Supporting Information

Goyal and Raichle 10.1073/pnas.1303453110

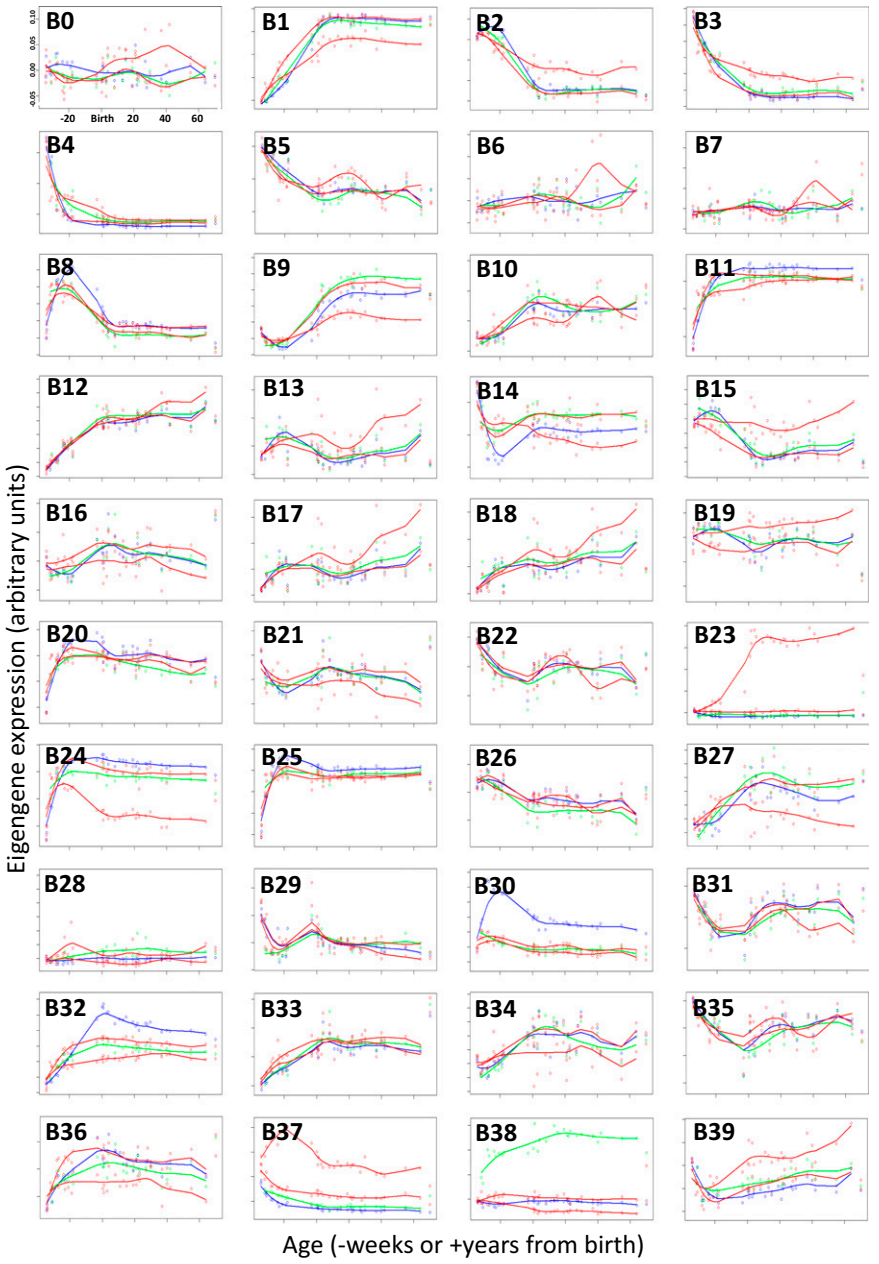

Fig. S1. Eigengene expression of all 40 clusters in the BrainSpan study after weighted gene coexpression network analysis (WGCNA). Dots represent actual eigengene expression values; lines are smoothed cubic splines. Expression is split regionally for the cortex (blue), striatum (green), thalamus (orange), and cerebellum (red).

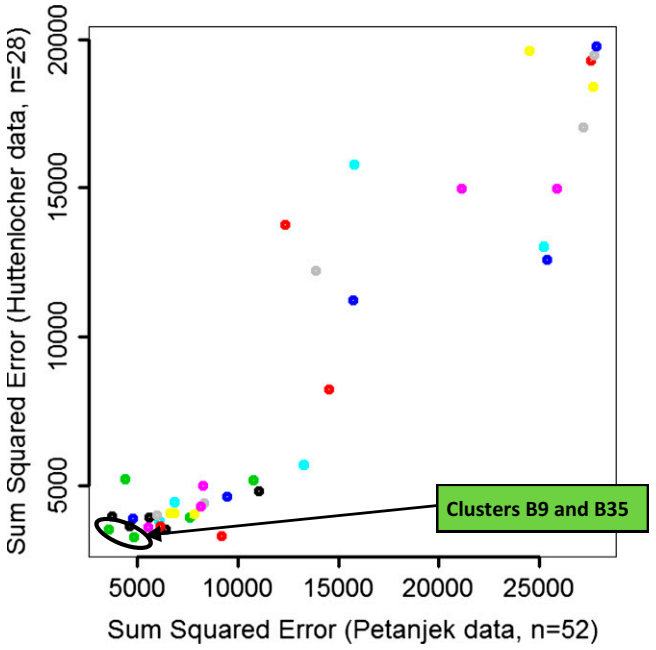

Fig. S2. Fit of estimated synaptic density for all 40 eigengenes using *Growth Rate* set to synaptic growth gene expression rather than to eigengene B1. Accuracy remains optimal when estimating *Elimination Rate* in model A with eigengenes B9 and B35 when *Growth Rate* is set to the average expression of synaptic growth genes, rather than to eigengene B1 (Fig. 3*A*). Again, B35 better fits the data of Petanjek et al. (1), whereas B9 better fits the data of Huttenlocher and Dabholkar (2), although the differences between the two are slight.

1. Petanjek Z, et al. (2011) Extraordinary neoteny of synaptic spines in the human prefrontal cortex. *Proc Natl Acad Sci USA* 108(32):13281–13286.
2. Huttenlocher PR, Dabholkar AS (1997) Regional differences in synaptogenesis in human cerebral cortex. *J Comp Neurol* 387(2):167–178.

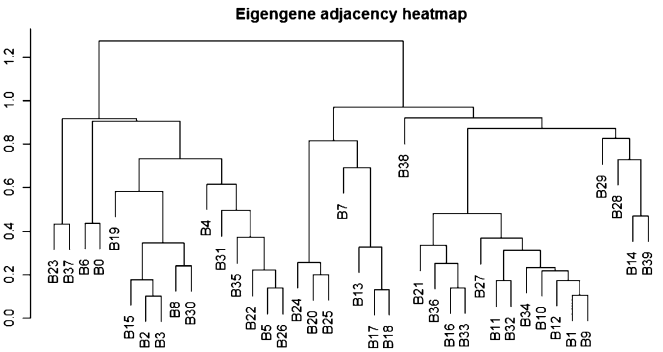

Fig. S3. Relationships among the 40 eigengenes derived from WGCNA of the BrainSpan study. Using plotEigengeneNetworks in the WGCNA R package, the correlational relationship among the 40 eigengenes of the BrainSpan data were determined and plotted on a dendrogram.

Other Supporting Information Files

Table S1 (DOCX)
Table S2 (DOCX)
Table S3 (DOCX)
Table S4 (DOCX)