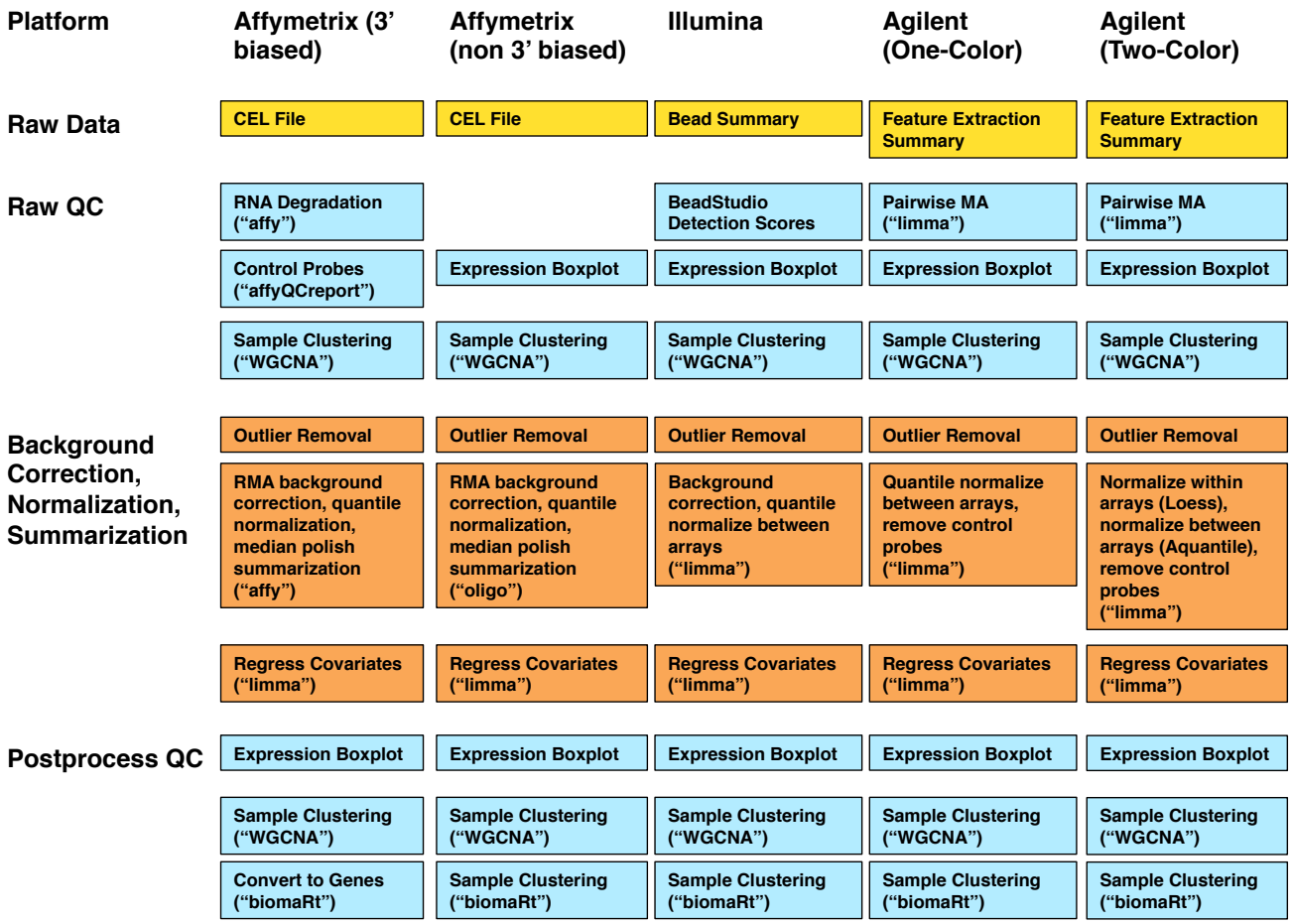
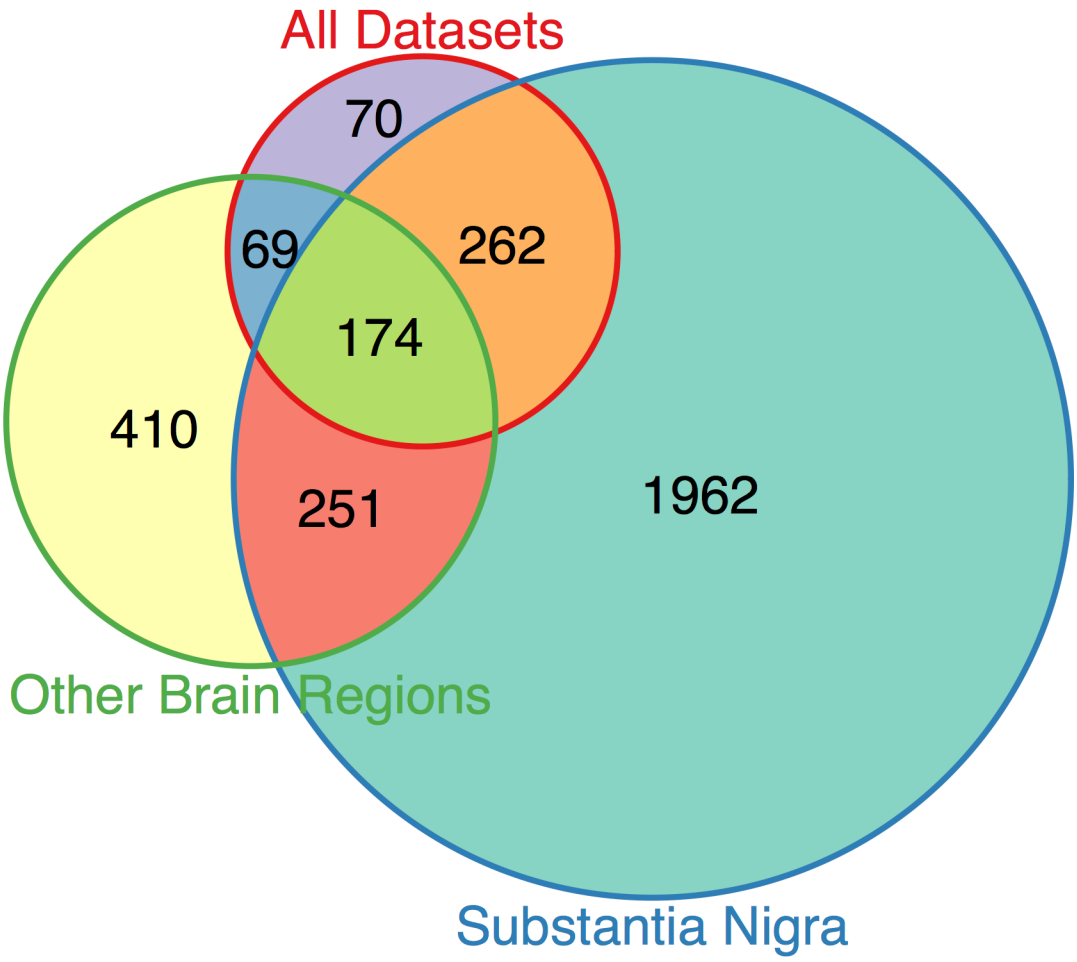
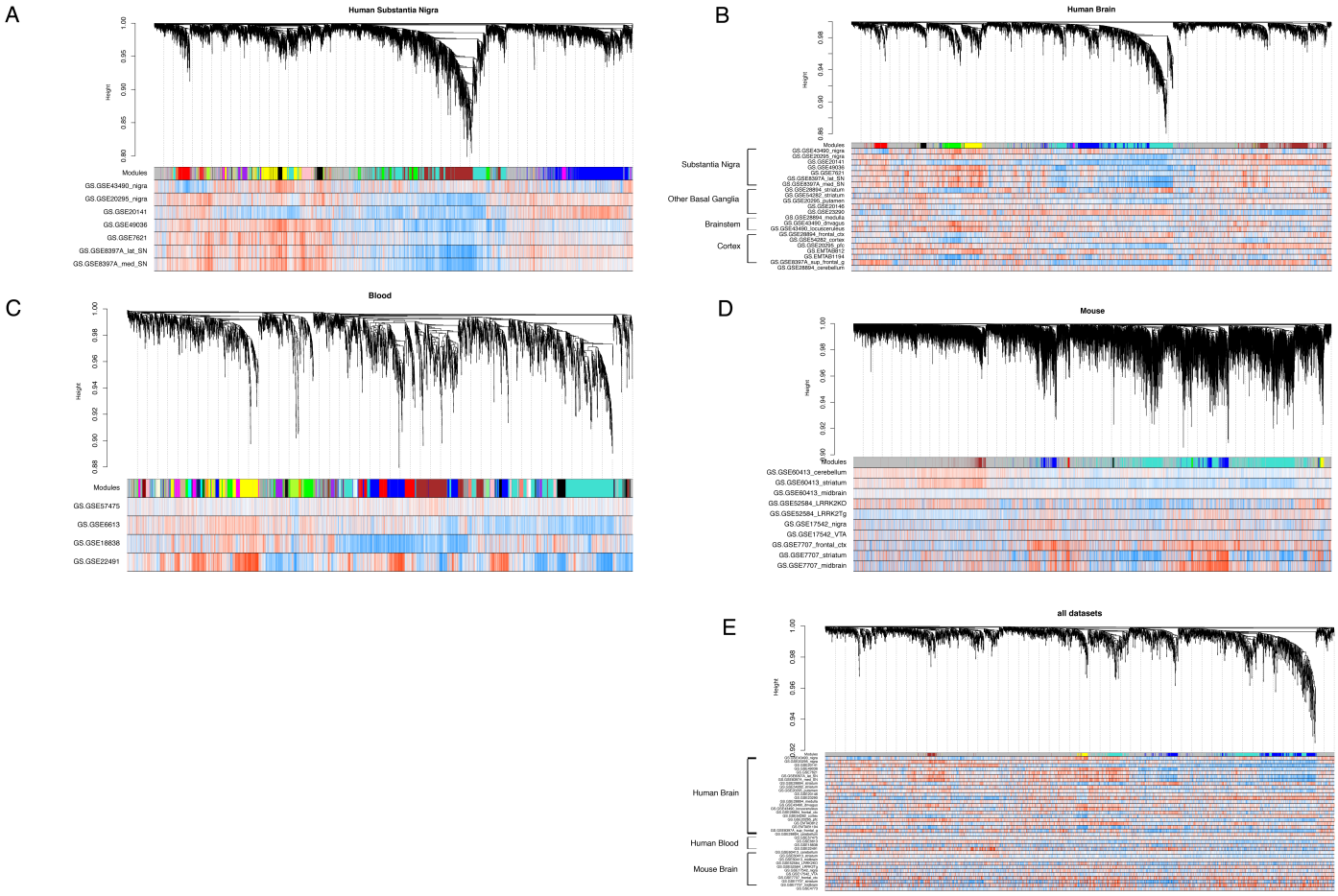
Supplementary Data for Chen J, Gene co-expression network analysis