Expanded View Figures

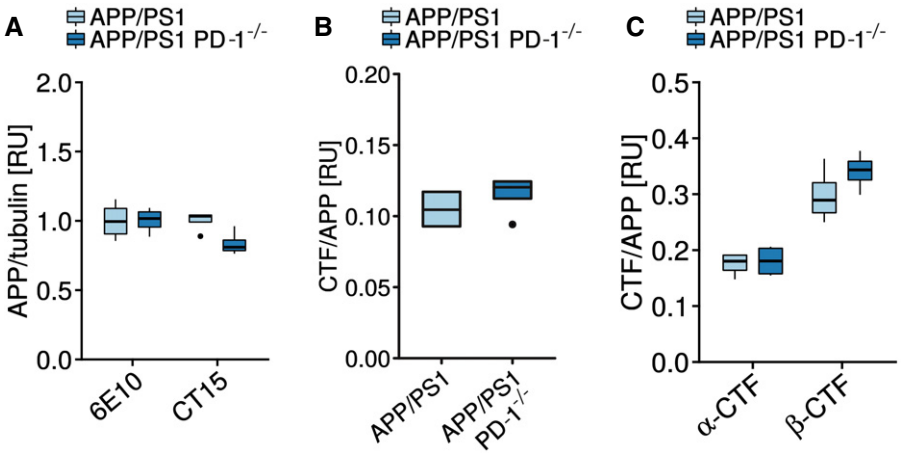

Figure EV1. APP expression is unaltered in APP/PS1 PD-1$^{-/-}$ mice.

A Quantification of the APP expression normalized to tubulin shown in Fig 4F (biological replicates with $n = 4$ mice per group, one-way ANOVA (df = 1, $F = 2.776$, $P = 0.122$), Tukey's *post hoc* test).

B Quantification of the 6E10 Western blot and the calculation of the APP C-terminal fragment (CTF)-to-APP ratio shown in Fig 4F (biological replicates with $n = 4$ mice per group, Student's *t*-test ($t = 0.9435$, df = 6), $P = 0.3818$).

C Quantification of the CT15 Western blot and the calculation of the APP α-C-terminal fragment (α-CTF)-to-APP and the APP β-C-terminal fragment (β-CTF)-to-APP ratio shown in Fig 4F (biological replicates with $n = 4$ mice per group, ANOVA (df = 1, $F = 1.184$, $P = 0.298$), Tukey HSD).

Data information: (A–C) Central bands represent median, boxes show interquartile range (IQR), and whiskers define the ± 1.5xIQR.

