

Supplementary Information for

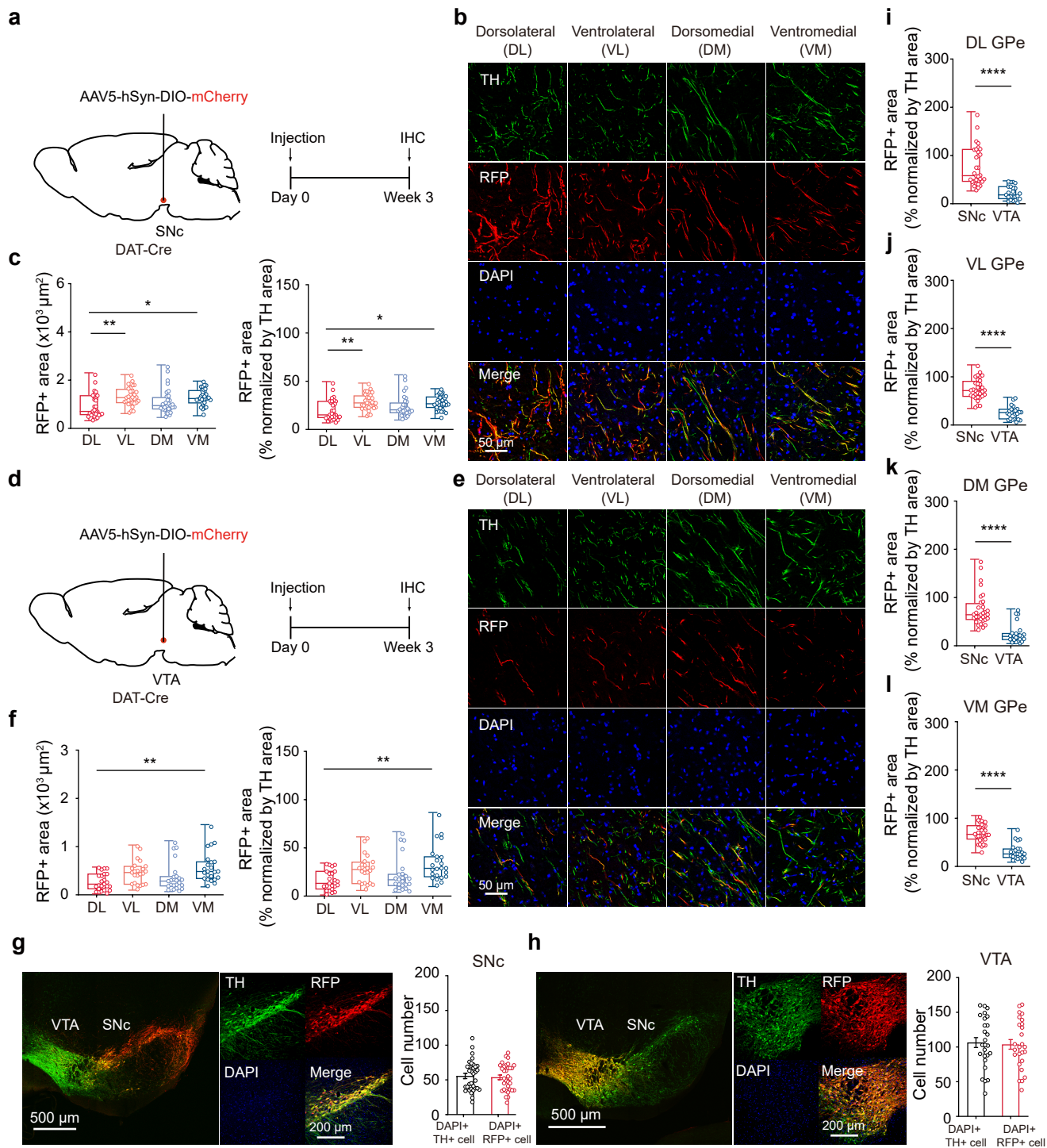
Distinct modes of dopamine modulation on

striatopallidal synaptic transmission

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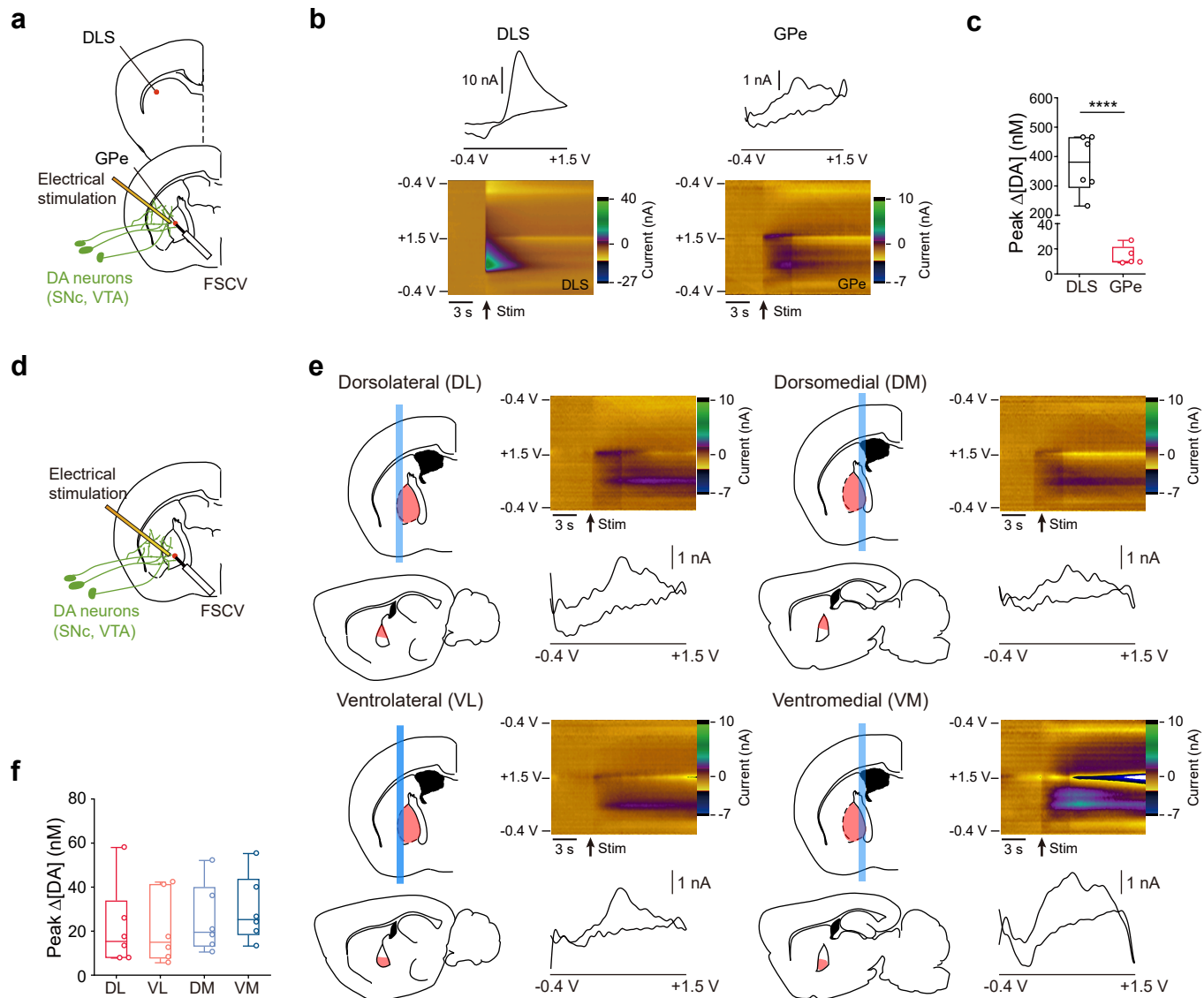
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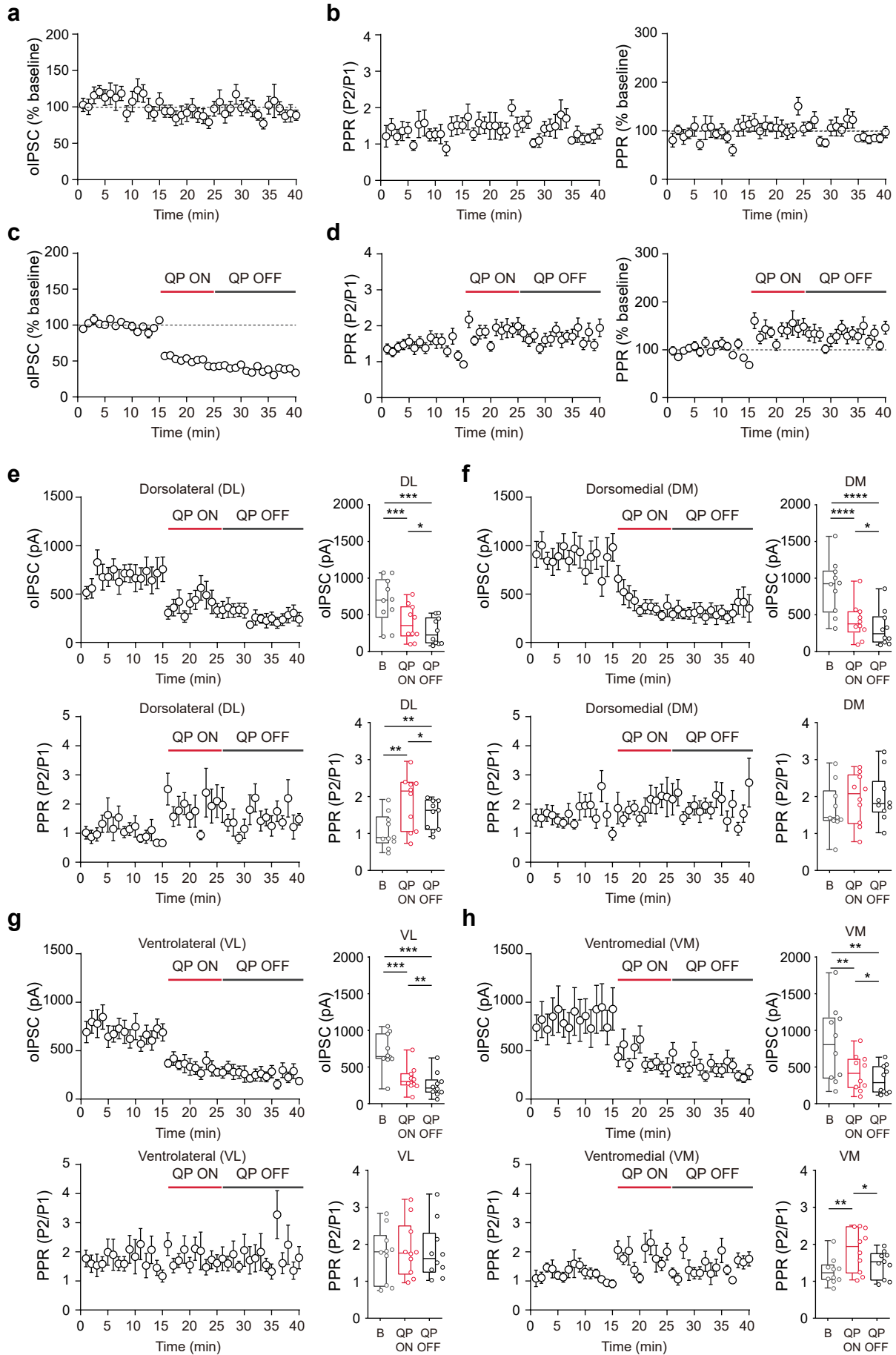
Supplementary Fig. 1 | The SNc is the principal source of the nigropallidal pathway projecting to the GPe

