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Mapping the genetic links of broad cognition and language to brain structure: A two-factor Genomic SEM analysis

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Research Article

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Abstract

Cognitive abilities share substantial genetic architecture, but it is unclear whether their genetic relationships with brain structure primarily reflect broad cognitive variation or domain-related components such as language. We used linkage disequilibrium score regression and Genomic Structural Equation Modeling to model correlated broad-cognition and language factors from 12 published cognitive GWAS. We first tested a frozen UK Biobank atlas of 114 imaging-derived phenotypes (66 hemisphere-specific cortical surface-area measures and 48 white-matter fractional-anisotropy measures), then prospectively triangulated the cortical results in 34 bilateral ENIGMA-3 surface-area GWAS. In UK Biobank, no direct cognition-versus-language brain covariance contrast survived within-family FDR correction, although broad cognition showed 12 cortical and 11 white-matter factor-specific FDR associations versus 2 cortical and 0 white-matter associations for language. In ENIGMA, 33/34 broad-cognition and 16/34 language associations survived the prespecified 68-test FDR. Two direct cortical contrasts survived the 34-region FDR: superior parietal cortex (cognition r_g = 0.197; language r_g=-0.012; P = 9.0×10^-5; q = 0.0031) and precuneus (cognition r_g = 0.251; language r_g = 0.074; P = 0.00185; q = 0.0315); superior parietal cortex also survived Bonferroni correction. Across 33 cortical regions shared by UK Biobank and ENIGMA, regional maps correlated r = 0.719 for cognition and r = 0.781 for language. Fixing the small Spelling residual variance to zero preserved every multiple-testing decision. Broad cognition therefore shows a highly distributed structural-brain genetic architecture, language a more selective pattern, and specific parietal regions show corrected evidence of stronger genetic coupling to broad cognition than to language.

Introduction

Individual cognitive tests are positively correlated at both phenotypic and genetic levels, motivating models of a broad general cognitive factor. Genome-wide analyses have likewise demonstrated extensive genetic sharing among diverse cognitive traits. De la Fuente et al. (2021) modeled seven UK Biobank cognitive tests and identified a broad dimension of genetic covariance, while Procopio et al. (2025) subsequently combined those seven measures with five GenLang reading- and language-related GWAS to construct a 12-indicator genomic-g model. At the same time, recent multivariate work has reinforced that cognition is not genetically unitary: reaction time, fluid reasoning, crystallized knowledge and language can show correlated yet distinguishable genetic architectures (Londono-Correa et al. 2026).

This distinction matters for imaging genetics. Cortical surface area and white-matter microstructure are heritable, highly polygenic phenotypes, and large UK Biobank and ENIGMA resources now provide genome-wide summary statistics for thousands of imaging-derived phenotypes (Elliott et al. 2018; Grasby et al. 2020; Smith et al. 2021). Multivariate analyses of cortical morphology have shown extensive genetic covariance among regions and have linked broad cognitive function particularly to a general surface-area factor (Grotzinger et al. 2023). Such findings suggest that many observed

cognition-brain genetic relationships may reflect distributed, domain-general architecture rather than isolated regional specificity.

Language provides an informative test of this problem because its genomic architecture is both strongly related to broader cognition and partly distinct from it. The GenLang Consortium meta-analyzed five quantitatively assessed reading- and language-related skills and reported significant SNP heritability across traits. A multivariate GenLang signal showed a genetic correlation of approximately 0.21 with surface area of the banks of the left superior temporal sulcus (STS), selected from a targeted set of language-relevant UK Biobank neuroimaging phenotypes (Eising et al. 2022). Thus, a language-brain genetic relationship is already established; the unresolved question is not whether language genetics relates to neuroanatomy, but whether a language-related genomic domain shows a systematically distinguishable structural-brain map when considered jointly with broader cognition.

The present study originated as an attempt to identify imaging phenotypes showing genetic specificity beyond a single genomic-g factor. Before extending that analysis, however, we audited the factor structure of the 12 cognitive GWAS. The single-factor model fit poorly relative to a correlated two-factor solution separating seven UK Biobank cognitive measures from five GenLang measures. We therefore pivoted prospectively to a more defensible question: across a frozen structural-imaging atlas, which phenotypes are genetically associated with broad UK Biobank cognition, with the GenLang language domain, or preferentially with one domain over the other?

