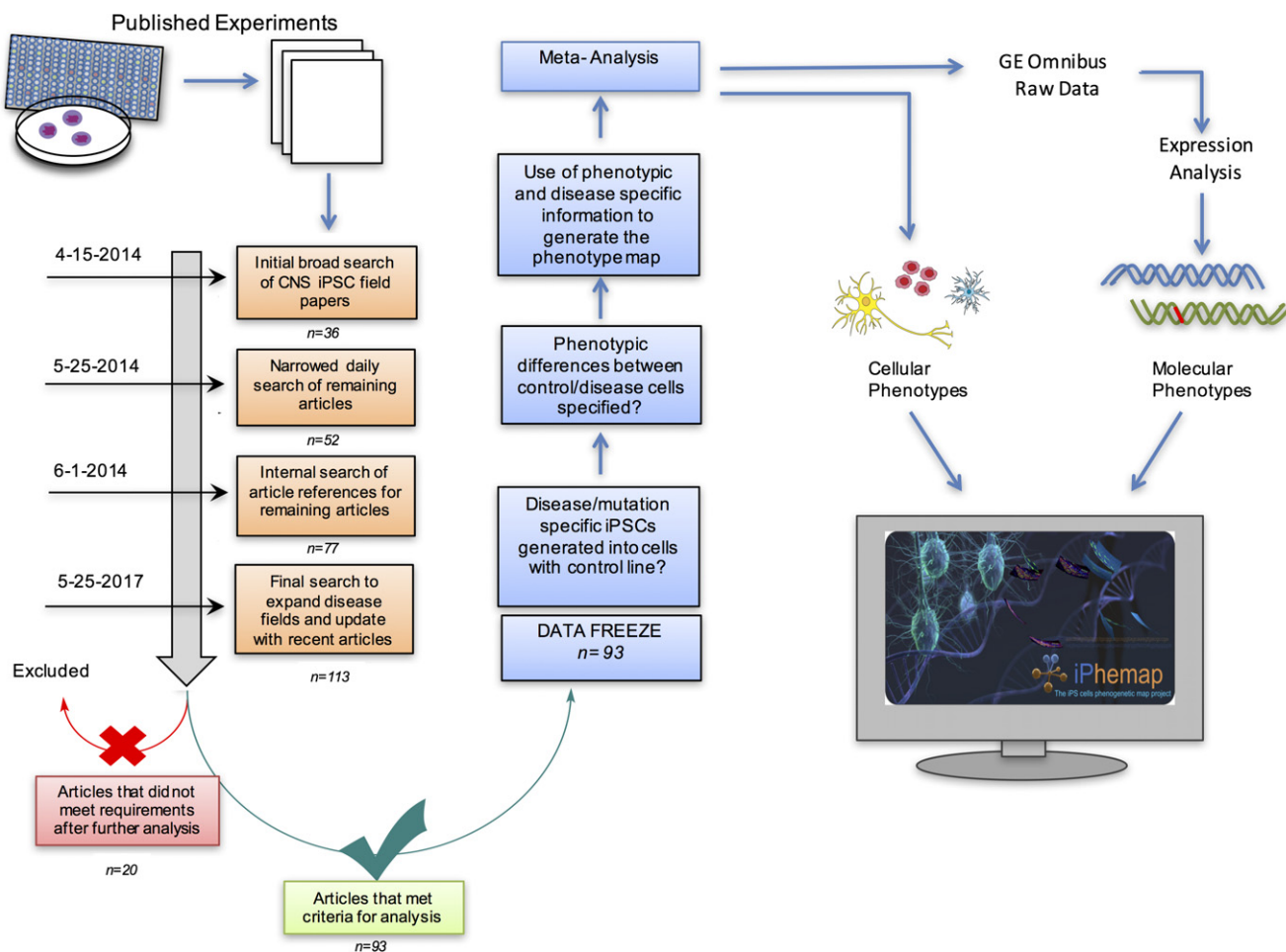# Expanded View Figures

Figure EV1. Diagram of meta-analysis flowchart showing our search for potential CNS iPSC papers spanned over three years.

