Science Advances
AAAS

Supplementary Materials for

Lineage tracing of stem cell–derived dopamine grafts in a Parkinson's model reveals shared origin of all graft-derived cells

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Sci. Adv. **10**, eadn3057 (2024)
DOI: 10.1126/sciadv.adn3057

The PDF file includes:

Other Supplementary Material for this manuscript includes the following:

List of Supplementary Materials

Figure S1

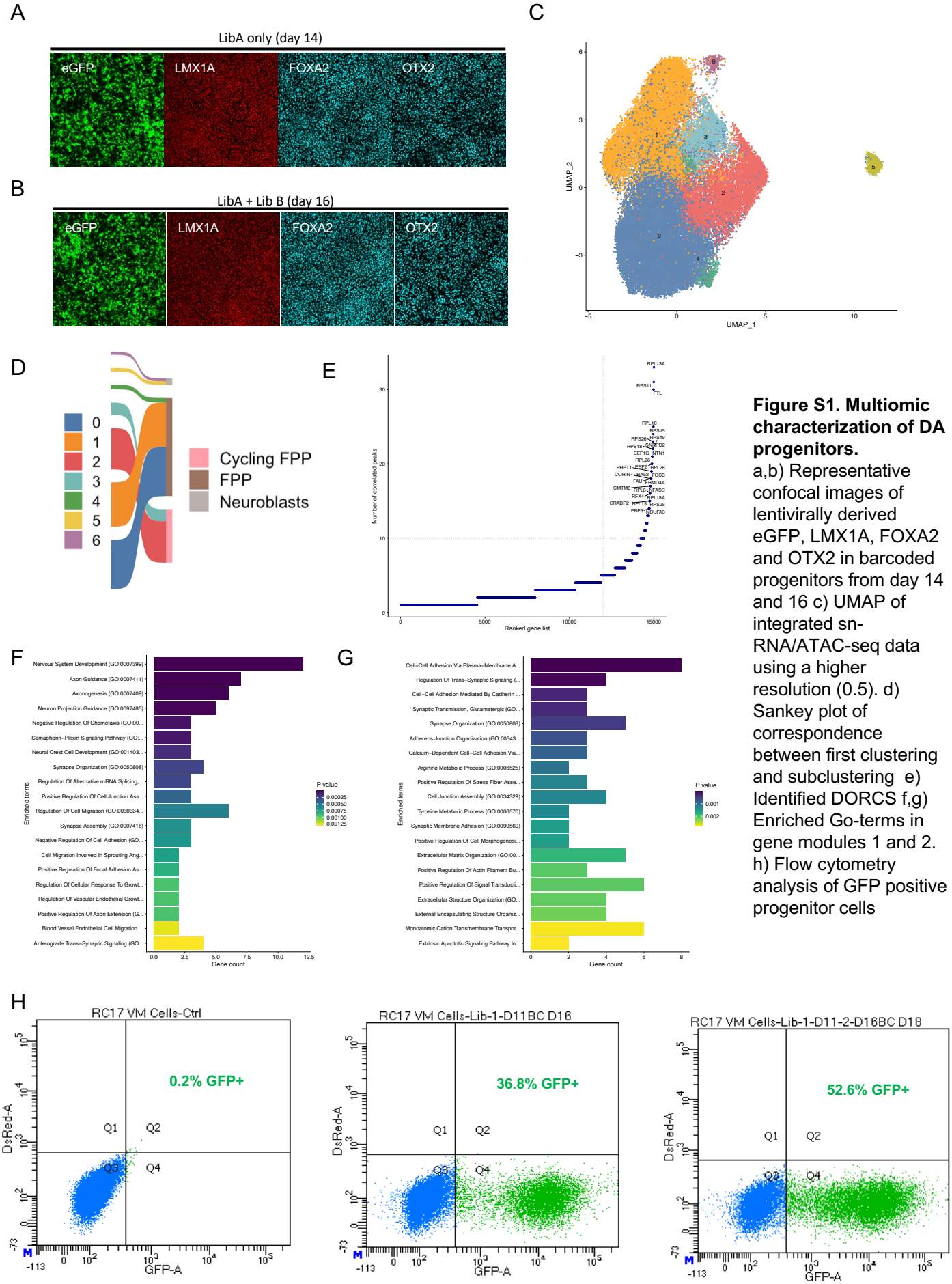
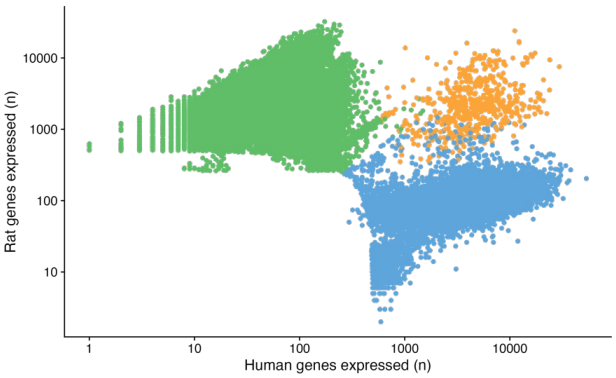