implicates microRNA processing in Parkinson's disease pathogenesis, *Parkinsonism & Related Disorders*



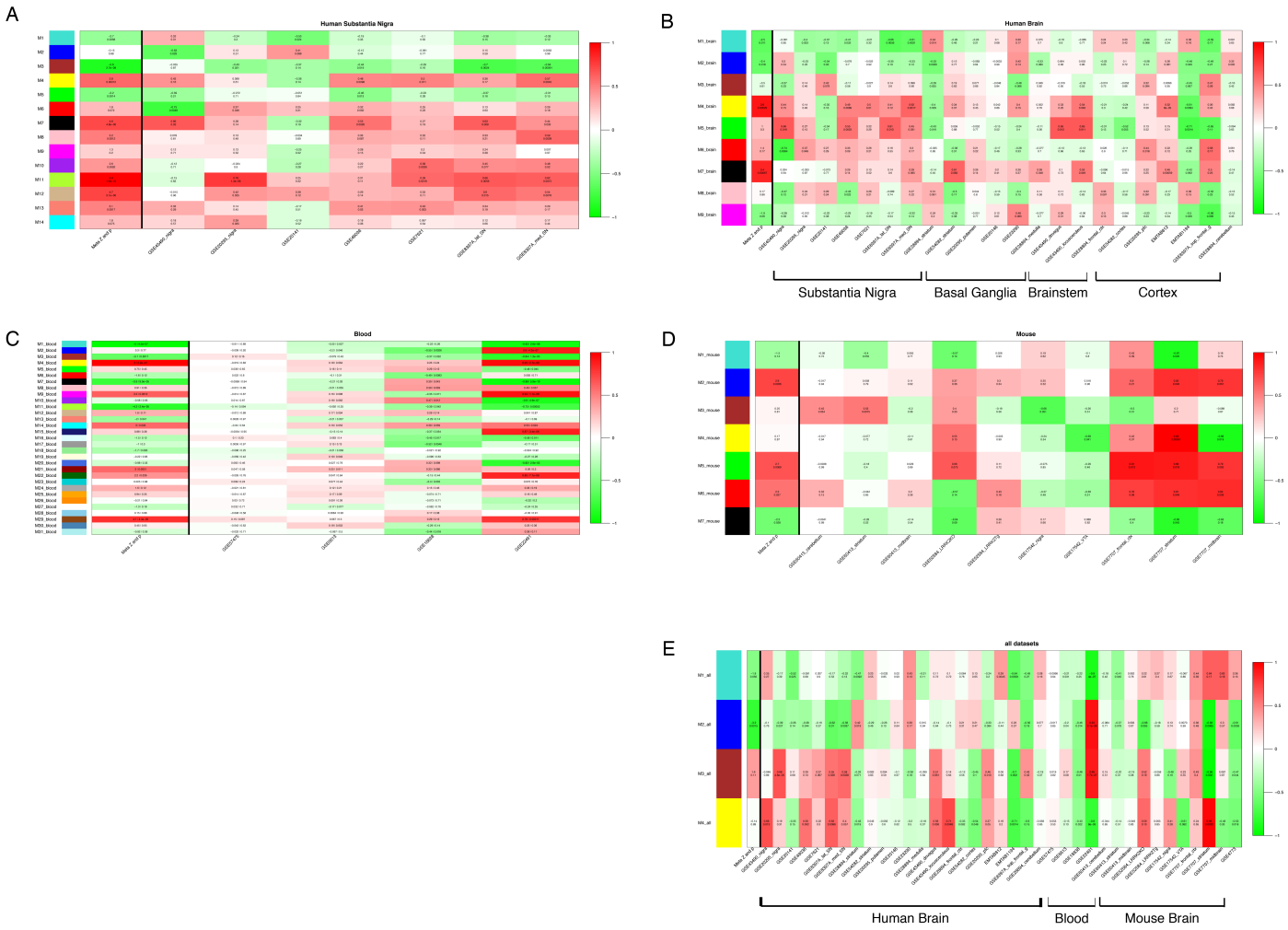
Supplementary Figure 1: Preprocessing pipelines for each platform. QC was first performed on raw data. Processing steps, including removal of outlier samples, background correction, normalization, summarization, and covariate regression, were then used to standardize data. Quality of the analysis-ready data was then assessed with post-processing QC. Relevant R/Bioconductor packages used in implementation are shown in parentheses.



