Regional Brain Hypometabolism Is Unrelated to Regional Amyloid Plaque Burden

Andre Altmann[1], Bernard Ng[1], Susan Landau[2], William Jagust[2], Michael D Greicius[1] for the Alzheimer's Disease Neuroimaging Initiative

Author affiliations:

1 FIND lab, Department of Neurology and Neurological Sciences, Stanford University, Stanford California, USA

2 Helen Wills Neuroscience Institute, University of California, Berkeley, Berkeley, California, USA

Figure S1: Cortex-wide changes in imaging biomarker intensities with different diagnosis. After correcting for age, sex, ICV, APOE-ε4 carrier status, and education, compared to healthy controls (HC), MCIs show reduced gray matter density (GM; left), reduced glucose metabolism (FDG; middle), but increased amyloid deposition (florbetapir; right) throughout the cortex.

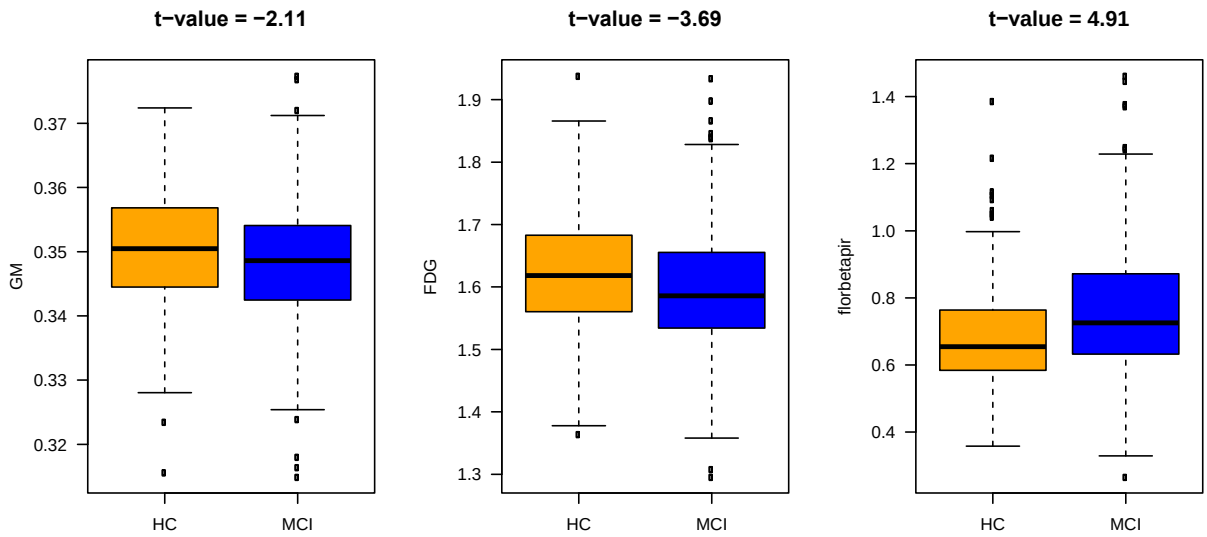


Figure S2: Overview of association results. The ROIs of interest are grouped by the five lobes. The ribbons in the center of the plot connect the ROIs belonging to the vDMN (blue) and the dDMN (light blue). The histogram in the innermost layer depicts the size for each ROI. The following three layers, from inward to outward, depict the association of regional florbetapir SUVR, FDG SUVR and gray matter with the current diagnosis. Each layer depicts the $-\log_{10}$ P-value of the association on the y-axis, black dots indicate significance after multiple testing correction ($P < 1.24\text{x}10^{-4}$), gray dots indicate nominal significance ($P \leq 0.05$) and white dots no significance. In addition, significant results are highlighted using a red background color: darker colors indicate stronger associations. The following three layers of blocks summarize the results for the regional association of amyloid plaque deposition and metabolism. The blocks represent, from inward to outward, significant ($P < 1.24\text{x}10^{-4}$) associations between regional amyloid and metabolism, significant after additional correction for global amyloid, significant in the permutation test. The color scheme for the first two rows of blocks is blue for negative associations and red for positive associations. In the third row purple blocks indicate the significant local association. Darker colors indicate stronger effects. Finally, boxes spanning the last three layers highlight ROIs with a significant association between global amyloid and regional metabolism.

