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A General Cognitive Ability Factor for the UK Biobank

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Franck Ramus

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23 is no conflict of interest.

24 **Data/Code Availability** - This research has been conducted using data from UK
25 Biobank, a major biomedical database (<http://www.ukbiobank.ac.uk/>). Restrictions apply to
26 the availability of these data, which were used under license for this study: application 46007.

27 Supplements and code available on
28 OSF: https://osf.io/49scv/?view_only=29e0ee6a1420461d81d234d94d549751

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30 tab” at <https://biobank.ctsu.ox.ac.uk/crystal/field.cgi?id=200>). The UK Biobank received
31 ethical approval from the Research Ethics Committee (reference 11/NW/0382) and the present
32 study was conducted based on application 46 007.

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68 [Highlights](#)

- 69 ● We provide 8 standardized cognitive scores relative to an age-matched UK population
- 70 ● We provide general intelligence (g) scores relative to the UK population
- 71 ● We estimate the quality of the g factor for individuals with missing data
- 72 ● We ran a g factor GWAS on UK Biobank individuals without brain data (N = 187,288)
- 73 ● We created g polygenic scores for subjects with brain data: 7.7% explained variance

74 **Abstract**

75 Our aim was to create a standardized measure of general intelligence (*g*) relative to the
76 UK population for UK Biobank participants and derive a *g* factor polygenic score for UK
77 Biobank participants with neuroimaging data.

78 We first created standardized cognitive test scores that were relative to the UK
79 population based on the participants' age, sex, and occupation. Using confirmatory factor
80 analysis, we extracted a *g* factor score from eight cognitive tests for all individuals who
81 completed at least one test (N= 501,650), explaining 29% of the variance in *g*. We estimated
82 the quality of the *g* factor for individuals with missing data.

83 Our *g* factor was highly correlated ($r > 0.85$) with alternative measures of intelligence
84 calculated in the UK Biobank and correlations between measures of intelligence and life and
85 health outcomes were similar.

86 We conducted a Genome-Wide Association Study (GWAS) on UK Biobank
87 participants with a *g* factor of good quality (N= 223,731) and identified 36 genetic loci that
88 were not previously linked to intelligence or cognitive performance. We ran a another GWAS
89 on UK Biobank participants with a *g*-factor of good quality but without neuroimaging data (N=
90 187,288). We used the results from the second GWAS to create a polygenic score for
91 individuals with neuroimaging data and their siblings (N= 40,871), explaining 7.7% of the
92 variance in *g*.

93 The present study provides cognitive and genetic scores for use by future UK Biobank
94 studies as control variables or to examine the genetic, brain, and environmental factors
95 underlying intelligence.

96

97

98

99 Introduction

100 Intelligence – our ability to learn, reason and solve problems (Arvey et al., 1994) – has
101 been of great interest to researchers in epidemiology, neuroscience, and genetics as it predicts
102 a wide array of educational, health, and social outcomes (e.g., Calvin et al., 2017; Deary et al.,
103 2007; Strenze, 2007). Given the numerous genetic, neural, and environmental factors that may
104 contribute to intelligence, large-scale studies are needed to identify the respective contribution
105 of these factors and their potential interactions on intelligence (for review see Deary et al.,
106 2019, 2021).

107 The UK Biobank is an ideal database to study the causes and consequences of
108 intelligence, with its cognitive, brain imaging, genetic, health, and environmental data on more
109 than 500,000 British middle-aged and older adults. Yet, numerous factors make the use of
110 cognitive tests in the UK Biobank difficult. First, not all participants completed the same
111 number of tests, and more recent tests have fewer participants (e.g., word production). Second,
112 those who completed the same number of tests did not necessarily complete the same
113 combination of tests. Across 501,650 participants with data on at least one of the eight cognitive
114 tests, we counted 80 different combinations of tests, with only 30,471 participants having
115 usable data on all eight tests. Third, the age at which a test was completed varies by test and
116 participant, with some participants completing a test as early as 38 years old and as late as 82
117 years old. Fourth, some participants completed certain tests several times. Finally, some tests
118 or similar tests with slight variations (e.g., 14 instead of 13 questions for Fluid Intelligence)
119 were completed at different locations: the assessment center on a touchscreen or autonomously
120 online, with one's device.

121 To maximize the number of participants included in their studies on intelligence in the
122 UK Biobank, some researchers estimated intelligence with a single test, either a Verbal
123 Numerical Reasoning (aka Fluid Intelligence) score or a reaction time score (Davies et al.,
124 2016; Kievit et al., 2018; Lee et al., 2018; Savage et al., 2018; Sniekers et al., 2017). Others
125 created a general intelligence (*g*) factor from 3 to 5 cognitive variables using Principal
126 Component Analysis (PCA) or Confirmatory Factor Analysis (CFA; (Cox et al., 2019a;
127 Hepsomali & Groeger, 2021; Lyall et al., 2016; Navrady et al., 2017). Thus, while the UK
128 Biobank test battery includes a diverse array of cognitive tests, these have been relatively
129 under-exploited up to now. Furthermore, most studies used test scores that were neither
130 adjusted for age nor standardized relative to a representative sample of the general population,
131 despite the acknowledged lack of representativeness of the UK Biobank sample (Fry et al.,

132 2017). As the UK Biobank continues to accrue data and attract new researchers, access to a
133 standardized general factor of intelligence for most UK Biobank participants will benefit future
134 studies that consider intelligence as a variable of interest or as a confounder.

135 Our study's aim was therefore to create a standardized general (*g*) factor for all UK
136 Biobank participants with at least one cognitive test that is relative to the UK population given
137 the participant's age, sex, and occupation. We first created standardized cognitive tests scores
138 relative to the UK population and then extracted a *g* factor score from these 8 cognitive tests
139 with CFA for individuals with data on at least one cognitive test. We estimated the quality of
140 the *g* factors for participants with missing data. We assessed the external validity of our *g* factor
141 by examining the correlation between our *g* factor and life outcomes.

142 Finally, we conducted genetic analyses to create a general intelligence polygenic score
143 (PGS) in the UK Biobank: We conducted a genome-wide association study (GWAS) of the *g*
144 factor score on the UK Biobank participants with a *g* factor of good quality and without
145 neuroimaging data ($N = 187,288$), and we assessed its predictive validity in the participants
146 with neuroimaging data ($N = 39,131$). We additionally conducted a GWAS of the *g* factor score
147 on the entire UK Biobank sample with a *g* factor of good quality to identify SNPs and genomic
148 loci that were not previously associated with intelligence or cognitive abilities.

149 By creating cognitive and polygenic scores in the UK Biobank, we offer more robust
150 measures of intelligence that foster homogeneity in intelligence research within the UK
151 Biobank, and deliver summary statistics and PGS for future studies interested in examining the
152 genetic associations of intelligence with neuroimaging, behavioral, and environmental
153 measures.