© 2021 The Authors

© 2021 The Authors

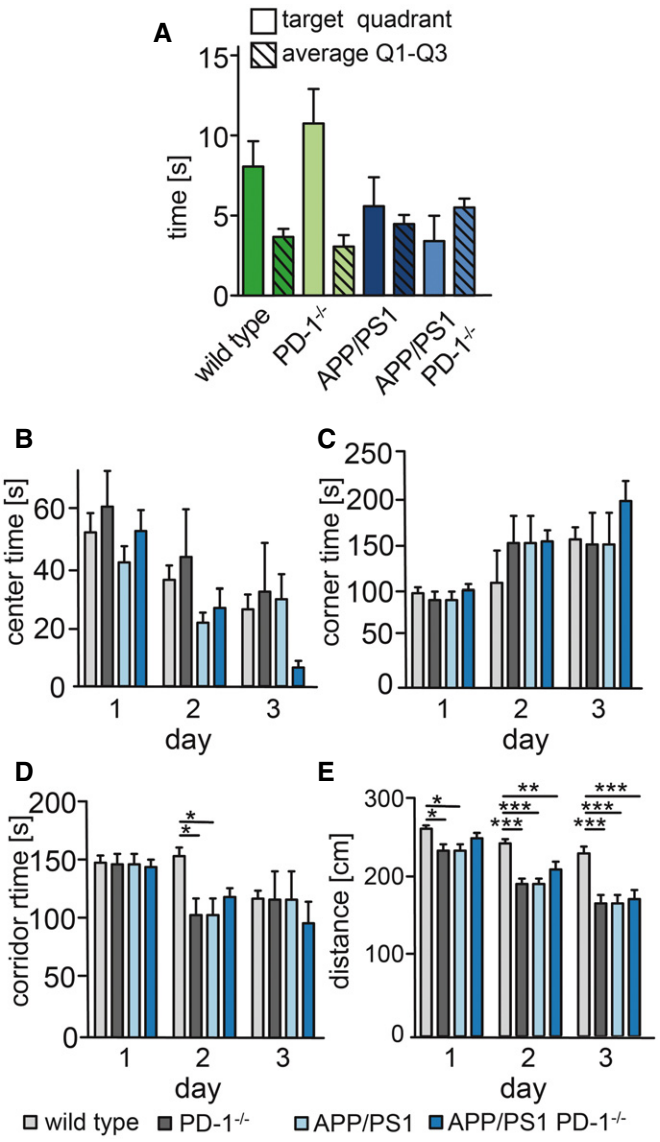

Figure EV2. Behavioral analysis of wild-type, PD-1$^{-/-}$, APP/PS1, and APP/PS1 PD-1$^{-/-}$ mice.

A Mice were tested one day after the last trial day for 30 s in the absence of the platform in quadrant 4. The time in the quadrants was measured and averaged for quadrants 1–3.

B–E Evaluation of the open field testing for (B) time spend in the center (center time) (ANOVA ($F = 0.83$, df = 6, $P = 0.54$), Bonferroni test), (C) corner time (ANOVA ($F = 0.47$, df = 6, $P = 0.93$), Bonferroni test), (D) corridor time (ANOVA ($F = 1.487$, df = 6, $P = 0.193$), Bonferroni test, $^{*}P < 0.05$), and (E) distance (ANOVA ($F = 0.83$, df = 6, $P = 0.54$), Bonferroni test, $^{*}P < 0.05$, $^{**}P < 0.01$, and $^{***}P < 0.001$).

Data information: For all panels: mean + SEM of biological replicates with $n = 12$ for wt, $n = 5$ for PD-1$^{-/-}$, $n = 7$ for APP/PS1, and $n = 5$ for APP/PS1 PD-1$^{-/-}$.

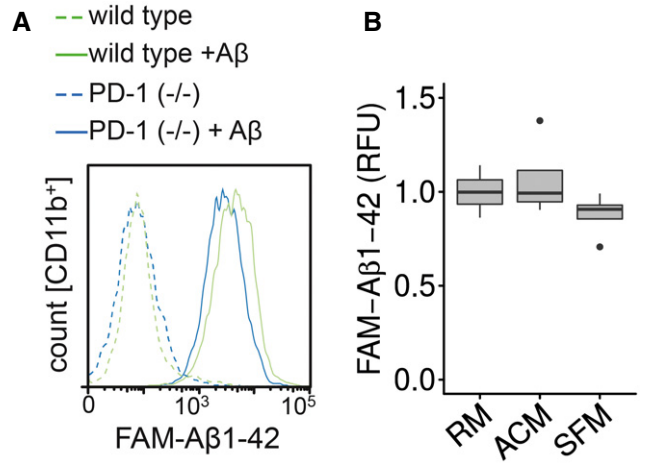

Figure EV3. Aβ phagocytosis in PD-1$^{-/-}$ microglial cells by flow cytometry.

A Microglia from wild-type or PD-1$^{-/-}$ mice were incubated with FAM-Aβ1-42, and the increase in fluorescence was measured in the CD11b^{+} cells.

B Microglia were preincubated for 1 h with regular medium (RM), astrocyte-conditioned medium (ACM), or serum-free medium (SFM) followed by the addition of 0.5 μM FAM-Aβ1-42 for 4 h (median (central band) with interquartile range (IQR; boxes) and ± 1.5xIQR (whiskers) of one experiment in technical quadruplicates, one-way ANOVA (df = 2, $F = 1.493$, $P = 0.275$), Tukey's HSD).