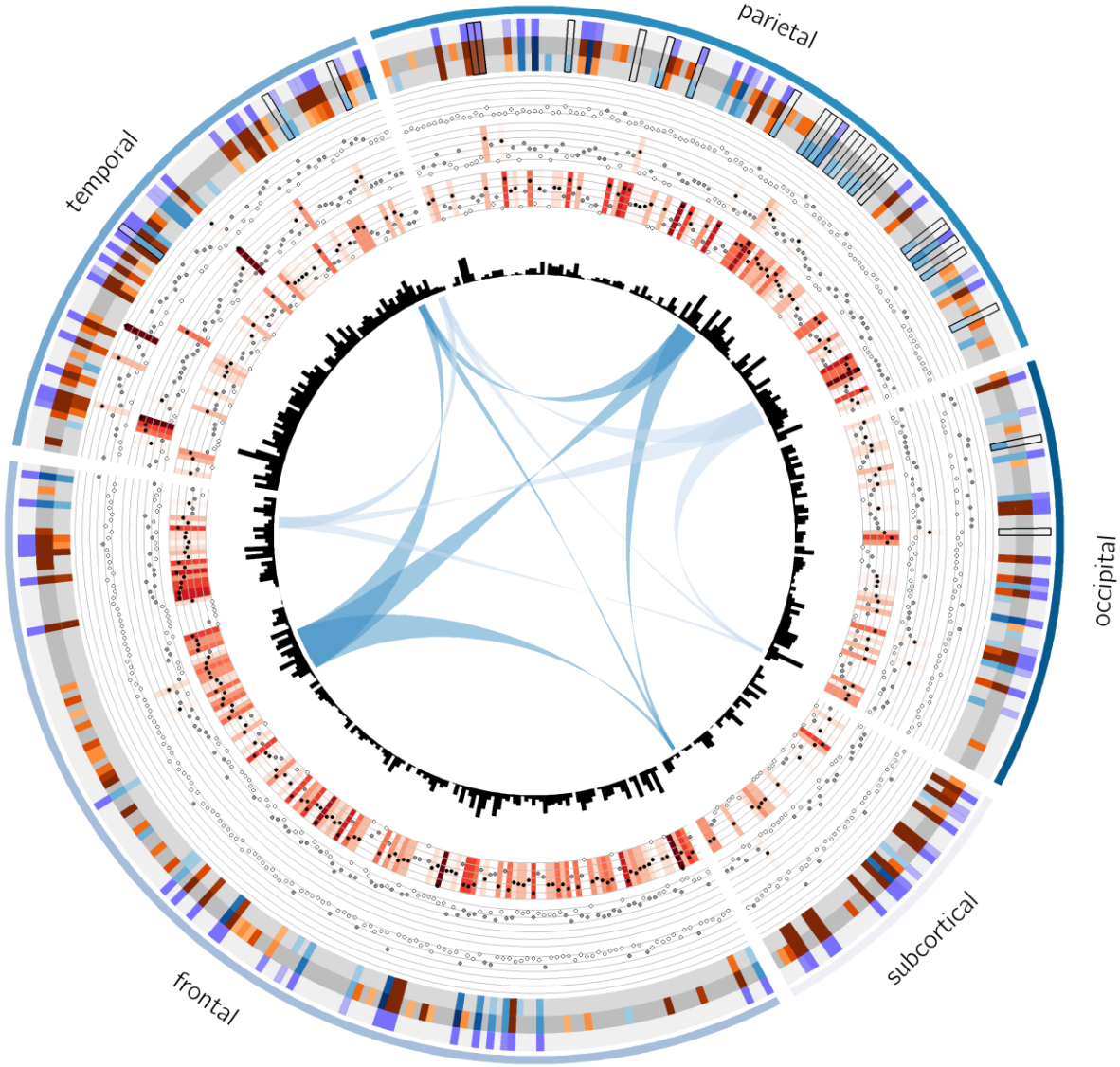

parietal
occipital
subcortical
frontal
temporal

Figure S3: Correlation of global amyloid and CSF Aβ. Scatter plot between global amyloid levels in the cortex (x-axis) and CSF Aβ levels (y-axis). Black points correspond to healthy subjects and blue points to MCI subjects. The red dashed horizontal line marks the 192 pg/ml CSF Aβ threshold below which CSF biomarker levels are considered abnormal (Shaw *et al.*, 2009) and the grey vertical dashed line marks the threshold beyond which an amyloid scan is considered amyloid positive (see methods).