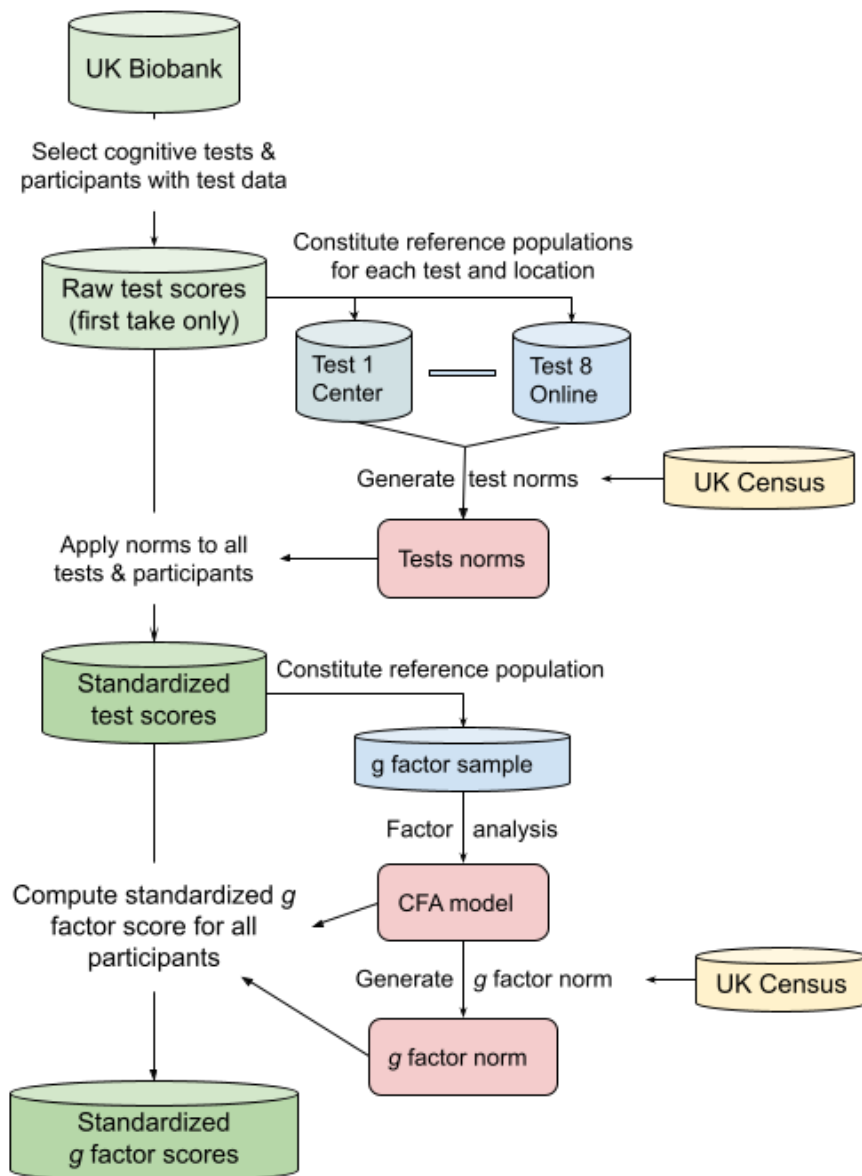
154

155 1. Methods

156 All analyses were performed in R (R Core Team, 2022). Supplemental Information,
 157 supplemental data, and code are anonymously available on the Open Science Framework
 158 (OSF): https://osf.io/49scv/?view_only=29e0ee6a1420461d81d234d94d549751 .

159 The standardization of cognitive test and g factor scores relative to the UK population
 160 are summarized in Figure 1.

161



162

163

164 **Figure 1.** G factor Creation Pipeline. Cylinders represent datasets; inputs are UK Biobank and
 165 UK census data; blue cylinders are subsets of data (standardization samples). Boxes represent
 166 produced norms and models. Arrows represent computations.

167

168 2.1. UK Biobank dataset and participants

169 The UK Biobank is an open-access large prospective study with phenotypic, genotypic,
170 and neuroimaging data from more than 500,000 participants. Participants were recruited
171 between 2006 and 2010, from the vicinity of 22 assessment centers in England, Wales, and
172 Scotland, with an age range for inclusion of 40–69 years (Sudlow et al., 2015). Data collection
173 continues up to date.

174 All participants provided informed consent (“Resources tab” at
175 <https://biobank.ctsu.ox.ac.uk/crystal/field.cgi?id=200>). The UK Biobank received ethical
176 approval from the Research Ethics Committee (reference 11/NW/0382) and the present study
177 was conducted based on application 46007.

178 Participants performed a variety of cognitive tests, either when visiting a UK Biobank
179 assessment center, or online during the online follow-up. Participants who did not complete
180 any of the cognitive tests retained for this study were excluded, yielding 501,650 participants
181 (excluded 843 participants).

182 The UK Biobank participants differ from the general UK population: they tend to be
183 healthier and to have a higher socioeconomic status (e.g., more likely to own property; Fry et
184 al., 2017; Keyes & Westreich, 2019), women are overrepresented and the distribution across
185 ages differs from the general population (ages 50–59 in 2001 overrepresented, while 30–39 are
186 underrepresented). To obtain an IQ score standardized with respect to the general population,
187 one needs to compensate for the difference between UK Biobank participants and the general
188 UK population.

189

190 2.2. Census data

191 UK 2001 census data (Office for National Statistics, 2011) was obtained from Casweb
192 (casweb.mimas.ac.uk). We selected tables ST033 and ST034, which provide occupation
193 categories for people currently in employment (ST033) and unemployed or economically
194 inactive (ST034), between 16 and 74 (ST033) or 64 (ST034) years of age, by sex.

195 Occupation was retained as a stratification variable because of its correlation with
196 intelligence (Schmidt & Hunter, 2004) and because it is available with a similar coding in the
197 UK Biobank and in the 2001 census (Standard Occupational Classification 2000 - SOC2000;
198 Office for National Statistics, 2000). We did not use the 2011 census because occupation was
199 coded using SOC2010, which differs notably from SOC2000, with no easy correspondence.

200 We matched participants to census characteristics using their age, country, and
 201 occupation on the day the census was conducted (April 29, 2001; Supplemental Section 1.1).

202

203 2.3. Cognitive Tests

204 2.3.1. Test Selection

205 UK Biobank participants could complete several cognitive tests every time they visited the UK
 206 Biobank assessment centers ([category 100026](#)) and during the online follow-up ([category 116](#)).

207 We used 8 cognitive tests to create the g factor (bolded tests in Table 1). Some participants
 208 completed some tests several times. We only considered the first occurrence of each test to best
 209 reflect the stable part of general intelligence, before aging and cognitive decline.

210

211 **Table 1.** *UK Biobank Cognitive Tests Considered for this Study.*

| Test (Included tests in bold) | UKB links (C: center, O: Online) | Description | Number of participan ts | Included or Excluded |
|--|---|---|--|-------------------------------------|
| FI - Fluid intelligence | C 100027 O 118 | Under a time limit of 2 minutes, answer a set of 13 (center) or 14 (online) numerical and verbal reasoning questions. | C=205,333 O=123,613 | Included |
| MAT - Matrix pattern completion | C 501 | Select the element that best completes matrix pattern blocks. 15 puzzles. | C=33,657 | Included |
| TWR - Tower rearranging | C 503 | Looking at an illustration of three pegs (towers), on which three differently-colored hoops have been placed, find how many moves it would take to rearrange the hoops into another specific position. 18 puzzles. | C=33,381 | Included |
| MEMN - Numeric memory | C 100029 O 120 | memorize 2 digits displayed on the screen. After they disappear for 3 seconds, enter them. Every time a sequence is correctly remembered, the next sequence is made one digit longer, up to a maximum of 12 digits. | C=82,865 O=111,062 | Included |

G factor for the UK Biobank

| | | | | |
|---|---|--|------------------------|---|
| MEMS - Pairs matching | C 100030 O 117 | memorize the position of matching pairs of cards. Once the cards are turned face down, find as many pairs as possible in the fewest tries. Up to 3 rounds, with an increasing number of pairs (3, 6, 8). | C=498,730 O=118,528 | Included |
| <i>MEMW - Paired associate learning</i> | C 506 | memorize 12 pairs of words shown for 30 seconds in total. After an interval (different test), see the first word of 10 of these pairs and select the matching second word from 4 alternatives. | C=34,045 | Excluded: ceiling effect |
| <i>MEMP - Prospective memory</i> | C 100031 | Early in the test session, the participant is shown "At the end of the games we will show you four colored shapes and ask you to touch the Blue Square. However, to test your memory, we want you to touch the Orange Circle instead." | C=211,952 | Excluded: only 1 question |
| <i>MEML - Lights pattern memory</i> | C 100028 | See pictures of houses which have some windows lit. After a 10-second delay, indicate which windows were lit. | C=3,714 (pilot only) | Excluded: too few participants |
| RT - Reaction time | C 100032 | Watch two cards on the screen. If they are the same, press a button-box as quickly as possible. | C=496,829 | Included |
| SDS - Symbol digit substitution | C 502 O 122 | Identify the digits attached to each symbol in a grid, by using another grid linking symbols to digits as a key. | C=33,679 O=118,466 | Included |
| TMT - Trail making | C 505 O 121 | Click sequentially on a set of digits in circles scattered around the screen (numeric path), then on a set of digits/letters (alphanumeric path). | C=34,045 O=104,028 | Included |
| <i>VOC - Picture vocabulary</i> | C 504 | Indicate which of 4 images is most closely related to a displayed word. Difficulty varies according to the correctness of the previous answers. | C=33,606 | Excluded: data not available in February 2022 |

| | | | | |
|------------------------------|--------------------------|--|----------------------|--------------------------------|
| <i>WRD - Word production</i> | C 100077 | State as many words beginning with the letter 'S' as possible within one minute. | C=3,744 (pilot only) | Excluded: too few participants |
|------------------------------|--------------------------|--|----------------------|--------------------------------|

212 *Note.* The numbers of participants are taken from UK Biobank's showcase, across all instances,
213 and include uncompleted tests.

