.003061	9.80E-69	0.229959771	129.6838
rs75664430	17	8.10E+06	C	G	0.751972	1.024	0.002296	3.60E-24	0.391361871	279.233

rs111527438	17	2.90E+07	T	C	0.648749	-0.987	0.002296	3.10E-09	0.444050752	346.8525
rs12941945	17	4.10E+07	A	G	0.832437	1.026	0.002551	3.00E-22	0.293861581	180.7176
rs2069536	17	7.40E+07	A	G	0.249795	1.015	0.002296	1.80E-10	0.38620912	273.2433
rs1143697	17	7.60E+07	T	C	0.536558	-0.986	0.002041	5.50E-12	0.483595014	406.6669
rs9952504	18	657458	A	G	0.958066	1.054	0.005357	2.40E-24	0.089336088	42.60065
rs3891167	18	658423	A	G	0.746565	1.044	0.002296	1.20E-70	0.41239514	304.7724
rs111811424	18	674579	C	T	0.913521	-0.962	0.003571	1.40E-27	0.146145087	74.32716
rs8088824	18	4.20E+07	C	T	0.236812	-0.974	0.002296	8.10E-28	0.343148355	226.8622
rs2276182	18	5.20E+07	C	G	0.596773	-0.977	0.002041	2.80E-30	0.459633019	369.377
rs6565924	18	7.50E+07	A	G	0.638554	-0.987	0.002041	2.90E-10	0.449758512	354.9551
rs35601737	19	1.30E+07	C	G	0.704101	1.014	0.002041	1.90E-10	0.428517635	325.6217
rs8105767	19	2.20E+07	A	G	0.70533	-0.968	0.002041	2.50E-50	0.389130112	276.6263
rs4530278	19	3.40E+07	G	T	0.40185	-0.986	0.002041	1.50E-11	0.467459327	381.1873
rs429358	19	4.50E+07	T	C	0.846031	-0.983	0.002806	3.80E-10	0.251816132	146.158
rs8102497	19	5.70E+07	G	A	0.568172	1.015	0.002041	1.40E-13	0.505649354	444.1828
rs1291143	20	3.60E+07	A	C	0.150974	-0.952	0.002806	1.80E-69	0.232430057	131.4988
rs55765053	20	6.20E+07	C	T	0.933938	-0.978	0.004082	3.6E-08	0.118083931	58.14481
rs3761121	20	6.20E+07	T	C	0.878032	-0.980	0.003061	7.30E-11	0.205785354	112.5185
rs8114049	20	6.20E+07	C	T	0.330913	1.043	0.002041	1.40E-85	0.481622927	403.4677
rs2259797	20	6.20E+07	T	C	0.907332	1.084	0.003571	1.30E-116	0.197734167	107.0313
rs35640778	20	6.20E+07	G	A	0.979243	1.232	0.007143	9.60E-195	0.06174761	28.57906
rs28502153	22	1.70E+07	C	A	0.622042	1.022	0.002041	1.20E-25	0.491362721	419.5091

SNP: SNP rsID; **CHR:** Chromosome of SNP; **BP:** Base-pair location of SNP (hg19); **A1:** Effect allele; **A2:** Other allele; **EAF:** Effect allele frequency; **BETA:** SNP effect estimate; **SE:** SE of SNP effect estimate; **pval:** P-value for effect allele on Telomere length.

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rsID	CHR	BP	A1	A2	EAF	BETA	SE	pval	R ²	F-Statistic
rs138895564	5	1.30E+06	C	T	0.990903	-0.835	0.010969	1.10E-59	0.012578	50.95611
rs33987166	5	1.30E+06	T	C	0.975189	-0.907	0.006633	8.00E-50	0.039778	165.7125
rs146546514	3	1.70E+08	C	A	0.983095	-0.923	0.008418	2.30E-22	0.028324	116.6052
rs7705526	5	1.30E+06	C	A	0.673422	-0.925	0.002296	2.40E-282	0.376317	2413.662
rs183553155	16	7.40E+07	G	A	0.989437	-0.931	0.010204	3.10E-12	0.018136	73.88732
rs139795227	1	9.30E+07	A	C	0.985979	-0.942	0.008673	6.70E-12	0.024522	100.561
rs79717857	5	1.30E+06	C	A	0.973921	-0.950	0.006633	3.80E-15	0.045872	192.3205
rs1291143	20	3.60E+07	A	C	0.150974	-0.952	0.002806	1.80E-69	0.23243	1211.323
rs1609812	11	5.20E+06	G	A	0.160214	-0.954	0.002806	3.90E-65	0.244949	1297.731
rs12615793	2	5.40E+07	G	A	0.859605	-0.956	0.002806	1.80E-55	0.220594	1132.182