© 2021 The Authors

© 2021 The Authors

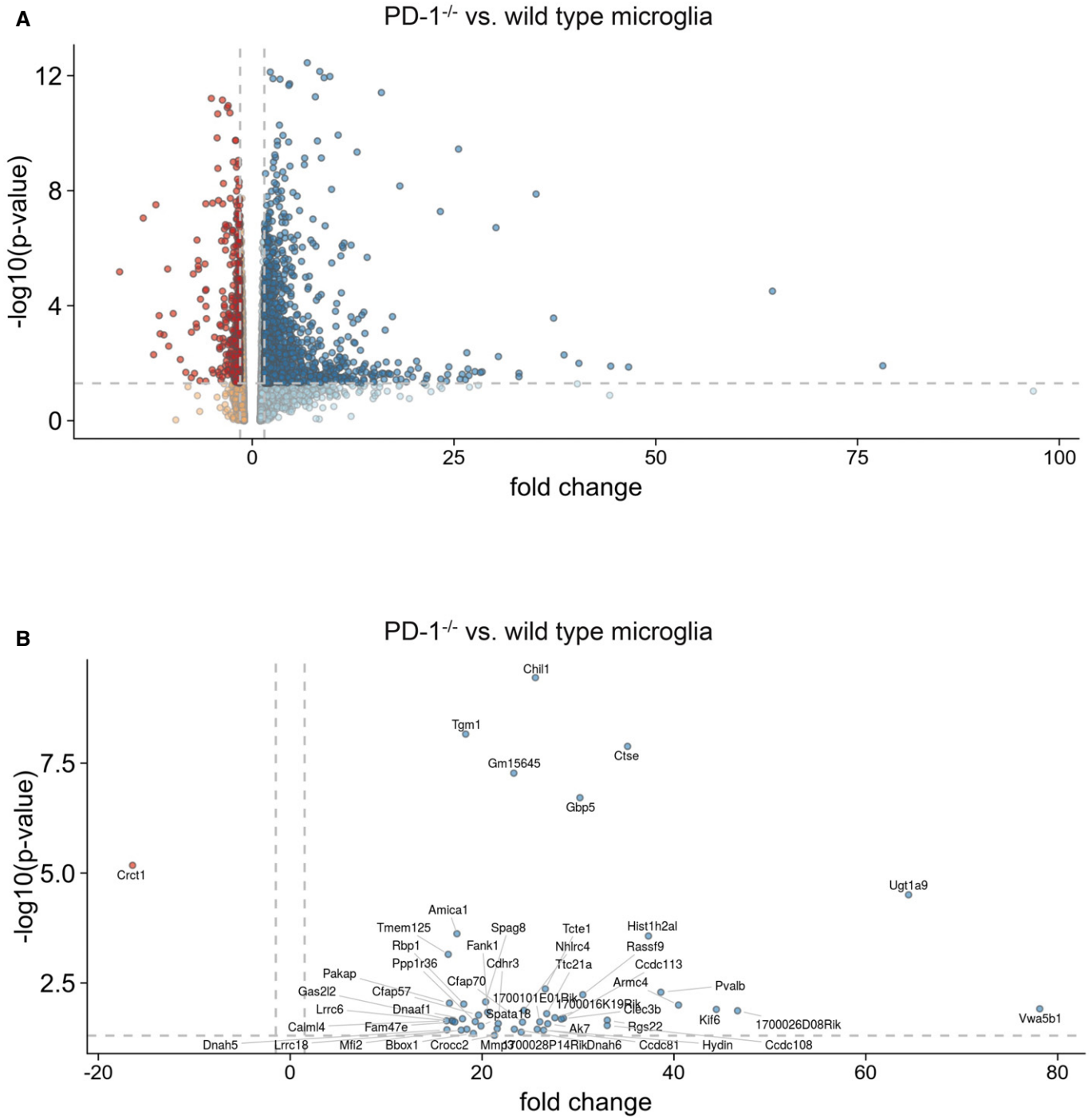

Figure EV4. Gene expression analysis of wild type and PD-1$^{-/-}$ microglia.

A Gene expression in microglia from wild-type or PD-1$^{-/-}$ mice presented as a Volcano plot. Dark data points represent more than 1.5 times up- or downregulated genes that have a *P*-value of 0.05 or less (one-way ANOVA, dashed lines represent fold change ± 1.5 and $P = 0.05$).

B Same as A but only the top 50 regulated genes are depicted (one-way ANOVA, dashed lines represent fold change ± 1.5 and $P = 0.05$).