214

215 **2.3.3. Obtaining Raw Scores**

216 To obtain a raw score for each test, we had to select between variables when several
217 measures were provided for a test and/or transform these measures. We excluded participants
218 with abnormal results (e.g., too many errors in the Symbol digit substitution test, indicating
219 non-compliance with the test instructions) or who did not finish the test. Retained measures,
220 transformations, and exclusion criteria are described in Table 2.

221

222 **Table 2.** *Raw scores Transformations for the Included Cognitive Tests*

| Test | Measures used | Raw score computation |
|---------------------------------|---|--|
| FI - Fluid intelligence | Number of correct answers [0-14] Fields 20016 (center) & 20191 (online) | Measure unchanged |
| MAT - Matrix pattern completion | Number of correct answers [0-15] Field 6373 (center only) | Measure unchanged |
| TWR - Tower rearranging | Number of correct answers [0-18] Field 21004 (center only) | Measure unchanged |
| MEMN - Numeric memory | Maximum number of digits remembered correctly [0-12] Fields 4282 (center) & 20240 (online) | Measure unchanged |
| MEMS - Pairs matching | Numbers of correct and incorrect matches in each round. The test has up to 3 rounds, with increasing difficulty (more pairs to remember). Access to a round is subject to a high score in the previous round. Fields 10136/398 (center) & 20131 (online) Fields 10137/399 (center) & 20132 (online) | Score computed as follows: - Each correct pair earns 2 points in rounds 1 and 2, 1 point in round 3 - Each incorrect pair loses 1 point - Within each round, negative scores are brought back to zero |

| | | |
|---------------------------------|---|--|
| SDS - Symbol digit substitution | Number of correct matches and number of attempts Fields 23324 (center) & 20159 (online) Fields 23323 (center) & 20195 (online) | Score = the number of correct matches Exclusion criteria: scores with more than 35 attempts and less than 65% correct matches (participants likely did not follow test instructions, for example by repeatedly entering the same digit). These outlier limits were computed as $\pm 3sd$ from the mean. |
| RT - Reaction time | Mean time to correctly identify matches Field 20023 (center only) | Score = $-\log(\text{mean time to correctly identify matches})$ Higher scores represent better performance No exclusion criteria because response times out of the 50ms to 2000ms range were already excluded. |
| TMT - Trail making | Duration to complete alphanumeric path trail Fields 6350 (center) & 20157 (online) | Score = $-\log(\text{duration to complete alphanumeric path trail})$ Higher scores represent better performance This measure had higher correlations with other tests than a measure based on a combination of the numeric and alphanumeric trails. |

223

224 **2.3.4. Standardization of test scores**

225 Standardization served two purposes: (1) to adjust for age effects (since intellectual
226 performance varies with age), and (2) to provide a test score relative to the UK population
227 (Figure 1). We created a common norming model for males and females. We simultaneously
228 performed two adjustments:

- 229 1. An age adjustment by using the semiparametric continuous norming method proposed
230 by Lenhard eand colleagues (2016). With this method, raw scores are modeled as a
231 function of both standard scores and an explanatory variable, age when taking the test
232 in this case.
- 233 2. A socio-demographic adjustment: by using standardization samples and computing
234 weights to apply to participants, to compensate for the socio-demographic differences
235 between the UK Biobank population and the complete UK population.

236

237 To do so, we first created standardization samples for each test and location
238 (online/center), with about 32,000 to 497,000 participants. Details regarding the
239 standardization sample creation and the number of participants in each sample are available in
240 Supplemental Section 1.2.

241 We then used cell weighting to adjust measures from the standardization samples to
242 reflect the UK population characteristics: For each standardization sample, we computed the
243 proportion of participants for each possible combination of country, sex, age range at census,
244 occupation status, and occupation SOC group. We compared the proportion of UK Biobank
245 participants in each cell to the 2001 census and created weights for each cell by dividing the
246 census proportion by the UK Biobank proportion. See Supplemental section 1.3. for details and
247 an example.

248 We used the *cNorm* package (Lenhard et al., 2018) to compute norming models on the
249 standardization samples with census weights, using the semiparametric continuous norming
250 method. We modeled raw scores as a function of standard scores (percentiles) and age at test
251 completion. Age at test completion is provided in [field 21003](#) for tests taken at the assessment
252 center and in fields [20134](#) to [20138](#) for tests taken online. This age differs from the age used to
253 compute census weighting factors, which is the participant's age on the day of the 2001 census.

254 We applied the norming models to the whole dataset and obtained standardized test
255 scores for all participants on the tests they took (Figure 1).

256 [2.4. G factor](#)

257 We created a *g* factor score for all participants who completed at least one of the eight cognitive
258 tests using confirmatory factor analysis (CFA). The *g* factor was standardized relative to the
259 UK population. We also evaluated the impact of missing test scores on the quality of the *g*
260 factor.

261 [2.4.1. CFA Parameters](#)

262 We performed a CFA with one-factor loading on the eight cognitive tests, using all
263 pairwise complete cases (i.e., data from all participants who performed at least two tests). First,
264 we checked whether the data was suitable for factor analysis by looking at the Kaiser, Meyer,
265 Olkin measure of sampling adequacy and Bartlett's test of sphericity. We then estimated the
266 CFA model with the *lavaan* R package (Rosseel, 2012). We used the full information
267 maximum likelihood (FIML) estimator to make use of all data points even for cases with
268 missing values, estimated the mean structure, and set the variance of the latent variable to 1 to

269 estimate each observed variable loading. Model fit was assessed using commonly used model
270 fit indices: the Tucker Lewis Index (TLI), the Comparative Fit Index (CFI), Standardized Root
271 Mean Square Residual (SRMR), and the Root Mean Square Error of Approximation (RMSEA).
272 Good fit was established with a CFI and TLI > 0.95 , a RMSEA < 0.06 and a SRMR < 0.08 (Hu
273 & Bentler, 1999). See Supplemental Section 1.4. for a discussion on the choice of factor
274 analysis.

275 **2.4.2. G Factor Score Standardization**

276 We created a standardization sample with 496,990 participants who had data for the
277 census variables: sex, age on census day, and occupation on census day (countries were
278 merged, see Supplement Section 1.3), to compute census weighting factors for these
279 participants (Figure 1).

280 We computed factor scores using the regression estimation method, which maximizes
281 validity (DiStefano et al., 2019). We then computed the weighted mean and weighted standard
282 deviation of these scores, using the census weighting factors. We subtracted the weighted
283 sample mean from the raw factor scores and divided the result by the weighted sample standard
284 deviation, to obtain factor scores with a general population mean of 0 and a standard deviation
285 of 1.

286 **2.4.3. Evaluation of the g Factor Score Quality in the Presence of Missing Data**

287 We examined how well a g factor score computed using a subset of tests (called partial
288 factor score) correlates with the factor score that would have been obtained from the full set of
289 eight tests (called full factor score) by looking at the correlation between the full and the partial
290 factor scores for each the 80 subsets of tests present in the data, in the 30,471 participants who
291 completed all the tests.

292

293

294 **2.5. Analyses**

295 In the following analyses, we included participants whose combination of cognitive
296 tests allowed for a correlation with the complete *g* factor of 0.70 or higher (N=261,701). This
297 threshold was chosen to maximize the robustness of the factor as well as the number of
298 participants for which we would generate a *g* factor.

299 **2.5.1. Correlations with Alternative estimates of *g* and Life outcomes**

300 We examined the external validity of our *g* measure by examining correlations in
301 complete cases between our *g* factor and FI, life and health outcomes expected to correlate with
302 intelligence (e.g., educational attainment, income, deprivation indices, etc., life and health
303 outcomes described in Supplemental Data S8). In brief, we selected well-being, household
304 income before taxes, highest qualification as well as the Townsend deprivation score – a
305 deprivation score of an individual’s postal code from the census data - and the index of multiple
306 deprivations that regroups several deprivation indices which vary by country. The latter include
307 subindices such as health, income, education, employment, and housing. The index of multiple
308 deprivations and its subindices come from a UK government qualitative study of deprived areas
309 in British local councils and are calculated separately for England, Wales, and Scotland.
310 Common multiple deprivation scores across countries were combined into a single variable for
311 the correlation matrix (Supplemental Data S8). We adjusted each measure for sex and age at
312 which the measure was reported.

313 **2.5.1. Genetic Analyses**

314 We conducted genetic analyses to (i) examine whether our measure of intelligence leads
315 to the identification of novel SNPs and genomic loci that were not previously associated with
316 cognitive performance (Lee et al., 2018) or intelligence (Savage et al., 2018) and to (ii) create
317 polygenic scores (PGS) for individuals with neuroimaging data for future UK Biobank studies.
318 A detailed overview of the genetic analyses is available in Supplemental Section 1.6.

