

Supplementary Information

Structural covariance networks are coupled to expression of genes enriched in supragranular layers of the human cortex

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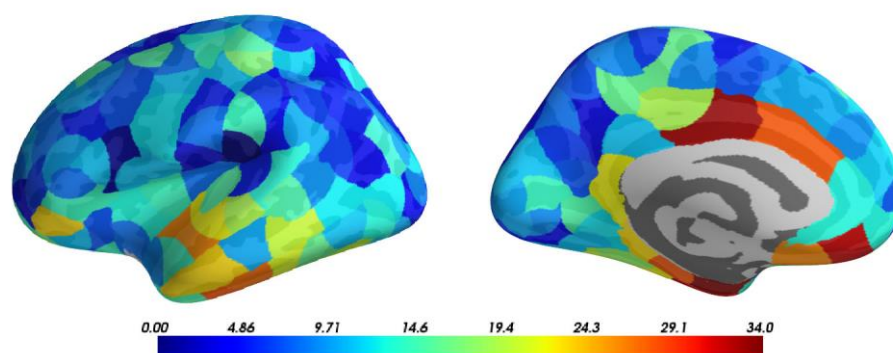


Figure S1: Number of AIBS samples in each cortical region.

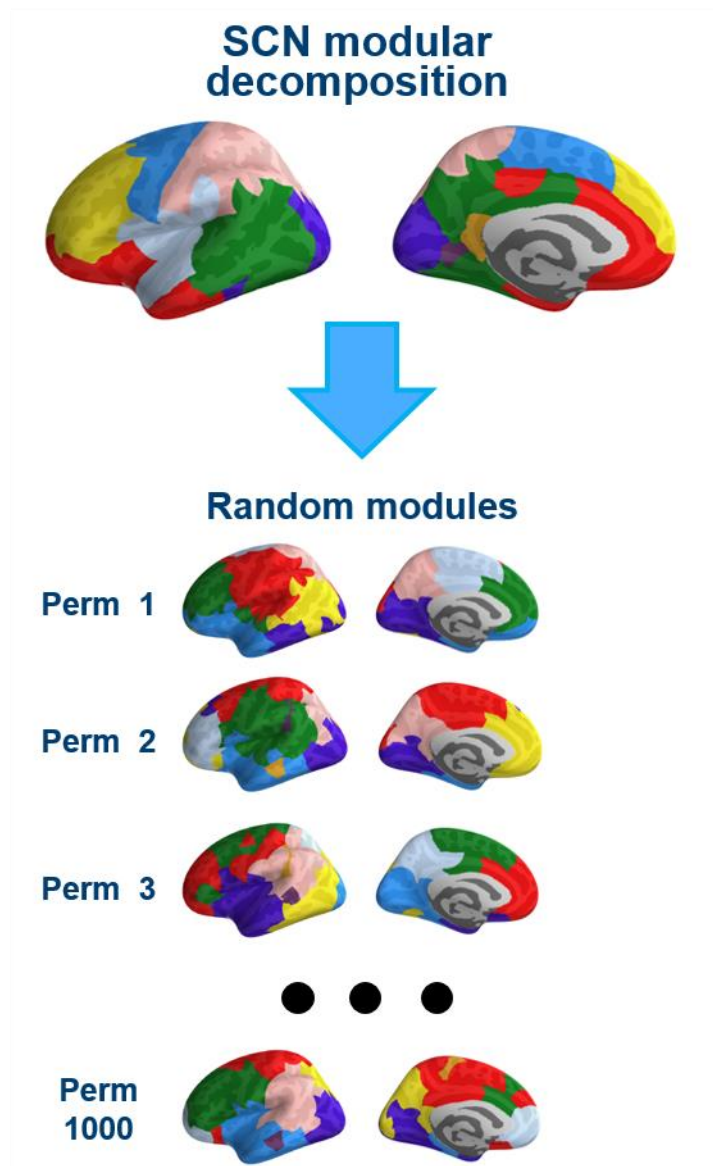


Figure S2: Random modular communities that preserve the number and size of modules, as well as the spatial contiguity of the empirical community partition.

