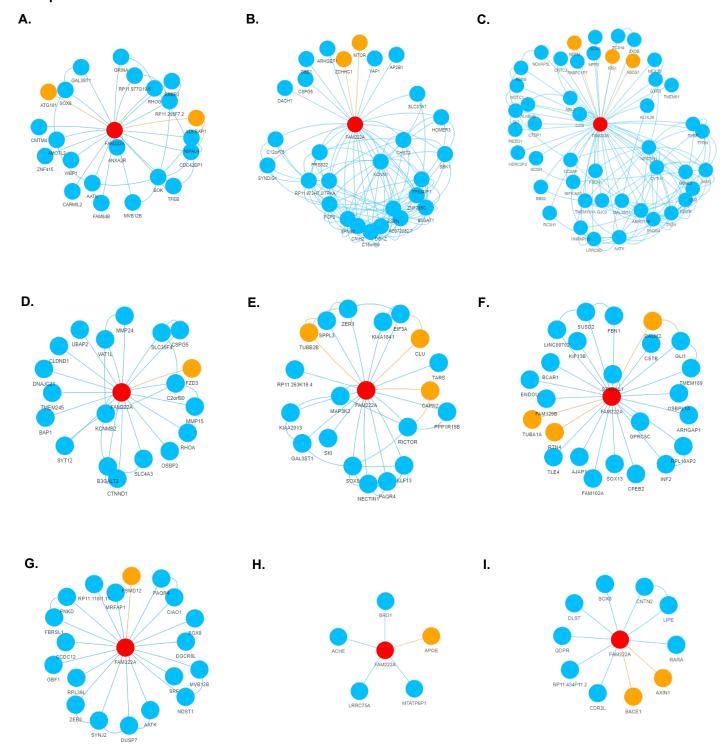
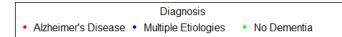
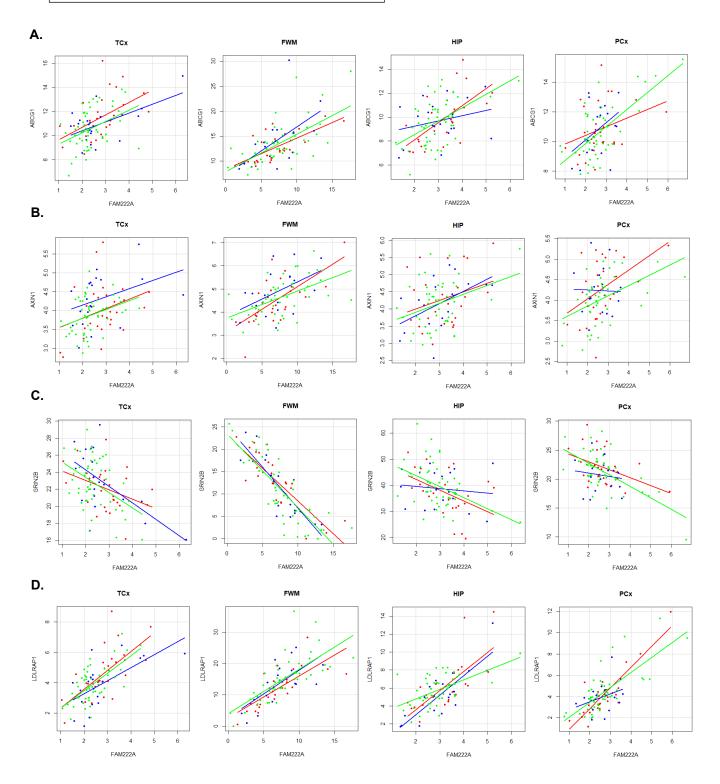
Supplementary Material

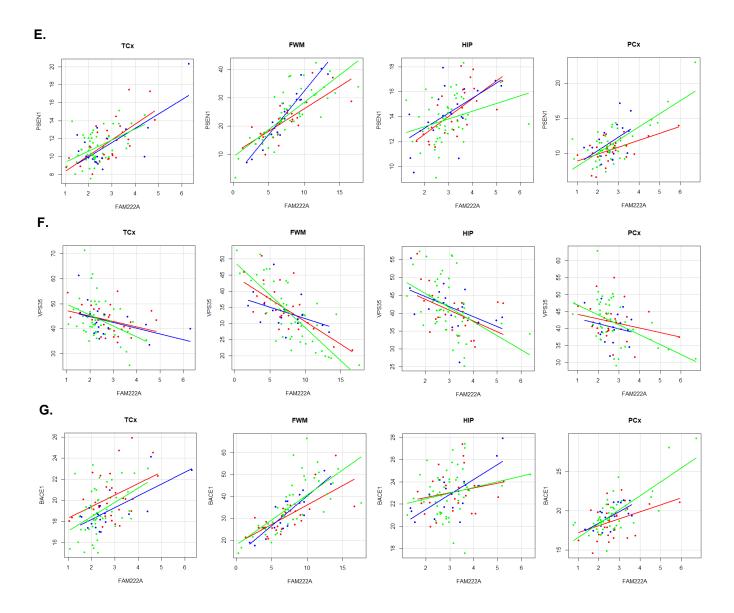
Gene Co-Expression Analysis of Multiple Brain Tissues Reveals Correlation of FAM222A Expression with Multiple Alzheimer's Disease-Related Genes



Supplementary Figure 1. Gene co-expression network of genes identified to be significantly co-expressed with *FAM222A* in hippocampus (A), cerebellum (B), substantia nigra (C), hypothalamus (D), spinal cord (E), putamen (basal ganglia) (F), caudate (G), nucleus accumbent (H), cortex (I).







Supplementary Figure 2. Scatterplot comparing expression levels between *ABCG1* (A), *AXIN1* (B), *GRIN2B* (C), *LDLRAP1* (D), *PSEN1* (E), *VPS35* (F), *BACE1* (G) with *FAM222A*. Clinical information of the donors are indicated in different colors. TCx, temporal neocortex; FWM: white matter of forebrain; HIP, hippocampus; PCx, parietal neocortex.