© 2021 The Authors

© 2021 The Authors

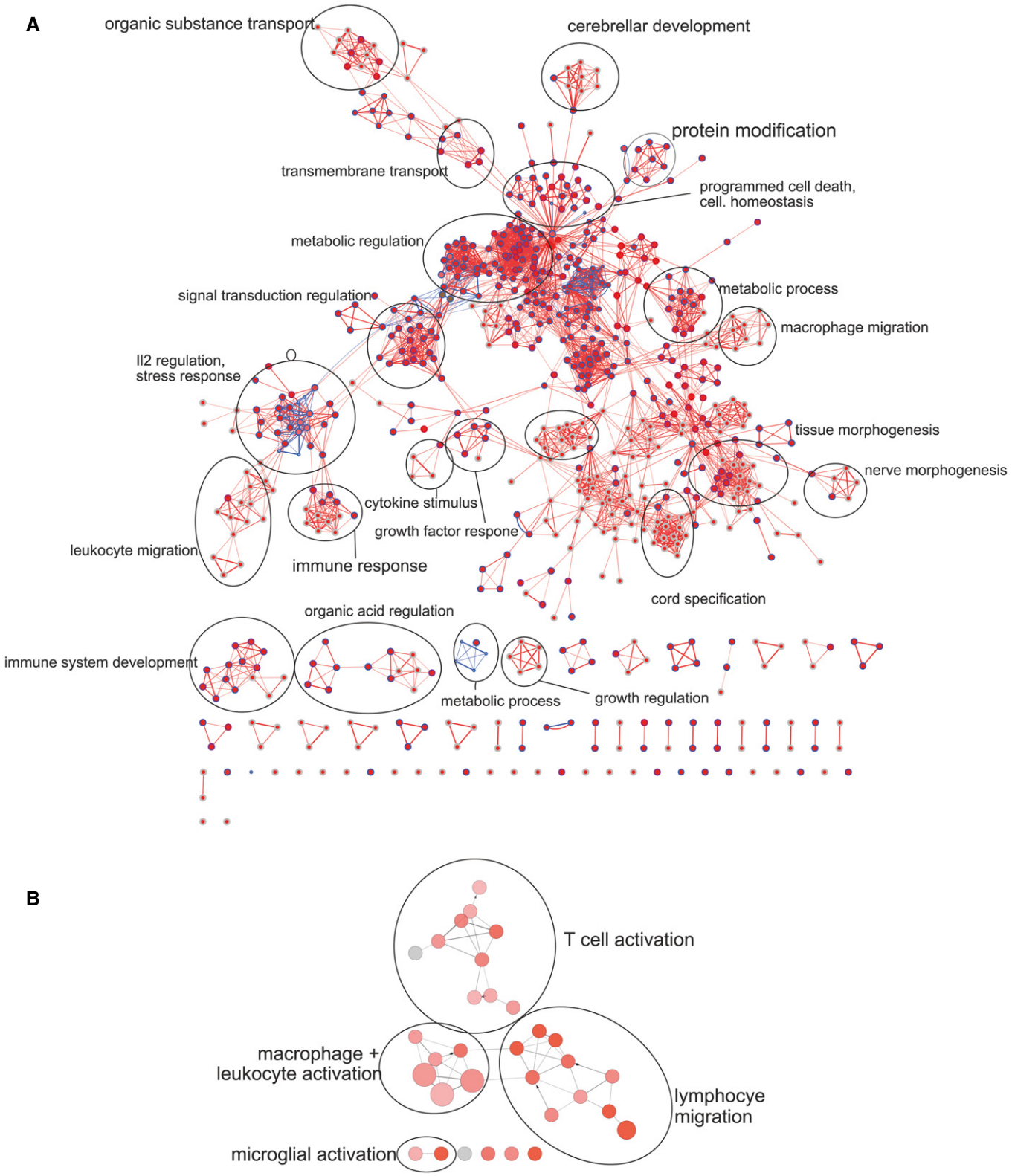

Figure EV5. Gene ontology (GO) enrichment analysis.

A Visualization of gene ontology enrichment analysis (GOEA) of DE genes (PD-1$^{-/-}$ vs. wild-type microglia: blue = downregulated genes, red = upregulated genes) using BiNGO and the EnrichmentMap plugin.

B ClueGO network analysis of "Immune System Process" GO terms of DE genes (PD-1$^{-/-}$ vs. wild-type microglia: red = upregulated genes).

© 2021 The Authors