a,d, A schematic illustrations describing the injection of AAV5-hSyn-DIO-mCherry virus into the SNc and VTA of DAT-Cre mice to selectively label dopaminergic axons from the SNc and VTA. **b,e**, Representative confocal images of TH+ dopaminergic and RFP+ axons originating from the SNc and VTA dopamine neurons. **c**, Summary statistics of virally expressed RFP+ axonal areas in the GPe subregions, originating from the SNc (left) (n = 32 images from 6 mice per each group, one-way ANOVA with Holm-Sidak's post-hoc multiple comparisons test; DL $935.72 \pm 89.33 \mu\text{m}^2$, VL $1322.18 \pm 70.73 \mu\text{m}^2$, DM $1096.91 \pm 92.89 \mu\text{m}^2$, VM $1284.85 \pm 62.93 \mu\text{m}^2$; $p = 0.0026$) and RFP+ areas normalized to the TH+ areas (right) (DL $20.17 \pm 1.93\%$, VL $28.50 \pm 1.53\%$, DM $23.64 \pm 2.0\%$, VM $27.69 \pm 1.36\%$). **f**, Summary statistics of virally expressed RFP+ axonal areas in the GPe subregions, originating from the VTA (left) (n = 23 images from 5 mice per each group, one-way ANOVA with Holm-Sidak's post-hoc multiple comparisons test; DL $273.04 \pm 37.82 \mu\text{m}^2$, VL $465.54 \pm 52.02 \mu\text{m}^2$, DM $369.82 \pm 65.53 \mu\text{m}^2$, VM $571.82 \pm 67.85 \mu\text{m}^2$; $p = 0.0029$) and RFP+ areas normalized to the TH+ areas (right) (DL $16.25 \pm 2.25\%$, VL $27.71 \pm 3.10\%$, DM $22.01 \pm 3.90\%$, VM $34.03 \pm 4.04\%$). **g,h**, Representative confocal images of TH+ dopamine neurons and RFP+ neurons in the SNc or VTA of DAT-Cre mice (left), and summary statistics of TH+ and RFP+ cell numbers (right) in the SNc (n = 33 images from 6 mice per each group, paired t-test; DAPI+ TH+ cell 55.64 ± 3.79 , DAPI+ RFP+ cell 53.73 ± 3.33) or in the VTA (n = 26 images from 5 mice per each group, paired t-test; DAPI+ TH+ cell 106.40 ± 7.16 , DAPI+ RFP+ cell 103.70 ± 6.94). **i-l**, Summary statistics of virally expressed RFP+ axonal areas normalized to the TH+ areas in the DL GPe (paired t-test; SNc $77.41 \pm 7.39\%$, VTA $22.59 \pm 3.13\%$), VL GPe (SNc $73.96 \pm 3.96\%$, VTA $26.04 \pm 2.91\%$), DM GPe (SNc $74.79 \pm 6.33\%$, VTA $25.21 \pm 4.47\%$), and VM GPe (SNc $69.20 \pm 3.39\%$, VTA $30.80 \pm 3.65\%$). The data are presented as box-and-whisker plots or mean $\pm$ SEM. * $p < 0.05$, ** $p < 0.01$, **** $p < 0.0001$.



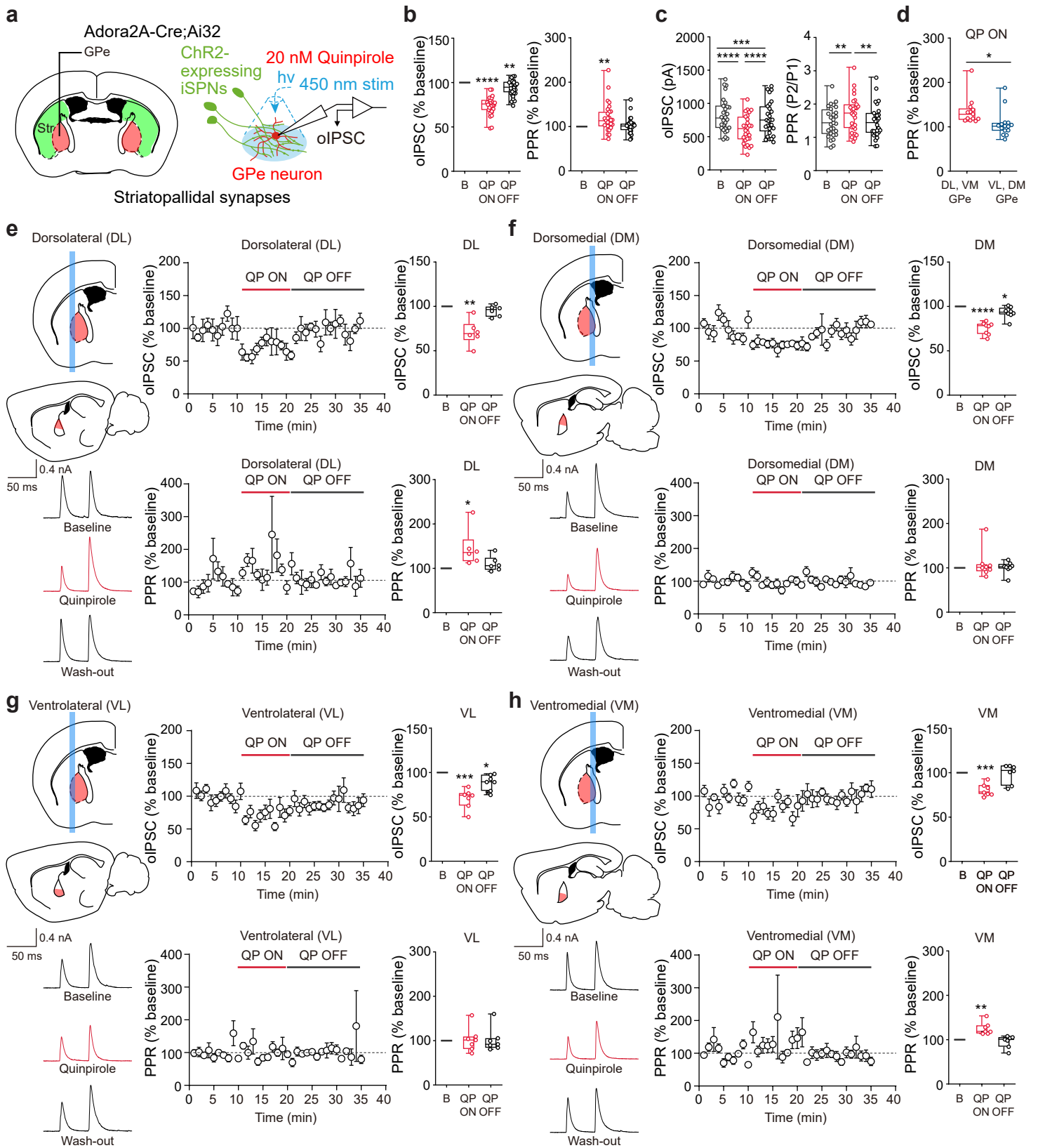
Supplementary Fig. 2 | Electrical stimulation of dopaminergic axons evokes measurable dopamine release in the GPe

a,d, Schematic illustrations describing the FSCV recording setup and electrical stimulation in the dorsolateral striatum (DLS) and GPe. **b**, Representative 2D voltammogram showing oxidation and reduction peaks of dopamine (top) and representative 3D color-coded voltammograms (bottom) in the DLS and GPe. **c**, Quantification of peak dopamine amplitude in the DLS and GPe ($n = 6$ slices from 2 mice for the DLS, $n = 5$ slices from 2 mice for the GPe, unpaired t-test; DLS 373.28 ± 40.15 nM, GPe 14.26 ± 3.41 nM; $p < 0.0001$). **e**, Schematic illustrations of the GPe subregions (left), representative 3D color-coded voltammograms (top), and 2D voltammogram showing oxidation and reduction peaks of dopamine (bottom) in the GPe subregions. **f**, Quantification of peak dopamine amplitude in the GPe subregions ($n = 6$ slices from 2 mice per each subregion, one-way ANOVA; DL 21.69 ± 7.77 nM, VL 21.20 ± 6.69 nM, DM 25.24 ± 6.47 nM, VM 29.82 ± 6.24 nM). The data are presented as box-and-whisker plots. **** $p < 0.0001$.