319 **2.5.1.1. Main Analyses**

320 In brief, we conducted the first *g* factor GWAS on all 223,731 UK Biobank participants
321 with good *g* factor quality (Full GWAS) to identify novel SNPs and a second *g* factor GWAS
322 on 187,288 individuals without neuroanatomical data or twins/siblings with neuroanatomical
323 data (No Neuroimaging GWAS) for the creation of PGSs. We removed participants with
324 neuroanatomical data and their siblings to maintain the independence of predictions and
325 prevent overfitting. GWASs were conducted with fastGWA (Jiang et al., 2021) on individuals
326 of British ancestry and we controlled for relatedness, sex, center, genotyping chip, birth year,

327 and the first 40 PCs of the PCA on the genetic variation of a population to adjust for population
328 stratification.

329 We conducted functional mapping and annotation analyses on the GWAS summary
330 statistics with FUMA to (i) report the genes associated with our *g* factor measure in the Full
331 GWAS and No Neuroimaging GWAS (Supplemental Data S1-4 on OSF) and (ii) identify the
332 genes associated with novel SNPs and genetic loci (Supplemental Data S6-7 on OSF). We
333 report the SNP2GENE analysis on the summary statistics from the Full and No Neuroanatomy
334 GWAS in the main text, the GENE2FUNC analysis of these summary statistics in
335 Supplemental Data S3-4, and the GENE2FUNC analyses of the novel SNPs and genomic loci
336 in text.

337 Using sBayesR (Lloyd-Jones et al., 2019), we created PGSs from the summary statistics of
338 the No Neuroanatomy GWAS for individuals with either neuroimaging data or siblings with
339 neuroimaging data to (i) assess the predictive power of genetic variance from the no
340 neuroanatomy GWAS on the *g* factor and to (ii) be returned to the UK Biobank for use by
341 future studies.

342 **2.5.1.2. Additional Analyses**

343 We conducted additional analyses to answer the following questions.

- 344 1. ***Does the *g* factor PGS explain more variance in *g* than the FI PGS?*** We ran a GWAS
345 of the verbal-numerical reasoning test score (also known as Fluid Intelligence) on
346 180,722 individuals without neuroanatomical data or twins/siblings with
347 neuroanatomical data (FI GWAS) and calculated FI PGS for individuals with
348 neuroimaging data with the GWAS and PGS parameters described above. We then
349 adjusted the FI PGS for sex, birth year, and the first 40 PCs and examined the
350 percentage of variance explained in *g* and FI, separately.
- 351 2. ***Once you control for environmental factors, what proportion of variance in *g* does***
352 ***the *g* PGS predict?*** To quantify to what extent the polygenic signal captures genetic
353 effects that pass through the environment (indirect genetic effects or genetic nurture;
354 Howe et al., 2021), we conducted family fixed-effects analyses. To do so, we first ran
355 a *g* factor GWAS on the sample from the No Neuroimaging GWAS without siblings
356 (No Family, No Neuroimaging GWAS). We used the summary statistics from this
357 GWAS to create polygenic scores for individuals with siblings and then adjusted the
358 PGS for sex, birth year, and the first 40 PCs. Finally, we ran the family fixed effects

359 model with and without controlling for genetic relatedness and reported the change in
360 explained variance of the PGS on the *g* factor when adjusting or not for sibling pairs.

361 3. *Do our g factor and FI measures have similar genetic correlations and heritabilities*
362 *as the g factor and Educational Attainment (EA) measures from Lee and colleagues*
363 *(2018)?* We examined whether the genetic influences underlying our *g* factor and FI
364 measure were similar to the genetic influences underlying the EA and the *g* factor (also
365 known as Cognitive Performance) reported by Lee and colleagues (2018). To do so, we
366 calculated the genetic correlations between our *g*-factor GWAS summary statistics, our
367 FI GWAS summary statistics, and the publicly available Educational Attainment (EA)
368 and *g* factor summary statistics. We additionally calculated the heritability estimates of
369 each summary statistics file to examine whether our *g* factor was more heritable than
370 our FI measure, previous *g* factor measures, and EA. These analyses were conducted
371 with linkage disequilibrium score regression using the *ldsc* function from the GSEM
372 package (Grotzinger et al., 2019).

373 4. *If had included participants with a poor g factor measure ($r < .7$), would the genetic*
374 *correlation and heritabilities be the same?* We conducted a GWAS on 307,009
375 individuals with a *g* factor measure and without neuroanatomical data or twins/siblings
376 with neuroanatomical data (Low Quality No Neuroimaging *g* factor GWAS). If the
377 genetic correlation and heritabilities were similar or better for this Low *g* Quality
378 GWAS compared to the No Neuroimaging GWAS, we should be able to use this larger
379 sample size to obtain more lead SNPs and better polygenic predictions.

380

381 **2.5.3. Correlations with Alternative estimates of *g*, Life outcomes, Neuroimaging, and** 382 **Genetic Measures**

383 We conducted additional correlational analyses on a subset of participants that had
384 neuroimaging data and PGSs. We examined correlations on complete cases between our *g*
385 factor and alternative measures of intelligence for the UK Biobank (FI alone, *g* factor with 4
386 tests...), life and health outcomes expected to correlate with intelligence (e.g., educational
387 attainment, income, deprivation indices, etc., life and health outcomes in Supplemental Data
388 S8 on OSF), Total Brain Volume (TBV; Williams et al., 2021), and the FI and *g* factor PGS in
389 individuals with neuroimaging data.

390 We compared our *g* factor score to alternate measures of intelligence by transforming
391 the cognitive variables and extracting the *g* factor as done by Cox and colleagues (2019b) and

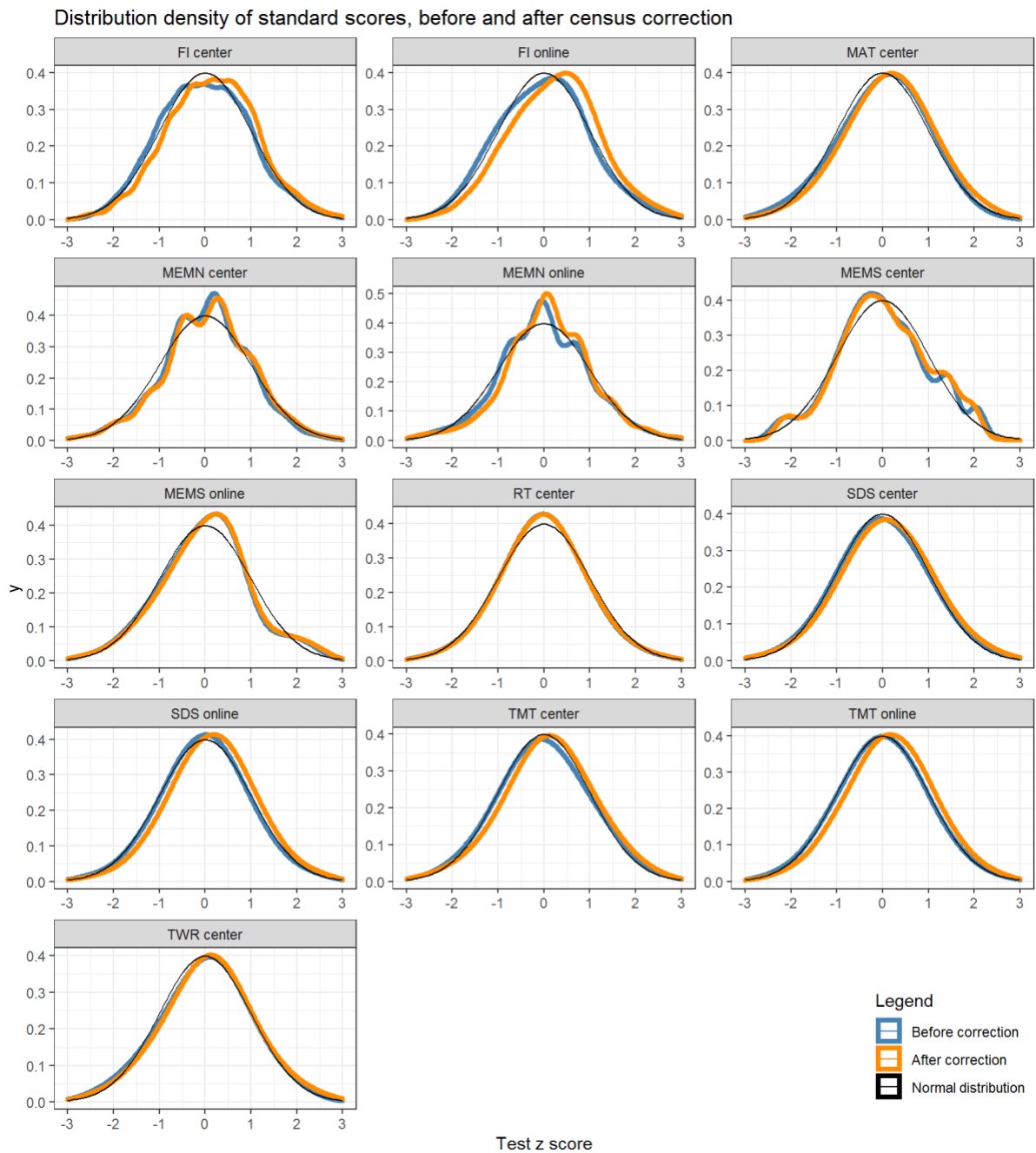
392 de Nooij and colleagues (2020), which used a different combination of cognitive tests and
393 factoring methods with a similar sample to the one we used to calculate PGSs. The authors
394 used cognitive tests completed at the center during the neuroimaging visit (Instance 2) and
395 included tests that were not initially available at the first center visit. Cox and colleagues (2019)
396 created a latent factor using CFA from the MAT, the SDS, the FI, and the TMT-B cognitive
397 tests, and de Nooij and colleagues (2020) extracted the first principal component of the
398 numerical memory, the FI, the SDS, the TMTB, the MAT, and the TWR cognitive tests.