rs154979	6	3.30E+07	C	A	0.971166	-0.957	0.006122	1.70E-13	0.051287	216.2527
rs138061125	7	1.60E+08	G	A	0.969815	-0.958	0.005867	2.60E-13	0.053723	227.1058
rs80324517	6	204031	G	A	0.951741	-0.961	0.004592	1.80E-17	0.084798	370.6399
rs111811424	18	674579	C	T	0.913521	-0.962	0.003571	1.40E-27	0.146145	684.6772
rs76219171	16	5.00E+07	G	A	0.941567	-0.965	0.004082	7.80E-17	0.102393	456.3202
rs115251750	5	1.30E+06	G	A	0.964935	-0.965	0.005357	4.50E-11	0.06297	268.822
rs11866592	16	7.50E+07	G	A	0.85802	-0.966	0.002806	1.30E-33	0.227172	1175.863
rs8105767	19	2.20E+07	A	G	0.70533	-0.968	0.002041	2.50E-50	0.38913	2548.19
rs79824385	18	4.20E+07	T	A	0.870276	-0.969	0.003061	7.90E-27	0.211793	1074.876
rs762679	8	4.90E+07	T	A	0.143499	-0.969	0.003061	1.40E-27	0.231036	1201.878
rs9990898	4	1.60E+08	T	C	0.857338	-0.970	0.002806	3.00E-26	0.230374	1197.398
rs5030755	17	1.80E+06	A	G	0.886658	-0.970	0.003316	6.20E-22	0.189286	933.9801
rs76666449	12	1.20E+08	T	C	0.899375	-0.970	0.003316	8.20E-19	0.170459	821.9904
rs11579626	1	1.50E+08	A	C	0.915118	-0.973	0.003827	1.30E-13	0.147187	690.4035
rs8088824	18	4.20E+07	C	T	0.236812	-0.974	0.002296	8.10E-28	0.343148	2089.779
rs1332941	13	4.20E+07	A	G	0.179534	-0.974	0.002806	5.90E-21	0.279675	1553.143
rs939916	11	202253	G	A	0.330033	-0.976	0.002041	6.60E-29	0.421497	2914.573
rs2276182	18	5.20E+07	C	G	0.596773	-0.977	0.002041	2.80E-30	0.459633	3402.579
rs73581419	14	2.20E+07	C	T	0.893395	-0.977	0.003061	1.30E-12	0.181917	889.5328
rs17677991	15	4.20E+07	C	G	0.657877	-0.978	0.002041	4.40E-26	0.430773	3027.247
rs55765053	20	6.20E+07	C	T	0.933938	-0.978	0.004082	3.6E-08	0.118084	535.6108
rs1957937	14	9.60E+07	A	T	0.83982	-0.979	0.002551	1.90E-14	0.257979	1390.765
rs1727302	12	1.20E+08	G	A	0.259019	-0.980	0.002296	8.40E-18	0.368805	2337.325
rs3761121	20	6.20E+07	T	C	0.878032	-0.980	0.003061	7.30E-11	0.205785	1036.483
rs5742915	15	7.40E+07	T	C	0.554171	-0.981	0.002041	1.60E-21	0.475706	3629.527
rs6669563	1	3.20E+07	G	A	0.562232	-0.982	0.002041	2.10E-19	0.474848	3617.063
rs12613375	2	5.90E+07	C	T	0.862288	-0.982	0.002806	9.10E-10	0.229097	1188.791
rs7012816	8	7.10E+07	G	A	0.870003	-0.982	0.002806	3E-09	0.218197	1116.447
rs13129697	4	9.90E+06	T	G	0.720832	-0.983	0.002296	1.50E-14	0.389013	2546.931
rs429358	19	4.50E+07	T	C	0.846031	-0.983	0.002806	3.80E-10	0.251816	1346.359
rs28711261	16	6.80E+07	A	G	0.867449	-0.983	0.003061	1.6E-08	0.222275	1143.275
rs10774625	12	1.10E+08	A	G	0.476428	-0.984	0.002041	1.70E-15	0.483177	3739.816
rs4742448	9	826585	C	G	0.530842	-0.985	0.002041	6.40E-14	0.483377	3742.805
rs4498805	1	1.10E+08	G	T	0.453368	-0.985	0.002041	5.70E-14	0.481002	3707.382
rs11646283	16	9.10E+06	T	C	0.589297	-0.985	0.002041	5.30E-14	0.469746	3543.768
rs2811491	3	1.30E+08	C	A	0.39223	-0.985	0.002041	8.90E-14	0.462681	3444.565

rs1907702	12	8.90E+07	G	A	0.233229	-0.985	0.002551	5.90E-10	0.347096	2126.599
rs4743037	9	1.10E+08	C	T	0.769126	-0.985	0.002296	5.10E-10	0.344646	2103.7
rs41269079	1	4.50E+07	T	A	0.811009	-0.985	0.002551	1.70E-09	0.297487	1693.945
rs4695407	4	4.90E+07	A	G	0.492157	-0.986	0.002041	1.50E-12	0.486075	3783.455
rs1143697	17	7.60E+07	T	C	0.536558	-0.986	0.002041	5.50E-12	0.483595	3746.081
rs56178008	2	2.90E+07	T	A	0.562503	-0.986	0.002041	9.70E-13	0.478597	3671.822
rs4530278	19	3.40E+07	G	T	0.40185	-0.986	0.002041	1.50E-11	0.467459	3511.372
rs10840270	11	9.60E+06	C	G	0.344316	-0.986	0.002296	1.30E-11	0.439058	3131.043
rs13062095	3	1.00E+08	T	C	0.672157	-0.986	0.002041	9.70E-11	0.428555	2999.975
rs1980240	15	5.70E+07	A	C	0.594757	-0.987	0.002041	2.20E-10	0.469671	3542.693
rs11556924	7	1.30E+08	C	T	0.624146	-0.987	0.002041	6.80E-10	0.457134	3368.503
rs6565924	18	7.50E+07	A	G	0.638554	-0.987	0.002041	2.90E-10	0.449759	3269.729
rs111527438	17	2.90E+07	T	C	0.648749	-0.987	0.002296	3.10E-09	0.444051	3195.091
rs6590343	11	1.30E+08	A	G	0.483615	-0.988	0.002041	1.50E-09	0.487619	3806.911
rs35671754	2	2.20E+08	G	T	0.704253	-0.988	0.002296	1.4E-08	0.406683	2741.921
rs12884911	14	6.50E+07	C	T	0.49667	1.013	0.002041	2.90E-11	0.513148	4216.294
rs2293579	11	4.70E+07	G	A	0.613726	1.013	0.002041	3.30E-10	0.486622	3791.753
rs9398196	6	1.10E+08	A	G	0.47995	1.014	0.002041	9.50E-13	0.513371	4220.065
rs8053839	16	4.80E+07	G	T	0.458038	1.014	0.002041	1.00E-11	0.510576	4173.124
rs10845387	12	1.20E+07	G	A	0.647334	1.014	0.002041	1.50E-11	0.46955	3540.984
rs35601737	19	1.30E+07	C	G	0.704101	1.014	0.002041	1.90E-10	0.428518	2999.519
rs8102497	19	5.70E+07	G	A	0.568172	1.015	0.002041	1.40E-13	0.505649	4091.665
rs869785	3	2.40E+07	T	C	0.327529	1.015	0.002041	4.40E-12	0.453923	3325.171
rs2069536	17	7.40E+07	A	G	0.249795	1.015	0.002296	1.80E-10	0.386209	2517.027
rs3768321	1	4.00E+07	G	T	0.810305	1.016	0.002551	1.10E-09	0.317418	1860.214
rs41272947	3	1.60E+08	G	A	0.458021	1.017	0.002041	5.90E-18	0.513646	4224.712
rs6776756	3	1.30E+08	G	A	0.402438	1.017	0.002041	1.10E-17	0.497597	3961.975
rs11190184	10	1.00E+08	G	C	0.71576	1.017	0.002296	1.10E-14	0.420968	2908.248
rs4758644	12	1.20E+08	A	C	0.269222	1.017	0.002296	2.70E-13	0.407091	2746.566
rs13230646	7	2.40E+07	T	C	0.751055	1.017	0.002296	8.90E-14	0.386875	2524.11
rs871134	4	7.00E+06	C	T	0.430968	1.018	0.002041	1.70E-19	0.508448	4137.732
rs66731853	1	2.10E+07	G	A	0.682696	1.018	0.002041	1.50E-16	0.449125	3261.373
rs1023767	8	9.60E+07	G	A	0.762405	1.018	0.002296	5.00E-15	0.375567	2405.956
rs12369950	12	2.50E+07	T	C	0.859325	1.018	0.003061	8.00E-10	0.250633	1337.921
rs61818036	1	1.50E+08	G	A	0.176391	1.019	0.002551	2.10E-12	0.301808	1729.185
rs762810	14	6.60E+07	C	A	0.647514	1.020	0.002041	4.30E-22	0.475109	3620.837