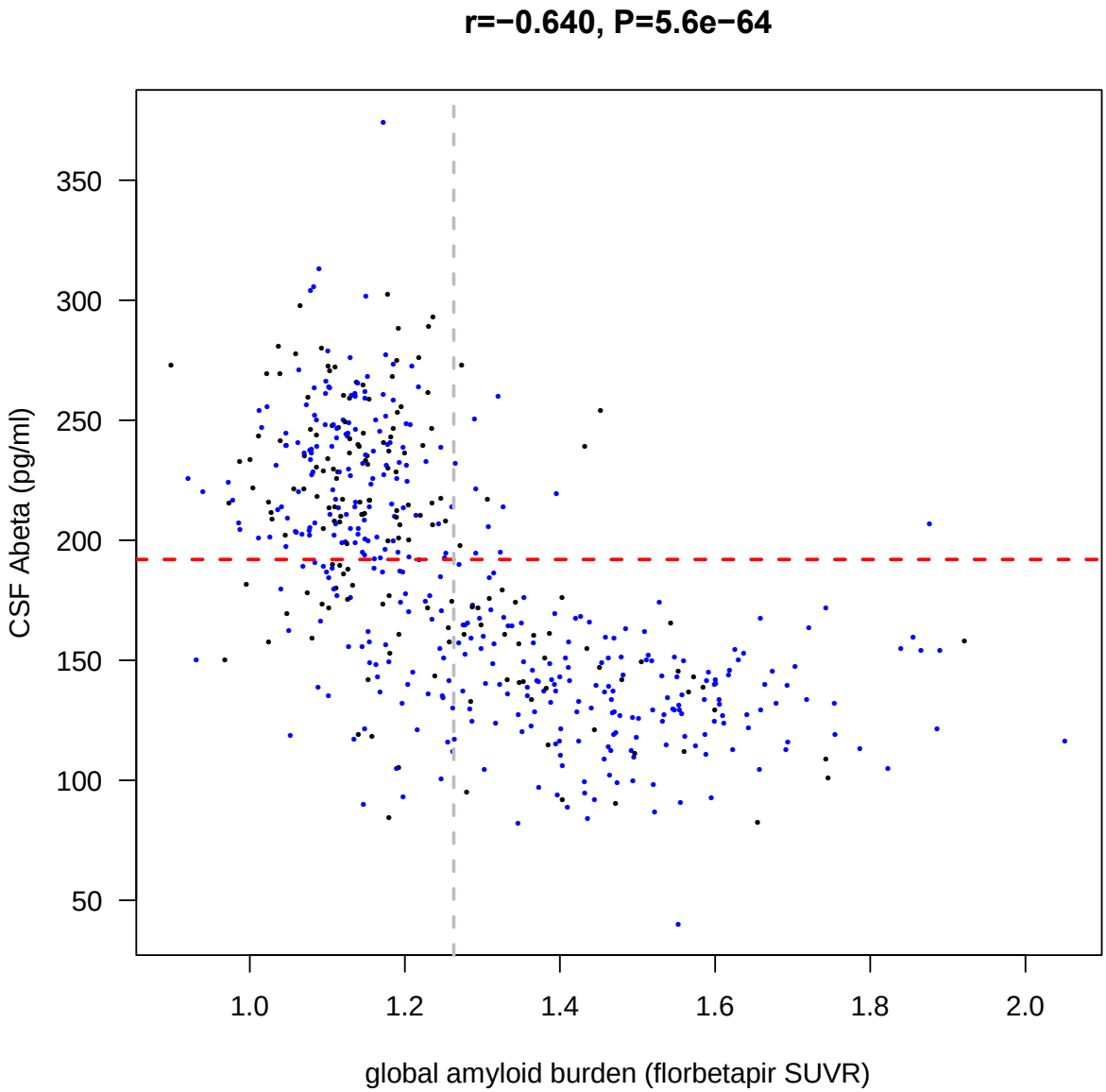


Figure S4: The default mode network. ROIs in our analysis belonging to the dorsal DMN (blue) and the ventral DMN (purple).