399 Since our *g* factor is adjusted for age, we created alternative *g* factors that are adjusted
400 for age in the CFA or after extracting the first PC. We additionally similarly controlled for sex
401 to examine whether differences between our *g* factor and the *g* alternatives could be explained
402 by sex differences.

403 2. Results

404 3.1. Cognitive Tests

405 We compared the distribution of the standard test scores before and after adjusting for
406 the difference between the UK Biobank population and the general UK population (Figure 2).
407 After adjusting for age and census weights, the distribution of the scores shifted to the right,
408 indicating a relatively higher score in the UK Biobank relative to the UK norm (Supplemental
409 Section 2.1.1). In some cases, the distribution was not normal because of its categorical nature
410 (e.g., MEMN) or because of threshold effects (e.g., MEMS). Correlations between standard
411 scores ranged from 0.07 (MEMN and RT) to 0.50 (TMT and SDS). TMT and FI had the highest
412 correlation coefficients with other cognitive tests (Supplemental Section 2.1.2).



413

414 **Figure 2.** The Distribution of Cognitive Tests Before (blue) and After (orange) correcting for

415 Sociodemographic Differences between the UK Biobank Population and the UK Population

416 (2001 Census). FI: Fluid Intelligence. RT: Reaction Time. MAT: Matrix Pattern Completion.

417 TWR: Tower Rearranging. MEMN: Numeric Memory. MEMS: Pair Matching. SDS: Symbol

418 Digit Substitution. TMT: Trail Making.

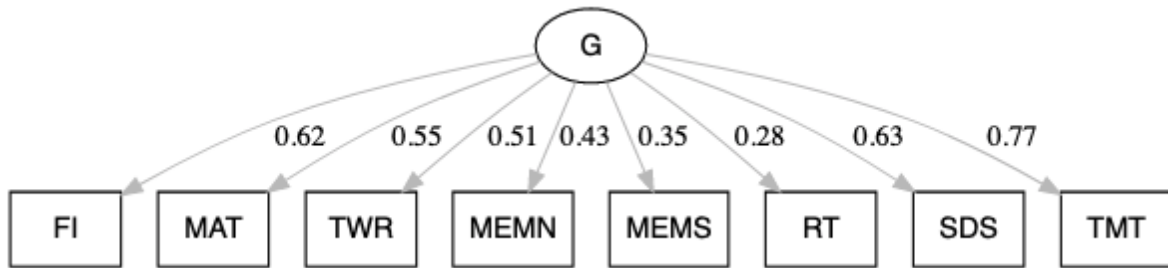
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420

421 3.2. CFA results

422 3.2.1. Model Fit

423 The CFA model fit on 501,650 participants (30,307 with complete data; N Women =
 424 272,955; N Men = 228,695) was good (CFI = 0.955, TLI = 0.938, RMSEA = 0.024, SRMR =
 425 0.028). The g factor accounted for 29% of the variance across cognitive tests and the loadings
 426 ranged from 0.77 (TMT) to 0.277 (RT) (Figure 3; Supplemental Section 2.1.3). Sex differences
 427 in cognitive and g factor scores are available in Supplemental Section 2.1.4.



428

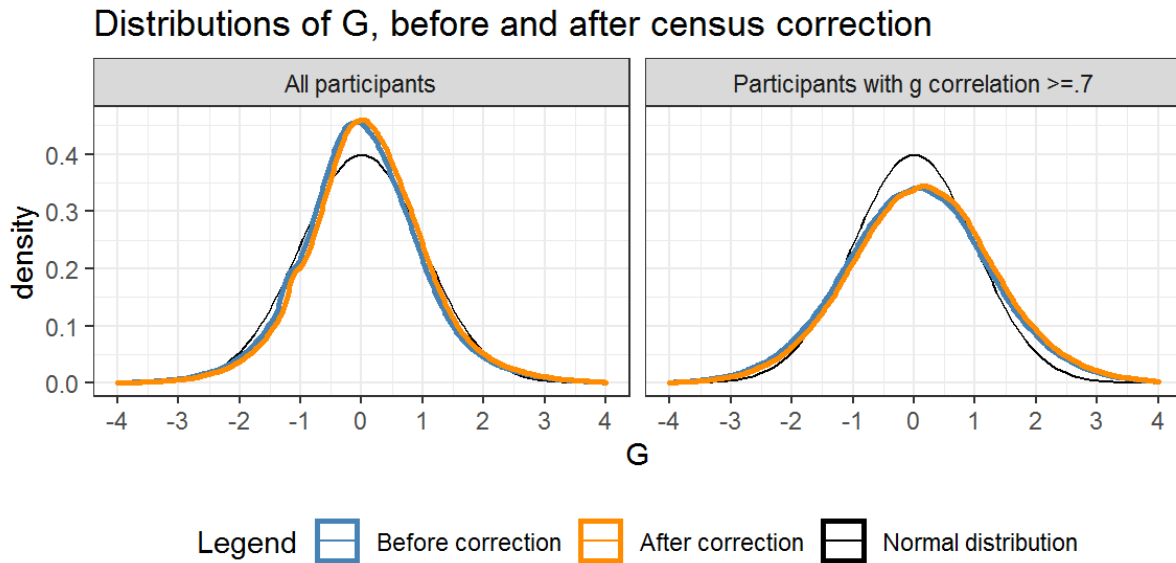
429 **Figure 3.** *Confirmatory Factor Analysis of UK Biobank Cognitive Tests.* Analyses were
 430 conducted with full information maximum likelihood with the lavaan package (Rosseel et al.,
 431 2021). Explained variance: 29%. FI: Fluid Intelligence. MAT: Matrix Pattern Completion.
 432 TWR: Tower Rearranging. MEMN: Numeric Memory. MEMS: Pair Matching. SDS: Symbol
 433 Digit Substitution. TMT: Trail Making. Loadings from completely standardized solutions (i.e.,
 434 standardized observed and latent variables).

435

436 3.2.2. Distribution of the g factor before and after census correction

437 We compared the distribution of the g factor scores before ($M = -0.004$, $sd = 0.993$)
 438 and after ($M = 0.086$, $sd = 1.001$) adjusting for the difference between the UK Biobank
 439 population and the general UK population ($d = 0.09$). After adjusting, the factor score
 440 distribution shifted to the right, indicating a relatively higher score in the UK Biobank relative
 441 to the UK norm (Figure 4; g distribution by job category in Supplemental Section 2.1.5).

442



443

444 **Figure 4.** *The Distribution of the g Factor Scores Before and After Census Correction for All*
 445 *Participants (left) and a Subset of Participants (right).* The subset of participants had a g factor
 446 score from a combination of subtests that allowed for a minimum correlation of 0.70 between
 447 the partial g factor score and the full g factor score.

