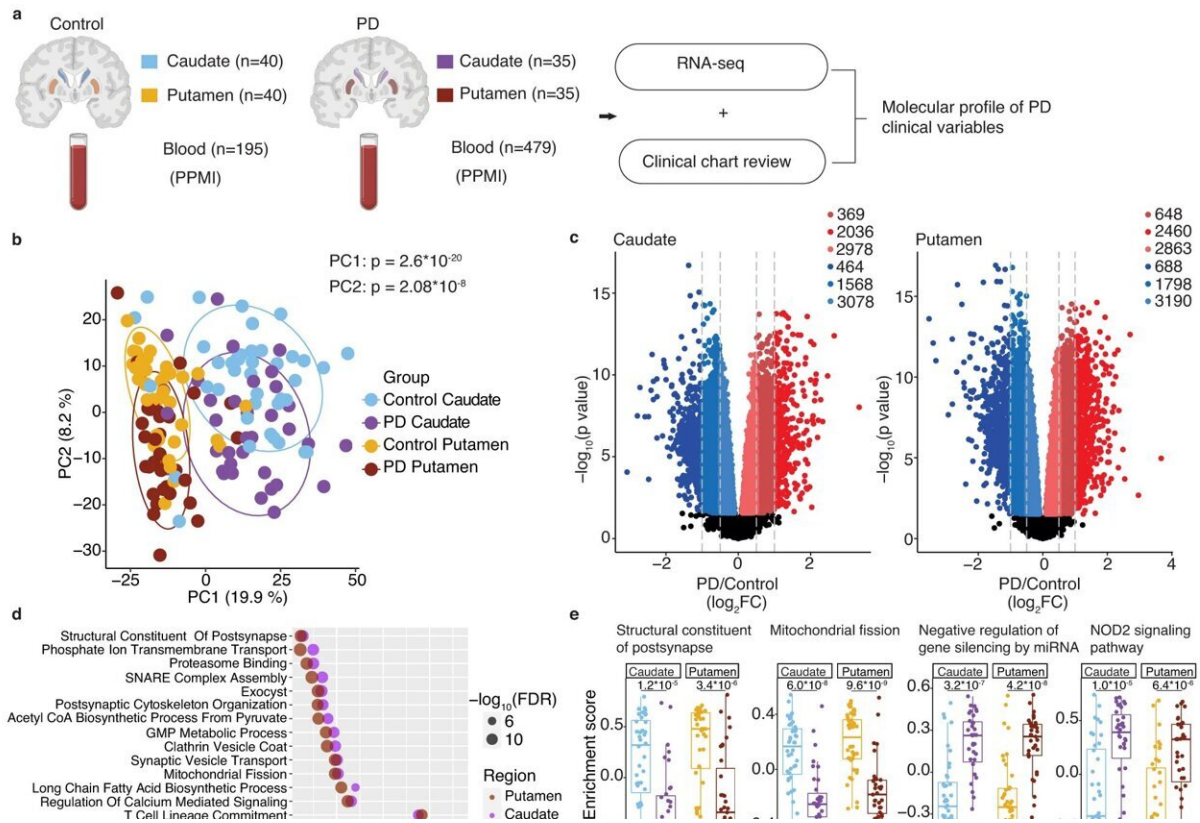# Researchers discover potential molecular indicators for Parkinson's symptoms

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Transcriptome patterns in PD caudate and putamen. **a** Overview of the study. Bulk RNA sequencing was performed in postmortem caudate and putamen from controls and PD patients. Antemortem blood transcriptome data was obtained from an independent cohort of subjects enrolled in the PPMI study. Clinical information was extracted from accompanying charts (postmortem donors) and open-access database (PPMI subjects) to determine molecular profiles associated with PD clinical variables. Parts of the image were created with BioRender.com. **b** Principal component analysis (PCA) shows the separation of caudate and

putamen regions of striatum along PC1 (p value: 2.6×10^{-20}, Kruskal–Wallis test). Healthy controls and PD are separated along PC2 (p value: 2.08×10^{-8}). Ellipses indicate confidence interval = 0.8 of indicated groups. **c** Volcano plot shows significantly changed RNAs in PD caudate and putamen compared to their respective controls. RNAs with significant changes in expression (determined by moderated *t*-tests with multiple test corrections using limma) with false discovery rate (FDR) 0.1, 0.5, and 1 are colored according to direction. **d** Bubble plot shows representative top significantly (FDR 0) and down ($\log_2$FC

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