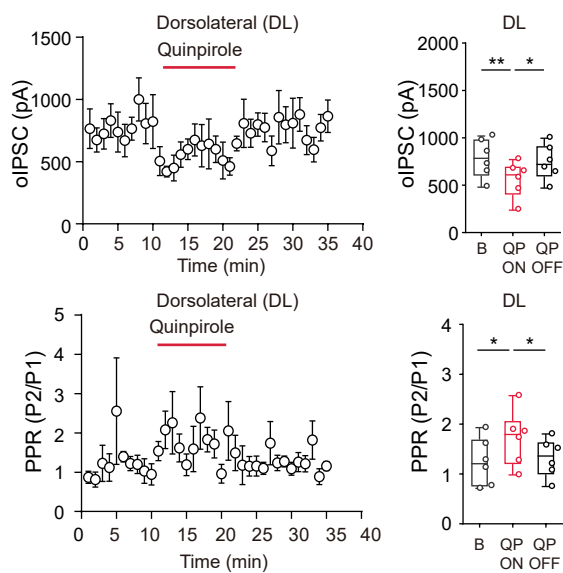
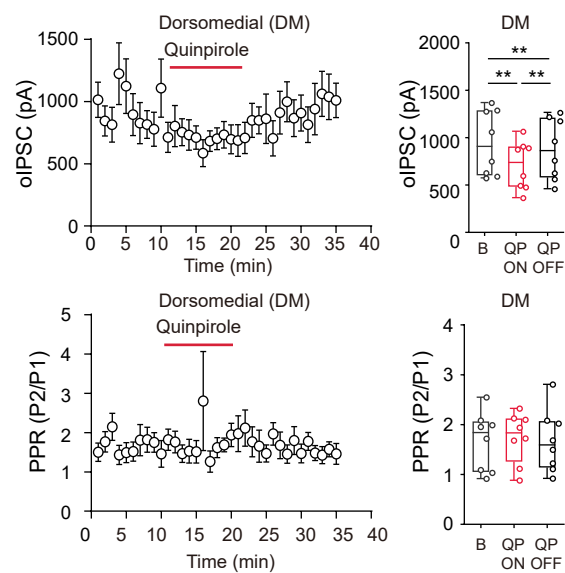
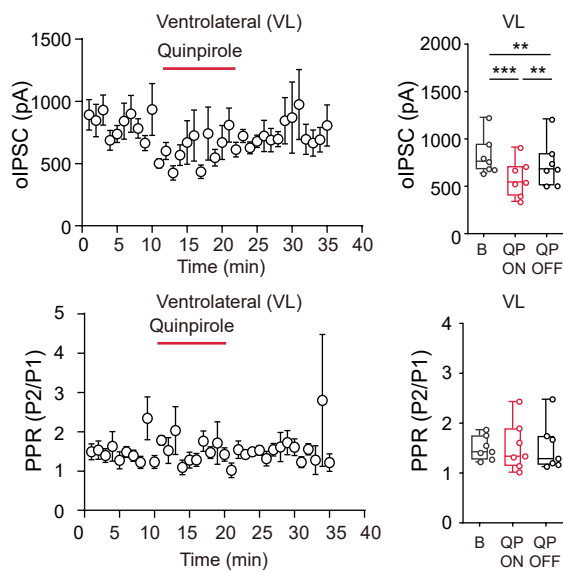
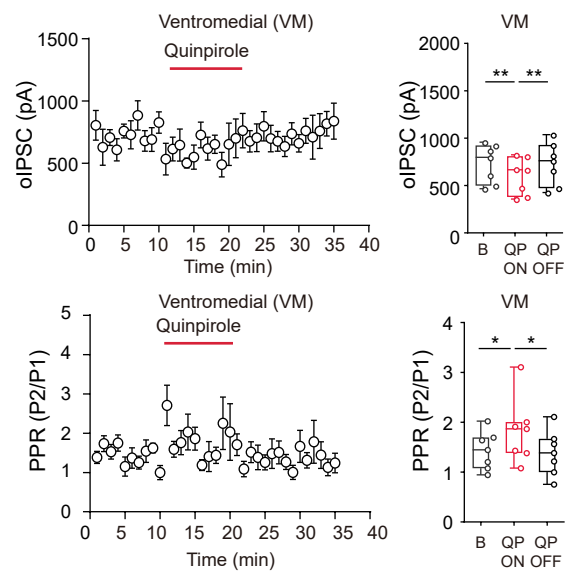
Supplementary Fig. 3 | Distinct dopaminergic modulation of striatopallidal synaptic transmission through D2-like receptors in the GPe subregions

a,b, Optogenetically evoked striatopallidal synaptic transmission (normalized oIPSC amplitude) and PPR plots. **c,d**, Normalized oIPSC amplitude, PPR plot (left), and normalized PPR plot (right) with the bath application of quinpirole (10 μ M). **e-h**, Absolute values of oIPSCs (top left), PPR plots (bottom left), and summary statistics of the absolute values of oIPSCs (top right) and PPRs (bottom right) in the GPe subregions. **e**, Summary statistics of absolute values of oIPSCs (repeated measures one-way ANOVA with Holm-Sidak's post-hoc multiple comparisons test; Baseline 687.91 ± 99.27 pA, QP ON 392.23 ± 75.84 pA, QP OFF 276.23 ± 57.86 pA; $p < 0.0001$) and PPRs (repeated measures one-way ANOVA with Holm-Sidak's post-hoc multiple comparisons test; Baseline 1.07 ± 0.15 , QP ON 1.87 ± 0.23 , QP OFF 1.51 ± 0.13 ; $p = 0.0014$) in the DL GPe. **f**, Summary statistics of absolute values of oIPSCs (repeated measures one-way ANOVA with Holm-Sidak's post-hoc multiple comparisons test; Baseline 880.68 ± 117.09 pA, QP ON 415.02 ± 77.89 pA, QP OFF 316.22 ± 76.99 pA, $p < 0.0001$) and PPRs (repeated measures one-way ANOVA with Holm-Sidak's post-hoc multiple comparisons test; Baseline 1.67 ± 0.21 , QP ON 1.95 ± 0.22 , QP OFF 1.98 ± 0.21 ; $p = 0.2845$) in the DM GPe. **g**, Summary statistics of absolute values of oIPSCs (repeated measures one-way ANOVA with Holm-Sidak's post-hoc multiple comparisons test; Baseline 706.24 ± 78.25 pA, QP ON 338.83 ± 53.94 pA, QP OFF 256.08 ± 51.93 pA, $p < 0.0001$) and PPRs (repeated measures one-way ANOVA with Holm-Sidak's post-hoc multiple comparisons test; Baseline 1.72 ± 0.23 , QP ON 1.87 ± 0.24 , QP OFF 1.80 ± 0.24 ; $p = 0.6651$) in the VL GPe. **h**, Summary statistics of absolute values of oIPSCs (repeated measures one-way ANOVA with Holm-Sidak's post-hoc multiple comparisons test; Baseline 810.73 ± 164.14 pA, QP ON 421.89 ± 77.75 pA, QP OFF 325.71 ± 61.63 pA, $p < 0.0001$) and PPRs (repeated measures one-way ANOVA with Holm-Sidak's post-hoc multiple comparisons test; Baseline 1.29 ± 0.12 , QP ON 1.85 ± 0.18 , QP OFF 1.47 ± 0.12 ; $p = 0.0013$) in the VM GPe. The data are presented as box-and-whisker plots or mean $\pm$ SEM. * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$, **** $p < 0.0001$.



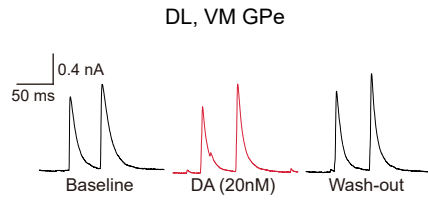
Supplementary Fig. 4 | Subregional pattern of dopamine modulation is reproduced by low-dose quinpirole application

a, A schematic illustration depicting electrophysiological recording of striatopallidal synaptic transmission during bath application of 20 nM quinpirole. **b**, Summary statistics of normalized values of optogenetically evoked oIPSCs (left) ($n = 28$ cells from 26 mice, one sample t-test; Baseline 100%, QP ON $74.60 \pm 1.95\%$, QP OFF $94.07 \pm 1.64\%$) and normalized values of optogenetically evoked PPRs (right) (Baseline 100%, QP ON $119.28 \pm 6.21\%$, QP OFF $101.90 \pm 3.45\%$) in GPe neurons during bath application of quinpirole (20 nM). **c**, Summary statistics of the absolute values of optogenetically evoked oIPSCs (left) (repeated measures one-way ANOVA with Holm-Sidak's post-hoc multiple comparisons test, Baseline 852.26 ± 47.80 pA, QP ON 619.57 ± 39.74 pA, QP OFF 776.85 ± 46.93 pA, $p < 0.0001$) and absolute values of optogenetically evoked PPRs (right) (Baseline 1.48 ± 0.08 , QP ON 1.71 ± 0.10 , QP OFF 1.49 ± 0.09 , $p = 0.0014$) in striatopallidal synaptic transmission during bath application of quinpirole (20 nM). **d**, Summary statistics of the normalized values of optogenetically evoked PPRs between DL/VM GPe subgroup and VL/DM GPe subgroup during bath application of quinpirole (20 nM) ($n = 13$ cells from 12 mice for the DL/VM GPe subgroup, $n = 15$ cells from 14 mice for the VL/DM GPe subgroup, unpaired t-test; DL/VM GPe $134.70 \pm 8.43\%$, VL/DM GPe $105.91 \pm 7.65\%$, $p = 0.0176$). **e-h**, Schematic illustrations of the GPe subregions (top left), representative recording traces (bottom left), oIPSC amplitude (top center) and PPR plots (bottom center) normalized to baseline during bath application of quinpirole (20 nM), and summary statistics of normalized oIPSCs (top right) and normalized PPRs (bottom right). **e**, Summary statistics of normalized oIPSCs ($n = 6$ cells from 6 mice, one sample t-test; Baseline 100%, QP ON $70.55 \pm 5.80\%$, QP OFF $95.01 \pm 2.51\%$) and normalized PPRs (Baseline 100%, QP ON $145.37 \pm 16.94\%$, QP OFF $110.34 \pm 6.95\%$) in the DL GPe. **f**, Summary statistics of normalized oIPSCs ($n = 8$ cells from 7 mice, one sample t-test; Baseline 100%, QP ON $75.49 \pm 2.48\%$, QP OFF $93.26 \pm 2.27\%$) and normalized PPRs (Baseline 100%, QP ON $109.08 \pm 11.61\%$, QP OFF $101.08 \pm 4.75\%$) in the DM GPe. **g**, Summary statistics of normalized oIPSCs ($n = 7$ cells from 7 mice, one sample t-test; Baseline 100%, QP ON $70.68 \pm 4.19\%$, QP OFF $88.94 \pm 3.34\%$) and normalized PPRs (Baseline 100%, QP ON $102.29 \pm 10.43\%$, QP OFF $101.56 \pm 10.28\%$) in the VL GPe. **h**, Summary statistics of normalized oIPSCs ($n = 7$ cells from 6 mice, one sample t-test; Baseline 100%, QP ON $80.96 \pm 2.65\%$, QP OFF $99.31 \pm 4.09\%$) and normalized PPRs (Baseline 100%, QP ON $125.56 \pm 5.36\%$, QP OFF $95.96 \pm 5.25\%$) in the VM GPe. The data are presented as box-and-whisker plots. * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$, **** $p < 0.0001$.