rs2306646	8	2.20E+07	G	C	0.440525	1.021	0.002041	3.30E-25	0.514069	4231.876
rs4731541	7	1.30E+08	C	G	0.375099	1.021	0.002041	1.40E-23	0.488908	3826.613
rs72801474	5	1.30E+08	G	A	0.911707	1.021	0.003571	3.90E-09	0.1679	807.1652
rs28502153	22	1.70E+07	C	A	0.622042	1.022	0.002041	1.20E-25	0.491363	3864.38
rs7218033	17	1.70E+06	C	T	0.746597	1.023	0.002296	1.00E-22	0.396192	2624.776
rs2056726	7	1.00E+08	G	A	0.785624	1.023	0.002551	7.90E-21	0.352694	2179.59
rs75664430	17	8.10E+06	C	G	0.751972	1.024	0.002296	3.60E-24	0.391362	2572.202
rs34003787	16	7.30E+07	C	T	0.912293	1.024	0.003571	1.90E-11	0.167898	807.1491
rs12941945	17	4.10E+07	A	G	0.832437	1.026	0.002551	3.00E-22	0.293862	1664.711
rs4919611	10	1.00E+08	C	A	0.112898	1.026	0.003316	5.10E-16	0.210995	1069.743
rs11769630	7	5.00E+07	T	A	0.927773	1.026	0.003827	4.30E-11	0.141174	657.5597
rs17185038	1	2.80E+07	C	G	0.93539	1.026	0.004082	2.10E-10	0.127323	583.6303
rs10112752	8	7.40E+07	G	A	0.569631	1.029	0.002041	9.50E-46	0.519581	4326.331
rs3093888	14	2.10E+07	G	A	0.94869	1.029	0.004592	1.50E-10	0.103168	460.1719
rs1985369	7	1.60E+08	A	G	0.131822	1.031	0.003061	3.60E-25	0.24353	1287.796
rs12572897	10	9.60E+07	G	A	0.869908	1.033	0.003061	3.60E-27	0.241295	1272.218
rs6030416	20	3.60E+07	T	G	0.135696	1.035	0.003061	1.50E-30	0.25107	1341.036
rs11557154	9	3.40E+07	C	T	0.86997	1.035	0.002806	1.10E-30	0.242164	1278.264
rs611646	11	1.10E+08	T	A	0.591315	1.038	0.002041	3.50E-73	0.520446	4341.335
rs932002	1	2.30E+08	C	T	0.849157	1.041	0.002806	7.30E-47	0.277515	1536.539
rs8114049	20	6.20E+07	C	T	0.330913	1.043	0.002041	1.40E-85	0.481623	3716.611
rs3891167	18	658423	A	G	0.746565	1.044	0.002296	1.20E-70	0.412395	2807.462
rs7790856	7	1.20E+08	C	T	0.710861	1.045	0.002296	1.80E-87	0.448889	3258.263
rs2303262	16	8.20E+07	C	T	0.222887	1.048	0.002551	2.90E-85	0.38056	2457.586
rs9952504	18	657458	A	G	0.958066	1.054	0.005357	2.40E-24	0.089336	392.4231
rs4724	17	7.80E+06	G	A	0.883402	1.057	0.003061	9.80E-69	0.22996	1194.605
rs182059586	16	1.50E+07	T	C	0.97489	1.059	0.006633	4.90E-17	0.054871	232.2397
rs61748181	5	1.30E+06	C	T	0.971072	1.061	0.005867	2.80E-23	0.063219	269.9568
rs78491606	3	7.30E+07	A	C	0.981567	1.079	0.007398	1.90E-24	0.042127	175.9286
rs9419958	10	1.10E+08	T	C	0.13861	1.084	0.003061	2.60E-167	0.280789	1561.743
rs2259797	20	6.20E+07	T	C	0.907332	1.084	0.003571	1.30E-116	0.197734	985.937
rs115451758	5	1.30E+06	G	A	0.989626	1.088	0.009949	6.70E-17	0.024289	99.58028
rs141379009	11	1.10E+08	T	G	0.974488	1.096	0.006378	8.70E-48	0.059767	254.2795
rs2293607	3	1.70E+08	T	C	0.757553	1.099	0.002296	<1.0E-314	0.44331	3185.512
rs144204502	17	7.60E+07	C	T	0.987438	1.106	0.008929	3.40E-28	0.030362	125.257
rs35640778	20	6.20E+07	G	A	0.979243	1.232	0.007143	9.60E-195	0.061748	263.2608

SNP: SNP rsID; **CHR:** Chromosome of SNP; **BP:** Base-pair location of SNP (hg19); **A1:** Effect allele; **A2:** Other allele; **EAF:** Effect allele frequency; **BETA:** SNP effect estimate; **SE:** SE of SNP effect estimate; **pval:** P-value for effect allele on Telomere length.

