Researchers identify a subtype of brain cells that die in Parkinson's patients

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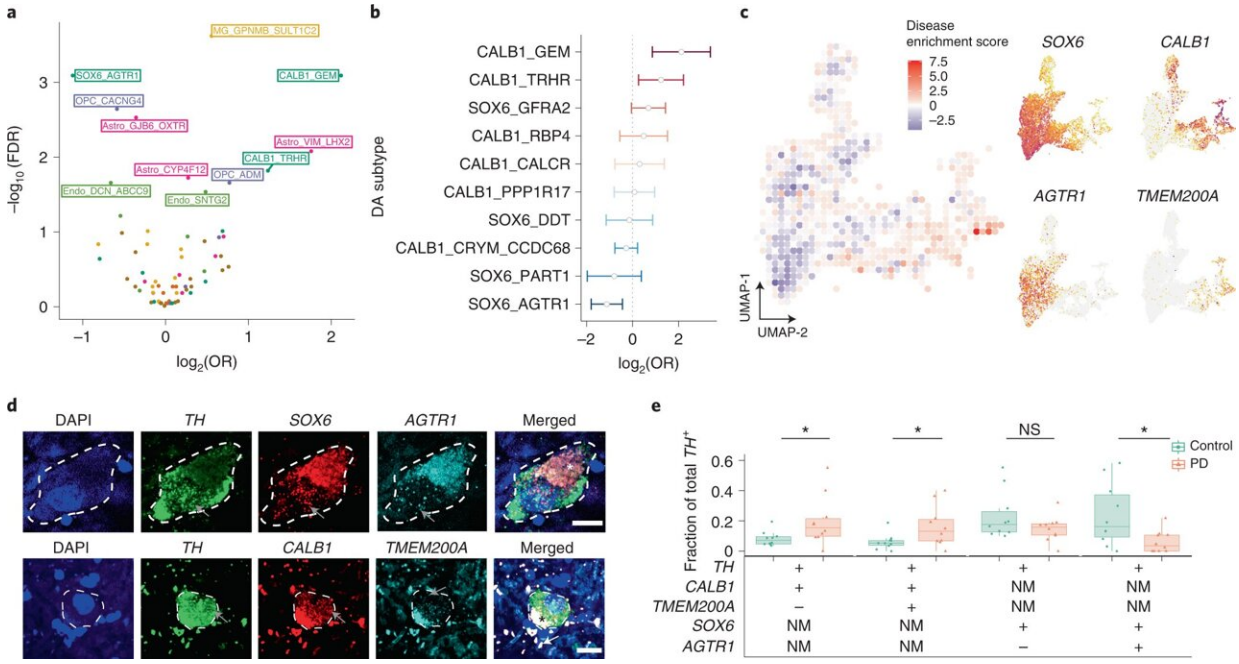

Quantification of DA subtype vulnerability to PD-associated degeneration. a, Volcano plot showing OR and FDR computed by MASC (Methods) for each of the 68 clusters identified in SNpc snRNA-seq analysis. Labeled clusters are those significantly (FDR-adjusted P 0.05, n = 22,048 DA neurons sampled across ten PD/LBD donors and eight neurotypical donors). c, Left: disease enrichment score (Methods) overlaid onto a binned UMAP representation of integrative analysis of both PD/LBD and control DA neurons (n = 10 PD/LBD individuals and n = 8 neurotypical controls). Right: expression of selected genes used to validate subtype vulnerability plotted on UMAP representation of DA neurons. d, Representative images of triple-positive cells for a disease-resistant DA population (TH^+/$CALB1^+$/$TMEM200A^+$) and a disease-vulnerable population

(TH$^+$/AGTR1$^+$/SOX6$^+$, bottom). White/black asterisks indicate neuromelanin-induced autofluorescence while white arrows show lipofuscin-induced autofluorescence; gray arrows indicate RNA puncta. Scale bars, 10 μm. e, Boxplot showing proportions of four DA populations across ten PD and ten control SNpc tissue donors, determined by counting smFISH images from the two staining procedures (3,258 and 2,081 DA neurons counted for first and second assay, respectively) described in d. Center line of the boxplot indicates the median value while upper and lower hinges indicate the first and third quartiles of data, respectively. Whisker distance between upper and lower hinges represent ≤1.5× interquartile range. All dots represent an individual case for each subtype as a fraction of total TH$^+$ cells counted. +, positive for marker; −, negative for marker; NM, not measured; NS, not significant. *P