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INTRODUCTION

- Functional connectivity is a heritable trait.
- Genetic factors can influence more than one trait at once.
- We wanted to map shared genetic influences in the human functional connectome.

METHODS

- Dataset:** 653 subjects from extended families of Mexican American ancestry (GOBS study).
- Imaging data:** rs-fMRI using a gradient-EPI BOLD sequence (TE/TR = 30/3,000 ms; flip angle = 90 ; isotropic 1.72 mm²) over 7.5 minutes. Subjects were instructed to lie with their eyes open and try not to fall asleep.
- Data processing:** functional image processing done using the NIAK software (v.7.2.2.0)
- Analysis:** Genetic analyses, covarying for age, sex and FD, carried out using the SOLAR software. Clustering performed using HAC-Ward in R (v. 3.3.0). All results corrected using FDR.
- Participants provided written informed consent, the study was approved by IRBs at the participating institutions.

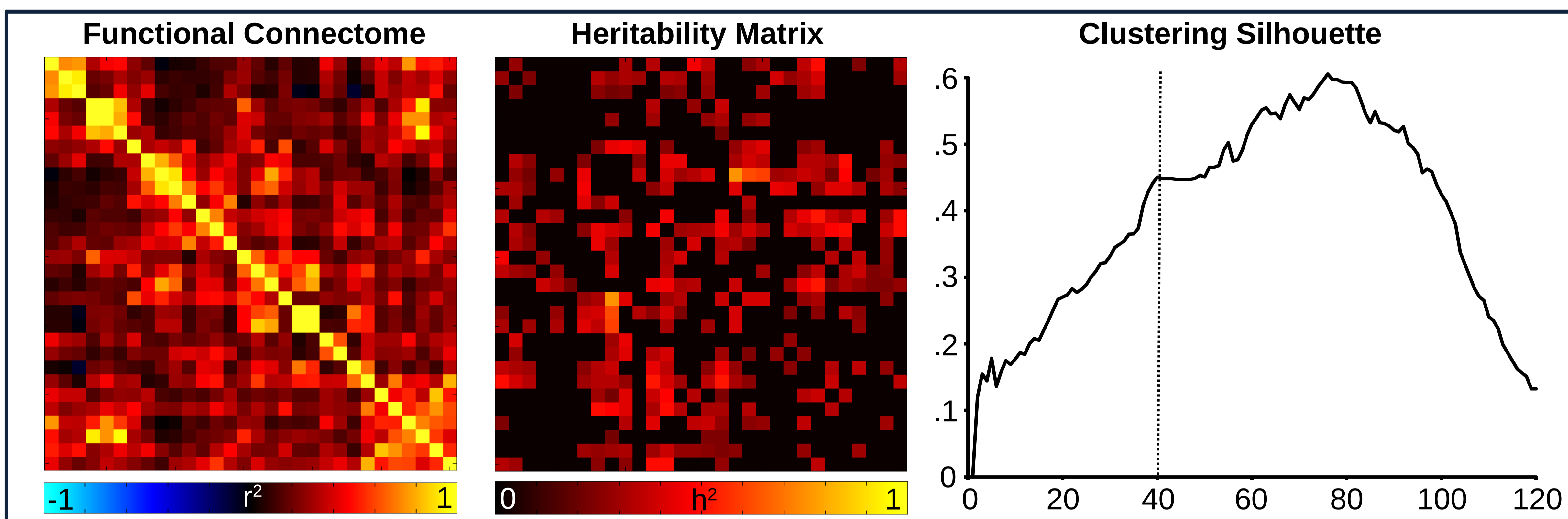
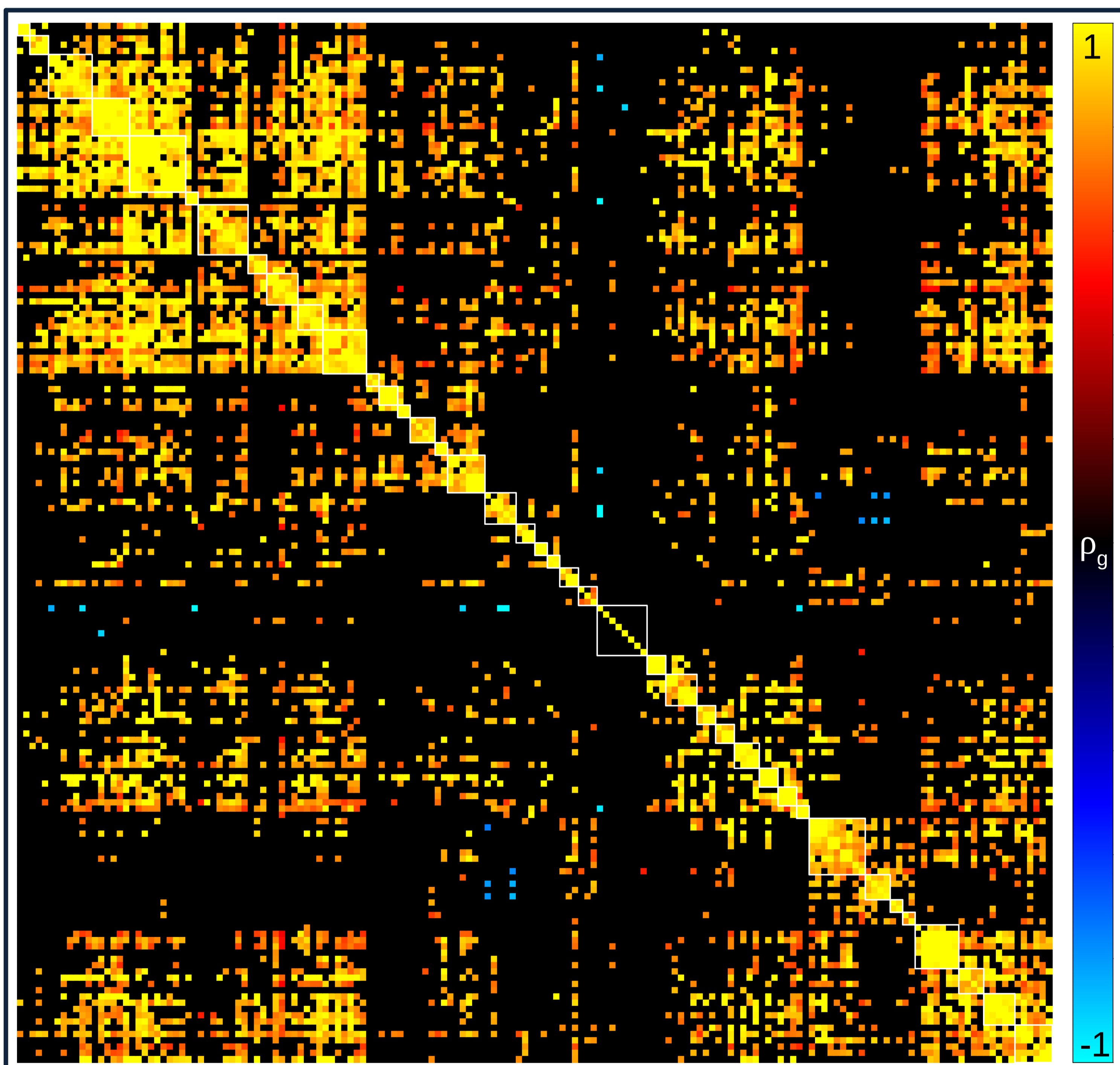


