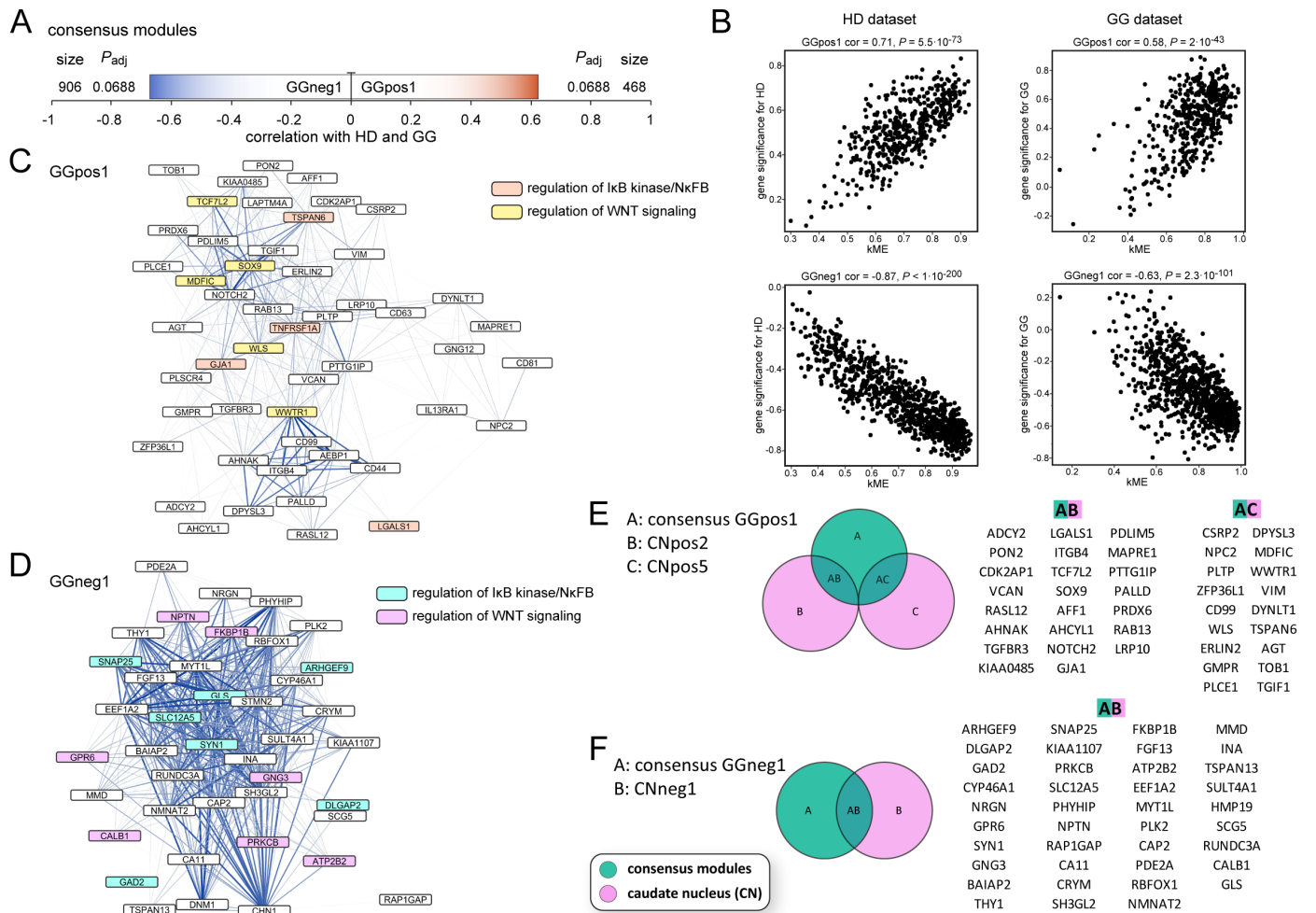




Additional data file 6. WGCNA analysis of the HD/GG consensus dataset. **(A)** Visualization of modules that are highly correlated with Huntington's (HD) and ganglioglioma (GG) disease state. Size is the number of genes for each module. P_{adj} gives the Benjamini Hochberg corrected significance value of correlation with HD/GG for each module. **(B)** Correlations of eigengene based connectivity (kME) versus the gene significance for HD and GG. cor = correlation. **(C and D)** Visualization of hub genes in HD/GG 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. **(E and F)** Hub gene comparison of HD/GG 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.