We tested this question across two prespecified imaging families: 66 hemisphere-specific Desikan-Killiany cortical surface-area phenotypes and 48 tract-based spatial statistics (TBSS) fractional-anisotropy phenotypes. The primary endpoint was a formal cognition-versus-language factor-brain genetic covariance contrast for each imaging phenotype, corrected separately within the two frozen imaging families. Factor-specific genetic correlations were secondary. We additionally evaluated a prespecified Heywood-case sensitivity and descriptive bilateral/map-level coherence. Finally, before viewing any ENIGMA results, we froze a 34-region bilateral cortical surface-area analysis for external triangulation.

Methods

Study design and analysis freeze

The analysis used only GWAS summary statistics. The systematic imaging extension was frozen before viewing results, with a manifest hash of SHA-256 7391faa4732f529d032bc3af61dd08c4e87f7973314fb1b500b264c9234dbbe2. The frozen families comprised 66 Desikan-Killiany regional cortical surface-area phenotypes (BIG40 IDs 0649–0681 and 0683–0715; hemisphere TotalSurface measures excluded) and 48 TBSS fractional-anisotropy phenotypes (BIG40 IDs 1452–1499), for 114 brain phenotypes in total. Two phenotypes (IDP_1487 and IDP_1493) had been inspected in an earlier 14-IDP pilot and were flagged as pilot overlap; the remaining

atlas phenotypes were not used to select the extension. The atlas is therefore a systematic extension within the same BIG40 cohort, not an independent replication.

Cognitive GWAS inputs

The cognitive input set matched the 12 traits used by Procopio et al. (2025). Seven UK Biobank GWAS from de la Fuente et al. (2021) represented a broad cognitive block: Matrix Pattern Recognition (N = 11,356), Pairs Matching/Memory (N = 331,679), Reaction Time (N = 330,024), Symbol Digit Substitution (N = 87,741), Trail Making Test B (N = 78,547), Tower Rearranging (N = 11,263), and Verbal-Numerical Reasoning (N = 171,304). Five European-ancestry GenLang GWAS from Eising et al. (2022) represented the language block: Phoneme Awareness (N = 12,411), Nonword Reading (N = 16,746), Nonword Repetition (N = 12,828), Spelling (N = 17,278), and Word Reading (N = 27,180). The labels 'broad cognition' and 'language' refer to these indicator blocks and should not be interpreted as perfectly pure psychometric constructs.

Table 1
Cognitive GWAS indicators.

Factor block	Indicator	GWAS N
Broad cognition	Matrix Pattern Recognition	11,356
Broad cognition	Memory / Pairs Matching	331,679
Broad cognition	Reaction Time	330,024
Broad cognition	Symbol Digit Substitution	87,741
Broad cognition	Trail Making Test B	78,547
Broad cognition	Tower Rearranging	11,263
Broad cognition	Verbal-Numerical Reasoning	171,304
Language	Phoneme Awareness	12,411
Language	Nonword Reading	16,746
Language	Nonword Repetition	12,828
Language	Spelling	17,278
Language	Word Reading	27,180

Brain imaging GWAS inputs

Brain summary statistics came from the expanded UK Biobank BIG40 resource (Smith et al. 2021). The cortical family consisted of regional cortical surface-area measures based on the Desikan-Killiany

parcellation (Desikan et al. 2006), with N = 31,968 per phenotype in the combined BIG40 release used here. The diffusion family consisted of all 48 BIG40 tract-based spatial statistics (TBSS) mean fractional-anisotropy phenotypes (Smith et al. 2006), with N = 31,356 per phenotype. The use of one cortical parcellation and one FA atlas was intended to avoid allowing multiple near-equivalent measures of the same anatomy to dominate the testing family.

LD Score regression and harmonization

Summary statistics were harmonized to HapMap3 SNPs and analyzed using the GenomicSEM implementation of multivariable LD Score regression (LDSC) (Bulik-Sullivan et al. 2015; Grotzinger et al. 2019). European LD scores were used. For each brain phenotype, LDSC estimated the genetic covariance matrix across the 12 cognitive indicators plus that brain phenotype, together with the sampling covariance matrix used by Genomic SEM. This framework explicitly accommodates sampling covariance arising from sample overlap among GWAS, which is relevant because the broad-cognition GWAS and BIG40 imaging GWAS both draw from UK Biobank. Brain phenotypes with nonpositive or nonfinite LDSC SNP heritability were prespecified for exclusion; all 114 atlas phenotypes passed this criterion (observed h2 range 0.064–0.350).

