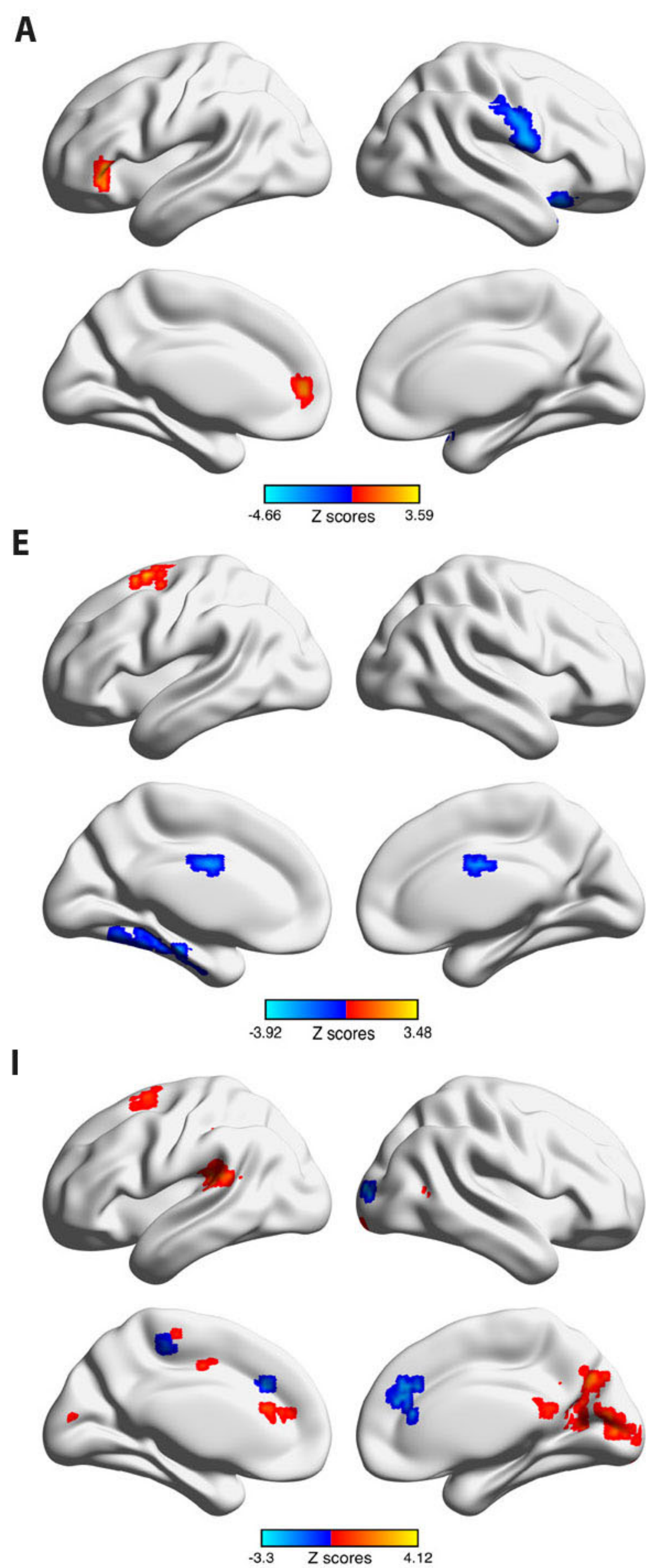