Figure S1. Multiomic characterization of DA progenitors. a,b) Representative confocal images of lentivirally derived eGFP, LMX1A, FOXA2 and OTX2 in barcoded progenitors from day 14 and 16 c) UMAP of integrated sn-RNA/ATAC-seq data using a higher resolution (0.5). d) Sankey plot of correspondence between first clustering and subclustering e) Identified DORCS f,g) Enriched Go-terms in gene modules 1 and 2. h) Flow cytometry analysis of GFP positive progenitor cells

Figure S2

A



B

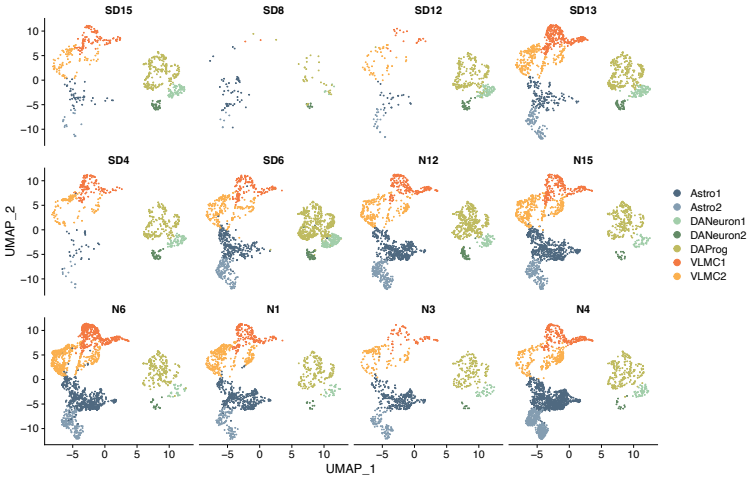


Figure S2. Graft quantification and quality control of snRNA-seq of grafted cells

a) Scatter plot of number of detected rat genes (y-axis) versus human genes (x-axis). Color indicates cell source with green = rat, yellow = human/rat doublet, blue=human. d) UMAP of individual samples of graft derived human cells. SD denotes spraque dawley rats (3 months) and N nude rats (6 months).

