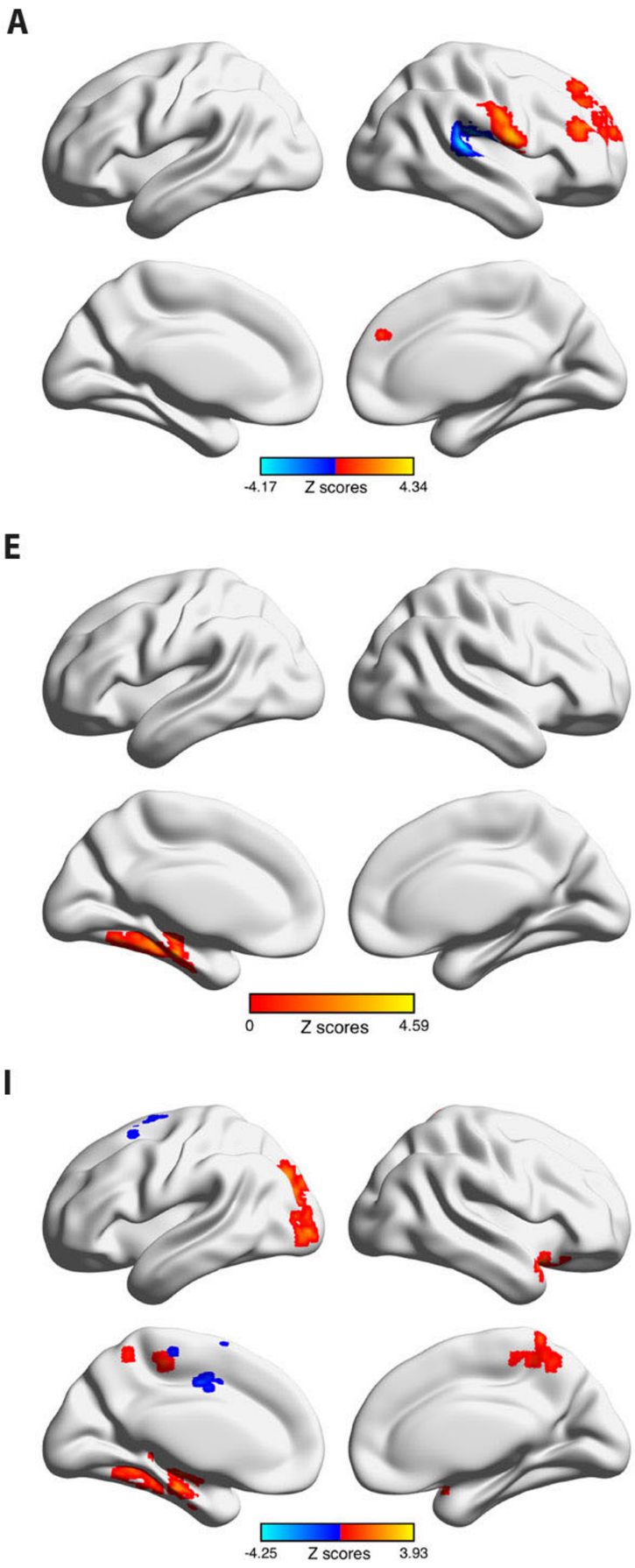
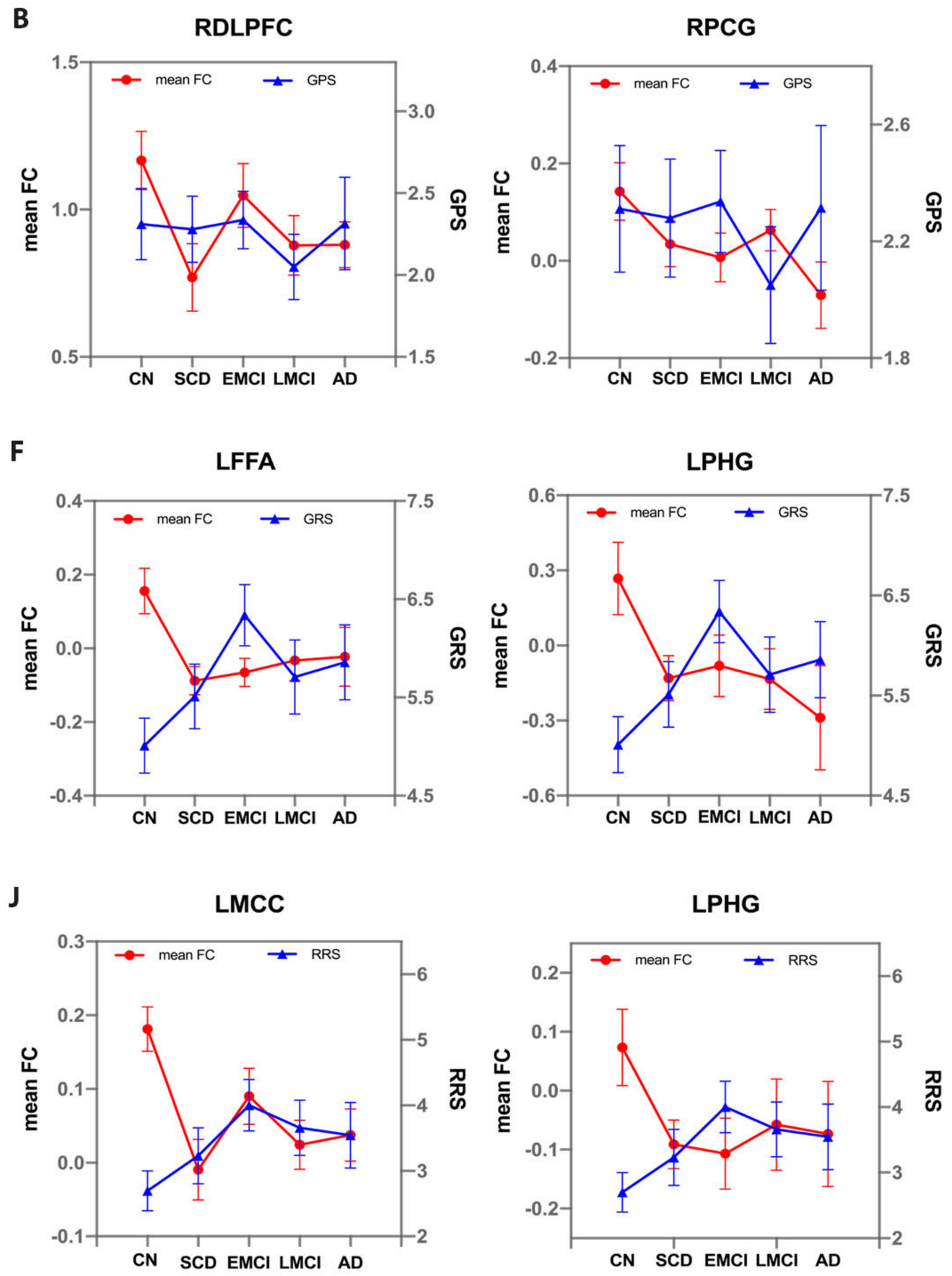
Figure 3. Interactive Effects Between Polygenic Scores and Disease on the Default Mode Network Across the AD Spectrum[a]

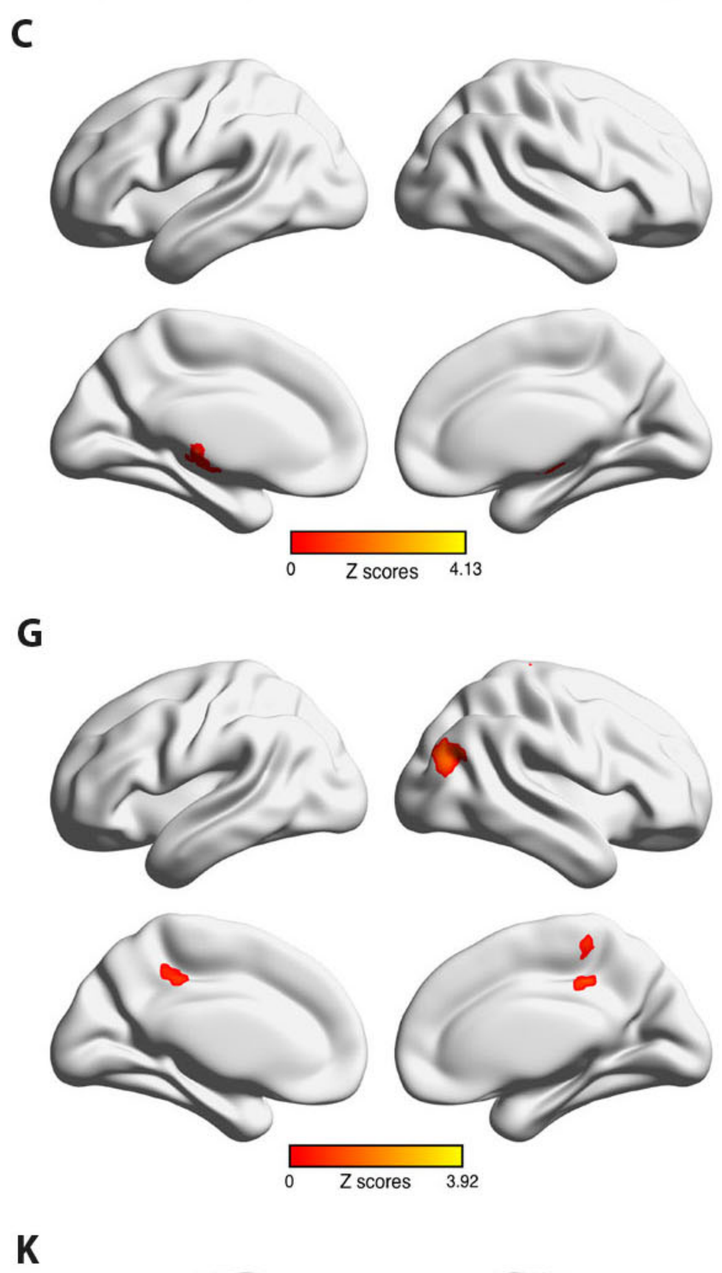
A, E, and I: Interactive effects between the GPS, GRS, and RRS, respectively, and disease on the anterior DMN in the AD spectrum.



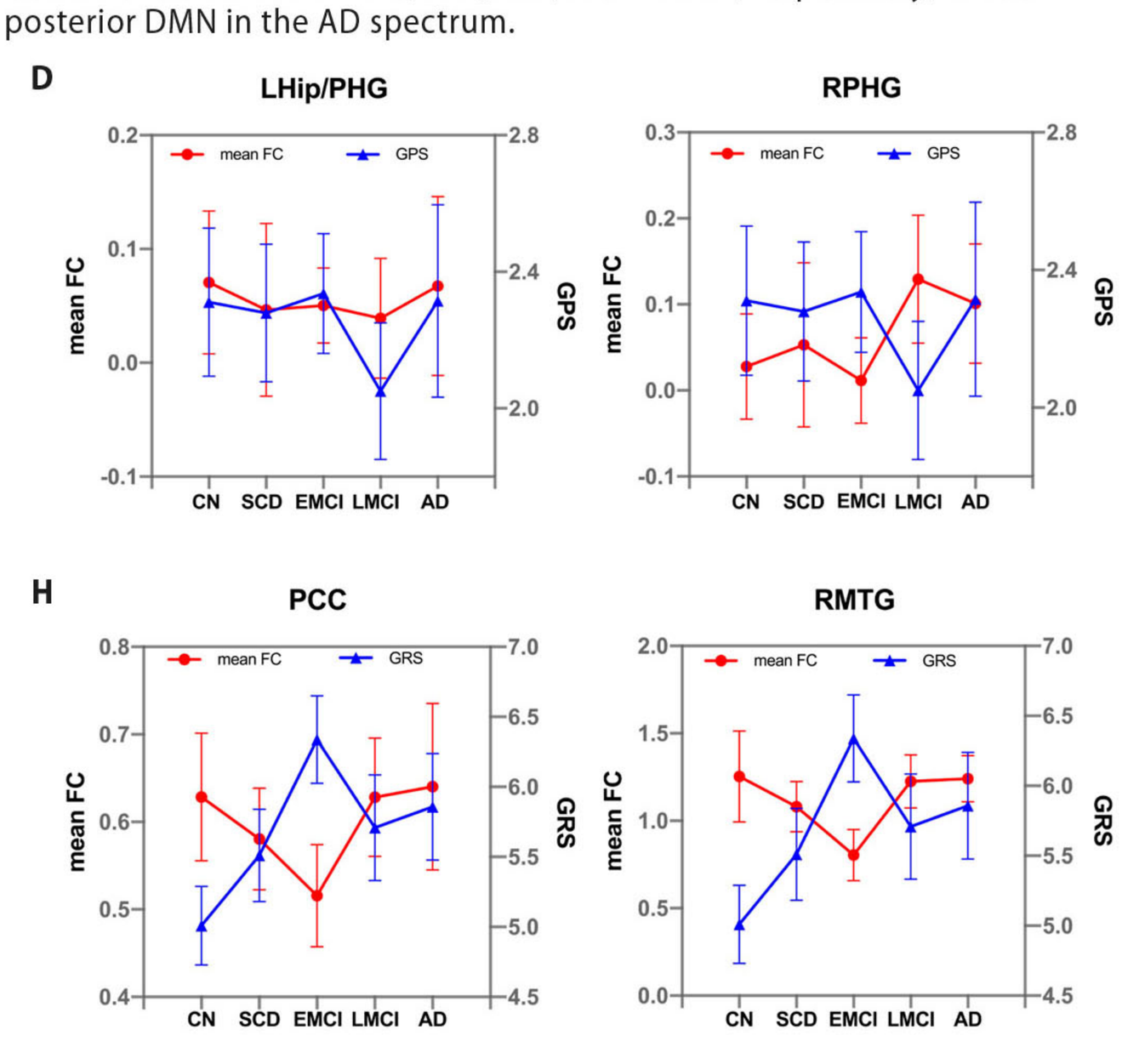