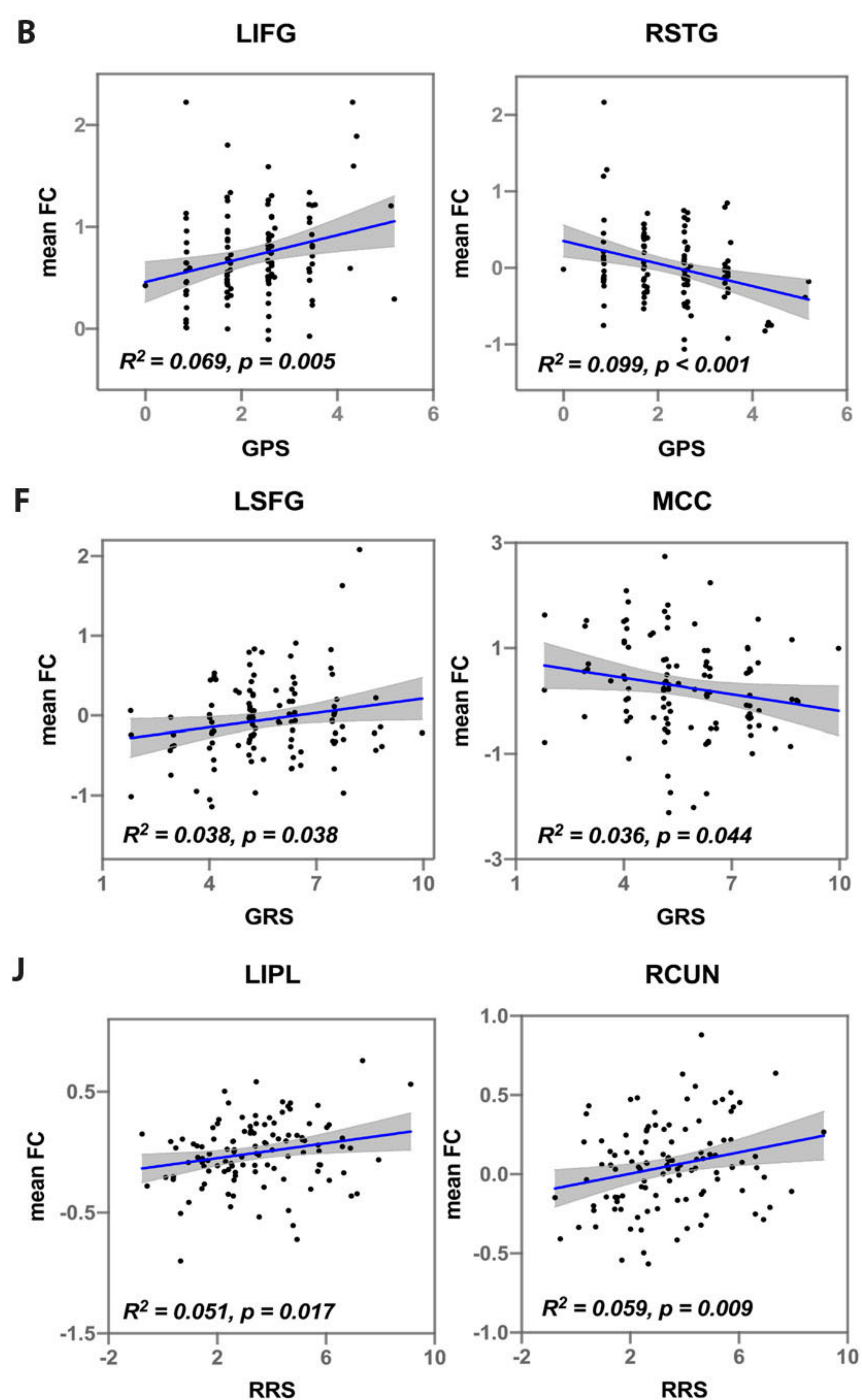