Factor-structure audit

Before systematic brain mapping, we compared four models using the already-computed 12-trait genetic covariance structure: (i) one factor across all 12 indicators; (ii) correlated UKB-cognition and GenLang-language factors; (iii) a UKB seven-indicator one-factor model; and (iv) a GenLang five-indicator one-factor model. Models were estimated in GenomicSEM using diagonally weighted least squares and unit-variance factor identification. The 12-indicator one-factor model fit poorly (chi-square = 867.40, df = 54, CFI = 0.855, SRMR = 0.193, AIC = 915.40). The correlated two-factor model fit substantially better (chi-square = 575.86, df = 53, CFI = 0.907, SRMR = 0.128, AIC = 625.86), with latent r_g = 0.579 (SE = 0.038). The two-factor model still showed imperfect absolute fit and was therefore treated as a pragmatic, better-fitting representation rather than a definitive psychometric decomposition.

Table 2
Factor-structure audit.

Model	χ^2	df	CFI	SRMR	AIC
One factor, 12 indicators	867.40	54	0.855	0.193	915.40
Two correlated factors	575.86	53	0.907	0.128	625.86
UKB7 one factor	96.81	14	0.969	0.088	124.81
GenLang5 one factor	8.47	5	0.997	0.071	28.47

Two-factor brain models

For each brain phenotype, the broad-cognition factor was defined by the seven UK Biobank indicators and the language factor by the five GenLang indicators; both latent variances were fixed to one and their covariance was freely estimated. The brain phenotype variance was estimated. Two factor-brain genetic covariance parameters were then estimated: a for broad cognition and b for language. The primary regional statistic was the model-defined contrast diff := a - b. This is a direct test of the difference between the two unstandardized factor-brain genetic covariances; it is not inferred from whether one factor-specific association is significant and the other is not. Standardized factor-brain genetic correlations (r_g) were retained as secondary effect-size estimates.

Multiplicity and sensitivity analyses

Primary cognition-versus-language contrast P values were corrected using the Benjamini-Hochberg false discovery rate (BH-FDR; Benjamini and Hochberg 1995) separately within the prospectively frozen cortical (66 tests) and TBSS-FA (48 tests) families. Bonferroni correction within each imaging family and correction across all 114 contrasts were retained as stringent sensitivity criteria. Factor-specific association P values were secondary and were corrected jointly across two factors times the size of each imaging family (132 cortical tests; 96 TBSS tests). The unconstrained two-factor model was primary. Because the factor audit yielded a small, nonsignificant negative residual variance for Spelling (estimate − 0.0134, SE = 0.0231, P = 0.563), every brain model was repeated with the Spelling residual variance fixed to zero.

Descriptive map-level analyses

To assess anatomical coherence without creating additional discovery endpoints, we calculated descriptive left-right correlations across the 33 homologous cortical region pairs, sign concordance across those pairs, and spatial correlations between the broad-cognition and language r_g maps within cortex and TBSS. These statistics were not assigned inferential P values because regional estimates are genetically and anatomically correlated and therefore do not represent independent observations.

Prospectively frozen ENIGMA analysis

Before viewing ENIGMA results, we froze a 34-region bilateral Desikan-Killiany cortical surface-area analysis. We used the principal all-European ENIGMA-3 regional surface-area summary statistics from Grasby et al. (2020), selecting the release without adjustment for global surface area and without genomic-control correction to best match the UK Biobank regional-area discovery phenotypes and LDSC workflow. The same 12 cognitive GWAS, LDSC reference data, and two-factor GenomicSEM specification were applied to every ENIGMA region. The primary endpoint was the broad-cognition-versus-language factor-brain covariance contrast, with BH-FDR across all 34 contrasts and Bonferroni correction as a

stringent sensitivity criterion. Factor-specific ENIGMA associations were secondary and corrected jointly across 68 tests (34 regions × 2 factors). Because the public all-European ENIGMA release may include UK Biobank participants, this analysis is interpreted as external triangulation rather than fully independent replication.

Software, reproducibility, and ethics

All analyses were scripted and executed using R 4.4.1 and GenomicSEM version 0.0.5. Per-IDP LDSC objects, parameter tables, frozen manifests, analysis scripts, and result tables were retained to allow full audit of the workflow. All analyses used de-identified, published or access-controlled GWAS summary statistics and involved no new participant contact or individual-level data.