(d)

rsID	CHR	BP	A1	A2	EAF	BETA	SE	pval	R ²	F-Statistic
rs138895564	5	1.30E+06	C	T	0.990903	-0.835	0.010969	1.10E-59	0.012578	50.95611
rs33987166	5	1.30E+06	T	C	0.975189	-0.907	0.006633	8.00E-50	0.039778	165.7125
rs146546514	3	1.70E+08	C	A	0.983095	-0.923	0.008418	2.30E-22	0.028324	116.6052
rs7705526	5	1.30E+06	C	A	0.673422	-0.925	0.002296	2.40E-282	0.376317	2413.662
rs183553155	16	7.40E+07	G	A	0.989437	-0.931	0.010204	3.10E-12	0.018136	73.88732
rs139795227	1	9.30E+07	A	C	0.985979	-0.942	0.008673	6.70E-12	0.024522	100.561
rs79717857	5	1.30E+06	C	A	0.973921	-0.950	0.006633	3.80E-15	0.045872	192.3205
rs1291143	20	3.60E+07	A	C	0.150974	-0.952	0.002806	1.80E-69	0.23243	1211.323
rs1609812	11	5.20E+06	G	A	0.160214	-0.954	0.002806	3.90E-65	0.244949	1297.731
rs12615793	2	5.40E+07	G	A	0.859605	-0.956	0.002806	1.80E-55	0.220594	1132.182
rs154979	6	3.30E+07	C	A	0.971166	-0.957	0.006122	1.70E-13	0.051287	216.2527
rs138061125	7	1.60E+08	G	A	0.969815	-0.958	0.005867	2.60E-13	0.053723	227.1058
rs80324517	6	204031	G	A	0.951741	-0.961	0.004592	1.80E-17	0.084798	370.6399
rs111811424	18	674579	C	T	0.913521	-0.962	0.003571	1.40E-27	0.146145	684.6772
rs76219171	16	5.00E+07	G	A	0.941567	-0.965	0.004082	7.80E-17	0.102393	456.3202
rs115251750	5	1.30E+06	G	A	0.964935	-0.965	0.005357	4.50E-11	0.06297	268.822
rs11866592	16	7.50E+07	G	A	0.85802	-0.966	0.002806	1.30E-33	0.227172	1175.863
rs8105767	19	2.20E+07	A	G	0.70533	-0.968	0.002041	2.50E-50	0.38913	2548.19
rs79824385	18	4.20E+07	T	A	0.870276	-0.969	0.003061	7.90E-27	0.211793	1074.876
rs762679	8	4.90E+07	T	A	0.143499	-0.969	0.003061	1.40E-27	0.231036	1201.878
rs9990898	4	1.60E+08	T	C	0.857338	-0.970	0.002806	3.00E-26	0.230374	1197.398
rs5030755	17	1.80E+06	A	G	0.886658	-0.970	0.003316	6.20E-22	0.189286	933.9801
rs76666449	12	1.20E+08	T	C	0.899375	-0.970	0.003316	8.20E-19	0.170459	821.9904
rs11579626	1	1.50E+08	A	C	0.915118	-0.973	0.003827	1.30E-13	0.147187	690.4035
rs8088824	18	4.20E+07	C	T	0.236812	-0.974	0.002296	8.10E-28	0.343148	2089.779
rs1332941	13	4.20E+07	A	G	0.179534	-0.974	0.002806	5.90E-21	0.279675	1553.143
rs939916	11	202253	G	A	0.330033	-0.976	0.002041	6.60E-29	0.421497	2914.573
rs2276182	18	5.20E+07	C	G	0.596773	-0.977	0.002041	2.80E-30	0.459633	3402.579
rs73581419	14	2.20E+07	C	T	0.893395	-0.977	0.003061	1.30E-12	0.181917	889.5328
rs17677991	15	4.20E+07	C	G	0.657877	-0.978	0.002041	4.40E-26	0.430773	3027.247
rs55765053	20	6.20E+07	C	T	0.933938	-0.978	0.004082	3.6E-08	0.118084	535.6108
rs1957937	14	9.60E+07	A	T	0.83982	-0.979	0.002551	1.90E-14	0.257979	1390.765
rs1727302	12	1.20E+08	G	A	0.259019	-0.980	0.002296	8.40E-18	0.368805	2337.325
rs3761121	20	6.20E+07	T	C	0.878032	-0.980	0.003061	7.30E-11	0.205785	1036.483

rs5742915	15	7.40E+07	T	C	0.554171	-0.981	0.002041	1.60E-21	0.475706	3629.527
rs6669563	1	3.20E+07	G	A	0.562232	-0.982	0.002041	2.10E-19	0.474848	3617.063
rs12613375	2	5.90E+07	C	T	0.862288	-0.982	0.002806	9.10E-10	0.229097	1188.791
rs7012816	8	7.10E+07	G	A	0.870003	-0.982	0.002806	3E-09	0.218197	1116.447
rs13129697	4	9.90E+06	T	G	0.720832	-0.983	0.002296	1.50E-14	0.389013	2546.931
rs429358	19	4.50E+07	T	C	0.846031	-0.983	0.002806	3.80E-10	0.251816	1346.359
rs28711261	16	6.80E+07	A	G	0.867449	-0.983	0.003061	1.6E-08	0.222275	1143.275
rs10774625	12	1.10E+08	A	G	0.476428	-0.984	0.002041	1.70E-15	0.483177	3739.816
rs4498805	1	1.10E+08	G	T	0.453368	-0.985	0.002041	5.70E-14	0.481002	3707.382
rs4742448	9	826585	C	G	0.530842	-0.985	0.002041	6.40E-14	0.483377	3742.805
rs11646283	16	9.10E+06	T	C	0.589297	-0.985	0.002041	5.30E-14	0.469746	3543.768
rs2811491	3	1.30E+08	C	A	0.39223	-0.985	0.002041	8.90E-14	0.462681	3444.565
rs1907702	12	8.90E+07	G	A	0.233229	-0.985	0.002551	5.90E-10	0.347096	2126.599
rs4743037	9	1.10E+08	C	T	0.769126	-0.985	0.002296	5.10E-10	0.344646	2103.7
rs41269079	1	4.50E+07	T	A	0.811009	-0.985	0.002551	1.70E-09	0.297487	1693.945
rs4695407	4	4.90E+07	A	G	0.492157	-0.986	0.002041	1.50E-12	0.486075	3783.455
rs1143697	17	7.60E+07	T	C	0.536558	-0.986	0.002041	5.50E-12	0.483595	3746.081
rs56178008	2	2.90E+07	T	A	0.562503	-0.986	0.002041	9.70E-13	0.478597	3671.822
rs4530278	19	3.40E+07	G	T	0.40185	-0.986	0.002041	1.50E-11	0.467459	3511.372
rs10840270	11	9.60E+06	C	G	0.344316	-0.986	0.002296	1.30E-11	0.439058	3131.043
rs13062095	3	1.00E+08	T	C	0.672157	-0.986	0.002041	9.70E-11	0.428555	2999.975
rs1980240	15	5.70E+07	A	C	0.594757	-0.987	0.002041	2.20E-10	0.469671	3542.693
rs11556924	7	1.30E+08	C	T	0.624146	-0.987	0.002041	6.80E-10	0.457134	3368.503
rs6565924	18	7.50E+07	A	G	0.638554	-0.987	0.002041	2.90E-10	0.449759	3269.729
rs111527438	17	2.90E+07	T	C	0.648749	-0.987	0.002296	3.10E-09	0.444051	3195.091
rs6590343	11	1.30E+08	A	G	0.483615	-0.988	0.002041	1.50E-09	0.487619	3806.911
rs35671754	2	2.20E+08	G	T	0.704253	-0.988	0.002296	1.4E-08	0.406683	2741.921
rs12884911	14	6.50E+07	C	T	0.49667	1.013	0.002041	2.90E-11	0.513148	4216.294
rs2293579	11	4.70E+07	G	A	0.613726	1.013	0.002041	3.30E-10	0.486622	3791.753
rs9398196	6	1.10E+08	A	G	0.47995	1.014	0.002041	9.50E-13	0.513371	4220.065
rs8053839	16	4.80E+07	G	T	0.458038	1.014	0.002041	1.00E-11	0.510576	4173.124
rs10845387	12	1.20E+07	G	A	0.647334	1.014	0.002041	1.50E-11	0.46955	3540.984
rs35601737	19	1.30E+07	C	G	0.704101	1.014	0.002041	1.90E-10	0.428518	2999.519
rs8102497	19	5.70E+07	G	A	0.568172	1.015	0.002041	1.40E-13	0.505649	4091.665
rs869785	3	2.40E+07	T	C	0.327529	1.015	0.002041	4.40E-12	0.453923	3325.171
rs2069536	17	7.40E+07	A	G	0.249795	1.015	0.002296	1.80E-10	0.386209	2517.027

