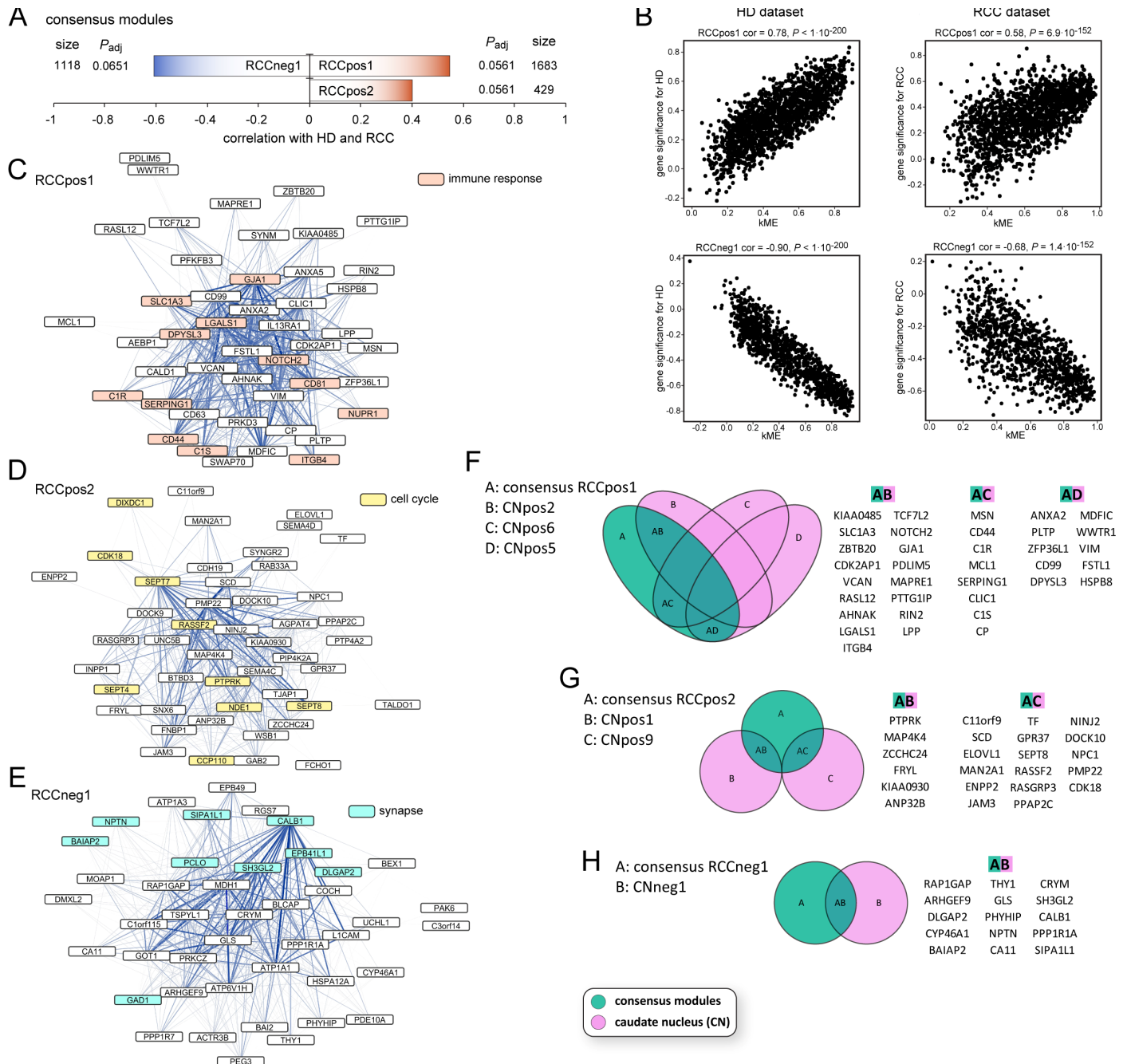




Additional data file 7. WGCNA analysis of the HD/RCC consensus dataset. **(A)** Visualization of modules that are highly correlated with Huntington's (HD) and renal cell carcinoma (RCC) disease state. Size is the number of genes for each module. P_{adj} gives the Benjamini Hochberg corrected significance value of correlation with HD/RCC for each module. **(B)** Correlations of eigengene based connectivity (kME) versus the gene significance for HD and RCC. The two modules with the highest absolute correlation are shown for each disease dataset. cor = correlation. **(C - E)** Visualization of hub genes in HD/RCC consensus network modules. The 50 most connected genes (nodes) and the 500 strongest gene-gene interactions (edges) in each module are shown. The width and the color saturation of the lines (edges) correspond to the weight of the interactions. **(F - H)** Hub gene comparison of HD/RCC consensus modules versus modules of the HD caudate nucleus (CN) dataset. Venn diagrams show the overlap of hub genes in the respective consensus modules with HD caudate nucleus modules. Only consensus modules with an overlap of 5 or more genes to CN modules are shown.