Results

Factor structure of the cognitive GWAS

The 12-indicator single-factor model did not provide an adequate representation of the genetic covariance matrix relative to the correlated two-factor alternative (Table 2). Moving from one factor to the two-factor model improved CFI by 0.052, reduced SRMR by 0.064, and reduced AIC by 289.54. The two latent factors remained substantially correlated (r_g = 0.579, SE = 0.038), supporting shared genetic architecture alongside meaningful domain structure. In the 114 subsequent brain models, the estimated cognition-language latent correlation was highly stable (mean r_g = 0.571; range 0.570–0.572).

Primary cognition-versus-language brain contrasts

All 114 brain phenotypes passed the prespecified positive-heritability criterion and yielded estimable two-factor models. No direct broad-cognition-versus-language covariance contrast survived within-family BH-FDR correction in either imaging family: 0/66 cortical surface-area phenotypes and 0/48 TBSS-FA phenotypes. The smallest cortical contrast P values occurred for left isthmus cingulate (P = 0.00247, q = 0.091), left frontal pole (P = 0.00277, q = 0.091), and left pars triangularis (P = 0.00503, q = 0.111), none of which met the prespecified $q < 0.05$ threshold. No TBSS contrast approached corrected significance.

Secondary factor-specific associations

In the prespecified secondary analysis, the broad-cognition factor showed 12 cortical and 11 TBSS associations surviving the joint factor-by-family FDR threshold, whereas the language factor showed 2 cortical and 0 TBSS associations. The strongest cortical broad-cognition associations included left precuneus (r_g = 0.120, P = 1.06×10^-4), left rostral middle frontal area (r_g = 0.128, P = 1.37×10^-4), left pars triangularis (r_g = 0.156, P = 1.40×10^-4), and right inferior parietal area (r_g = 0.142, P = 1.50×10^-4). The strongest white-matter broad-cognition associations included left anterior limb of the internal capsule (r_g = 0.141, P = 7.8×10^-6), right anterior limb of the internal capsule (r_g = 0.123, P = 1.23×10^-4), and left superior longitudinal fasciculus (r_g = 0.130, P = 2.02×10^-4).

The two cortical language associations surviving the same secondary FDR scheme were left banks of the STS ($r_g = 0.208$, $P = 6.57\times10^{-4}$) and left frontal pole ($r_g=-0.274$, $P = 0.00212$). The positive left-STS estimate closely matches the previously reported GenLang association with this phenotype ($r_g \approx 0.21$; Eising et al. 2022), providing a useful positive-control observation rather than a novel regional discovery. Importantly, unequal numbers of factor-specific significant associations do not themselves establish a statistically significant difference between factors; the direct covariance contrasts remained the primary inferential test and were null after correction.

Table 3
Frozen atlas decision counts.

Imaging family	Direct domain contrasts, FDR	Broad-cognition associations, FDR	Language associations, FDR
Cortical surface area (n = 66)	0	12	2
TBSS FA (n = 48)	0	11	0

Map-level coherence

The cortical factor-specific maps showed substantial bilateral coherence. Across 33 homologous Desikan-Killiany pairs, left-right correlations were $r = 0.735$ for broad cognition and $r = 0.825$ for language, with same-sign estimates in 30/33 pairs for each map. By contrast, the broad-cognition and language maps were only moderately correlated with one another (cortical $r = 0.376$; TBSS $r = 0.412$). These values are descriptive and are not treated as independent-region hypothesis tests.

Sensitivity analysis

Fixing the Spelling residual variance to zero reproduced the complete UK Biobank multiple-testing decision pattern: 0 corrected cortical domain contrasts, 0 corrected TBSS domain contrasts, 12 cortical broad-cognition associations, 11 TBSS broad-cognition associations, 2 cortical language associations, and 0 TBSS language associations. The same sensitivity analysis also preserved every ENIGMA decision: 2/34 direct contrasts at FDR $q < 0.05$ (1/34 Bonferroni), 33/34 cognition associations at FDR $q < 0.05$ (29/34 Bonferroni), and 16/34 language associations at FDR $q < 0.05$ (1/34 Bonferroni). Across ENIGMA regions, the maximum absolute change was < 0.000012 for cognition r_g and < 0.000675 for language r_g. The negative observed-variance warnings present in the unconstrained ENIGMA models disappeared after fixing the Spelling residual to zero, while the covariance-matrix smoothing warning remained; substantive estimates and conclusions were unchanged.

