

Supporting Information for
Genetic Effects on Structural and Functional Properties of
Sensorimotor-Association Axis of Cortical Organization are
Selectively Distinct.

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Figures S1 to S4

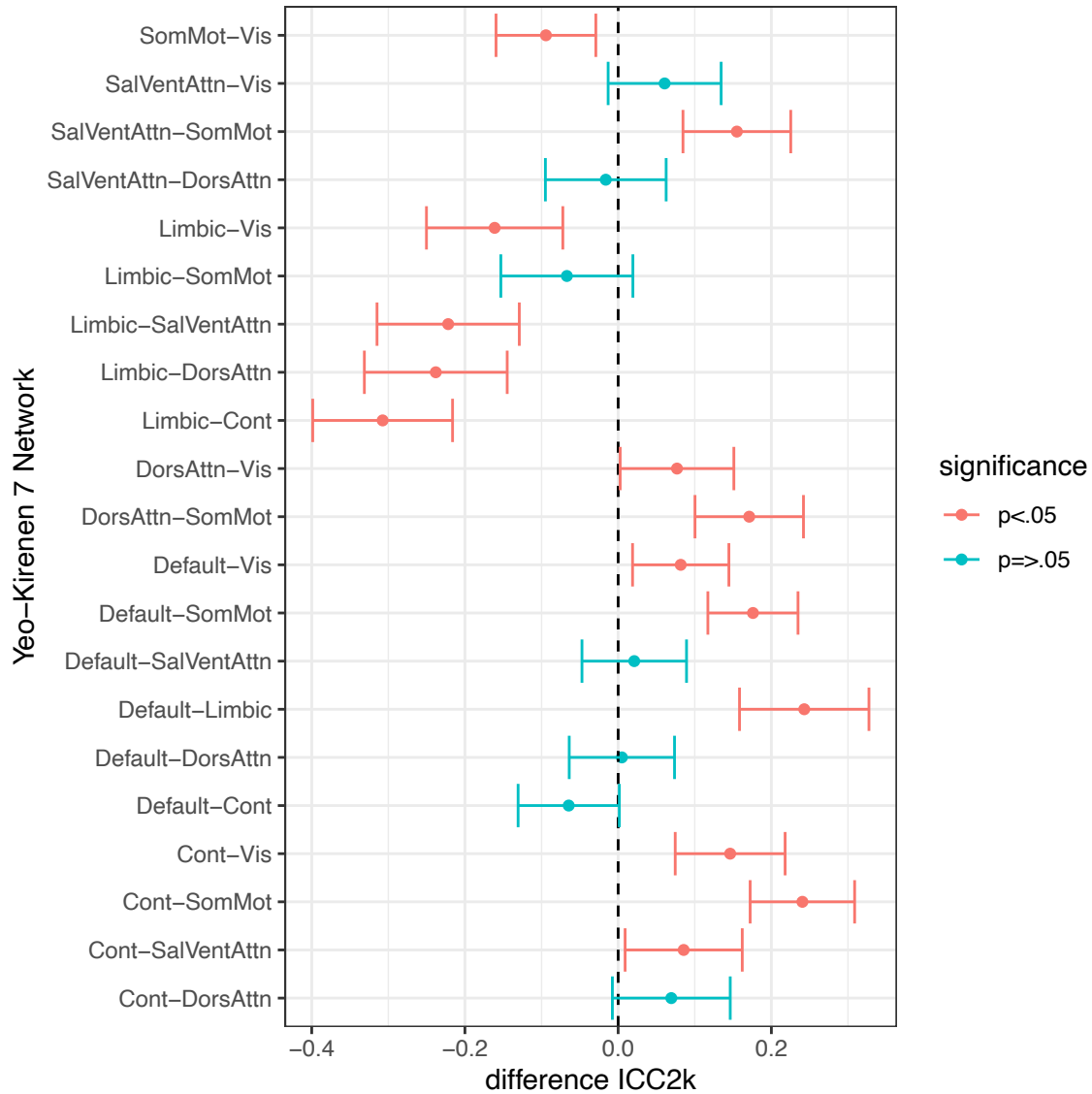


Figure S1. Heterogeneity of parcel-wise S-A measurement error across cortical networks. Differences between averaged parcel-wise inter-individual differences in S-A functional loadings across functional network pairs. The colours indicate the significance of the difference obtained during post-hoc comparisons via Tukey's Honest Significant Difference testing. Note that negative differences indicate that the first network (e.g., SomMot) of a pair (e.g., SomMot-Vis) displays, on average, lower inter-individual variance compared to the second network of the pair (e.g., Vis).