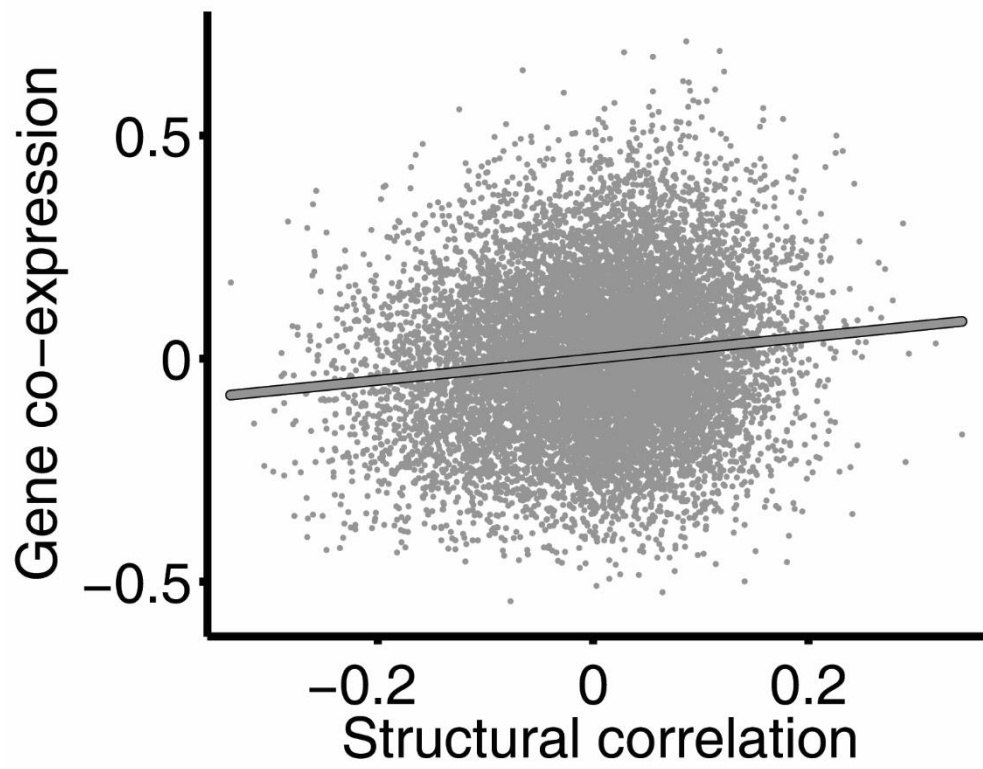


Figure S3: Scatterplot of gene co-expression versus structural covariance after regressing out the effect of the inter-regional distance.

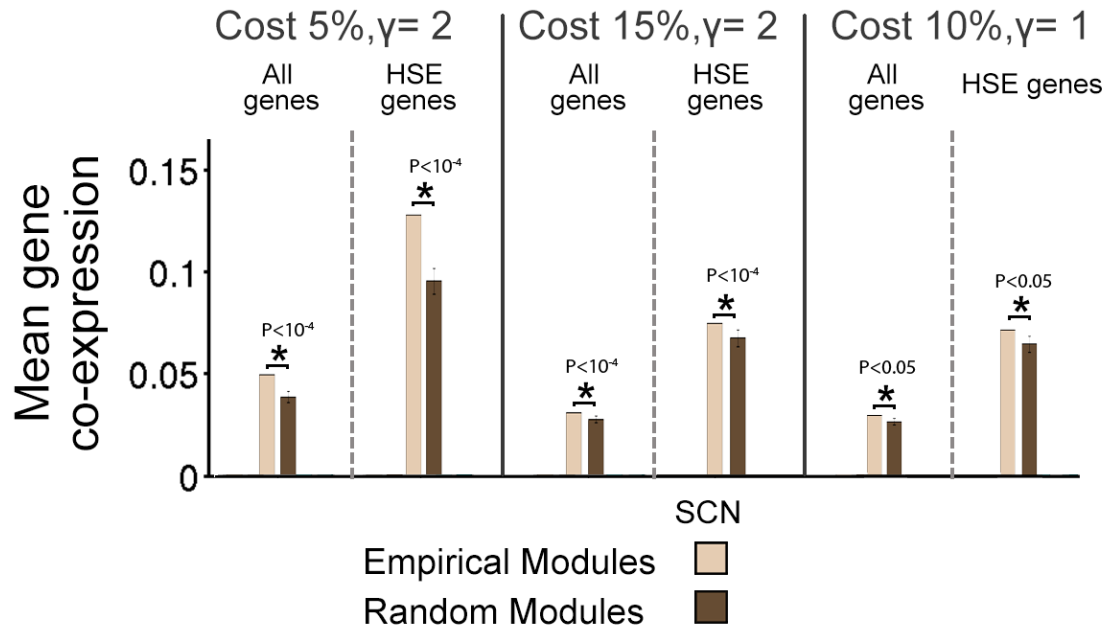


Figure S4: Mean gene co-expression between nodes located in the same SCN module for the empirical modules (light colors) and the random null modules (dark colors). Results replicated for different SCN costs (5%, 10% and 15%) and modularity resolution parameters ($\gamma=1$ and $\gamma=2$).

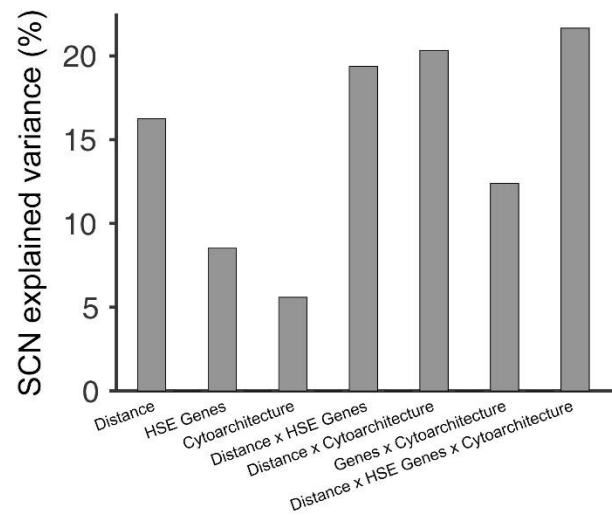


Figure S5: HSE gene expression has effects on structural covariation that are additive to the effects of connection distance. First column represents the SCN variance explained (R^2) by inter-regional distance using the log value of the inter-regional distance. Second and third column show the SCN variance explained by HSE gene expression and VE. The rest of the columns display the SCN variance explained by a linear multiple regression using combinations of variables.

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