Figure S3

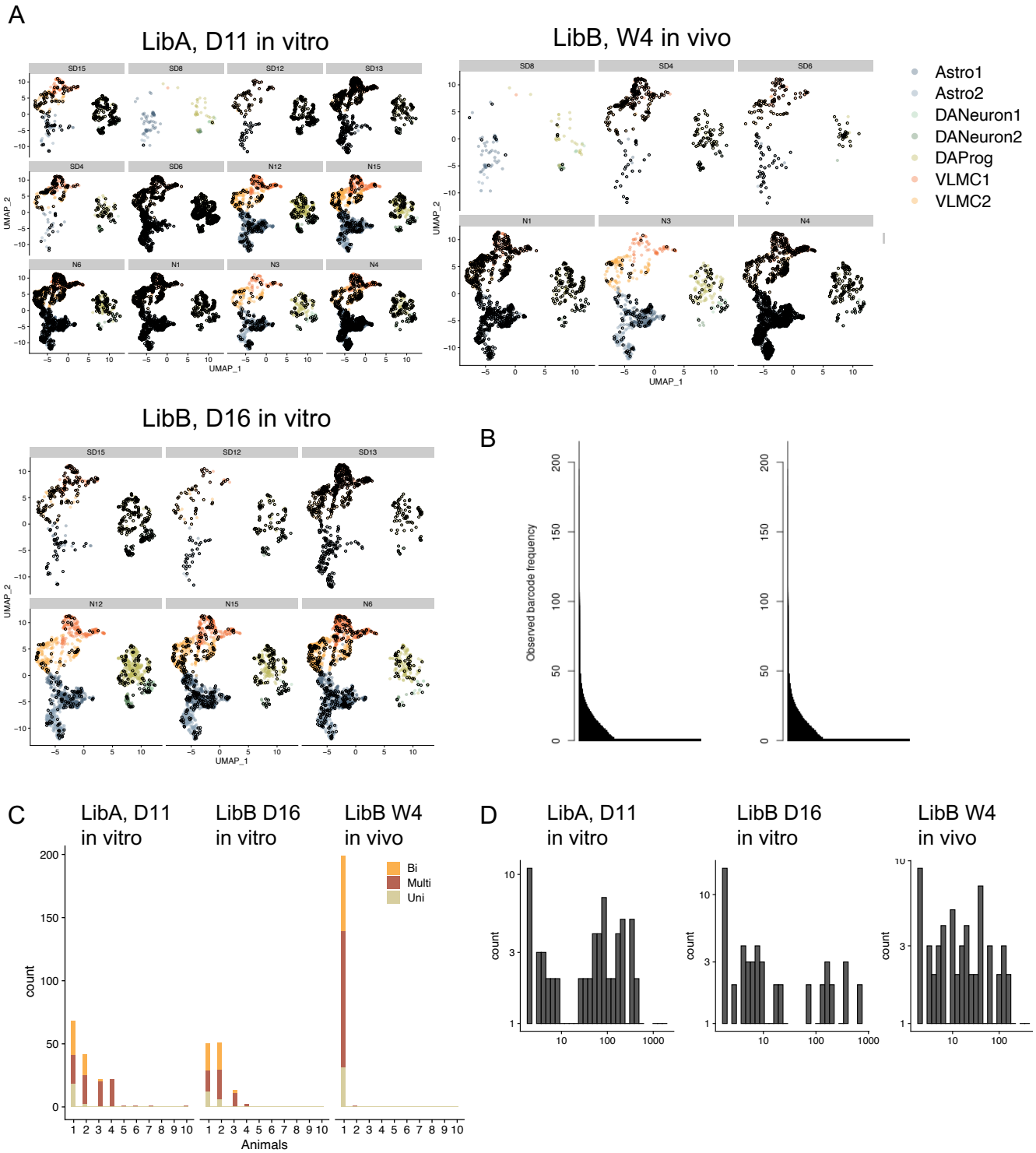


Figure S3 – Barcode detection and clone statistics
a) UMAP of individual samples of graft derived human cells with cells containing at least one viral barcode marked in black for the three different groups. b) Observed barcode frequency in the library as identified by sequencing of the viral pool. c) Frequency of clones per animal. X-axis denotes number of animals that the clone occurred in. Colored by potency. d) Clone sizes for the three different experiments.