rs3768321	1	4.00E+07	G	T	0.810305	1.016	0.002551	1.10E-09	0.317418	1860.214
rs41272947	3	1.60E+08	G	A	0.458021	1.017	0.002041	5.90E-18	0.513646	4224.712
rs6776756	3	1.30E+08	G	A	0.402438	1.017	0.002041	1.10E-17	0.497597	3961.975
rs11190184	10	1.00E+08	G	C	0.71576	1.017	0.002296	1.10E-14	0.420968	2908.248
rs4758644	12	1.20E+08	A	C	0.269222	1.017	0.002296	2.70E-13	0.407091	2746.566
rs13230646	7	2.40E+07	T	C	0.751055	1.017	0.002296	8.90E-14	0.386875	2524.11
rs871134	4	7.00E+06	C	T	0.430968	1.018	0.002041	1.70E-19	0.508448	4137.732
rs66731853	1	2.10E+07	G	A	0.682696	1.018	0.002041	1.50E-16	0.449125	3261.373
rs1023767	8	9.60E+07	G	A	0.762405	1.018	0.002296	5.00E-15	0.375567	2405.956
rs12369950	12	2.50E+07	T	C	0.859325	1.018	0.003061	8.00E-10	0.250633	1337.921
rs61818036	1	1.50E+08	G	A	0.176391	1.019	0.002551	2.10E-12	0.301808	1729.185
rs762810	14	6.60E+07	C	A	0.647514	1.020	0.002041	4.30E-22	0.475109	3620.837
rs2306646	8	2.20E+07	G	C	0.440525	1.021	0.002041	3.30E-25	0.514069	4231.876
rs4731541	7	1.30E+08	C	G	0.375099	1.021	0.002041	1.40E-23	0.488908	3826.613
rs72801474	5	1.30E+08	G	A	0.911707	1.021	0.003571	3.90E-09	0.1679	807.1652
rs28502153	22	1.70E+07	C	A	0.622042	1.022	0.002041	1.20E-25	0.491363	3864.38
rs7218033	17	1.70E+06	C	T	0.746597	1.023	0.002296	1.00E-22	0.396192	2624.776
rs2056726	7	1.00E+08	G	A	0.785624	1.023	0.002551	7.90E-21	0.352694	2179.59
rs75664430	17	8.10E+06	C	G	0.751972	1.024	0.002296	3.60E-24	0.391362	2572.202
rs34003787	16	7.30E+07	C	T	0.912293	1.024	0.003571	1.90E-11	0.167898	807.1491
rs12941945	17	4.10E+07	A	G	0.832437	1.026	0.002551	3.00E-22	0.293862	1664.711
rs4919611	10	1.00E+08	C	A	0.112898	1.026	0.003316	5.10E-16	0.210995	1069.743
rs11769630	7	5.00E+07	T	A	0.927773	1.026	0.003827	4.30E-11	0.141174	657.5597
rs17185038	1	2.80E+07	C	G	0.93539	1.026	0.004082	2.10E-10	0.127323	583.6303
rs10112752	8	7.40E+07	G	A	0.569631	1.029	0.002041	9.50E-46	0.519581	4326.331
rs3093888	14	2.10E+07	G	A	0.94869	1.029	0.004592	1.50E-10	0.103168	460.1719
rs1985369	7	1.60E+08	A	G	0.131822	1.031	0.003061	3.60E-25	0.24353	1287.796
rs12572897	10	9.60E+07	G	A	0.869908	1.033	0.003061	3.60E-27	0.241295	1272.218
rs6030416	20	3.60E+07	T	G	0.135696	1.035	0.003061	1.50E-30	0.25107	1341.036
rs11557154	9	3.40E+07	C	T	0.86997	1.035	0.002806	1.10E-30	0.242164	1278.264
rs611646	11	1.10E+08	T	A	0.591315	1.038	0.002041	3.50E-73	0.520446	4341.335
rs932002	1	2.30E+08	C	T	0.849157	1.041	0.002806	7.30E-47	0.277515	1536.539
rs8114049	20	6.20E+07	C	T	0.330913	1.043	0.002041	1.40E-85	0.481623	3716.611
rs3891167	18	658423	A	G	0.746565	1.044	0.002296	1.20E-70	0.412395	2807.462
rs7790856	7	1.20E+08	C	T	0.710861	1.045	0.002296	1.80E-87	0.448889	3258.263
rs2303262	16	8.20E+07	C	T	0.222887	1.048	0.002551	2.90E-85	0.38056	2457.586

