Fig. S1. Module preservation across different datasets. (A) Preservation median rank and (B) preservation $Z_{summary}$ scores of various modules.
**Fig. S2.** GO enrichment analysis for the genes in the AD metastable network. This analysis identifies specific components of the ubiquitin–proteasome and endosomal–lysosomal systems in the regulation of the metastable subproteome.
Fig. S3. KEGG pathways enriched in the AD metastable network.

Fig. S4. Correspondence between the modules of the VC dataset (GSE44771) and the consensus modules. Each row of the table corresponds to one of the modules of the VC dataset (labeled by color as well as text), and each column corresponds to one consensus module. Numbers in the table indicate the gene counts in the intersections of the corresponding modules. Coloring of the table encodes $-\log(p)$, with $p$ being the Fisher’s exact test $P$ value for the overlap of the two modules. The table indicates that most of the modules of the VC dataset have a consensus counterpart.

Fig. S5. Consensus eigengene networks for the dorsolateral PFC and the VC. (A) Heatmap of the preservation network, defined as one minus the absolute difference of the eigengene networks in the two datasets. (B) Mean preservation of adjacency for each of the eigengenes to all other eigengenes. $D$ denotes the mean preservation of eigengene networks among the datasets. $D^{1/2} = \text{mean}_{ij} r_{ij}^{1/2}$ (Materials and Methods).
Fig. S6. Network representation of the AD metastable network showing the hub genes and the main components of the protein homeostasis system linked with the AD metastable subproteome. This analysis reveals in particular the importance of the ubiquitin–proteasome (red) and trafficking (green) systems in the regulation of aggregation-prone proteins in AD. The top 10% of the hub gene interactions are visualized, with those genes involved in at least 50 interactions shown in the center. The sizes of the nodes correspond to their degrees of connectivity. The metastable genes are shown in blue. Dataset S1, Table S7 reports the names of the metastable genes according to the numerical labels shown here.
Fig. S7. Consensus eigengene networks and their differential analysis. (A–C) Dendrograms (clustering trees) of the consensus MEs in the three datasets. (D, H, and L) Eigengene network heatmaps. Red denotes high adjacency (positive correlation), and blue denotes low adjacency. (G, J, and K) Heatmaps of the preservation network, defined as one minus the absolute difference of the eigengene networks in the two datasets. (E, F, and I) Mean preservation of adjacency for each of the eigengenes to all other eigengenes.

Other Supporting Information Files

Dataset S1 (XLSX)