Pipeline includes our inclusion and exclusion criteria for selection of candidate papers; 93 of which met these requirements and were examined in our study.
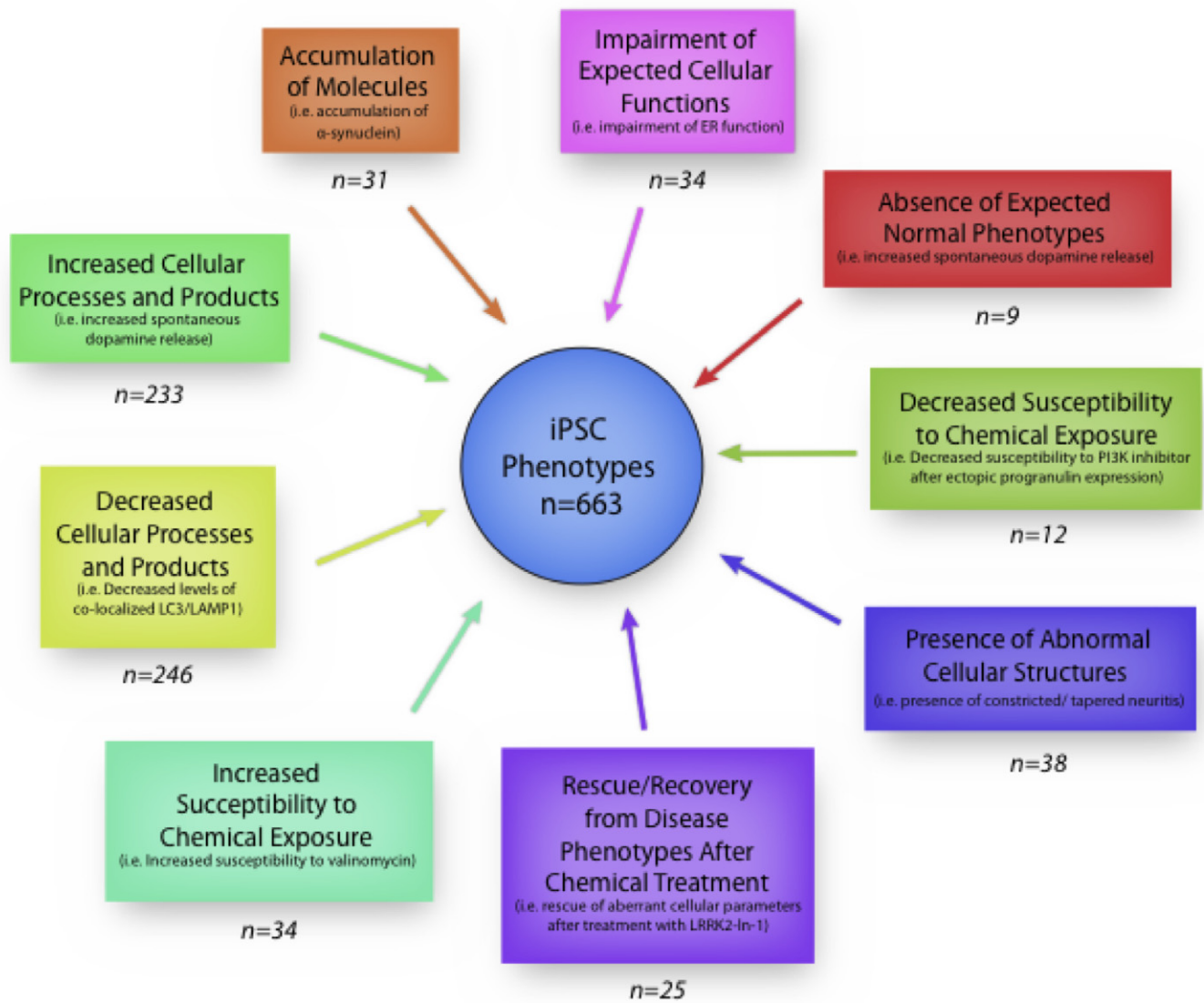
Figure EV2.   Taxonomy of phenotype classes established to classify our 663 phenotypes.