Figure S4

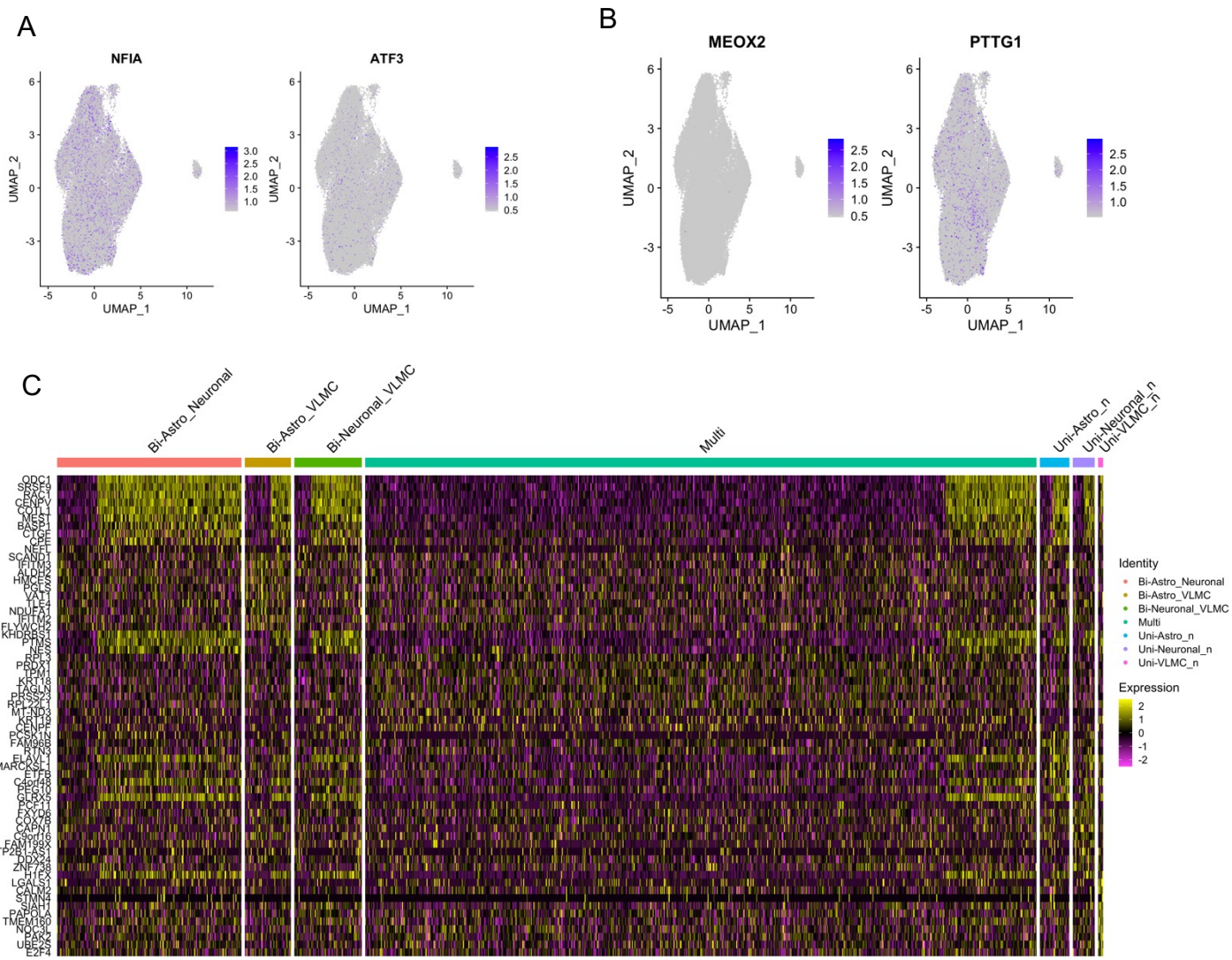


Figure S4 – Differentially expressed genes in progenitors
a,b) UMAP plots showing the expression of NFIA , ATF3, MEOX2 and PTTG1 across different progenitor cell types. The color gradient from gray to blue represents the expression levels of the genes, with higher expression indicated by darker shades of blue. c) Top ten differentially expressed genes per clone cell type in the progenitors. The heatmap uses a color gradient from purple to yellow, representing low to high expression levels, respectively.

Supplementary table caption

Table S1. Gene regulatory networks – transcription factors and targets

This table presents the summarized results of the gene regulatory network (GRN) analysis. For each transcription factor (TF) and target gene pair, the table includes the estimated effect size (estimate), the number of genomic regions (n_regions), the number of genes (n_genes), the number of transcription factors (n_tfs) involved, and the specific genomic regions analyzed. Additionally, the table provides the p-value (pval) and adjusted p-value (padj) for the statistical significance of each interaction.

Table S2. Gene regulatory networks – gene ontology analysis of gene modules

Gene ontology (GO) analysis conducted on gene modules identified within the gene regulatory networks. Each row represents a distinct GO term with the associated overlap between the genes in the module and the GO term, the p-value indicating the significance of the enrichment, the adjusted p-value after multiple testing correction, and additional statistical metrics. The specific genes contributing to the enrichment of each GO term are also listed.

Table S3. Simulation clone potency

Simulated and observed frequencies of different potency types (Bi, Multi, Uni) for various samples (LvLib1 D11 in vitro, LvLib2 D16 in vitro, etc.). The simulated frequency is expressed as a percentage with an associated standard deviation, and the observed frequency is provided as a raw count.