ENIGMA analysis

All 34 ENIGMA cortical regions had positive SNP heritability (range $h^2=0.125–0.346$) and yielded estimable two-factor models. Broad cognition showed positive genetic correlations in 34/34 regions; 33/34 survived the prespecified 68-test FDR and 29/34 survived Bonferroni correction. Language showed positive genetic correlations in 32/34 regions; 16/34 survived the 68-test FDR and only banks of

the superior temporal sulcus survived Bonferroni correction. Four direct cognition-versus-language contrasts were nominally significant, and two survived the prespecified 34-region FDR (Table 4). Superior parietal cortex showed the strongest domain contrast: broad cognition r_g = 0.197 versus language r_g=-0.012 (P = 9.0×10^-5, q = 0.0031), which also survived Bonferroni correction (adjusted P = 0.0031). Precuneus also showed stronger coupling to cognition (r_g = 0.251) than language (r_g = 0.074; P = 0.00185, q = 0.0315), although its Bonferroni-adjusted P was 0.0629. Thirty of 34 covariance contrasts favored cognition over language. Mean factor-specific genetic correlations across the 34 regions were 0.181 for cognition and 0.115 for language. Across the 33 regions shared with the hemisphere-resolved UK Biobank cortical atlas, ENIGMA and UK Biobank regional maps were strongly concordant (Pearson r = 0.719 for cognition and r = 0.781 for language). These map-level correlations are treated as descriptive because cortical regions are not independent and the ENIGMA release may overlap UK Biobank. Mean model fit across ENIGMA regions was CFI = 0.900 and SRMR = 0.121.

Table 4
ENIGMA regions with cognition-versus-language contrasts surviving FDR correction.

Region	Cognition r_g	Language r_g	Contrast P	FDR q	Bonferroni P	Sensitivity q
Superior parietal	0.197	-0.012	9.04e-05	0.0031	0.0031	0.0032
Precuneus	0.251	0.074	0.00185	0.0315	0.0629	0.0323

Discussion

The principal finding is that cognition and language show overlapping but non-identical neurogenetic architectures. In the frozen 114-phenotype UK Biobank discovery atlas, no individual cognition-versus-language brain covariance contrast survived correction. However, the prospectively frozen ENIGMA cortical triangulation sharpened this picture: superior parietal cortex and precuneus showed corrected evidence of stronger genetic coupling to broad cognition than to language, with superior parietal cortex surviving Bonferroni correction. These findings therefore refine, rather than overturn, the conservative UK Biobank result: domain differentiation appears limited region by region, but reproducible parietal exceptions emerge when cortical surface area is tested in a bilateral ENIGMA framework.

The factor-specific maps were highly structured. Broad cognition showed a distributed pattern of corrected associations in both cortical surface area and white-matter FA in UK Biobank, and this cortical ubiquity was even clearer in ENIGMA, where 33 of 34 regions survived the prespecified factor-specific FDR. Language associations were more selective: 16 of 34 ENIGMA regions survived FDR and only banks of the superior temporal sulcus survived Bonferroni correction. This asymmetry should not be conflated with a global statistical test of one factor being stronger than the other, but it supports the interpretation that broad cognition is coupled to a more spatially pervasive structural-brain genetic architecture.

The language findings provide an internal validity check. In the UK Biobank atlas, the positive genetic correlation between language and left banks-of-STS surface area ($r_g = 0.208$) closely matched the approximately 0.21 correlation previously reported by Eising et al. (2022). In ENIGMA, the bilateral banks-of-STS association was again prominent (language $r_g = 0.276$, $P = 4.9\times10^{-5}$) and was the only language association surviving Bonferroni correction across the 68 factor-specific tests. Because this relationship was already reported using GenLang-related analyses, it is not a novel discovery here; rather, its recovery supports the validity of the present pipeline.

Several features argue against interpreting the broader cognition pattern as a collection of isolated false-positive regions. The UK Biobank cortical cognition map was strongly bilaterally coherent, with a left-right regional correlation of 0.735 and same-sign effects in 30 of 33 homologous pairs. More importantly, the frozen ENIGMA and UK Biobank cortical maps showed strong spatial correspondence across 33 shared regions (Pearson $r = 0.719$ for cognition and $r = 0.781$ for language). The two corrected ENIGMA domain contrasts were also anatomically consistent with the UK Biobank hemisphere-specific estimates: both precuneus hemispheres and both superior-parietal hemispheres showed positive cognition and weak or negative language associations, with nominal direct contrasts in the same direction. Because the public ENIGMA release may include UK Biobank participants, these observations are best viewed as convergent triangulation rather than independent replication.