Phenotype classes include definitions and examples from our analysis. Colors of each phenotype class are preserved through all of the Figures.
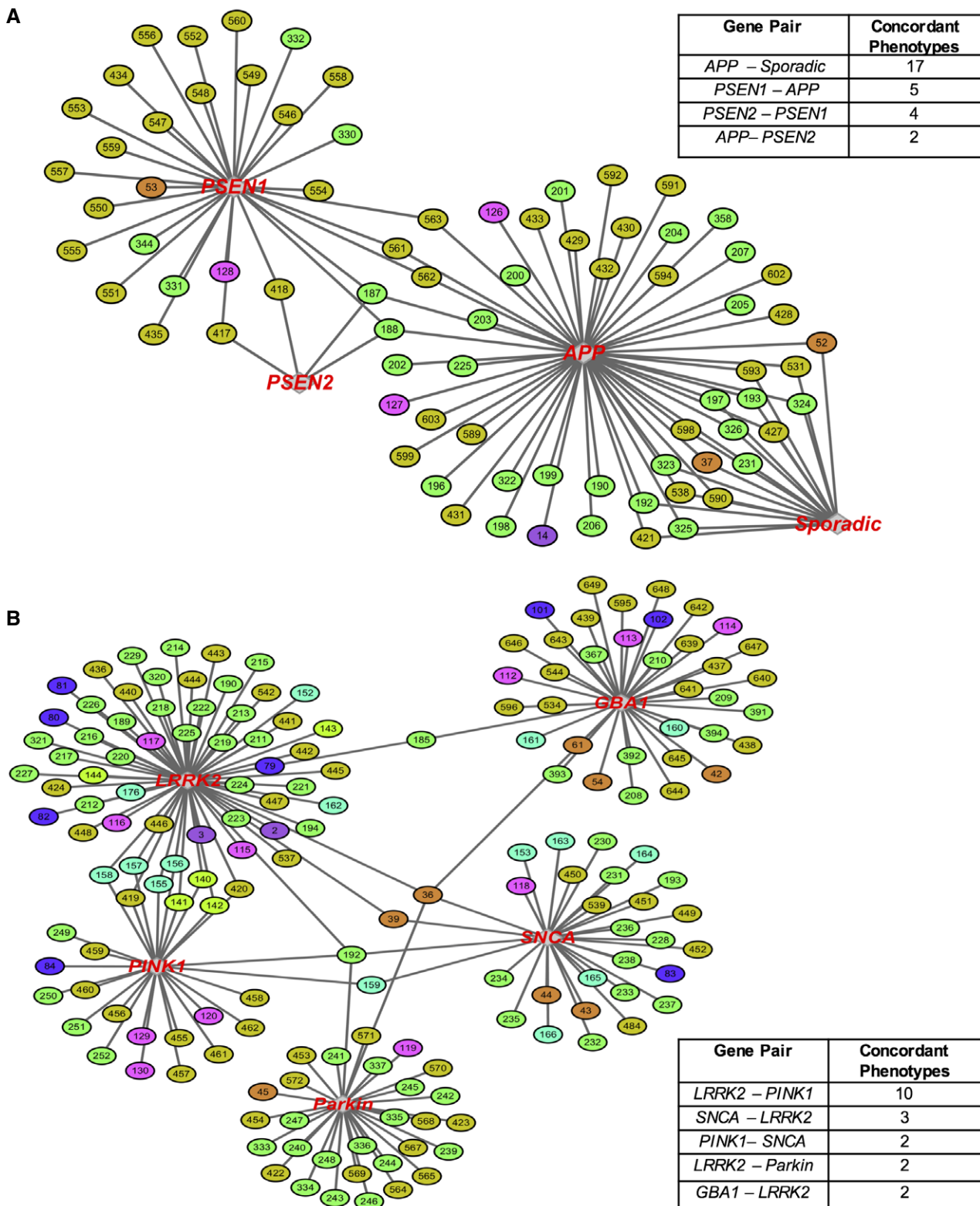
Figure EV3. Phenogenetic networks of genes linked to Alzheimer's and Parkinson's disease reveal concordant phenotypes.

