

Supplementary Table 1: Age and sex adjusted linear regressions of burden (sum of variants with minor allele frequency ≤ 0.05) against childhood and late-life general cognitive ability (Moray House Test).

1921 childhood MHT				1921 late-life MHT			
	b	SE	P		b	SE	P
Intercept	68.33	11.28	<0.001	Intercept	70.46	9.90	<0.001
Age	7.82	1.95	<0.001	Age	-1.18	0.86	0.17
Sex (Female)	0.16	1.13	0.89	Sex (Female)	-2.87	1.00	0.004
Burden	-0.038	0.020	0.055	Burden	-0.017	0.018	0.34

1936 childhood MHT				1936 late-life MHT			
	b	SE	P		b	SE	P
Intercept	47.73	7.49	<0.001	Intercept	69.58	5.52	<0.001
Age	7.48	1.36	<0.001	Age	-1.47	0.33	<0.001
Sex (Female)	1.75	0.76	0.021	Sex (Female)	-0.39	0.56	0.48
Burden	7.5×10^{-4}	0.013	0.95	Burden	-9.1×10^{-3}	9.8×10^{-3}	0.36

MHT: Moray House Test scores, b: unstandardised beta, SE: standard error, P: P-value.

Supplementary Table 2: Age and sex adjusted linear regressions of burden (sum of variants with minor allele frequency ≤ 0.05) against late-life fluid cognitive ability factors.

1921 late-life g			
	b	SE	P
Intercept	1.09	0.92	0.24
Age	-0.14	0.079	0.075
Sex (Female)	-0.27	0.093	0.004
Burden	-1.6×10^{-3}	1.6×10^{-3}	0.32

1936 late-life g			
	b	SE	P
Intercept	0.19	0.61	0.76
Age	-0.32	0.037	<0.001
Sex (Female)	-0.057	0.062	0.35
Burden	-2.9×10^{-4}	1.1×10^{-3}	0.79

g: fluid general cognitive ability, b: unstandardised beta, SE: standard error, P: P-value.

Supplementary Table 3: LBC1936 age- and sex-adjusted linear regressions of SNP annotation subcategory burden (sum of variants with minor allele frequency ≤ 0.01) against cognitive ability.

	b	SE	P
<i>All variants* : n_{SNPs} 47,967</i>			
childhood MHT	2.4x10 ⁻³	0.021	0.91
late-life MHT	-0.012	0.016	0.43
g	1.8x10 ⁻³	1.7x10 ⁻³	0.29
<i>Missense variants: n_{SNPs} 43,644</i>			
childhood MHT	9.7x10 ⁻³	0.023	0.68
late-life MHT	-6.6x10 ⁻³	0.017	0.70
g	2.7x10 ⁻³	1.9x10 ⁻³	0.16
<i>Splicing variants: n_{SNPs} 1,875</i>			
childhood MHT	-0.30	0.14	0.039
late-life MHT	-0.27	0.11	0.011
g	-0.010	0.012	0.39
<i>Stop variants: n_{SNPs} 865</i>			
childhood MHT	-0.27	0.22	0.22
late-life MHT	-0.25	0.16	0.11
g	-0.016	0.017	0.37

SNP: single nucleotide polymorphism, g: fluid general cognitive ability, MHT: Moray House

Test scores, b: unstandardised beta, SE: standard error, P: P-value.

* synonymous, missense, splicing, and stop variants

Supplementary Table 4: LBC1936 age- and sex-adjusted linear regressions of SNP annotation subcategory burden (sum of variants with minor allele frequency ≤ 0.05) against cognitive ability.

	b	SE	P
<i>All variants* : n_{SNPs} 57,145</i>			
childhood MHT	5.0x10 ⁻³	0.011	0.66
late-life MHT	-2.6x10 ⁻³	8.4x10 ⁻³	0.76
g	-4.2x10 ⁻⁴	9.3x10 ⁻⁴	0.65
<i>Missense variants: n_{SNPs} 51,333</i>			
childhood MHT	2.0x10 ⁻³	0.014	0.89
late-life MHT	-8.1x10 ⁻³	0.010	0.43
g	1.7x10 ⁻⁵	1.1 x10 ⁻³	0.99
<i>Splicing variants: n_{SNPs} 2,167</i>			
childhood MHT	-0.051	0.084	0.55
late-life MHT	-0.064	0.062	0.30
g	-0.012	6.8 x10 ⁻³	0.072
<i>Stop variants: n_{SNPs} 939</i>			
childhood MHT	0.027	0.15	0.86
late-life MHT	-5.8x10 ⁻⁴	0.11	0.99
g	4.5x10 ⁻³	0.012	0.71

SNP: single nucleotide polymorphism, g: fluid general cognitive ability, MHT: Moray House

Test scores, b: unstandardised beta, SE: standard error, P: P-value.

* synonymous, missense, splicing, and stop variants

Supplementary Table 5: LBC1921 age- and sex-adjusted linear regressions of SNP annotation subcategory burden (sum of variants with minor allele frequency ≤ 0.01) against cognitive ability.

	b	SE	P
<i>All variants: n_{SNPs} 37,514</i>			
childhood MHT	-0.052	0.032	0.10
late-life MHT	-9.1x10 ⁻³	0.028	0.74
g	1.5x10 ⁻³	2.6x10 ⁻³	0.56
<i>Missense variants: n_{SNPs} 34,113</i>			
childhood MHT	-0.039	0.035	0.27
late-life MHT	-4.8x10 ⁻³	0.031	0.88
g	-1.0x10 ⁻³	2.8x10 ⁻³	0.72
<i>Splicing variants: n_{SNPs} 1,471</i>			
childhood MHT	-0.25	0.21	0.24
late-life MHT	-0.050	0.19	0.80
g	-8.2x10 ⁻³	0.018	0.64
<i>Stop variants: n_{SNPs} 616</i>			
childhood MHT	-0.54	0.35	0.12
late-life MHT	-0.31	0.31	0.31
g	-0.023	0.029	0.42

SNP: single nucleotide polymorphism, g: fluid general cognitive ability, MHT: Moray House

Test scores, b: unstandardised beta, SE: standard error, P: P-value.

* synonymous, missense, splicing, and stop variants

Supplementary Table 6: LBC1921 age- and sex-adjusted linear regressions of SNP annotation subcategory burden (sum of variants with minor allele frequency ≤ 0.05) against cognitive ability.

	b	SE	P
<i>All variants* : n_{SNPs} 46,468</i>			
childhood MHT	-0.042	0.017	0.16
late-life MHT	-0.021	0.015	0.16
g	1.7×10^{-3}	1.4×10^{-3}	0.22
<i>Missense variants: n_{SNPs} 41,600</i>			
childhood MHT	-0.036	0.021	0.085
late-life MHT	-0.020	0.018	0.26
g	-1.8×10^{-3}	1.7×10^{-3}	0.30
<i>Splicing variants: n_{SNPs} 1,753</i>			
childhood MHT	-0.068	0.12	0.57
late-life MHT	0.16	0.11	0.14
g	4.8×10^{-3}	9.8×10^{-3}	0.62
<i>Stop variants: n_{SNPs} 692</i>			
childhood MHT	-0.42	0.22	0.060
late-life MHT	-0.25	0.20	0.20
g	-0.013	0.018	0.48

SNP: single nucleotide polymorphism, g: fluid general cognitive ability, MHT: Moray House

Test scores, b: unstandardised beta, SE: standard error, P: P-value.

* synonymous, missense, splicing, and stop variants