
Supplementary information

Dopamine drives persistent remodelling of the maternal brain

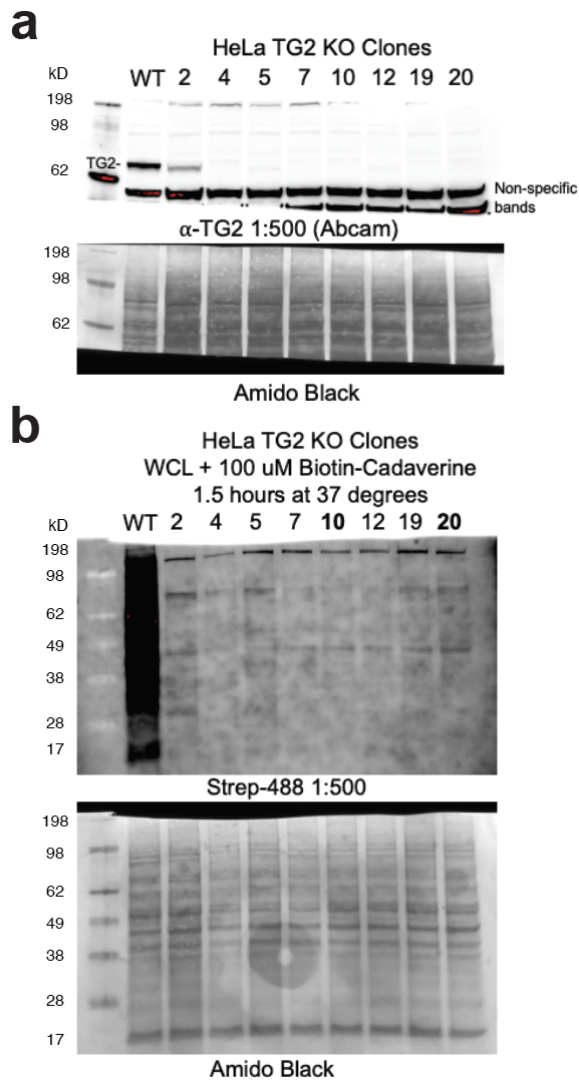
In the format provided by the
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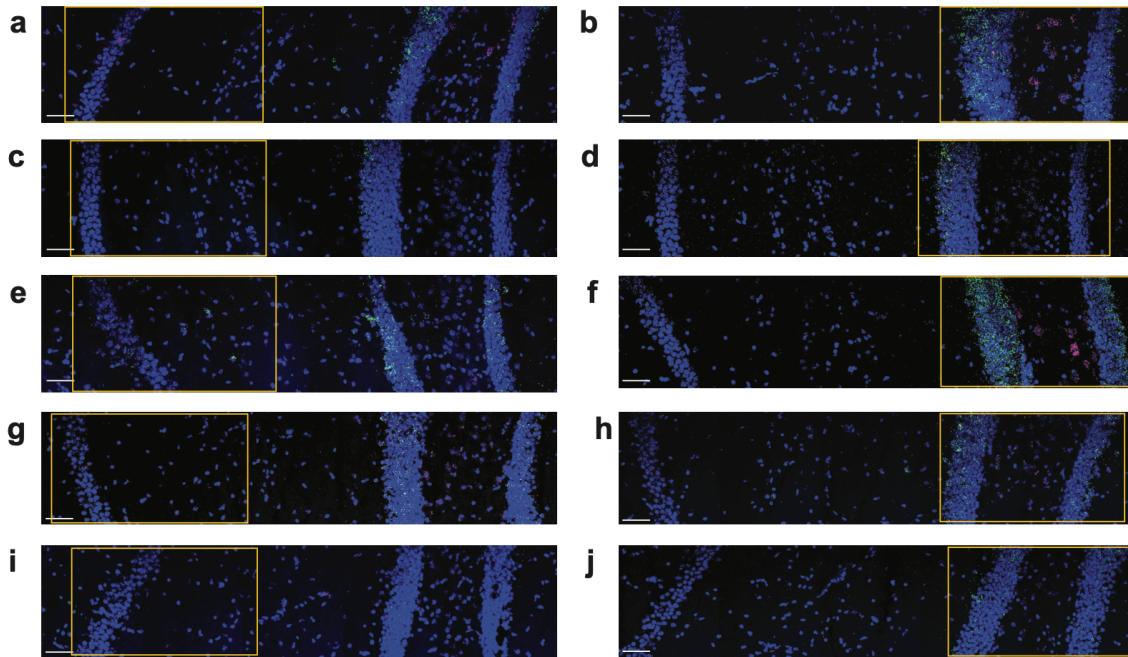
Dopamine drives persistent remodeling of the maternal brain