Figure 1. Matrices of (A) average functional connectivity, (B) heritability and (C) silhouette analysis of the genetic clustering of heritable functional connections.

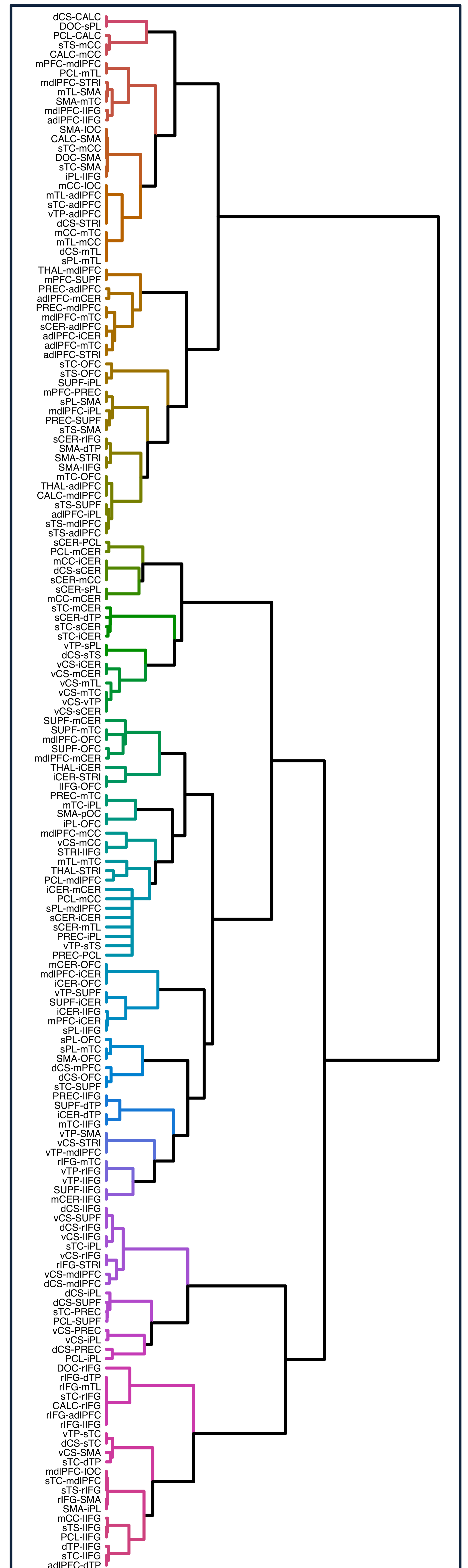


Results

- Genetic correlations are strong: many pairs of connections exhibit full pleiotropy.
- Shared genetic influences are widespread: 22% of possible genetic correlations are significant.
- Genetic correlations are also found between clusters of shared genetic influence.

Figure 2. Matrix of significant genetic correlations among heritable functional connections. 40 clusters are highlighted on the diagonal.

Figure 3. Dendrogram of the hierarchical clustering of heritable functional connections. Branches are colored according to the 40 cluster threshold.



CONCLUSIONS

- The same genetic factors influence functional connections both within and between resting-state networks.
- Genetic liability to common disorders might involve groups of connections under shared genetic influences.
- Negative genetic correlations often involve the cerebellum.

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