rs9952504	18	657458	A	G	0.958066	1.054	0.005357	2.40E-24	0.089336	392.4231
rs4724	17	7.80E+06	G	A	0.883402	1.057	0.003061	9.80E-69	0.22996	1194.605
rs182059586	16	1.50E+07	T	C	0.97489	1.059	0.006633	4.90E-17	0.054871	232.2397
rs61748181	5	1.30E+06	C	T	0.971072	1.061	0.005867	2.80E-23	0.063219	269.9568
rs78491606	3	7.30E+07	A	C	0.981567	1.079	0.007398	1.90E-24	0.042127	175.9286
rs9419958	10	1.10E+08	T	C	0.13861	1.084	0.003061	2.60E-167	0.280789	1561.743
rs2259797	20	6.20E+07	T	C	0.907332	1.084	0.003571	1.30E-116	0.197734	985.937
rs115451758	5	1.30E+06	G	A	0.989626	1.088	0.009949	6.70E-17	0.024289	99.58028
rs141379009	11	1.10E+08	T	G	0.974488	1.096	0.006378	8.70E-48	0.059767	254.2795
rs2293607	3	1.70E+08	T	C	0.757553	1.099	0.002296	<1.0E-314	0.44331	3185.512
rs144204502	17	7.60E+07	C	T	0.987438	1.106	0.008929	3.40E-28	0.030362	125.257
rs35640778	20	6.20E+07	G	A	0.979243	1.232	0.007143	9.60E-195	0.061748	263.2608

SNP: SNP rsID; **CHR:** Chromosome of SNP; **BP:** Base-pair location of SNP (hg19); **A1:** Effect allele; **A2:** Other allele; **EAF:** Effect allele frequency; **BETA:** SNP effect estimate; **SE:** SE of SNP effect estimate; **pval:** P-value for effect allele on Telomere length.

Table A2. Variants used in the genetic instrument for Parkinson's disease risk

SNP	CHR	BP	A1	A2	EAF	BETA	SE	P	R ²	F-Statistic
rs11578699	1	171719769	T	C	0.1949	-0.0704	0.012	4.47E-09	0.001555	24.88349
rs114138760	1	154898185	C	G	0.0112	0.2812	0.0478	4.19E-09	0.001751	28.02507
rs6658353	1	161469054	C	G	0.5011	0.065	0.0094	6.1E-12	0.002112	33.81515
rs4653767	1	226916078	T	C	0.7196	0.0833	0.0104	1.38E-15	0.0028	44.85442
rs10797576	1	232664611	T	C	0.1403	0.1114	0.0133	6.84E-17	0.002994	47.96289
rs11557080	1	205737739	A	G	0.1389	0.1315	0.0135	2.5E-22	0.004137	66.34922
rs76763715	1	155205634	T	C	0.9953	-0.7467	0.0765	1.59E-22	0.005216	83.76138
rs823118	1	205723572	T	C	0.566	0.1066	0.0094	1.11E-29	0.005583	89.67682
rs35749011	1	155135036	A	G	0.0169	0.6068	0.0342	1.72E-70	0.012235	197.8564
rs2042477	2	96000943	A	T	0.2422	-0.0657	0.0116	1.38E-08	0.001584	25.34991
rs76116224	2	18147848	A	T	0.9042	0.1104	0.0194	1.27E-08	0.002112	33.79982
rs11683001	2	102396963	A	T	0.337	0.0705	0.0098	8.04E-13	0.002221	35.55622
rs57891859	2	135464616	A	G	0.7185	0.0807	0.0107	4.55E-14	0.002634	42.19161
rs1474055	2	169110394	T	C	0.1312	0.1796	0.0137	2.54E-39	0.007354	118.3314
rs1450522	3	161077630	A	G	0.6742	-0.0616	0.0099	5.01E-10	0.001667	26.67191
rs11707416	3	151108965	A	T	0.3672	-0.0627	0.0097	1.13E-10	0.001827	29.23659
rs12497850	3	48748989	T	G	0.6476	0.0636	0.0099	1.36E-10	0.001846	29.54526
rs6808178	3	28705690	T	C	0.3794	0.0658	0.0096	8.09E-12	0.002039	32.63439
rs55961674	3	122196892	T	C	0.1722	0.0861	0.0126	9.98E-12	0.002113	33.83078