The study has important limitations. First, the broad-cognition and language labels reflect heterogeneous GWAS indicator blocks rather than perfectly matched psychometric batteries. The UK Biobank cognitive measures were collected in middle-to-older adulthood and varied greatly in sample size, whereas the GenLang traits were meta-analyzed across younger cohorts and instruments. Second, the correlated two-factor model improved substantially over a single genomic-g model but did not achieve perfect absolute fit; ENIGMA brain models averaged CFI = 0.900 and SRMR = 0.121. Third, GenomicSEM reported covariance-matrix smoothing warnings in every ENIGMA model. The unconstrained models also showed negative observed-residual warnings, but these disappeared when the small Spelling residual was fixed to zero and every multiple-testing decision was preserved, arguing against substantive dependence on that Heywood feature. Fourth, the public ENIGMA all-European release may include UK Biobank participants, limiting claims of independence. Fifth, the descriptive map-level correlations do not account for anatomical dependence among cortical regions and should not be interpreted as inferential replication statistics.

The prospectively frozen ENIGMA analysis materially strengthens the cortical component without changing the discovery hypothesis after the fact. Its value lies in three convergent observations: a nearly ubiquitous broad-cognition cortical signal, recovery of the established banks-of-STS language association, and corrected parietal domain contrasts that align directionally with the frozen UK Biobank atlas. A fully independent ENIGMA-only release excluding UK Biobank would remain the strongest replication test if such summary statistics become available, but the current triangulation already demonstrates that the principal spatial architecture is not unique to the hemisphere-resolved BIG40 analysis framework.

In conclusion, broad cognition and language were genetically correlated but better represented as distinguishable latent domains than as a single genomic-g factor. Across a frozen 114-phenotype UK Biobank structural-brain atlas, broad cognition showed a substantially more distributed factor-specific association pattern than language, although no direct regional domain contrast survived correction. Prospectively frozen ENIGMA cortical triangulation reproduced the distributed cognition architecture, showed strong map-level concordance with UK Biobank, and identified corrected cognition-greater-than-language contrasts in superior parietal cortex and precuneus. Together, these findings support a largely shared structural-brain genetic architecture with selective parietal differentiation between broad cognition and language.

Declarations

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Competing interests

The author declares no competing interests and has no relevant financial or non-financial interests to disclose.

Author contributions

Baptiste Dumoulin conceived and designed the study, curated the datasets, developed and executed the analyses, interpreted the results, prepared the figures and tables, wrote the manuscript, and approved the final version.

Data availability

This study analyzed published or access-controlled GWAS summary statistics from UK Biobank/de la Fuente et al. (2021), GenLang/Eising et al. (2022), the Oxford BIG40 resource (Smith et al. 2021), and ENIGMA-3 (Grasby et al. 2020). Access to the original summary statistics is subject to the terms of the respective data providers and consortia; raw ENIGMA summary statistics are therefore not redistributed. Non-restricted derived ENIGMA result tables supporting the manuscript are provided as Online Resources 1 and 2. Additional derived tables will be deposited with the analysis code in a persistent public repository during peer review, and the permanent identifier will be added to the manuscript before publication.

Code availability

Custom R and PowerShell scripts used for data harmonization, LDSC, Genomic SEM, multiplicity correction, sensitivity analyses, and figure generation are available from the corresponding author during peer review and will be archived in a persistent public repository (OSF or Zenodo), with a permanent identifier added before publication.

AI use declaration

OpenAI ChatGPT (GPT-5.6 Sol) was used as an AI-assisted tool for code drafting and debugging, workflow organization, manuscript structuring, and language editing. All analyses were executed locally by the author, and all code, statistical outputs, references, interpretations, and manuscript text were reviewed and verified by the author. The author takes full responsibility for the submitted work.

Ethics approval

Not applicable. This secondary analysis used de-identified aggregate GWAS summary statistics from previously approved studies and involved no new participant recruitment or individual-level data.

Consent to participate

Not applicable.

Consent to publish

Not applicable.