448

449 **3.2.4. G Factor Quality**

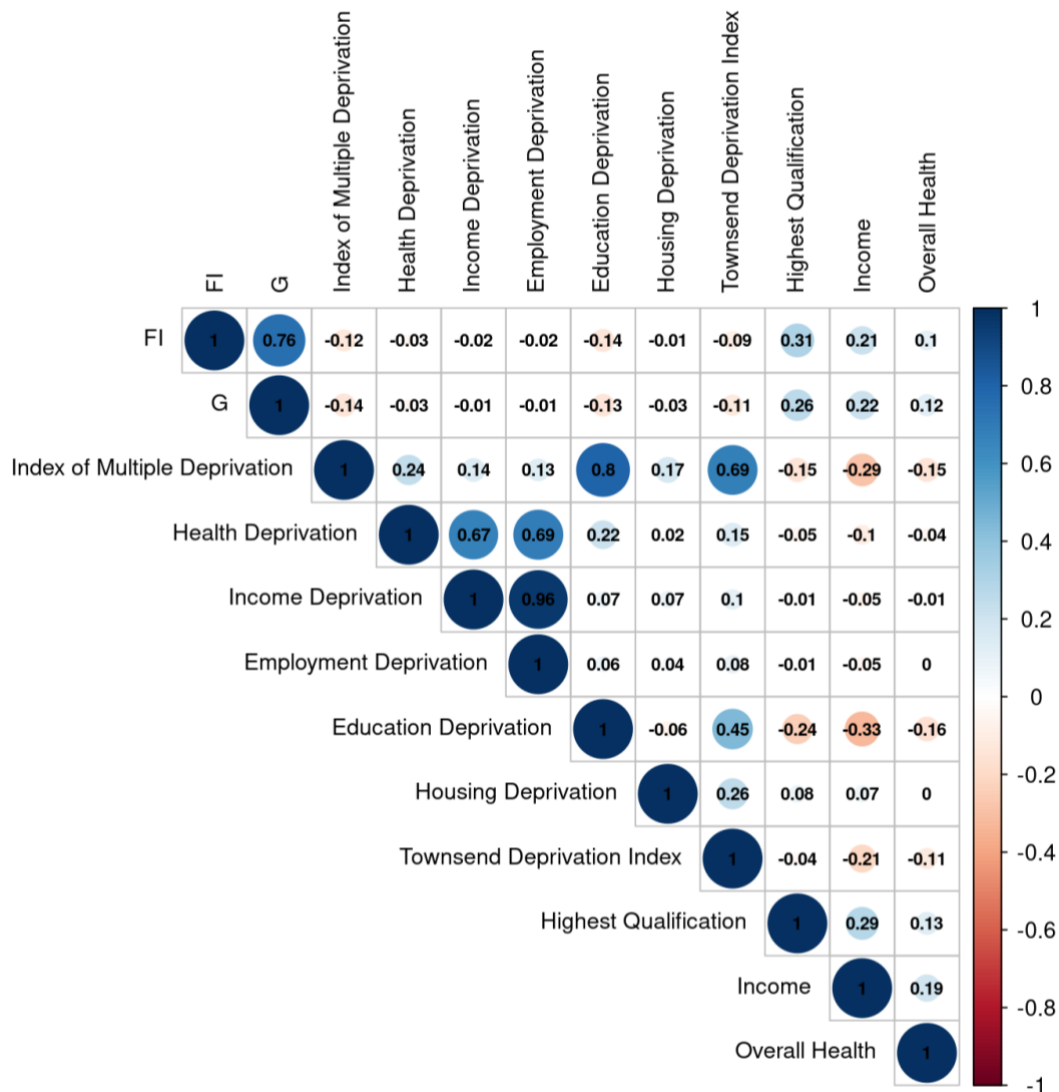
450 The quality of the g factor and the number of individuals for each possible combination
 451 of completed tests are available in Supplemental Section 2.1.6. For example, if we select
 452 participants with any of the first 73 cognitive test combinations observed in the UK Biobank,
 453 the worst factor scores of these participants would have a correlation of 0.70 with the ideal, 8-
 454 tests factor scores, and the number of available participants will be over 261,701.

455

456 3.3. Analysis of Individuals with a g Factor Quality over 0.70

457 3.3.1. Correlations: Alternative g factors and Life outcomes

458 We examined the external validity of our g measure by examining the association in
 459 complete cases between our g factor measure, FI (which is often used as a proxy of g in most
 460 studies), and life outcomes collected at the first center visit or online to estimate correlation
 461 coefficients on a larger number of participants (Figure 5). We removed well-being to include
 462 more participants because it was poorly correlated to our g factor (Figure S9).



463
 464 **Figure 5.** Correlation between age and sex-adjusted g factor Scores and Health and Life
 465 Outcomes. Pearson correlation coefficients were estimated on 181,327 individuals without
 466 missing data. All measures are adjusted for age at which the measure was taken and sex. G
 467 corresponds to the g factor of individuals with a combination of cognitive tests that allowed for
 468 a correlation of 0.70 or higher between their actual g factor and what their g factor would have
 469 been if they had completed all tests. FI: Fluid Intelligence.

470

471 **3.3.2. Genetic Analyses**472 **3.3.2.1. Main Results**

473 We identified 150 approximately independent SNPs attaining genome-wide
 474 significance in the full sample GWAS and 100 in the No Neuroanatomy Sample GWAS (Table
 475 3). There were 127 genomic risk loci associated with the *g* factor in the Full GWAS and 84
 476 genomic risk loci with the *g* factor in the No Neuroanatomy GWAS ($P < 5 \times 10^{-8}$; Supplemental
 477 Data S1-S2 on OSF). See Figure S3 for the Manhattan and QQ-plots.

478 We found 37 novel SNPs and 36 novel genetic loci (rs10182628 and rs7595241 mapped
 479 to the same loci; Supplemental Data S5 on OSF) that were not within ± 250 kb of the genome-
 480 wide significant SNPs associated with Lee's *g* factor (Cognitive Performance in Lee et al.,
 481 2018) and Savage's *g* factor (Intelligence in Savage et al., 2018) and SNPs previously
 482 associated with cognitive ability or educational attainment based on the GWAS catalog.

483

484 **Table 3.** *No Neuroimaging and Full Sample GWAS Results.*

| <i>GWAS Sample</i> | <i>N</i> | <i>Mean χ^2</i> | <i>LD Score Intercept</i> | <i>Ratio (SE)</i> | <i># Lead SNPs</i> | <i># Loci</i> | <i>h² (SE)</i> |
|------------------------|----------|---------------------------------|---------------------------|--------------------|--------------------|---------------|---------------------------|
| <i>Full</i> | 223,731 | 1.93 | 1.046 (0.017) | 0.049 (0.018) | 150 | 127 | 0.201 (0.008) |
| <i>No Neuroanatomy</i> | 187,288 | 1.76 | 1.032 (0.015) | 0.0412 (0.0191) | 100 | 84 | 0.197 (0.009) |

485 *N.B.* *N*, GWAS sample size; mean χ^2 , mean GWAS χ^2 statistics across HapMap3 SNPs with
 486 MAF greater than 0.01; LD score intercept, the estimate of the intercept from an LD score
 487 regression using HapMap3 SNPs with MAF greater than 0.01; no. lead SNPs, number of
 488 approximately independent (pairwise $r^2 < 0.1$) FUMA lead SNPs; no. loci, number of
 489 associated loci. H², heritability estimated from the ldsc function in the Genomic SEM package.

490

491 The positional annotation of candidate SNPs indicated that the majority of independent lead
 492 SNPs were located in the intronic, mRNA intronic, and intergenic regions in the Full and No
 493 Neuroanatomy GWAS (Supplemental Data S1-S2 on OSF).

494 From the 37 novel lead SNPs, we pinpointed 90 genes (44 protein-coding genes) by
495 positional, eQTL, and chromatin interaction mapping in the *g* factor Full GWAS. MAGMA
496 Tissue expression in the SNP2GENE analyses revealed that associated genes were highly
497 expressed in several brain regions (Figure S4). The heatmap of gene expression showed that
498 RIMS4, SEZ6, and SLC24A2 were highly expressed in the brain, whereas PLEKHB1 was
499 highly expressed in the brain amongst other tissues (Figure S5). Several of these genes were
500 previously associated with the cognitive dimension dimensional psychopathology among other
501 traits (Figure S6).

502 We created PGS for 40,871 individuals with either neuroimaging data or siblings with
503 neuroimaging data and *g* factor quality greater than $r \geq 0.70$. Of the 39,131 individuals with
504 neuroimaging data, 24,229 had a *g* factor quality of $r = 1$ (Table S5).

505 We adjusted the *g* and FI values for sex, year of birth, and the first 40 genetic PCs. The
506 *g* factor PGS created from the No Neuroanatomy GWAS explained 7.7% of the variance in the
507 *g* factor, whereas the FI created from the No Neuroanatomy GWAS explained 6.6% of the
508 variance in FI.