rs73038319	3	18361759	A	C	0.9592	-0.1693	0.0235	5.94E-13	0.002243	35.91591
rs10513789	3	182760073	T	G	0.8112	0.1485	0.0121	1.22E-34	0.006755	108.6312
rs6825004	4	77110365	C	G	0.6912	0.0622	0.0102	1.17E-09	0.001652	26.42457
rs62333164	4	170583157	A	G	0.3264	-0.0638	0.01	2E-10	0.00179	28.64177
rs34025766	4	17968811	A	T	0.1589	-0.0839	0.0133	2.87E-10	0.001882	30.11214
rs13117519	4	114369065	T	C	0.1744	0.0875	0.0123	9.82E-13	0.002205	35.29548
rs4101061	4	77147969	A	G	0.7107	-0.0912	0.0102	4.97E-19	0.00342	54.8202
rs6854006	4	77198054	T	C	0.3632	-0.0912	0.0097	5.82E-21	0.003847	61.69372
rs4698412	4	15737348	A	G	0.5529	0.1035	0.0094	2.06E-28	0.005296	85.04846
rs873786	4	925376	T	C	0.0988	-0.1731	0.0182	1.79E-21	0.005336	85.6888
rs5019538	4	90636630	A	G	0.6792	-0.1565	0.0124	1.13E-36	0.010673	172.3254
rs34311866	4	951947	T	C	0.8065	-0.2126	0.012	9.98E-70	0.014107	228.5654
rs356182	4	90626111	A	G	0.6278	-0.2774	0.0105	3.89E-154	0.035962	595.8605
rs11950533	5	134199105	A	C	0.102	-0.0916	0.0158	7.16E-09	0.001537	24.5903
rs26431	5	102365794	C	G	0.7025	0.0621	0.0103	1.57E-09	0.001612	25.78965
rs1867598	5	60137959	A	G	0.9019	-0.1554	0.0156	2.52E-23	0.004273	68.55159
rs9261484	6	30108683	T	C	0.2451	-0.0635	0.0112	1.62E-08	0.001492	23.87025
rs997368	6	112243291	A	G	0.8049	0.0714	0.0119	1.84E-09	0.001601	25.6165
rs12528068	6	72487762	T	C	0.2844	0.0657	0.0103	1.63E-10	0.001757	28.114
rs4140646	6	27738801	A	G	0.2081	0.0833	0.0121	5.62E-12	0.002287	36.61466
rs75859381	6	133210361	T	C	0.9673	-0.2207	0.0341	1.04E-10	0.003081	49.37216
rs112485576	6	32578772	A	C	0.163	-0.1676	0.0153	6.96E-28	0.007665	123.3761
rs76949143	7	66009851	A	T	0.0507	-0.1432	0.0253	1.43E-08	0.001974	31.59249
rs199351	7	23300049	A	C	0.5939	0.1016	0.0096	5.25E-26	0.004979	79.93369
rs2280104	8	22525980	T	C	0.3604	0.0556	0.0098	1.16E-08	0.001425	22.79767
rs2086641	8	130901909	T	C	0.7225	-0.0605	0.0107	1.81E-08	0.001468	23.4789
rs620513	8	16697593	T	G	0.2682	-0.0856	0.0108	2.72E-15	0.002876	46.07633
rs1293298	8	11712443	A	C	0.7444	0.093	0.0114	3.99E-16	0.003291	52.74644
rs6476434	9	34046391	T	C	0.7336	-0.0615	0.0106	6.58E-09	0.001478	23.6491
rs10756907	9	17727065	A	G	0.7666	-0.0926	0.011	5.06E-17	0.003068	49.16483
rs13294100	9	17579690	T	G	0.3422	-0.0859	0.01	8.72E-18	0.003322	53.23945
rs10748818	10	104015279	A	G	0.8514	-0.079	0.013	1.05E-09	0.001579	25.26512
rs72840788	10	121415685	A	G	0.2155	0.0763	0.0113	1.57E-11	0.001968	31.50455
rs896435	10	15557406	T	C	0.6892	0.0735	0.0101	3.41E-13	0.002314	37.05403
rs117896735	10	121536327	A	G	0.0166	0.4354	0.0394	2.36E-28	0.006189	99.48091
rs7938782	11	10558777	A	G	0.8776	0.087	0.0145	2.12E-09	0.001626	26.01666
rs12283611	11	83487277	A	C	0.4148	-0.0645	0.0102	2.61E-10	0.00202	32.32725

rs3802920	11	133787001	T	G	0.2054	0.1073	0.0117	6.26E-20	0.003758	60.25762
rs7134559	12	46419086	T	C	0.404	-0.0539	0.0098	3.96E-08	0.001399	22.37904
rs11610045	12	133063768	A	G	0.4896	0.0601	0.0094	1.77E-10	0.001805	28.88777
rs76904798	12	40614434	T	C	0.1444	0.1439	0.013	1.52E-28	0.005117	82.15154
rs10847864	12	123326598	T	G	0.364	0.1478	0.0115	1.47E-37	0.010114	163.2114
rs34637584	12	40734202	A	G	0.0015	2.4289	0.0937	3.61E-148	0.017672	287.3627
rs9568188	13	49927732	T	C	0.7397	0.0617	0.0108	1.15E-08	0.001466	23.45122
rs4771268	13	97865021	T	C	0.2295	0.0675	0.0112	1.45E-09	0.001611	25.78051
rs12147950	14	37989270	T	C	0.4376	-0.0529	0.0096	3.54E-08	0.001377	22.03235
rs3742785	14	75373034	A	C	0.7866	0.0707	0.0118	1.92E-09	0.001678	26.85003
rs979812	14	88464264	T	G	0.4421	0.061	0.0093	6.19E-11	0.001836	29.37397
rs11158026	14	55348869	T	C	0.3245	-0.0842	0.0102	1.66E-16	0.003108	49.80173
rs2251086	15	61997385	T	C	0.1417	-0.1186	0.0137	6.08E-18	0.003421	54.8397
rs6500328	16	50736656	A	G	0.5985	0.0586	0.0097	1.82E-09	0.00165	26.40527
rs2904880	16	28944396	C	G	0.3094	-0.065	0.0106	7.87E-10	0.001806	28.89261
rs6497339	16	19277493	A	T	0.4536	0.063	0.0095	2.76E-11	0.001967	31.48824
rs3104783	16	52636242	A	C	0.4343	0.0668	0.0094	1.29E-12	0.002193	35.10027
rs10221156	16	52969426	A	G	0.0932	-0.1156	0.0179	1.08E-10	0.002259	36.16208
rs11150601	16	30977799	A	G	0.6442	0.0907	0.0099	5.12E-20	0.003771	60.46588
rs12600861	17	7355621	A	C	0.6484	-0.0565	0.0099	1.01E-08	0.001456	23.28357
rs12951632	17	40741013	T	C	0.7349	0.0642	0.0106	1.4E-09	0.001606	25.69415
rs666463	17	76425480	A	T	0.8328	0.076	0.0128	3.2E-09	0.001609	25.73544
rs2269906	17	42294337	A	C	0.6531	0.0631	0.0102	6.24E-10	0.001804	28.87056
rs61169879	17	59917366	T	C	0.1641	0.082	0.0134	9.28E-10	0.001845	29.5203
rs11658976	17	44866805	A	G	0.5802	-0.0624	0.0113	3.52E-08	0.001897	30.35583
rs850738	17	42434630	A	G	0.6056	-0.071	0.0105	1.29E-11	0.002408	38.55803
rs117615688	17	43798308	A	G	0.067	-0.2324	0.0288	6.71E-16	0.006752	108.5924
rs62053943	17	43744203	T	C	0.1552	-0.27	0.0155	3.58E-68	0.019116	311.3034
rs1941685	18	31304318	T	G	0.4983	0.0531	0.0094	1.69E-08	0.00141	22.55096
rs8087969	18	48683589	T	G	0.5496	-0.0578	0.0102	1.41E-08	0.001654	26.46354
rs12456492	18	40673380	A	G	0.6816	-0.0983	0.0099	3.8E-23	0.004194	67.27648
rs55818311	19	2341047	T	C	0.6937	-0.0696	0.0111	4.18E-10	0.002059	32.95038
rs77351827	20	6006041	T	C	0.1275	0.0802	0.0139	8.87E-09	0.001431	22.89152
rs2248244	21	38852361	A	G	0.2828	0.0714	0.0107	2.74E-11	0.002068	33.10118

SNP: SNP rsID; **CHR:** Chromosome of SNP; **BP:** Base-pair location of SNP (hg19); **A1:** Effect allele; **A2:** Other allele; **EAF:** Effect allele frequency; **BETA:** SNP effect estimate; **SE:** SE of SNP effect estimate; **pval:** P-value for effect allele on Telomere length.