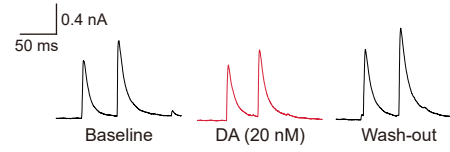
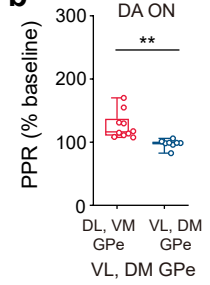
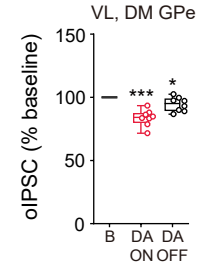
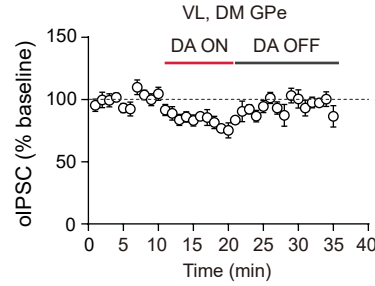
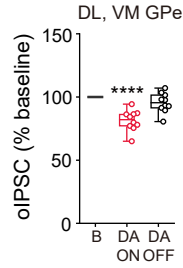
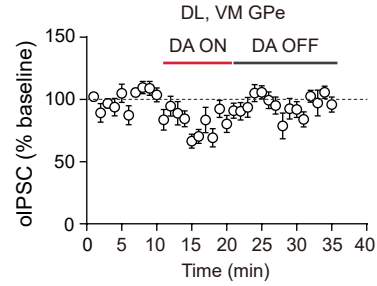
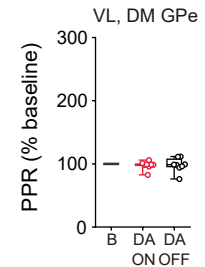
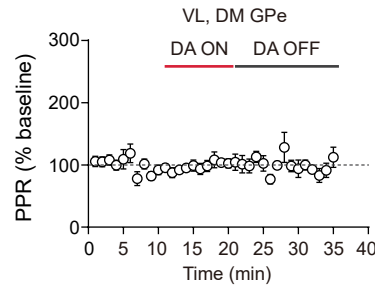
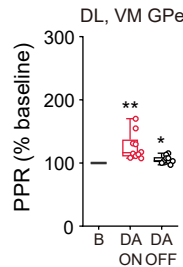
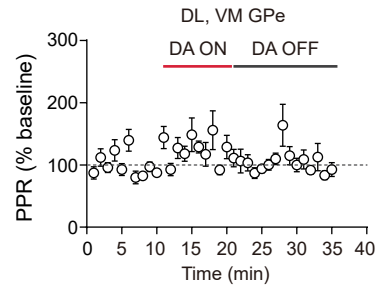
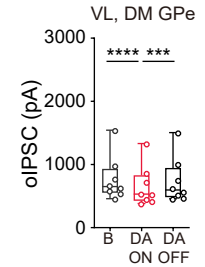
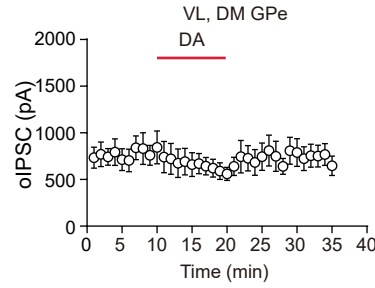
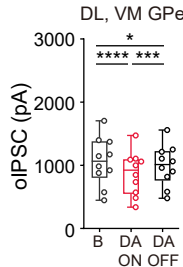
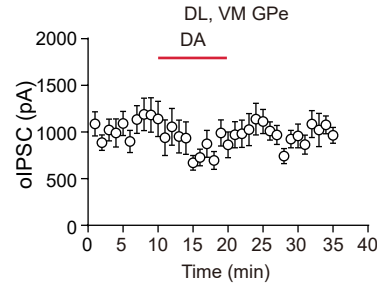
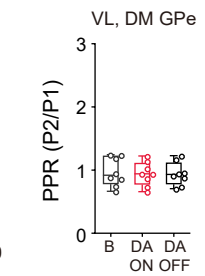
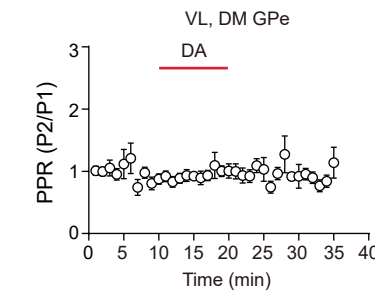
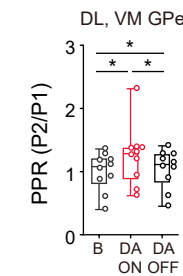
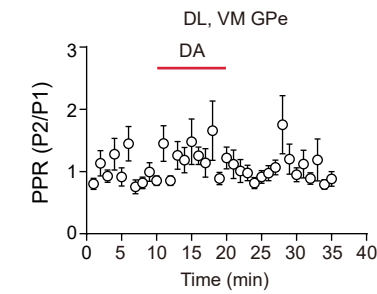
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Supplementary Fig. 5 | Absolute values of oIPSCs and PPRs reflecting region-specific modulation patterns during bath-application of low-dose quinpirole

a-d, Absolute values of oIPSCs (top left), PPR plots (bottom left), and summary statistics of the absolute values of oIPSCs (top right) and PPRs (bottom right) in the GPe subregions. **a**, Summary statistics of absolute values of oIPSCs (repeated measures one-way ANOVA with Holm-Sidak's post-hoc multiple comparisons test; Baseline 779.76 ± 83.83 pA, QP ON 558.64 ± 77.16 pA, QP OFF 736.90 ± 76.13 pA; $p = 0.0020$) and PPRs (repeated measures one-way ANOVA with Holm-Sidak's post-hoc multiple comparisons test; Baseline 1.24 ± 0.19 , QP ON 1.72 ± 0.22 , QP OFF 1.32 ± 0.16 ; $p = 0.0064$) in the DL GPe. **b**, Summary statistics of absolute values of oIPSCs (repeated measures one-way ANOVA with Holm-Sidak's post-hoc multiple comparisons test; Baseline 944.36 ± 121.17 pA, QP ON 711.28 ± 90.50 pA, QP OFF 880.81 ± 112.97 pA, $p = 0.0003$) and PPRs (repeated measures one-way ANOVA with Holm-Sidak's post-hoc multiple comparisons test; Baseline 1.67 ± 0.21 , QP ON 1.74 ± 0.18 , QP OFF 1.67 ± 0.22 ; $p = 0.2371$) in the DM GPe. **c**, Summary statistics of absolute values of oIPSCs (repeated measures one-way ANOVA with Holm-Sidak's post-hoc multiple comparisons test; Baseline 821.89 ± 78.11 pA, QP ON 588.53 ± 74.10 pA, QP OFF 740.29 ± 91.19 pA, $p < 0.0001$) and PPRs (repeated measures one-way ANOVA with Holm-Sidak's post-hoc multiple comparisons test; Baseline 1.50 ± 0.09 , QP ON 1.54 ± 0.19 , QP OFF 1.53 ± 0.18 ; $p = 0.8824$) in the VL GPe. **d**, Summary statistics of absolute values of oIPSCs (repeated measures one-way ANOVA with Holm-Sidak's post-hoc multiple comparisons test; Baseline 731.52 ± 77.25 pA, QP ON 598.01 ± 73.40 pA, QP OFF 728.83 ± 85.34 pA, $p = 0.0013$) and PPRs (repeated measures one-way ANOVA with Holm-Sidak's post-hoc multiple comparisons test; Baseline 1.43 ± 0.14 , QP ON 1.83 ± 0.25 , QP OFF 1.386 ± 0.170 ; $p = 0.0061$) in the VM GPe. The data are presented as box-and-whisker plots or mean $\pm$ SEM. * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$, **** $p < 0.0001$.