B, F, and J: Linear trends depicted by line charts represent the significant interactive effects of the GPS, GRS, and RRS, respectively, and disease on the anterior DMN in the AD spectrum.



C, G, and K: Interactive effects between the GPS, GRS, RRS, and disease, respectively, on the posterior DMN in the AD spectrum.



D, H, and L: Linear trends depicted by line charts represent the significant interactive effects of the GPS, GRS, RRS, and disease, respectively, on the posterior DMN in the AD spectrum.



[a]A bright 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, CN = cognitively normal, DMN = default mode network, EMCI = early amnestic mild cognitive impairment, FC = functional connectivity, GPS = genetic protective score, GRS = genetic risk score, LFFA = left fusiform area, LHip/PHG = left hippocampus/parahippocampal gyrus, LMCC = left middle cingulate cortex, LMCI = late mild cognitive impairment, LPHG = left parahippocampal gyrus, PCC = posterior cingulate cortex, RDLPFC = right dorsolateral prefrontal cortex, RMOG = right middle occipital gyrus, RMTG = right middle temporal gyrus, RPCG = right precentral gyrus, RPCL = right paracentral lobule, RPHG = right parahippocampal gyrus, RRS = relative risk score, RSTG = right superior temporal gyrus, SCD = subjective cognitive decline.