Table A3. Variants used in the genetic instrument for Parkinson's disease age at onset.

SNP	CHR	BP	A1	A2	EAFF	BETA	SE	P	R2	F-Statistic
rs356203	4	90666041	G	A	0.37	-0.626	0.089	1.90E-12	0.182693	1946.051
rs34311866	4	951947	C	T	0.26	-0.613	0.107	9.62E-09	0.143361	1456.971

SNP: SNP rsID; **CHR:** Chromosome of SNP; **BP:** Base-pair location of SNP (hg19); **A1:** Effect allele; **A2:** Other allele; **EAFF:** Effect allele frequency; **BETA:** SNP effect estimate; **SE:** SE of SNP effect estimate; **pval:** P-value for effect allele on Telomere length.

Table A4. Variants used in the genetic instrument for Parkinson's disease continuous motor subtype.

SNP	CHR	BP	A1	A2	EAFF	BETA	SE	P	R ²	F-Statistic
rs113942635	3	75446661	T	C	0.01	0.81	0.18	8.00E-06	0.012991	1.350142
rs2913614	5	5224692	A	T	0.54	0.15	0.03	6.33E-06	0.011178	1.159609
rs77942836	11	103916643	A	G	0.02	-0.53	0.12	8.11E-06	0.011011	1.14212
rs80164227	18	5197857	A	G	0.97	-0.43	0.1	9.15E-06	0.010761	1.115897
rs79890063	21	20786475	A	C	0.12	-0.22	0.04	6.96E-07	0.010222	1.059417
rs17488950	13	110127965	T	C	0.07	-0.27	0.06	1.46E-06	0.009492	0.982982
rs9626407	22	46008464	A	G	0.04	-0.35	0.07	1.97E-06	0.009408	0.974244
rs116917617	12	62440045	T	C	0.98	-0.46	0.1	2.11E-06	0.008295	0.857995
rs11644635	16	15972631	T	C	0.39	-0.13	0.03	3.14E-06	0.008041	0.831539
rs10109703	8	8387903	A	C	0.64	-0.13	0.03	1.44E-06	0.007788	0.805119
rs2301857	4	5418485	T	C	0.12	-0.19	0.04	6.60E-07	0.007624	0.788117
rs117238693	10	56421400	T	C	0.98	0.43	0.1	8.04E-06	0.007248	0.748941
rs12242050	10	103048995	T	G	0.76	-0.14	0.03	8.44E-07	0.00715	0.738742
rs6958272	7	5794044	T	C	0.92	-0.22	0.05	3.01E-06	0.007124	0.736078
rs66792854	7	132040533	A	G	0.06	0.25	0.06	9.96E-06	0.00705	0.728328
rs118076379	17	72542970	A	G	0.01	0.59	0.13	9.49E-06	0.006892	0.711932
rs2336592	11	132873644	C	G	0.63	-0.12	0.03	7.82E-06	0.006713	0.693307
rs2717804	7	148211886	A	G	0.36	-0.12	0.03	2.67E-06	0.006636	0.685223
rs538015403	19	14878196	A	G	0.02	-0.41	0.09	2.56E-06	0.00659	0.680441
rs7834008	8	22906180	T	C	0.79	0.14	0.03	5.98E-06	0.006503	0.671477
rs9483680	6	134657949	A	C	0.9	-0.19	0.04	7.02E-06	0.006498	0.670929
rs56242312	2	57141732	A	G	0.9	-0.19	0.04	8.18E-06	0.006498	0.670929
rs72636490	13	87927123	A	C	0.08	-0.21	0.05	8.59E-06	0.006492	0.670255
rs143548133	2	72300987	T	C	0.01	0.57	0.13	7.02E-06	0.006433	0.664176
rs76377494	4	86019236	T	C	0.07	-0.22	0.05	1.89E-06	0.006302	0.65053
rs17015314	1	105497011	A	G	0.88	-0.17	0.04	7.90E-06	0.006104	0.629965
rs75477320	14	47229012	T	C	0.13	0.16	0.04	9.07E-06	0.005791	0.597476

rs6535273	4	82616045	T	C	0.39	0.11	0.02	1.37E-06	0.005757	0.593995
rs7257687	19	45887928	T	C	0.03	-0.3	0.07	8.30E-06	0.005238	0.540147
rs2892663	4	116121350	T	C	0.5	0.1	0.02	5.73E-06	0.005	0.515481
rs1552340	3	142015590	A	G	0.42	0.1	0.02	9.73E-06	0.004872	0.50222

SNP: SNP rsID; **CHR:** Chromosome of SNP; **BP:** Base-pair location of SNP (hg19); **A1:** Effect allele; **A2:** Other allele; **EAF:** Effect allele frequency; **BETA:** SNP effect estimate; **SE:** SE of SNP effect estimate; **pval:** P-value for effect allele on Telomere length.

Table A5. Variants used in the genetic instrument for Parkinson's disease binary motor subtype.

rsID	CHR	BP	A1	A2	EAF	BETA	SE	P	R ²	F-Statistic
rs116504637	1	47557933	T	G	0.74	0.35	0.07	9.83E-07	0.047138	22.64309
rs11949046	5	161678799	T	C	0.89	0.54	0.11	1.57E-06	0.057095	27.71576
rs78926797	16	19502663	A	C	0.6	-0.3	0.06	2.08E-06	0.0432	20.66603
rs6932127	6	125107499	T	C	0.89	-0.46	0.1	3.01E-06	0.041431	19.78334
rs55971529	11	22583068	A	G	0.97	-1.08	0.23	3.95E-06	0.067884	33.3346
rs988295487	1	77190938	C	G	0.96	-0.84	0.18	4.98E-06	0.05419	26.22469
rs13330839	16	82279626	A	G	0.87	-0.47	0.1	7.00E-06	0.049968	24.07378

SNP: SNP rsID; **CHR:** Chromosome of SNP; **BP:** Base-pair location of SNP (hg19); **A1:** Effect allele; **A2:** Other allele; **EAF:** Effect allele frequency; **BETA:** SNP effect estimate; **SE:** SE of SNP effect estimate; **pval:** P-value for effect allele on Telomere length.