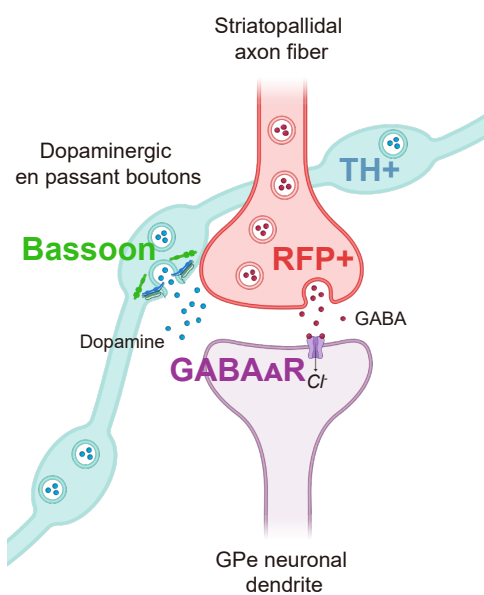
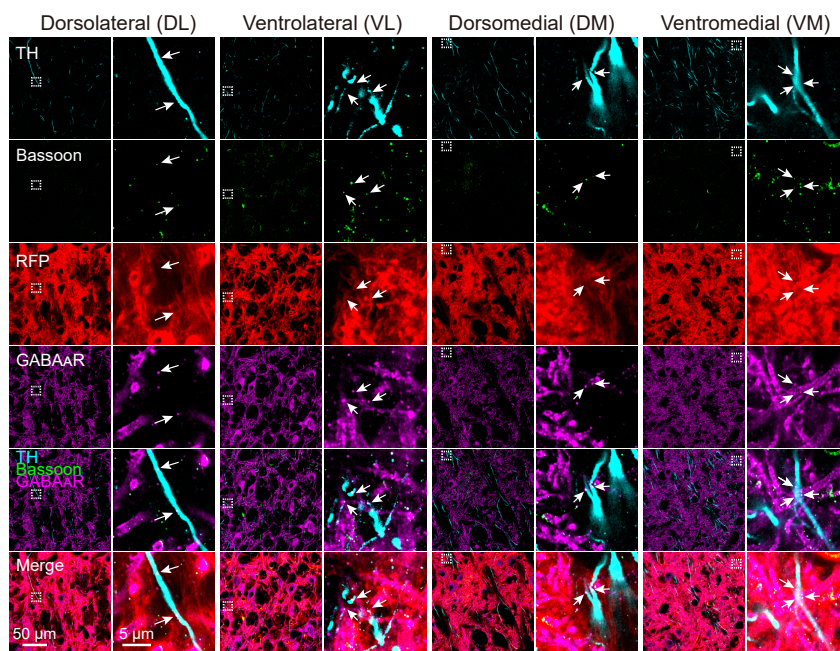
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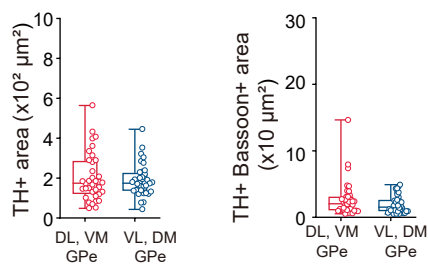
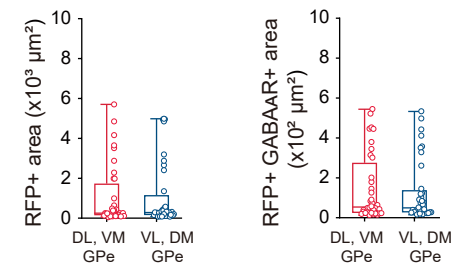
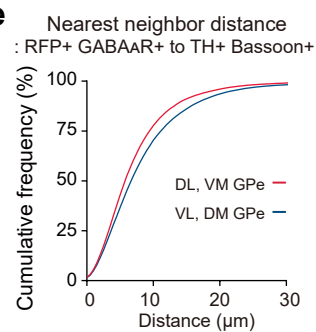
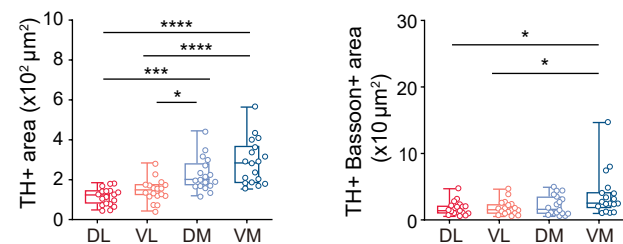
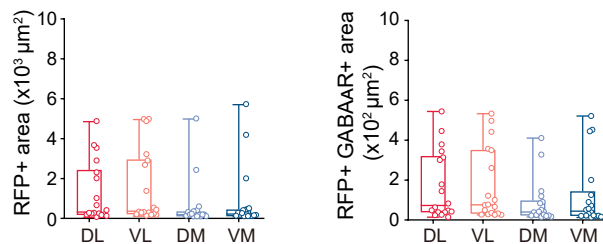
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Supplementary Fig. 6 | The subregional patterns of dopamine modulation is reproduced by low-dose dopamine application in adult mice

a, Representative recording traces of optogenetically evoked oIPSCs during bath application of dopamine (20 nM) in adult mice, comparing the DL/VM GPe and VL/DM GPe subgroups. **b**, Summary statistics of the normalized values of optogenetically evoked PPRs between DL/VM GPe subgroup and VL/DM GPe subgroup during bath application of dopamine (20 nM) ($n = 10$ cells from 8 mice for the DL/VM GPe subgroup, $n = 8$ cells from 7 mice for the VL/DM GPe subgroup, unpaired t-test; DL/VM GPe $125.96 \pm 6.70\%$, VL/DM GPe $97.64 \pm 2.39\%$, $p = 0.0023$). **c**, oIPSC amplitude plots normalized to baseline and summary statistics of normalized oIPSCs in the DL/VM GPe subgroup (left) ($n = 10$ cells from 8 mice, one sample t-test; Baseline 100%, QP ON $81.41 \pm 2.57\%$, QP OFF $95.54 \pm 2.43\%$) and VL/DM GPe subgroup (right) ($n = 8$ cells from 7 mice, one sample t-test; Baseline 100%, QP ON $83.68 \pm 2.29\%$, QP OFF $94.43 \pm 1.98\%$) during bath application of dopamine (20 nM) in adult mice. **d**, PPR plots normalized to baseline and summary statistics of normalized PPRs in the DL/VM GPe subgroup (left) ($n = 10$ cells from 8 mice, one sample t-test; Baseline 100%, QP ON $125.96 \pm 6.70\%$, QP OFF $105.35 \pm 1.81\%$) and VL/DM GPe subgroup (right) ($n = 8$ cells from 7 mice, one sample t-test; Baseline 100%, QP ON $97.64 \pm 2.39\%$, QP OFF $98.32 \pm 3.93\%$) during bath application of dopamine (20 nM) in adult mice. **e**, Absolute values of oIPSC plots and summary statistics of the absolute values of oIPSCs in the DL/VM GPe subgroup (left) (repeated measures one-way ANOVA with Holm-Sidak's post-hoc multiple comparisons test; Baseline 1059.75 ± 120.98 pA, QP ON 870.55 ± 108.66 pA, QP OFF 993.67 ± 101.38 pA; $p < 0.0001$) and VL/DM GPe subgroup (right) (repeated measures one-way ANOVA with Holm-Sidak's post-hoc multiple comparisons test; Baseline 773.41 ± 123.63 pA, QP ON 654.26 ± 112.44 pA, QP OFF 738.08 ± 126.87 pA; $p < 0.0001$) during bath application of dopamine (20 nM) in adult mice. **f**, Absolute values of PPR plots and summary statistics of the absolute values of PPRs in the DL/VM GPe subgroup (left) (repeated measures one-way ANOVA with Holm-Sidak's post-hoc multiple comparisons test; Baseline 1.05 ± 0.10 , QP ON 1.25 ± 0.15 , QP OFF 1.04 ± 0.10 ; $p = 0.0180$) and VL/DM GPe subgroup (right) (repeated measures one-way ANOVA with Holm-Sidak's post-hoc multiple comparisons test; Baseline 1.03 ± 0.08 , QP ON 0.94 ± 0.07 , QP OFF 0.94 ± 0.06 ; $p = 0.5064$) during bath application of dopamine (20 nM) in adult mice. The data are presented as box-and-whisker plots or mean $\pm$ SEM. * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$, **** $p < 0.0001$.

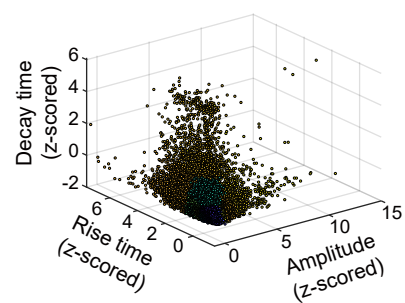
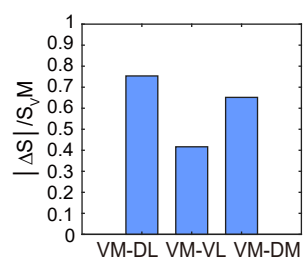
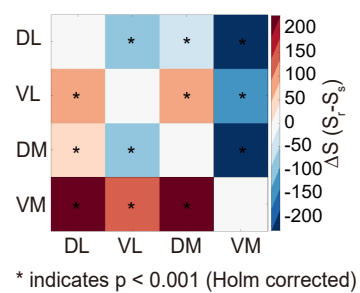
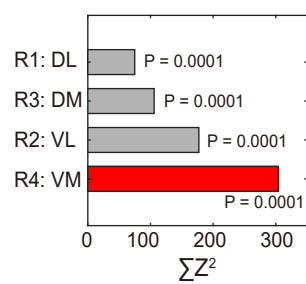
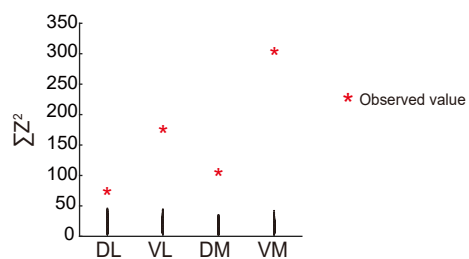
a**b**