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Figures

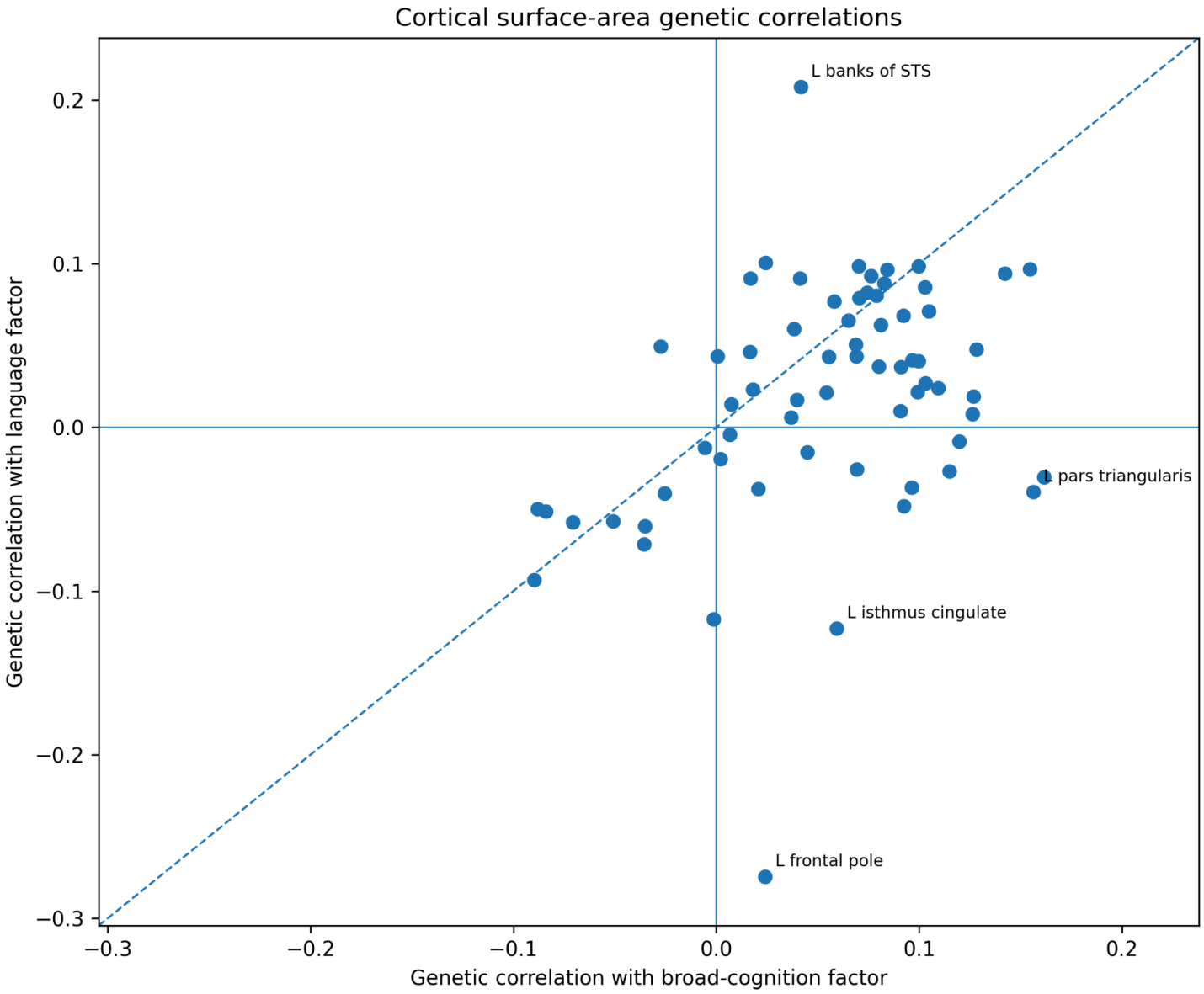


Figure 1

Cortical surface-area genetic correlations with the broad-cognition and language factors. The dashed diagonal denotes equality of the two standardized genetic-correlation estimates and is not a significance boundary. Labels are restricted to the two language FDR hits and the three smallest raw domain-contrast P values. No individual direct domain contrast survived the prespecified cortical FDR correction.