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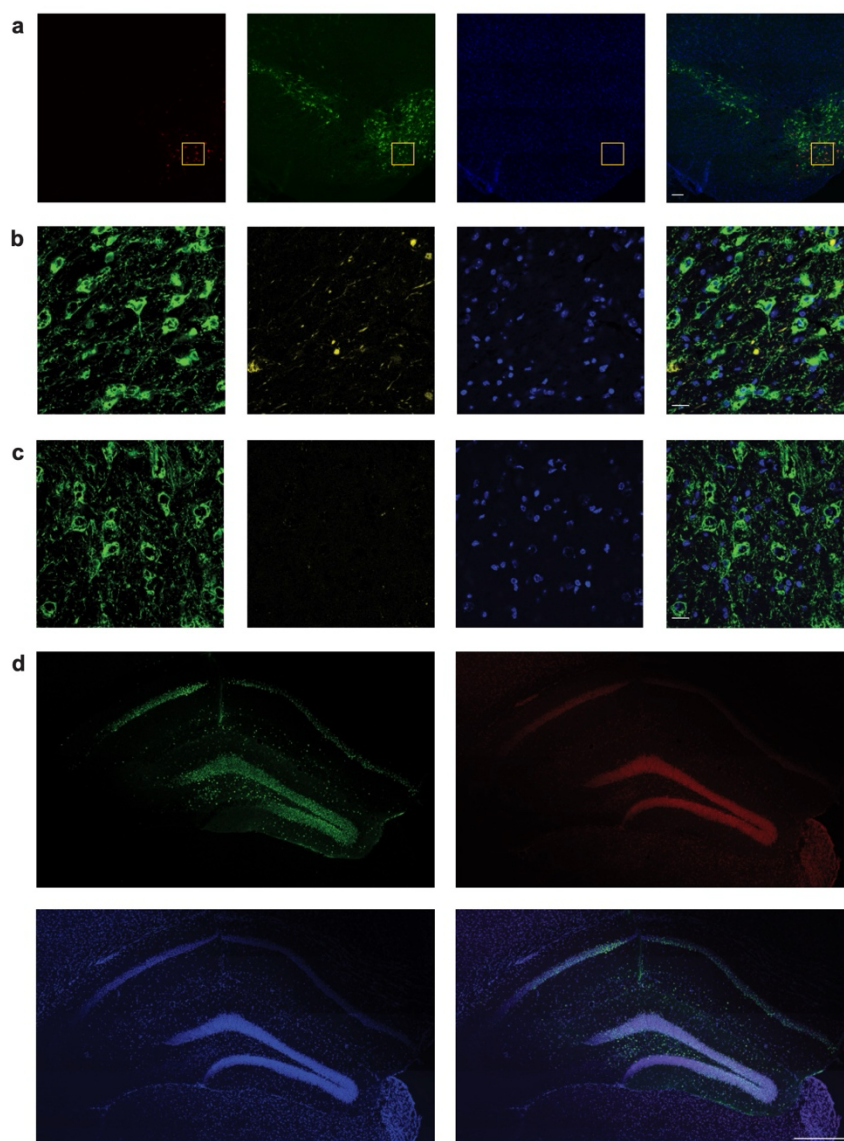
Supplementary Figure 1. Uncropped blots related to Extended Data Figure 8

Western blots related to (a) Extended Data Fig 8a, (b) Extended Data Fig 8b. The images shown in Extended Data Fig. 8 are presented in uncropped form. Amido Black staining, used as a loading control, was performed on the same blot.



Supplementary Figure 2. Uncropped RNAscope images related to Figures 2 and 4.

Full tiled RNAscope images related to **(a)** Fig 2i (NP CA1), **(b)** Fig 2j (NP DG), **(c)** Fig 2i (Control RE CA1), **(d)** Fig 2j (Control RE DG), **(e)** Fig 2i (Stress RE CA1), **(f)** Fig 2j (Stress RE DG), **(g)** Fig 4g (NP-mCherry CA1), **(h)** Fig 4h (NP-mCherry DG), **(i)** Fig 4g (NP-hM4Di CA1), **(j)** Fig 4h (NP-hM4Di DG). Scale bars, 50 μ m. Yellow boxes indicate representative images presented in the Figures.