RFP+ GABAAR+ co-localization: Striatopallidal GABAergic synapse
 TH+ Bassoon+ co-localization: Presynaptic marker for DA bouton

c**d****e****f****g**

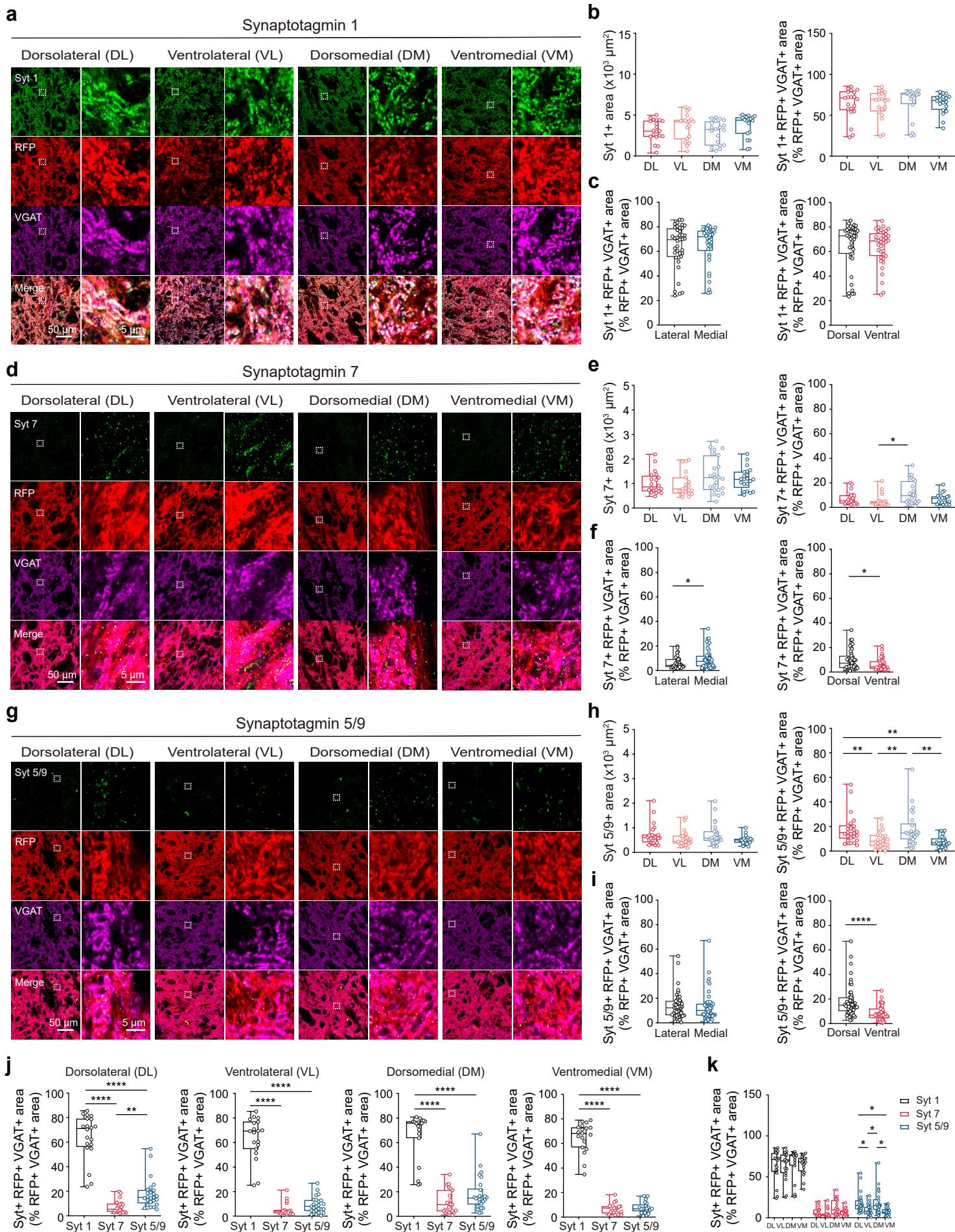
Supplementary Fig. 7 | The spatial relationship between putatively functional DA boutons and striatopallidal synapses

a, A schematic illustration depicting fluorescently labeled striatopallidal axons (RFP), GABA_AR, dopaminergic axons (TH), and Bassoon. **b**, Representative enhanced confocal images of striatopallidal GABAergic synapses and presynaptic markers for DA boutons. **c**, Summary statistics of TH⁺ area (left) (n = 36 images from 3 mice per GPe subgroup, unpaired t-test; DL/VM GPe $202.39 \pm 20.02 \mu\text{m}^2$, VL/DM GPe $188.73 \pm 13.40 \mu\text{m}^2$) and Bassoon⁺ area colocalized with TH⁺ area (right) (DL/VM GPe $27.22 \pm 4.44 \mu\text{m}^2$, VL/DM GPe $19.59 \pm 2.17 \mu\text{m}^2$). **d**, Summary statistics of RFP⁺ area (left) (n = 36 images from 3 mice per GPe subgroup, unpaired t- test; DL/VM GPe $1054.57 \pm 25.72 \mu\text{m}^2$, VL/DM GPe $1071.03 \pm 26.91 \mu\text{m}^2$) and GABA_AR⁺ area colocalized with RFP⁺ area (right) (DL/VM GPe $146.65 \pm 28.12 \mu\text{m}^2$, VL/DM GPe $128.39 \pm 25.75 \mu\text{m}^2$). **e**, Cumulative plot for the nearest neighbor distance from striatopallidal GABAergic synapses (RFP⁺ GABA_AR⁺) to presynaptic DA boutons (TH⁺ Bassoon⁺) in the GPe subgroups. **f**, Summary statistics of TH⁺ area (left) (n = 18 images from 3 mice per GPe subregion, one-way ANOVA with Holm-Sidak's post-hoc multiple comparisons test; DL $117.81 \pm 10.12 \mu\text{m}^2$, VL $149.48 \pm 13.27 \mu\text{m}^2$, DM $227.99 \pm 19.54 \mu\text{m}^2$, VM $286.98 \pm 26.57 \mu\text{m}^2$; $p < 0.0001$) and Bassoon⁺ area colocalized with TH⁺ area (right) (DL $16.99 \pm 2.48 \mu\text{m}^2$, VL $17.76 \pm 2.59 \mu\text{m}^2$, DM $21.42 \pm 3.50 \mu\text{m}^2$, VM $37.45 \pm 7.93 \mu\text{m}^2$; $p = 0.0092$). **g**, Summary statistics of RFP⁺ area (left) (n = 18 images from 3 mice per GPe subregion, one-way ANOVA with Holm-Sidak's post-hoc multiple comparisons test; DL $1264.99 \pm 360.26 \mu\text{m}^2$, VL $1541.13 \pm 436.08 \mu\text{m}^2$, DM $600.92 \pm 286.49 \mu\text{m}^2$, VM $844.15 \pm 370.57 \mu\text{m}^2$; $p = 0.2776$) and GABA_AR⁺ area colocalized with RFP⁺ area (right) (DL $170.50 \pm 40.21 \mu\text{m}^2$, VL $172.17 \pm 42.68 \mu\text{m}^2$, DM $84.60 \pm 26.12 \mu\text{m}^2$, VM $122.81 \pm 39.67 \mu\text{m}^2$; $p = 0.3013$). The data are presented as box-and-whisker plots. * $p < 0.05$, *** $p < 0.001$, **** $p < 0.0001$.

a**b****c****d****e**

Supplementary Fig. 8 | A clustering analysis on Sr^{2+} -induced quantal responses in the GPe subregions

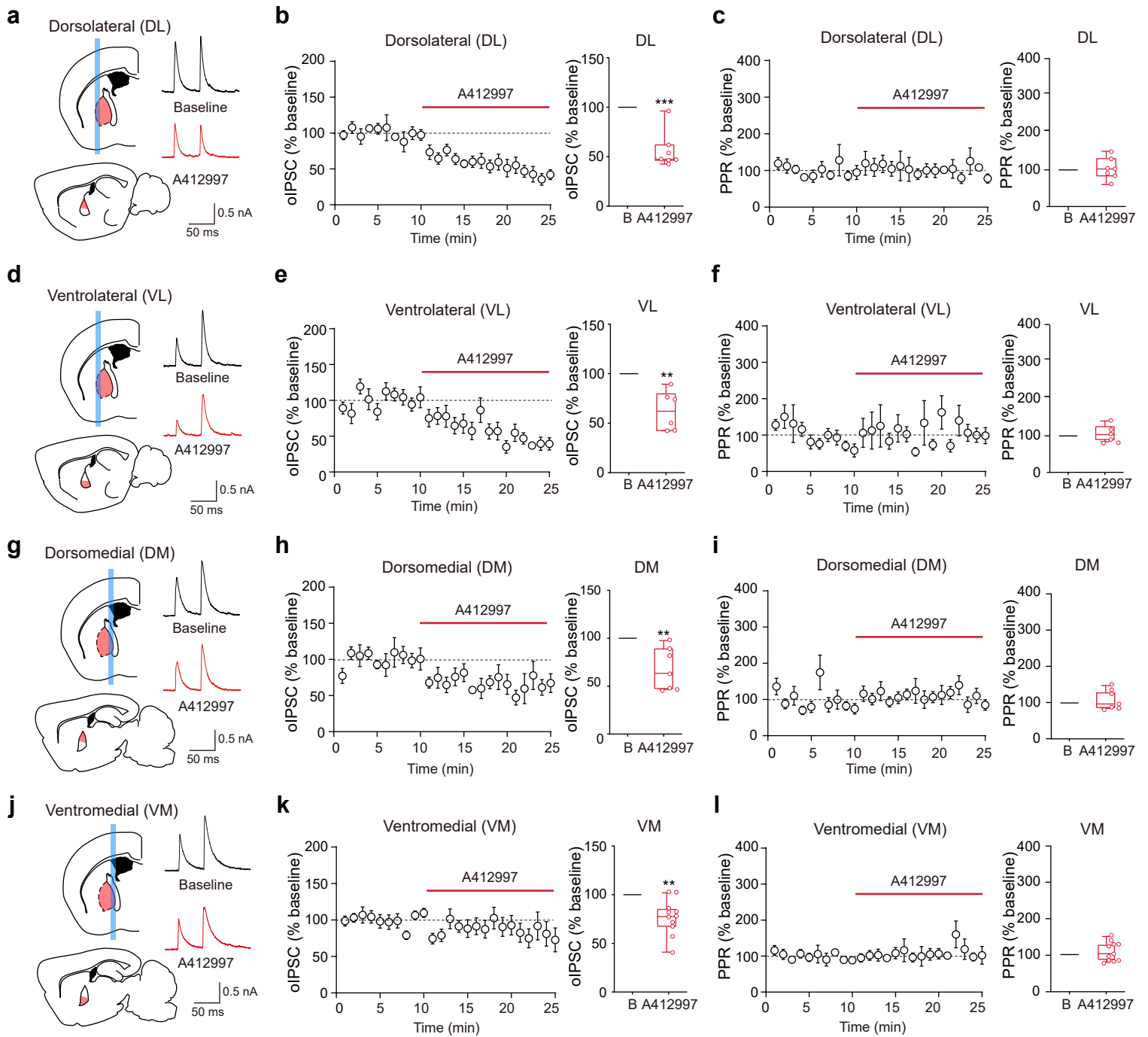
a, A representative 3D plot showing z-scored miniature IPSC features (amplitude, rise time, and decay constant) used for recursive k-means clustering. **b**, A bar graph showing cumulative χ^2 contributions (ΣZ^2) across GPe subregions. **c**, A heatmap showing pairwise contrasts (ΔS) between GPe subregions, with significant differences (Holm-corrected $p < 0.001$). **d**, Horizontal bars ranking GPe subregions by their ΣZ^2 contributions, annotated with permutation p value. **e**, Permutation cloud plots overlaying observed ΣZ^2 values (red stars) on 10,000 null draws (gray).



