Supplementary Tables

Table S1. Related to Figure 4: Tab 1, list of genes differentially expressed between all AD-BXDs relative to all Ntg-BXDs. Tabs 2-3, Gene ontology (GO) terms significantly enriched among differentially expressed genes (adjusted p-value < 0.05), as identified by ranked gene set enrichment analysis (GSEA).*See spreadsheet

Table S2. Related to Figure 5: List of AD transcriptional signature genes identified by Hargis and Blalock (2017) as the top 10% commonly upregulated and downregulated genes across human AD datasets and their expression profile across mouse and human datasets.*See spreadsheet

Table S3. Related to Figure 5: List of genes differentially expressed in late-stage mouse AD (between 14m AD-BXDs and 14m Ntg-BXDs) and in mouse normal aging (between 6m Ntg-BXDs and 14m Ntg-BXDs) as identified by DESeq2.*See spreadsheet

Table S4. Related to Figure 5: List of GO terms significantly enriched among differentially expressed genes in mouse AD (Tab 1) or mouse normal aging (Tab 2). For comparison, we identified those pathways containing enough genes to be identified in each set (Tab 3) for use in graphing relative enrichment in mouse AD vs mouse normal aging.*See spreadsheet

Table S5. Related to Figure 1 and STAR Methods: Data used for comparing mutated human *APP* and *PSEN1* (i.e. 5XFAD transgene expression) and endogenous mouse *App* and *Psen1* across genetic backgrounds.