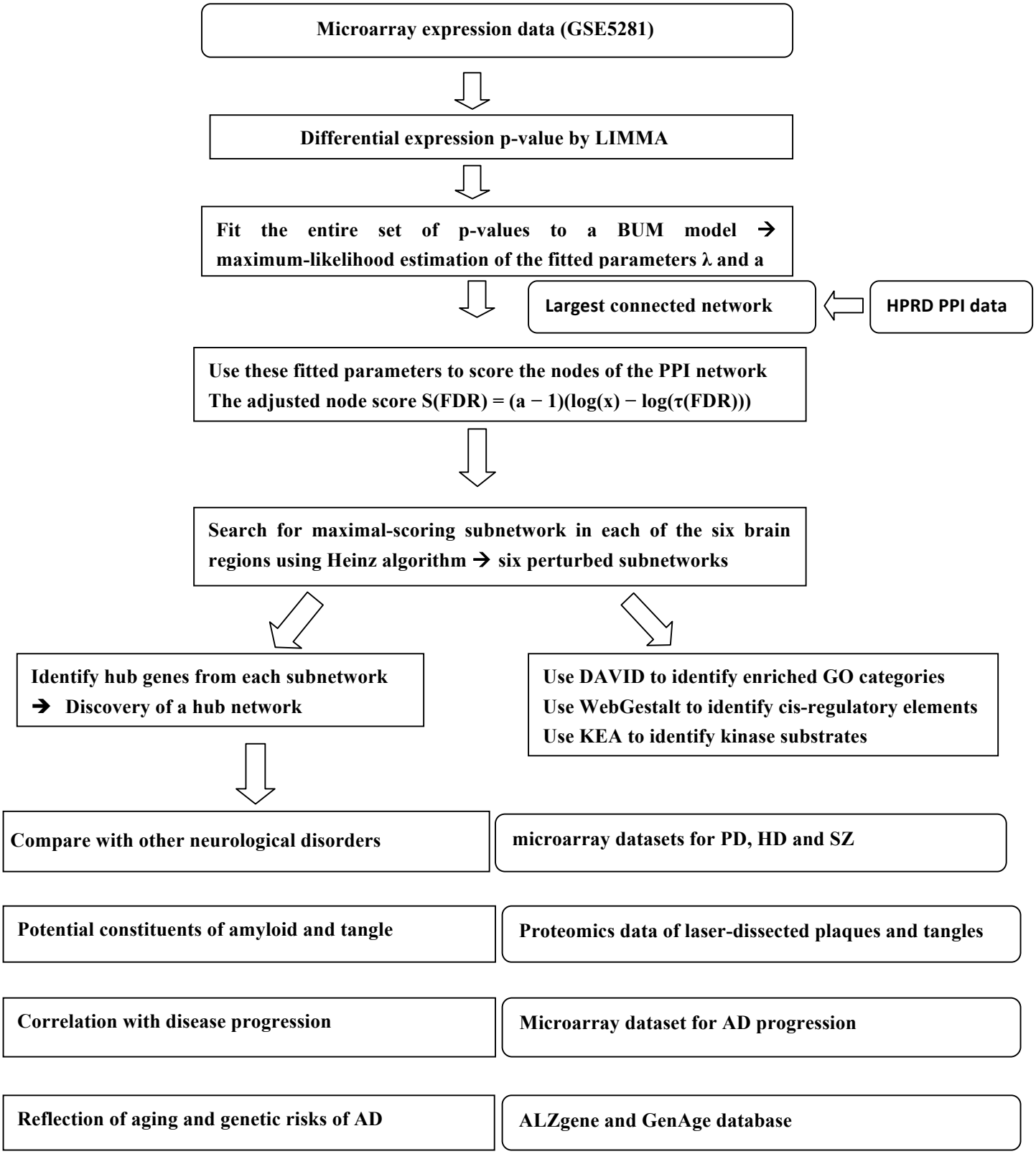
Microarray expression data (GSE5281)
Differential expression p-value by LIMMA
Fit the entire set of p-values to a BUM model → maximum-likelihood estimation of the fitted parameters λ and a
Largest connected network
HPRD PPI data
Use these fitted parameters to score the nodes of the PPI network
The adjusted node score S(FDR) = (a − 1)(log(x) − log(τ(FDR)))
Search for maximal-scoring subnetwork in each of the six brain regions using Heinz algorithm → six perturbed subnetworks
Identify hub genes from each subnetwork
→ Discovery of a hub network
Use DAVID to identify enriched GO categories
Use WebGestalt to identify cis-regulatory elements
Use KEA to identify kinase substrates
Compare with other neurological disorders
microarray datasets for PD, HD and SZ
Potential constituents of amyloid and tangle
Proteomics data of laser-dissected plaques and tangles
Correlation with disease progression
Microarray dataset for AD progression
Reflection of aging and genetic risks of AD
ALZgene and GenAge database

Figure S1