509 3.3.2.2. Additional Analyses

510 1. *Does the g factor PGS explain more variance in g than the FI PGS?* The *g* factor PGS
511 created from the No Neuroanatomy GWAS explained 1.7% more variance in *g* than the
512 FI PGS created from the No Neuroanatomy GWAS, which explained 6.0% of the
513 variance in the *g* factor. The *g* factor PGS created from the No Neuroanatomy GWAS
514 explained 5.8% of the variance in FI.

515 2. *Once you control for environmental factors, what proportion of variance in g does*
516 *the g PGS predict?* The family fixed-effect analysis on the PGS from the No Family,
517 No Neuroimaging GWAS summary statistics when adjusting for sex, year of birth, and
518 the first 40 genetic principal components, showed a decrease in explained variance from
519 6.6% to 3.2% and a reduction of 17% in the beta. See Supplemental Section 2.2.4. for
520 additional PGS analyses.

521 3. *Do our g factor and FI measures have similar genetic correlations and heritabilities*
522 *as the g factor and Educational Attainment (EA) measures from Lee and colleagues*
523 *(2018)?* The SNP heritability of the present *g* factor was similar to the heritability of
524 Lee's *g* factor ($h^2 = 0.199$, $SE = 0.008$) and greater than Lee's EA ($h^2 = 0.151$, $SE =$
525 0.004 ; Table 3 and S10). Lee's *g* factor was highly correlated to our various estimates

526 of the g factor 0.92-0.93, suggesting that they capture common genetic influences
527 (Figure S8).

528 4. ***Do participants with a low-quality g factor estimate ($r < .7$) impact the results?*** We
529 found that the heritability of the Low-Quality No Neuroimaging GWAS ($h^2 = 0.127$,
530 $SE = 0.005$) was much lower than the heritability of the No Neuroimaging GWAS (h^2
531 $= 0.197$, $SE = 0.008$; Table S10) and that the genetic correlation between the Low-
532 Quality No Neuroimaging GWAS and the No Neuroimaging GWAS was of 0.98
533 (Figure S8), suggesting that although both GWASs are measuring overlapping genetic
534 effects, the Low-Quality No Neuroimaging GWAS has more measurement error. The
535 genetic correlations of the Low-Quality No Neuroimaging GWAS were lower with
536 Lee's g factor (0.87 vs. 0.93) and EA (0.5 vs. 0.55), suggesting that doubling the sample
537 size by including g factor estimates of lower quality is counterproductive for the
538 GWAS.

539

540 **3.3.3. Correlations: Alternative g factors, Life outcomes, Neuroimaging, and Genetic** 541 **Measures**

542 We conducted separate correlation analyses on our g factor with the alternative g
543 factors, neuroimaging, and PGSs because these data were only available for participants who
544 visited the center for the neuroimaging visit.

545 The alternative g factors were created from cognitive tests scores from their
546 neuroimaging visit and cognitive tests that were only available at the second visit. The
547 correlation between our study's g factor (adjusted for age, not sex) and the cognitive tests
548 ranged from 0.25 (RT) to 0.84 (TMT), whereas the age-adjusted g factors from previous studies
549 ranged from about 0.16 (RT) to 0.71 (MAT; Figure S11).

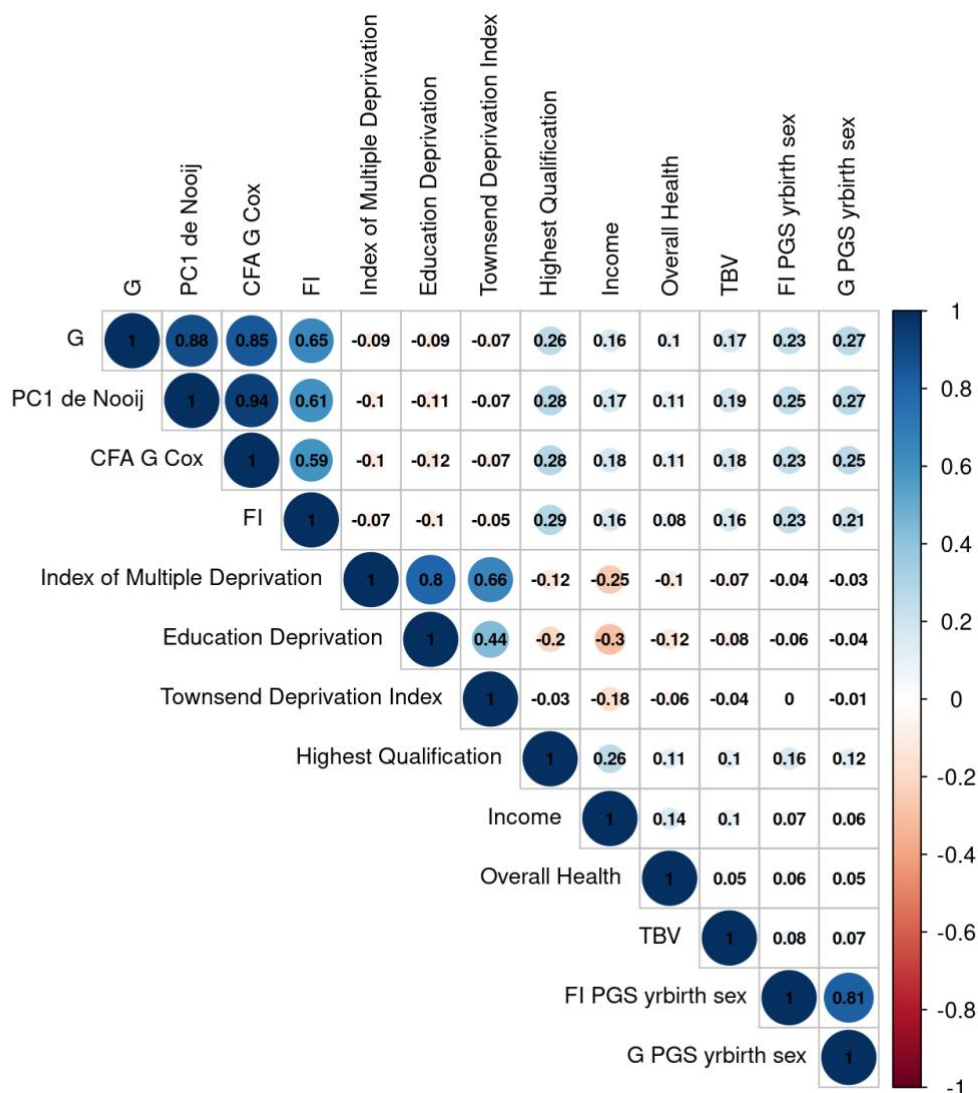
550 Correlation coefficients between our study's g factor and alternative g factors were high
551 (0.85 to 0.89; Figure S12). The alternative g factor measures were more correlated to the
552 highest qualification achieved ($r = 0.26$ - 0.29 vs. $r = 0.24$) and income ($r = 0.18$ - 0.19 vs. $r =$
553 0.16) than the present g factor because the cognitive tests included in the alternative g factors
554 were the cognitive tests with the highest correlations with highest qualification and income
555 (Figure S13).

556 The g factor from the present study and the g factors calculated as done by previous
557 studies were highly correlated after adjusting for the age of test completion and sex. The g
558 factors positively correlated with the PGS, highest qualifications, income before tax, overall

G factor for the UK Biobank

559 health, and total brain volume, and negatively with the deprivation indices (Figure 6). We also
560 looked at the correlation coefficients of the *g* factors with well-being and additional deprivation
561 indices, which reflect the degree of housing, employment, education, etc. deprivation in an
562 area. However, these correlations were small and therefore reported in Figure S14.

563



564

565 **Figure 6.** Correlation between age and sex-adjusted G Factor Scores, selected Life and Health
 566 Outcomes, Total Brain Volume (TBV), and sex and year of birth adjusted Polygenic Scores
 567 (PGS). Pearson correlation coefficients were estimated on 18,976 individuals without missing
 568 data. We included all life and health variables with an $r \geq 0.1$ with g except for the
 569 Townsend Deprivation Index. CFA: Confirmatory Factor Analysis. PC1: 1st Principal
 570 Component. G: General Factor for intelligence. G corresponds to the g factor of individuals
 571 with a combination of cognitive tests that allowed for a correlation of 0.70 or higher between
 572 their actual g factor and what their g factor would have been if they had completed all tests. FI:
 573 Fluid Intelligence. Income: Income before tax. PGS were adjusted for sex and birth year (yr
 574 birth).