Figure 2. Main Effect of Polygenic Scores on the Default Mode Network Across the AD Spectrum^a

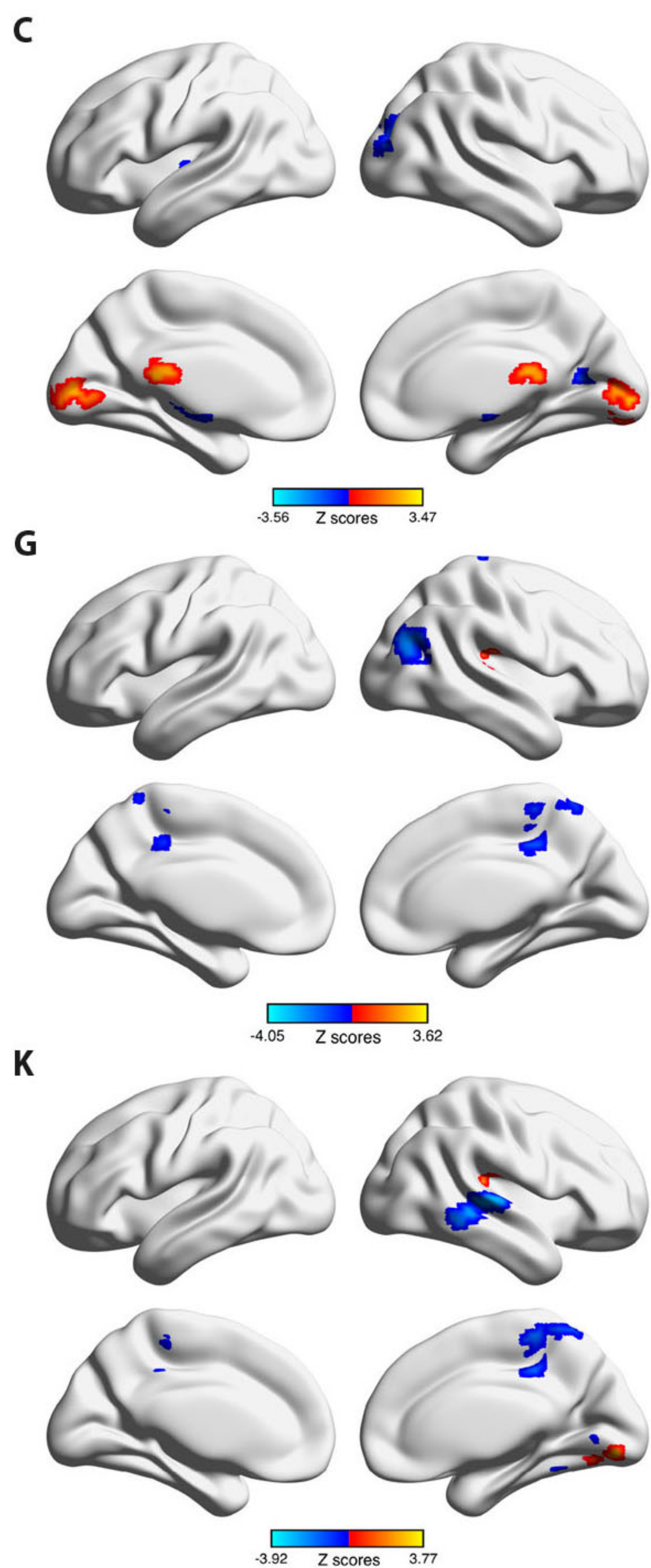
A, E, and I: Brain regions depicting the main effects of GPS, GRS, and RRS on the anterior DMN.