Supplementary Fig. 9 | Regional variations in the expression of synaptotagmin subtypes at striatopallidal axon terminals in the subregions of the GPe

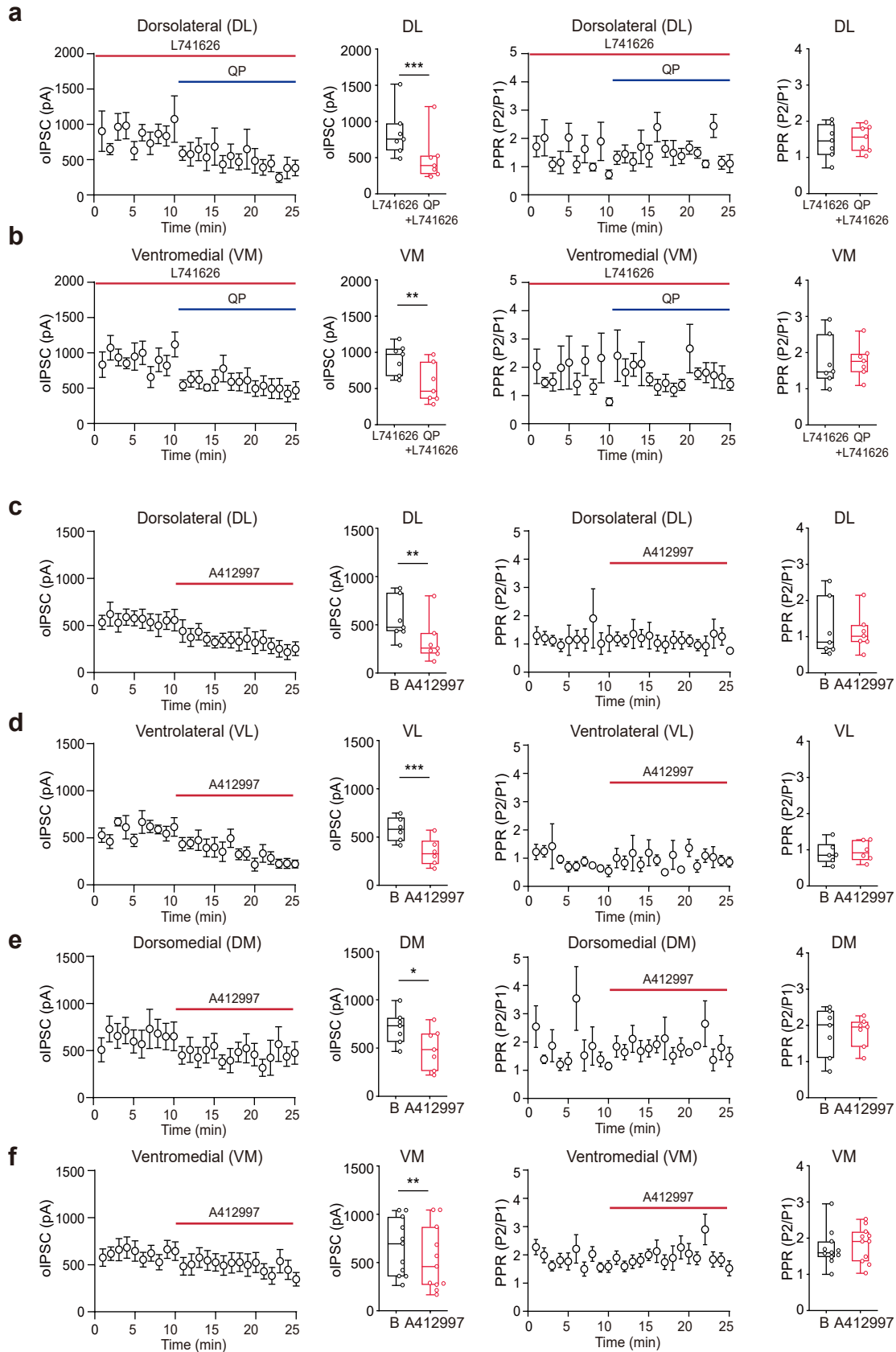
a,d,g, Representative enhanced confocal images of synaptotagmins (1, 7, 5/9), RFP, and VGAT immunofluorescence in the GPe subregions of Adora2A-Cre;Ai9 mice. **b,e,h**, Summary statistics of synaptotagmin⁺ area (left) and synaptotagmin⁺ area on striatopallidal GABAergic presynaptic terminals, normalized to the total area of striatopallidal GABAergic presynaptic terminals (right) in the GPe subregions. **c,f,i**, Summary statistics of synaptotagmin⁺ area on striatopallidal GABAergic presynaptic terminals, normalized to the total area of striatopallidal GABAergic presynaptic terminals in the lateral-medial GPe (left) and dorsal-ventral GPe (right). **b**, Summary statistics of synaptotagmin 1⁺ area (left) (n = 20 images from 3 mice per GPe subregion, one-way ANOVA; DL $3104.4 \pm 286.2 \mu\text{m}^2$, VL $3589.3 \pm 365.3 \mu\text{m}^2$, DM $2906 \pm 321 \mu\text{m}^2$, VM $3700 \pm 324.4 \mu\text{m}^2$; p = 0.2599) and normalized synaptotagmin 1⁺ RFP⁺ VGAT⁺ area (right) (DL $64.3 \pm 4.1\%$, VL $63.7 \pm 3.9\%$, DM $65.7 \pm 4.5\%$, VM $65.1 \pm 2.8\%$; p = 0.9859). **c**, Summary statistics of normalized synaptotagmin 1⁺ area in the lateral-medial GPe (left) (n = 40 images from 6 mice per GPe subgroup, unpaired t-test; lateral GPe $64.0 \pm 2.8\%$, medial GPe $65.4 \pm 2.6\%$) and dorsal-ventral GPe (right) (dorsal GPe $65 \pm 3\%$, ventral GPe $64.4 \pm 2.4\%$). **e**, Summary statistics of synaptotagmin 7⁺ area (left) (n = 20 images from 3 mice per GPe subregion, one-way ANOVA; DL $1026.3 \pm 101.7 \mu\text{m}^2$, VL $969.3 \pm 114.2 \mu\text{m}^2$, DM $1349.5 \pm 151.8 \mu\text{m}^2$, VM $1192 \pm 97.6 \mu\text{m}^2$; p = 0.1129) and normalized synaptotagmin 7⁺ RFP⁺ VGAT⁺ area (right) (DL $7.4 \pm 1.2\%$, VL $5.6 \pm 1.2\%$, DM $11.7 \pm 2.0\%$, VM $6.6 \pm 0.9\%$; p = 0.0174). **f**, Summary statistics of normalized synaptotagmin 7⁺ area in the lateral-medial GPe (left) (n = 40 images from 6 mice per GPe subgroup, unpaired t-test; lateral GPe $6.1 \pm 0.8\%$, medial GPe $9.2 \pm 1.2\%$) and dorsal-ventral GPe (right) (dorsal GPe $9.7 \pm 1.2\%$, ventral GPe $6.1 \pm 0.8\%$). **h**, Summary statistics of synaptotagmin 5/9⁺ area (left) (n = 25 images from 3 mice per GPe subregion, one-way ANOVA; DL $698.1 \pm 84.7 \mu\text{m}^2$, VL $554 \pm 60 \mu\text{m}^2$, DM $722 \pm 86.8 \mu\text{m}^2$, VM $500.5 \pm 32.9 \mu\text{m}^2$; p = 0.0733) and normalized synaptotagmin 5/9⁺ RFP⁺ VGAT⁺ area (right) (DL $18.0 \pm 2.4\%$, VL $9.1 \pm 1.3\%$, DM $18.2 \pm 2.8\%$, VM $7.7 \pm 0.9\%$; p = 0.0001). **i**, Summary statistics of normalized synaptotagmin 5/9⁺ area in the lateral-medial GPe (left) (n = 50 images from 6 mice per GPe subgroup, unpaired t-test; lateral GPe $13.5 \pm 1.5\%$, medial GPe $13.1 \pm 1.6\%$) and dorsal-ventral GPe (right) (dorsal GPe $18.1 \pm 1.8\%$, ventral GPe $8.4 \pm 0.8\%$). **j**, Summary statistics of synaptotagmin (1, 7, 5/9)⁺ area on striatopallidal GABAergic presynaptic terminals, normalized to the total area of striatopallidal GABAergic presynaptic terminals in the DL GPe (one-way ANOVA; Syt-1 $64.3 \pm 4.1\%$, Syt-7 $7.4 \pm 1.2\%$, Syt-5/9 $18.0 \pm 2.4\%$; p < 0.0001), VL GPe (Syt-1 $63.7 \pm 3.9\%$, Syt-7 $5.6 \pm 1.2\%$, Syt-5/9 $9.1 \pm 1.3\%$; p <