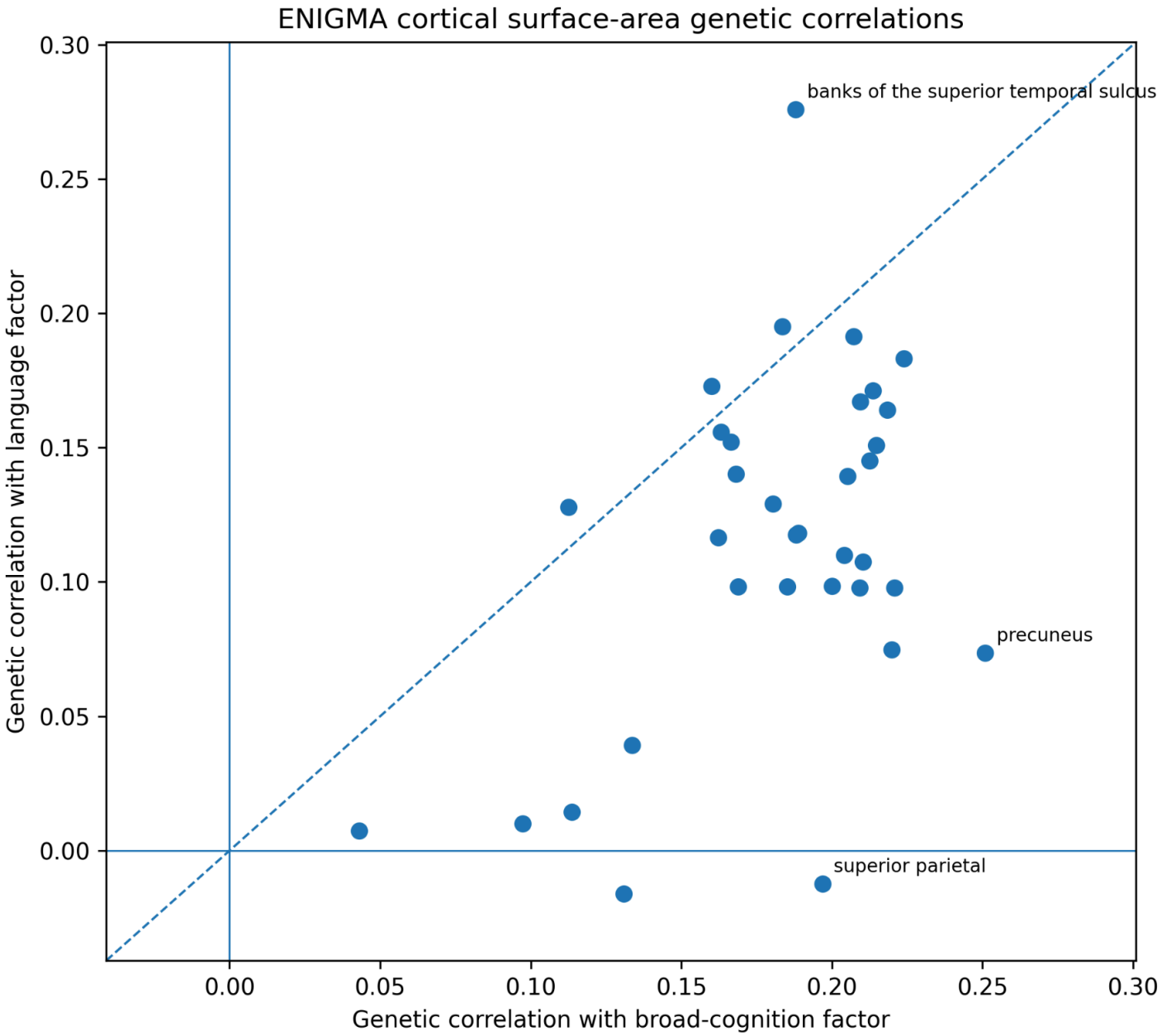


Figure 2

ENIGMA cortical surface-area genetic correlations with the broad-cognition and language factors. The dashed diagonal denotes equality of the two standardized genetic-correlation estimates and is not a significance boundary. Superior parietal cortex and precuneus survived the prespecified 34-region FDR for the direct cognition-versus-language covariance contrast; banks of the superior temporal sulcus was the only language association surviving Bonferroni correction across the 68 factor-specific tests.

Supplementary Files

This is a list of supplementary files associated with this preprint. Click to download.

- ENIGMA34TWOFACTORSUMMARY.csv
- ENIGMA34TWOFACTORALLRESULTS.csv