A, B A nuanced phenogenetic network view of genes associated with (A) Alzheimer's disease and (B) Parkinson's disease. The number of concordant phenotypes shared by gene pairs of AD and PD is outlined in tables, with *APP-Sporadic* and *APP-PSEN1* having the most in AD and *LRRK2-PINK1* in PD.
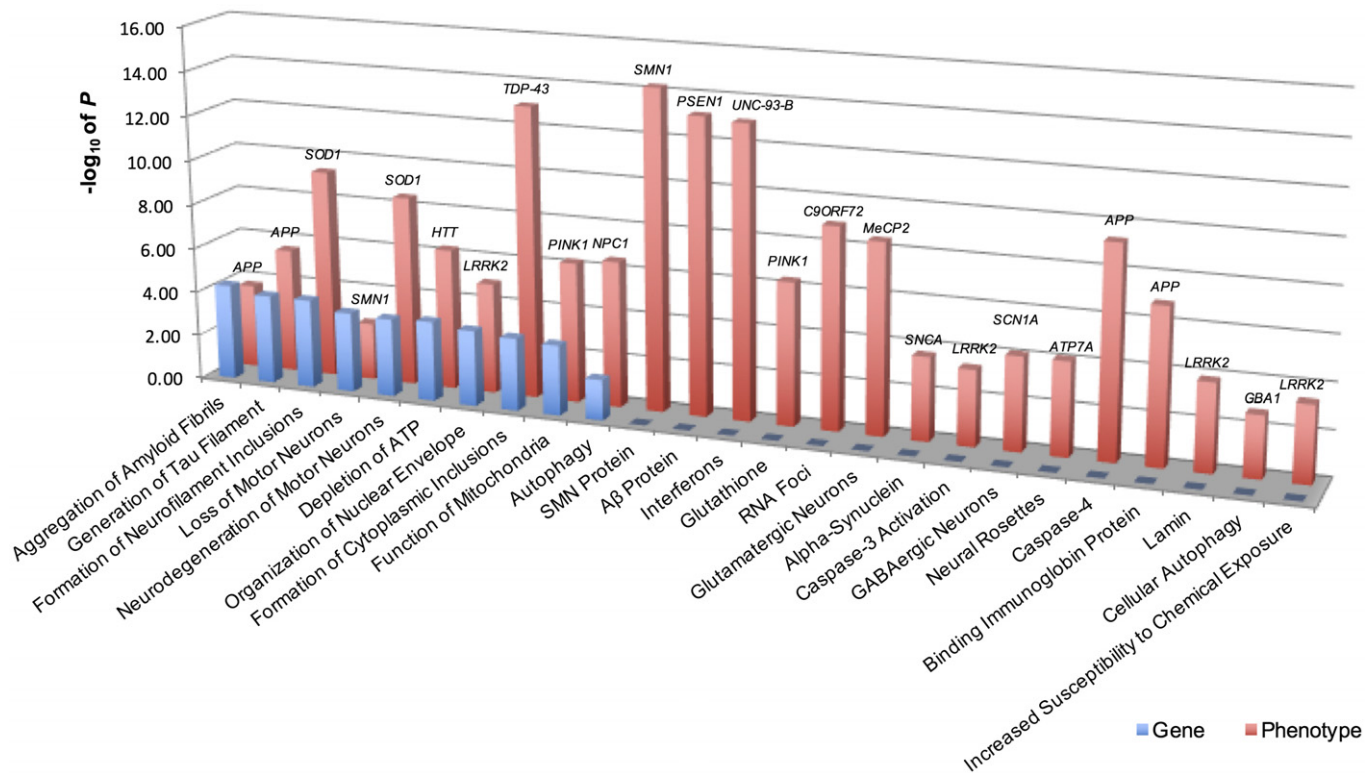
Figure EV4. Comparison between phenotype and gene ontology.

Pairwise statistical comparison of functional annotations derived from well-established gene ontologies and phenotype ontology, which notably includes several novel phenotype ontology terms, $n = 15$, that have yet to be reported in gene ontologies.