575 Discussion

576 We aimed to create a robust measure of general intelligence for all UK Biobank
577 participants. We created an age-standardized *g* factor measure relative to the UK population
578 for about 500,000 UK Biobank participants, with an estimation of the *g* factor's quality for
579 each participant, allowing researchers to select their sample based on their quality
580 requirements. We examined correlations between the present study's *g* factor, alternative
581 measures of intelligence, and life outcomes. Our *g* factor was highly correlated with alternative
582 *g* factor measures of intelligence in the UK Biobank and their correlations with life and health
583 outcomes were similar. The GWASs and functional analyses on our new measure of general
584 intelligence revealed novel SNPs that were either associated with genes related to the cognitive
585 dimension of psychopathology or genes that were not previously associated with intelligence,
586 cognitive ability, or educational attainment. Finally, our study provides a PGS for about 38,000
587 UK Biobank individuals with neuroimaging data that explained 7.7% of the variance in the
588 intelligence score.

589 There was a high correlation between our *g* factor and the alternative *g* factor measures
590 derived using methods from previous UK Biobank studies. Although *g* factors differed in terms
591 of the included cognitive tests, and in some cases, in terms of the captured variance, they were
592 highly similar ($r = 0.85-0.94$). This is consistent with the high level of common measurement
593 reported across different cognitive tests, providing further support for a common underlying
594 component of intelligence (Johnson et al., 2004; Kaufman, 2012).

595 The *g* factor from the present study and alternative *g* factor measures were similarly
596 correlated to life outcomes, such as household income before tax or highest qualification (i.e.,
597 level of education) when adjusting for age and sex. The slightly higher correlations between
598 the alternative *g* factor measures and the highest qualification achieved compared to our *g*
599 factor could be explained by the tests used to create the alternative *g* factors, which correlated
600 the most with the highest qualification. Therefore, some outcomes, such as the highest
601 qualification, may not be as highly correlated to general intelligence as previously thought and
602 may be more correlated with specific cognitive tests. However, the main advantage of our *g*
603 factor is that it was calculated on all of the 500 000 UK Biobank participants with a measure
604 of its quality.

605 Consistent with a previous meta-analysis (Veenhoven & Choi, 2012), we did not find
606 a correlation between our *g* measure and well-being. Although the studies in this meta-analysis
607 have been criticized for their limited measure of well-being, as they solely focused on life

608 satisfaction, another study with a larger range of well-being measures found that the positive
609 association between IQ and well-being disappeared after controlling for socioeconomic status
610 (SES; Altaras Dimitrijević et al., 2018).

611 We report a negative correlation between our *g* factor and the Townsend Index, an SES
612 measure that reflects a person's material deprivation based on unemployment rates, non-car
613 ownership, non-homeownership, and household overcrowding in their postal code. This
614 negative correlation coincides with the negative correlation between neighborhood deprivation
615 and educational attainment (Garner & Raudenbush, 1991), as well as previous findings that
616 childhood IQ remains stable across old age (Deary et al., 2000), predicts later SES outcomes
617 (Deary et al., 2005). We additionally found a negative correlation between our *g* factor and the
618 index of multiple deprivation of the area where a person resides, which was largely explained
619 by the negative correlation between the *g* factor and the education deprivation index of the area
620 where a person resides. The education deprivation index was measured by a score reflecting
621 child and adolescent school performance (e.g., English, math, and science exams Stage 3
622 exams) and adult skills (e.g., the proportion of adults with no or low qualifications) in a given
623 geographical area.

624 The GWASs led to the identification of novel SNPs that were not previously associated
625 with cognitive performance or intelligence. These SNPs were not associated with genes related
626 to educational attainment, or cognitive ability, although some were associated with genes
627 involved in the cognitive domain of psychopathology (McCoy et al., 2018). For instance, the
628 PLEKHB1 (Pleckstrin Homology Domain Containing B1) protein-coding gene was prioritized
629 by eQTL and positional mapping. This gene is associated with neurological diseases and the
630 cognitive dimension of psychopathology (McCoy et al., 2018).

631 The *g* PGS created from the No Neuro GWAS summary statistics explained 7.7% of
632 the variance in the *g* factor of individuals with neuroimaging data and siblings with
633 neuroimaging data. Lee and colleagues (2018) similarly found that their CP PGS created from
634 their GWAS summary statistics explained 7% of the variance in CP for individuals in the
635 Wisconsin Longitudinal Study, a study that used cognitive tests with similar properties to their
636 discovery GWAS. However, they found that the CP PGS from the summary statistics of their
637 multi-trait analysis GWAS (MTAG) of CP, which yielded more significant SNPs, explained
638 9.7% of the variance in CP for individuals in the Wisconsin Longitudinal Study.

639
640

641 The FI PGS explained 1.7% less variance in *g* than the PGS of the *g* factor, suggesting
642 that the *g* PGS is a better genetic predictor of *g*. The genetic correlations between FI and the *g*
643 factor were high, suggesting that FI and *g* have very similar genetic influences. The *g* factor
644 and FI PGSs also similarly correlated with total brain volume, the most correlated brain
645 measure to intelligence (Deary et al., 2021). Taken together, our findings suggest that a
646 common genetic component to FI and the *g* factor may explain the genetic association between
647 intelligence and TBV. Although the FI PGS may be sufficient when investigating global brain
648 size associations with intelligence, the *g* factor PGS still explains a larger range of variance in
649 general intelligence than FI and its use should be favored when controlling for the genetic
650 components of intelligence.

651 The present study has several limitations. First, the selection of cognitive tests currently
652 available in the UK Biobank severely underrepresents verbal ability. Indeed, of the 8 tests that
653 could be considered in the present study, only 2 were verbal: the FI test (verbal-numerical
654 reasoning) and the numeric memory test (digit span). These imbalances are currently being
655 corrected by the addition of new tests (picture vocabulary and word production), which will
656 become available later, and which would justify a new calculation of the *g* factor once they are
657 taken by a sufficient number of participants.

658 The underrepresentation of verbal skills may partly explain why men were found to
659 have a slightly higher *g* factor than women ($d = -0.13$). Another non-exclusive explanation may
660 be that male and female UK populations are unequally sampled in the UK Biobank, with
661 women representing 54.4% of the entire sample. Thus women with lower general intelligence
662 may have been oversampled compared to men with lower intelligence. Finally, participants
663 were born between 1934 and 1971 (median: 1950), a period when UK women may still have
664 had inferior higher education opportunities, and therefore fewer opportunities to fully develop
665 their intellectual potential. These three considerations suggest that the UK Biobank is not a
666 suitable database to reliably estimate sex differences in cognitive abilities, and potentially in
667 other phenotypes associated with cognitive ability.

668 We were limited when correcting for the socio-demographic imbalance in the UK
669 Biobank. Due to occupation coding constraints, we had to use the 2001 census data, instead of
670 the 2011 census data, and we only determine the occupation on census day of 71.5% of
671 participants. Moreover, we were limited by the number of variables on which we adjusted the
672 UK Biobank sample. Adjusting additional variables, such as years of education would have
673 improved the adjustment.

674

675 Finally, the *g* factor score was calculated from different subsets of tests and although
676 we took the first instance of a test, some tests were taken at different ages. Therefore, although
677 we attempted to provide a *g* factor measure of pre-aging adult intelligence, some test scores
678 may already be influenced by cognitive decline. One study reported that most UK Biobank
679 cognitive tests show reasonable stability over time except for the visual memory task (pairs-
680 matching; Lyall et al., 2016), while another study found declines in cognitive abilities before
681 65 years of age were small (Cornelis et al., 2019). Considering that the majority of participants
682 were 64 years or younger and that the median age was 60, our *g* factor measure likely reflects
683 pre-cognitive-decline intelligence scores.

684 The present study provides cognitive tests scores and a *g* factor score for UK Biobank
685 participants that are adjusted for age and relative to the UK population, as well as a *g* PGS for
686 UK Biobank individuals with neuroimaging data that explained 7.7% of the variance in the *g*
687 factor. The behavioral and genetic scores from this study will enable the simultaneous
688 investigation of the associations between the brain, genes, and intelligence, which are currently
689 rare in the present literature (Deary et al., 2021). Taken together, the present study offers robust
690 measures of intelligence that will foster homogeneity in intelligence research within the UK
691 Biobank and provides summary statistics and PGSs for future studies interested in examining
692 the genetic associations of intelligence with neuroimaging, behavioral, and environmental
693 measures.

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