Supplementary Figures 1 - 2

Druggable transcriptomic pathways revealed in Parkinson's patient-derived midbrain neurons

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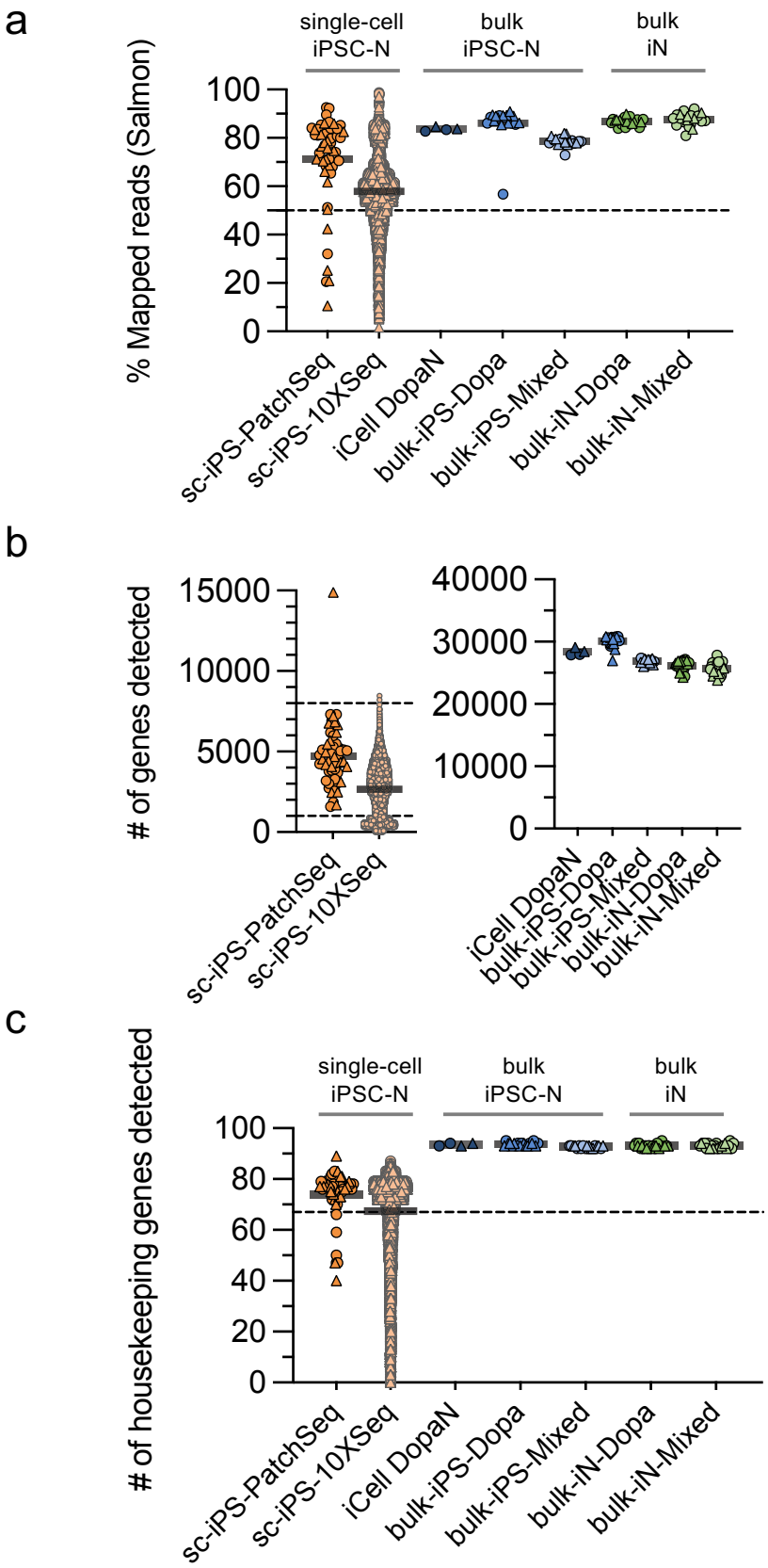
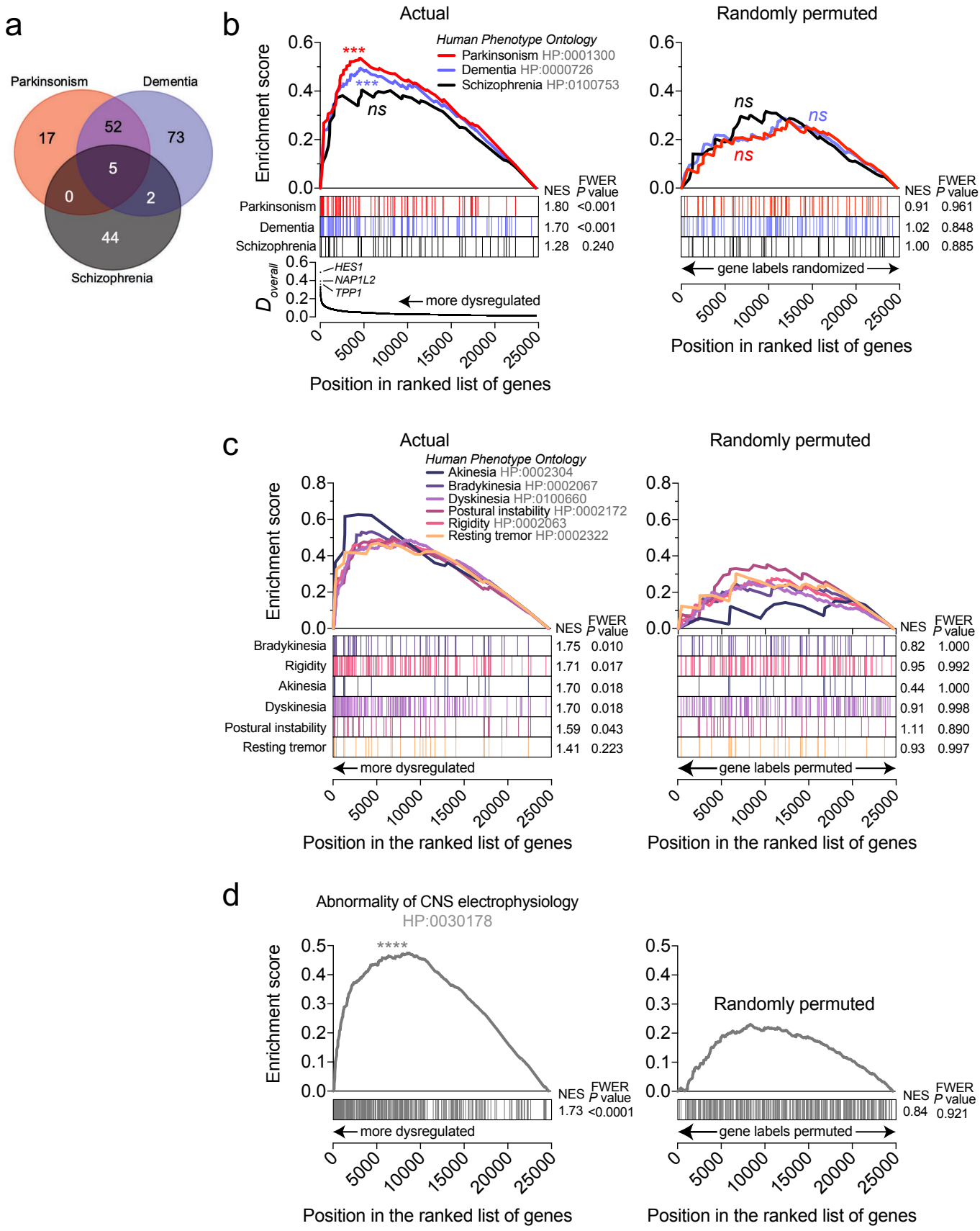


Supplementary Figure 1. Quality control metrics (percentage of mapped reads (**a**), number of genes detected (**b**) and number of housekeeping genes expressed (**c**)) for each single-cell or bulk RNA-seq library. Horizontal dotted lines indicate critical thresholds for sample inclusion/exclusion (refer to Methods for details).



Supplementary Figure 2. a Venn analysis of genes annotated to the Human Phenotype Ontologies for Parkinsonism, Dementia and Schizophrenia reveals substantial overlap between parkinsonism and dementia genes. **b-d** Significant associations of the dysregulated PD transcriptome with Parkinsonism (**b**), PD clinical symptoms ontology (**c**) and abnormality of central nervous system electrophysiology (**d**) is completely abolished upon random permutation of gene labels, effectively destroying the gene-dysregulation score relationship.