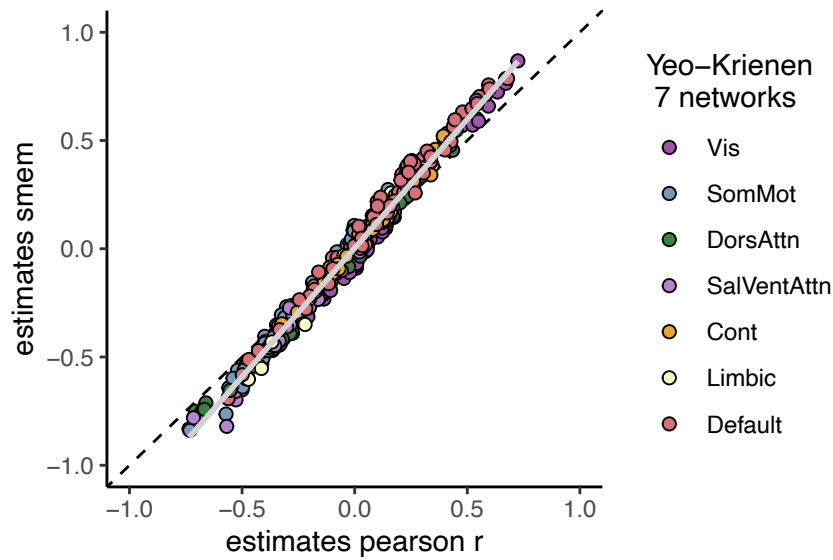


Figure S2. *The structural Measurement Error Model de-attenuates downward biases.* The scatter plot represents the relationship between correlations between regional functional gradient loadings and geodesic distance estimated following the classic Pearson correlation approach and the Structural Measurement Error Model (SMEM) approach. The grey line represents the deviation from the expected relationship between the two approaches under no estimated difference. As can be seen, negative and positive downward biases tend to be de-attenuated.

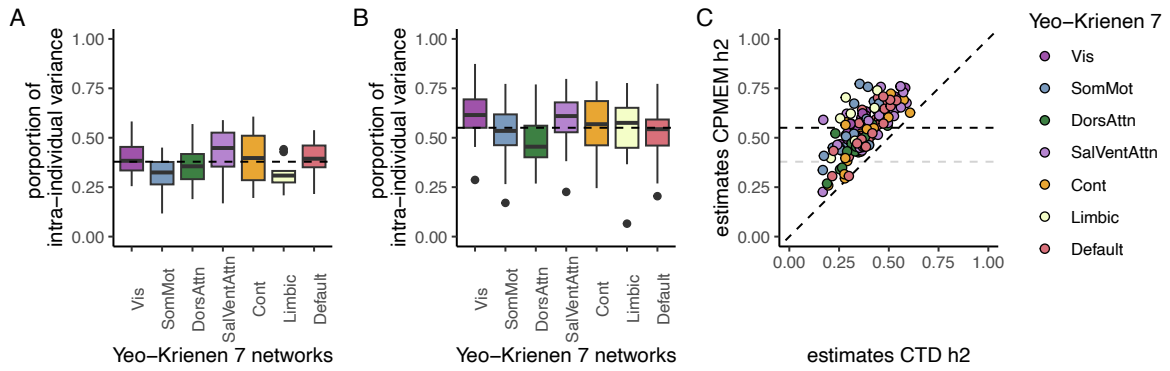
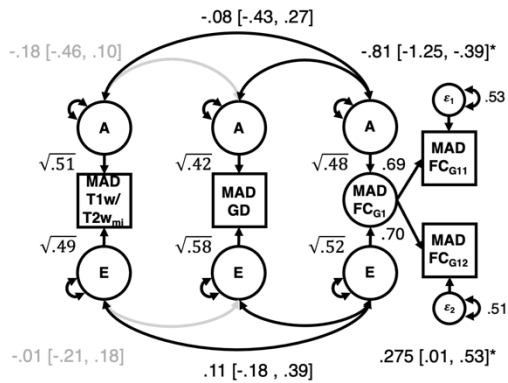


Figure S3. *Univariate twin AE models accounting for measurement error boost heritability estimation.* Parcel-wise twin heritability (h^2_{twin}) estimates for models with good fit indices. **A** Box plot of the h^2_{twin} stratified per Yeo-Krienen 7 functional networks. **B** Box plot of the h^2_{twin} stratified per Yeo-Krienen 7 functional networks obtained from the model accounting for inter-individual differences. Note that the mean of the heritability is higher. **C** scatter plot showing the increase of the h^2_{twin} estimate per parcel for parcels that had good fit indices in both models.

A Multivariate model for overall within-individual S-A axis MAD accounting for ICV



B Multivariate model for S-A axis ρ similarity indices accounting for ICV

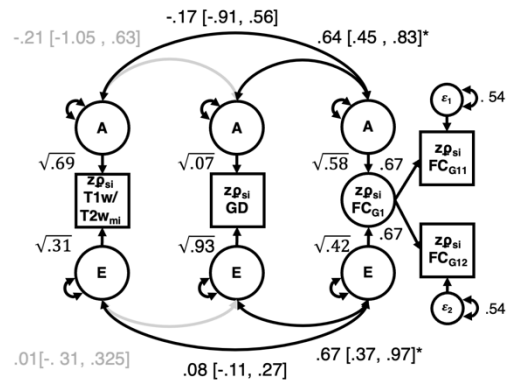


Figure S4. Association between MAD scores and ρ similarity indices are robust to intra-cranial value as a possible confounder. Simplified graphical representation of the multivariate twin-informed structural equation model (SEM) for overall within-individual median absolute deviations (MAD) and ρ similarity indices after regressing out ICV as a covariate from each S-A property. Note the minimal impact of ICV on estimates of interest. *Notes on measurement model:* Squares represent the measured phenotypes; The circle is the latent component; the double-headed arrows within the circle represent the variance associated with the latent components; one-headed arrows are the paths (here, all set to 1). double-headed arrows between circles represent covariances; Path coefficients for the measurement error model are estimate