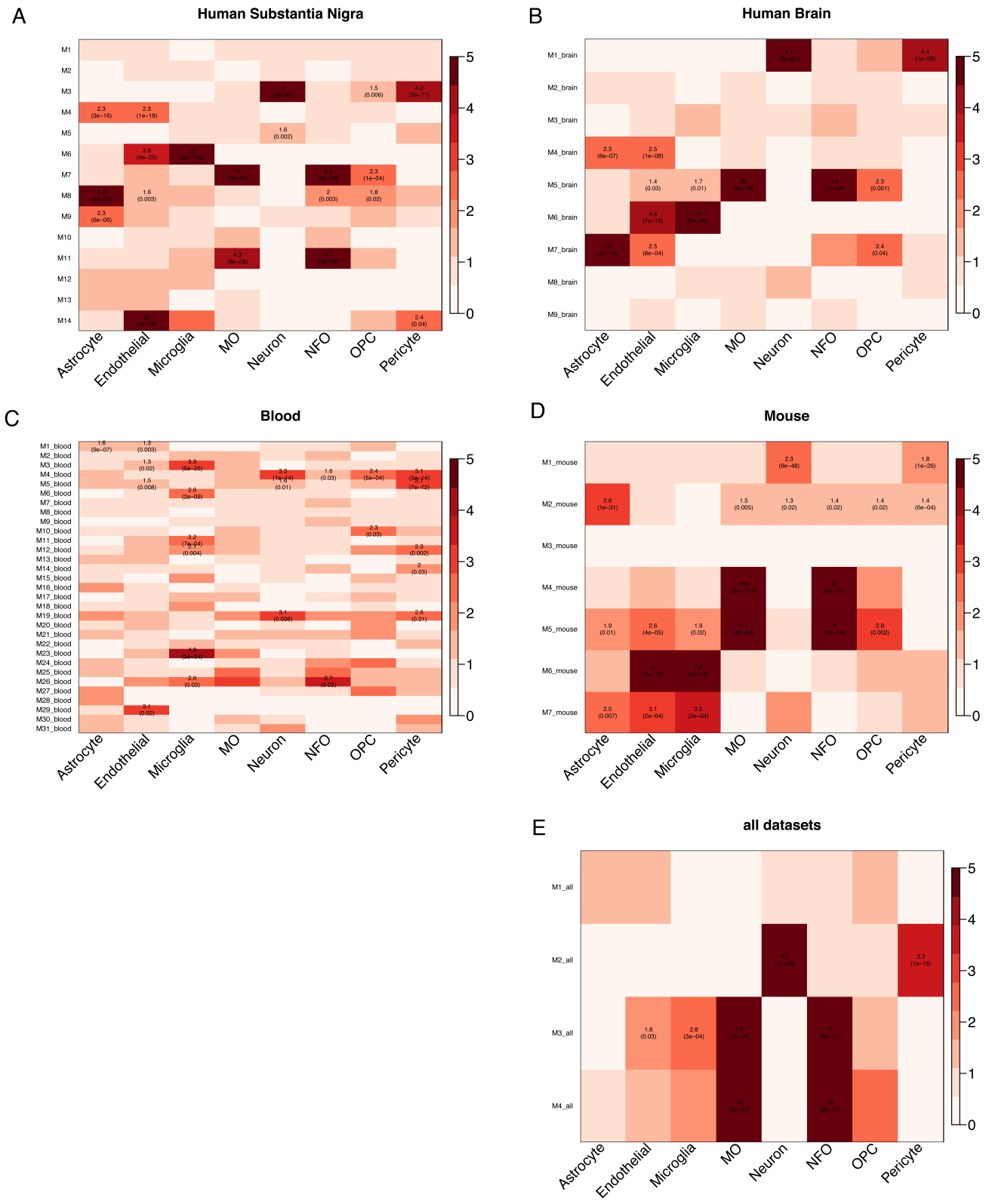
Supplementary Figure 2: Overlap of differential expression among substantia nigra, other brain regions, blood, and all datasets.



Supplementary Figure 3: WGCNA assigns modules (colorbar) based on clustering of gene topological overlap and tree cutting of the resultant dendrogram in a) human substantia nigra datasets; b) human brain datasets; c) human peripheral blood datasets; d) mouse datasets; and e) all datasets. Below each dendrogram, the correlation of each gene's expression level with Parkinson's disease status is shown. Red hues indicate positive correlation, blue hues indicate negative correlation, and the intensity of the coloration corresponds to the magnitude of correlation.



Supplementary Figure 4: Correlation of module eigengene with Parkinson's disease for a) human substantia nigra datasets; b) human brain datasets; c) blood datasets; d) mouse brain datasets; and e) all datasets.



Supplementary Figure 5: Enrichment of cell marker genes in eight cell types for modules in a) human substantia nigra datasets; b) human brain datasets; c) blood datasets; d) mouse brain datasets; and e) all datasets. MO: mature oligodendrocyte; NFO: newly-formed oligodendrocyte; OPC: oligodendrocyte precursor cell