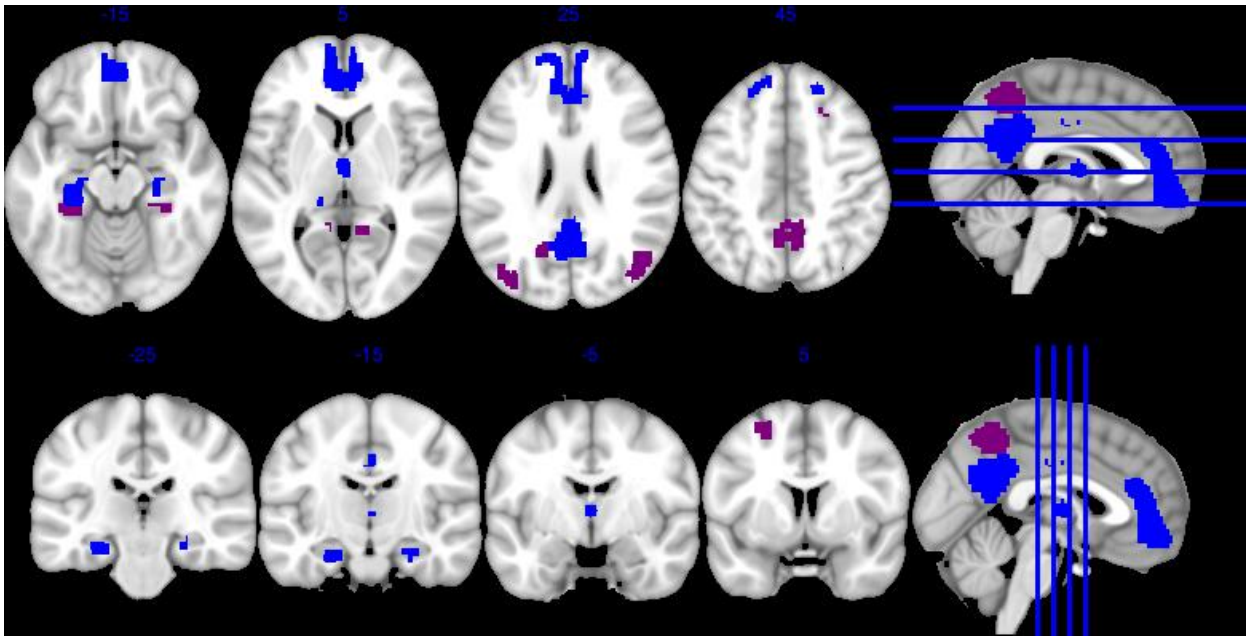
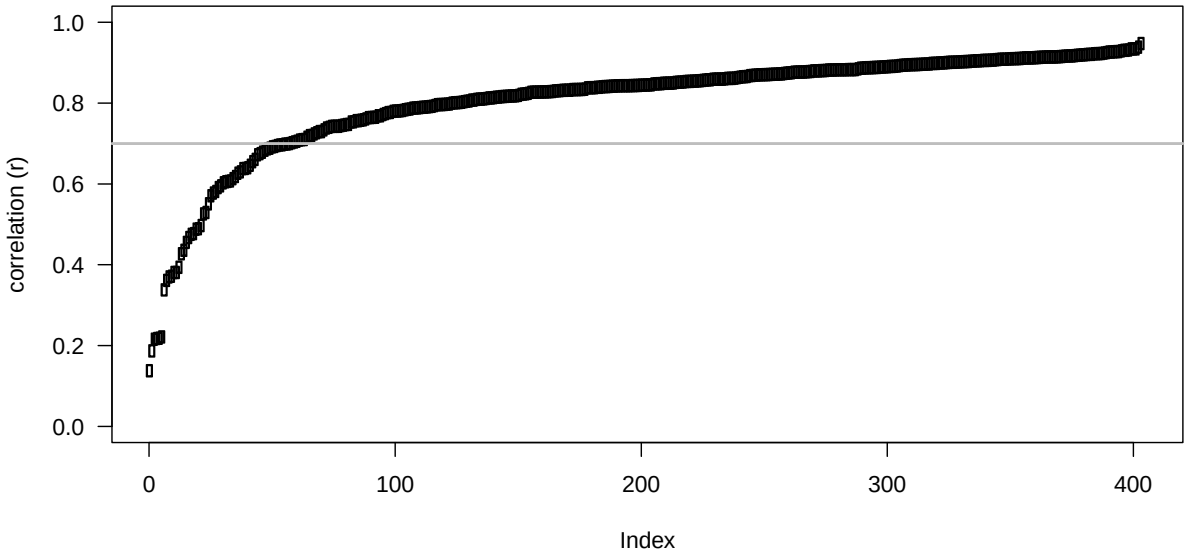


Figure S5: Correlation of regional amyloid with global amyloid. The 404 ROIs are ordered with respect to their Pearson's correlation to the global level of amyloid burden. The horizontal line marks r = 0.7.



References

Shaw LM, Vanderstichele H, Knapik-Czajka M, Clark CM, Aisen PS, Petersen RC, et al. Cerebrospinal fluid biomarker signature in Alzheimer's disease neuroimaging initiative subjects. Annals of neurology. 2009;65(4):403-13.