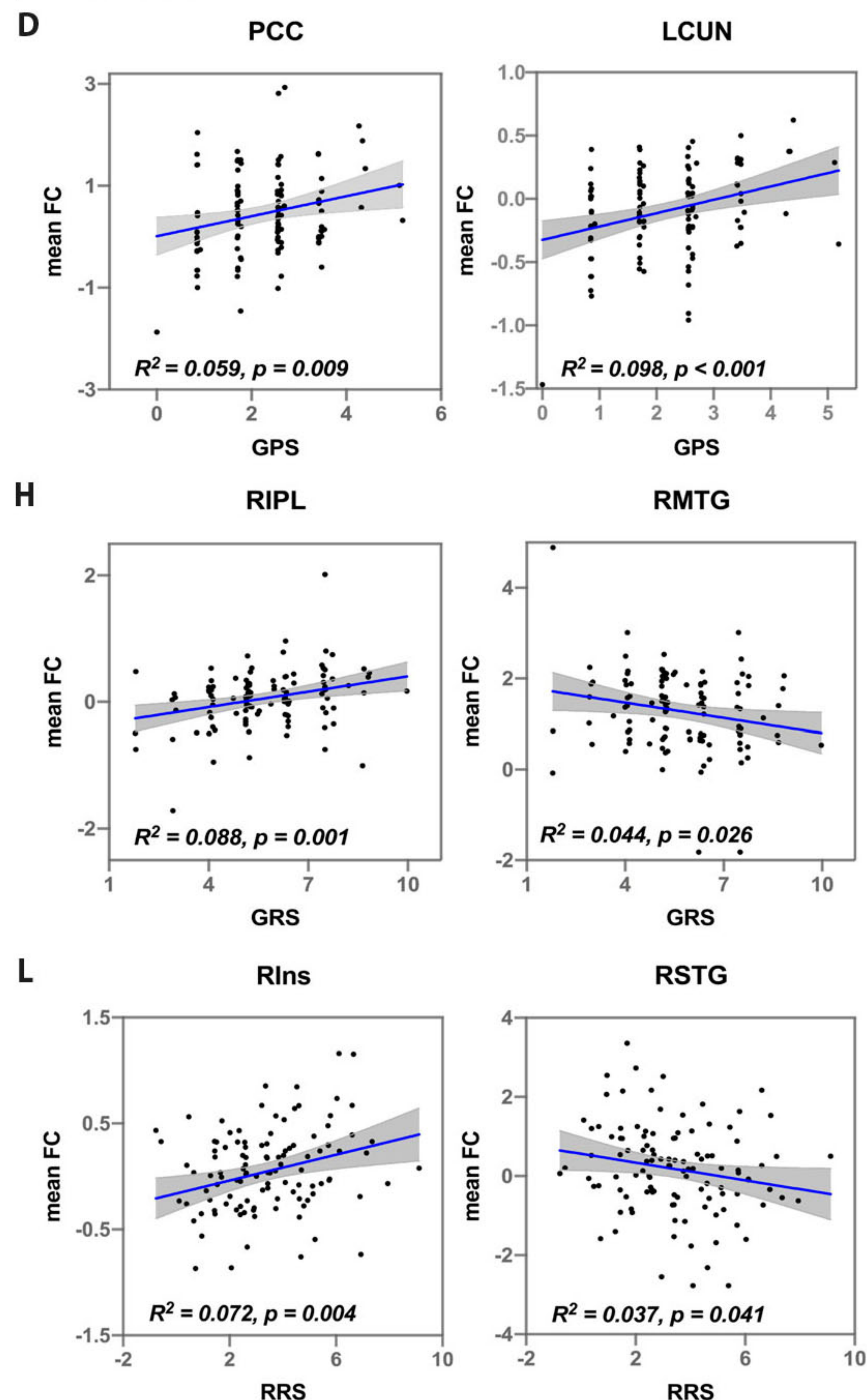
B, F, and J: Representative brain regions with significant correlations between the GPS, GRS, and RRS, respectively, with averaged functional connectivity of the anterior DMN.



C, G, and K: Brain regions showing the main effects of the GPS, GRS, and RRS, respectively, on the posterior DMN.



D, H, and L: Representative brain regions with significant correlations between the GPS, GRS, and RRS with averaged functional connectivity of the posterior DMN.



^aA red color indicates a positive correlation, and a blue color indicates a negative correlation between polygenic scores and functional connectivity strength of the DMN. The color bar indicates z scores.

Abbreviations: AD = Alzheimer's disease, DMN = default mode network, FC = functional connectivity, GPS = genetic protective score, GRS = genetic risk score, LCUN = left cuneus, LIFG = left inferior frontal gyrus, LIPL = left inferior parietal lobule, LSFG = left superior frontal gyrus, MCC = middle cingulate cortex, PCC = posterior cingulate cortex, RCUN = right cuneus, RIns = right insula, RIPL = right inferior parietal lobule, RMTG = right middle temporal gyrus, RRS = relative risk score.