Supplementary Figure 3. Uncropped microscopy images related to Figures 4, 5 and Extended Data 9. Confocal images related to (a) Fig 4a-b; Scale bar, 100 μm , (b) Extended Data 9a (rTH-mCherry); Scale bar, 20 μm , (c) Extended Data 9a (rTH-hM4Di); Scale bar, 20 μm , (d) Fig 5b; Scale bar, 400 μm . Yellow boxes indicate representative images presented in the Figures.

Legends for Supplementary Tables 1-19

Supplementary Table 1. DESeq2 results for bulk RNA-seq of 11 brain regions, comparing NP vs. RE related to Figure 1 and Extended Data Figure 1.

Supplementary Table 2. DESeq2 results for bulk RNA-seq of 11 brain regions, adjusted for cell composition, comparing NP vs. RE related to Figure 1 and Extended Data Figure 1.

Supplementary Table 3. DESeq2 results for bulk RNA-seq of dHF across reproductive events (NP, Mating + No Pregnancy, Mating + Pregnancy + Birth, Pup Sensitized, RE) related to Extended Data Figure 3.

Supplementary Table 4. DESeq2 results for bulk RNA-seq of dHF across reproductive timepoints (7.5dpc, 17.5dpc, 2dpp, 21dpp, NP, RE) related to Extended Data Figure 4.

Supplementary Table 5. DESeq2 results for bulk RNA-seq of vHF across reproductive timepoints (7.5dpc, 17.5dpc, 2dpp, 21dpp, NP, RE) related to Extended Data Figure 4.

Supplementary Table 6. DESeq2 results for bulk RNA-seq of mPFC across reproductive timepoints (7.5dpc, 17.5dpc, 2dpp, 21dpp, NP, RE) related to Extended Data Figure 4.

Supplementary Table 7. DESeq2 results for bulk RNA-seq in dHF examining effect of late postpartum stress (NP, Control RE, Stress RE) related to Figure 2 and Extended Data Figure 5.

Supplementary Table 8. DESeq2 results for bulk RNA-seq in dHF examining effect of early postpartum stress (NP, Control RE, Early Stress RE) related to Extended Data Figure 6.

Supplementary Table 9. Diffbind results for H3K4me3Q5dop CUT&RUN-seq in dHF examining effect of parity (Control RE vs. NP) related to Figure 3 and Extended Data Figure 8.

Supplementary Table 10. Diffbind results for H3K4me3Q5dop CUT&RUN-seq in dHF examining effect of postpartum stress (Control RE vs. Stress RE) related to Figure 3 and Extended Data Figure 8.

Supplementary Table 11. Clinical, demographic, and parity information for donors of human postmortem dorsal subiculum tissues.

Supplementary Table 12. DESeq2 results for bulk RNA-seq in human dorsal subiculum examining effect of parity (Parous vs. NP) related to Figure 3 and Extended Data Figure 8.

Supplementary Table 13. Diffbind results for H3K4me3Q5dop CUT&RUN-seq in human dorsal subiculum examining effect of parity (Parous vs. NP) related to Figure 3 and Extended

Data Figure 8.

Supplementary Table 14. DESeq2 results for bulk RNA-seq in dHF examining effect of chronic chemogenetic suppression of VTA-dHF projection (NP-mCherry, NP-hM4Di, RE-mCherry, RE-hM4Di) related to Figure 4 and Extended Data Figure 9.

Supplementary Table 15. Diffbind results for H3K4me3Q5dop CUT&RUN-seq in dHF examining effect of chronic chemogenetic suppression of VTA-dHF projection (NP-mCherry vs. NP-hM4Di) related to Figure 4 and Extended Data Figure 9.

Supplementary Table 16. Diffbind results for H3K4me3Q5dop CUT&RUN-seq examining effect of postpartum stress in virally manipulated dHF (Control RE H3.3WT vs. Stress RE H3.3WT) related to Figure 5 and Extended Data Figure 10.

Supplementary Table 17. Diffbind results for H3K4me3Q5dop CUT&RUN-seq examining effect of H3.3Q5A in postpartum stress dHF (Stress RE H3.3WT vs. Stress RE H3.3Q5A) related to Figure 5 and Extended Data Figure 10.

Supplementary Table 18. DESeq2 results for bulk RNA-seq in dHF examining effect of H3.3Q5A in postpartum stress (Control RE H3.3WT, Stress RE H3.3WT, Stress RE H3.3Q5A) related to Figure 5 and Extended Data Figure 10.

Supplementary Table 19. Fisher's exact test ($p > 0.05$) results for estrous stage distributions across groups for all behavioral assays. All staging information is available in the Source Data file.