0.0001), DM GPe (Syt-1 $65.7 \pm 4.5\%$, Syt-7 $11.7 \pm 2.0\%$, Syt-5/9 $18.2 \pm 2.8\%$; $p < 0.0001$), and VM GPe (Syt-1 $65.1 \pm 2.8\%$, Syt-7 $6.6 \pm 1.0\%$, Syt-5/9 $7.7 \pm 1.0\%$; $p < 0.0001$). **k**, Summary statistics of synaptotagmin (1, 7, 5/9)+ area on striatopallidal GABAergic presynaptic terminals, normalized to the total area of striatopallidal GABAergic presynaptic terminals in the GPe subregions (ordinary two-way ANOVA with Holm-Sidak's post-hoc multiple comparisons test; Syt-1, DL $64.3 \pm 4.1\%$, VL $63.7 \pm 3.9\%$, DM $65.6 \pm 4.4\%$, VM $65.1 \pm 2.8\%$; Syt-7, DL $7.4 \pm 1.2\%$, VL $5.6 \pm 1.2\%$, DM $11.7 \pm 2.0\%$, VM $6.6 \pm 0.9\%$; Syt-5/9, DL $18.0 \pm 2.4\%$, VL $9.1 \pm 1.3\%$, DM $18.2 \pm 2.8\%$, VM $7.7 \pm 0.9\%$; GPe subregion, $p = 0.0149$, synaptotagmin subtype, $p < 0.0001$, interaction, $p = 0.2354$). The data are presented as box-and-whisker plots. * $p < 0.05$, ** $p < 0.01$, **** $p < 0.0001$.



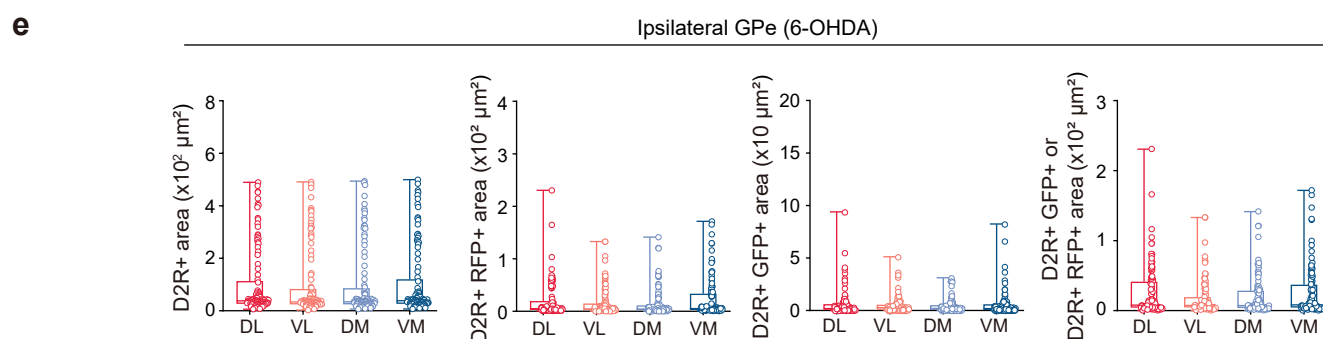
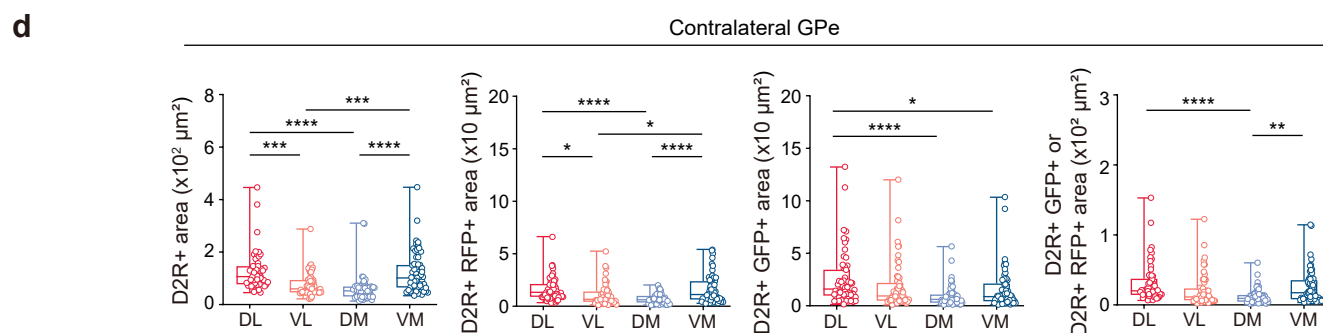
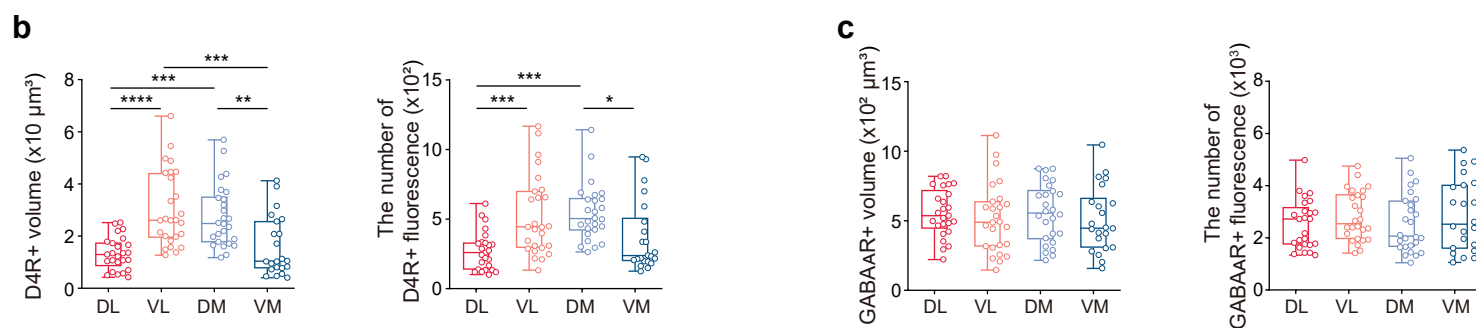
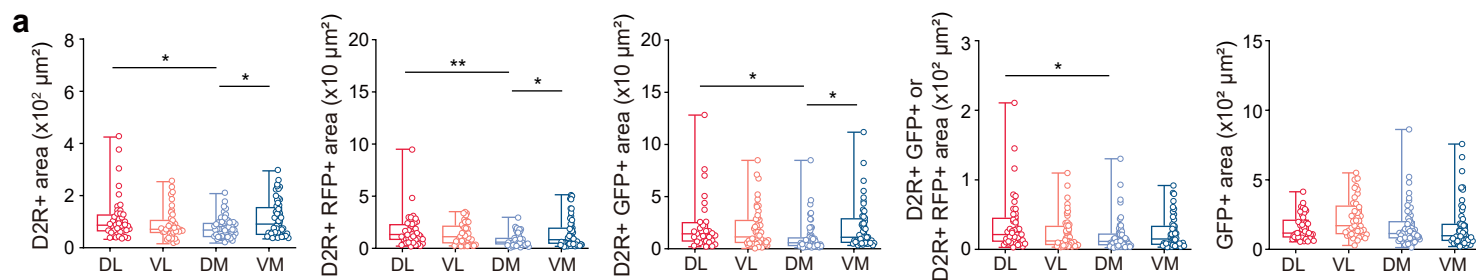
Supplementary Fig. 10 | The selective D4R agonist A-412997 universally attenuates striatopallidal transmission across all subregions of the GPe, without affecting the PPR

a,d,g,j, Schematic illustrations of the GPe subregions and representative recording traces before and after the bath application of A-412997 (100 nM). **b,e,h,k**, Normalized oIPSC amplitude plots (left) and summary statistics of normalized oIPSCs (right) in the GPe subregions. **c,f,i,l**, Normalized PPR plots (left) and summary statistics of normalized PPR (right) in the GPe subregions. **b,c**, Summary statistics of normalized oIPSCs (n = 7 cells from 4 mice, one sample t-test; Baseline 100%, A-412997 $56.44 \pm 7.04\%$) and PPRs (Baseline 100%, A-412997 $103.02 \pm 10.93\%$) in the DL GPe. **e,f**, Summary statistics of normalized oIPSCs (n = 6 cells from 6 mice, one sample t-test; Baseline 100%, A-412997 $62.47 \pm 8.17\%$) and PPRs (Baseline 100%, A-412997 $107.85 \pm 8.15\%$) in the VL GPe. **h,i**, Summary statistics of normalized oIPSCs (n = 7 cells from 4 mice, one sample t-test; Baseline 100%, A-412997 $67.77 \pm 8.13\%$) and PPRs (Baseline 100%, A-412997 $107.65 \pm 9.13\%$) in the DM GPe. **k,l**, Summary statistics of normalized oIPSCs (n = 11 cells from 7 mice, one sample t-test; Baseline 100%, A-412997 $75.54 \pm 5.39\%$) and PPRs (Baseline 100%, A-412997 $109.47 \pm 7.89\%$) in the VM GPe. The data are presented as box-and-whisker plots. **p < 0.01, ***p < 0.001.



Supplementary Fig. 11 | Absolute values of oIPSCs and PPRs reflecting D2R- and D4R-mediated modulation in the GPe

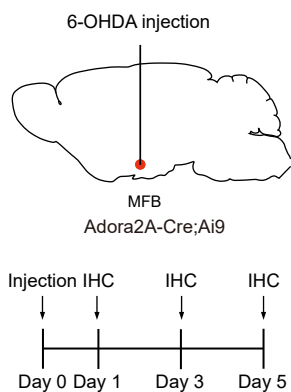
a-f, Absolute values of oIPSC plots, summary statistics (left) and absolute values of PPR plots, summary statistics (right) in the GPe subregions. **a**, Summary statistics of absolute values of oIPSCs (paired t-test; L-741626 841.87 ± 126.70 pA, L-741626 + QP 497.17 ± 124.82 pA; $p = 0.0003$) and PPRs (paired t-test; L-741626 1.44 ± 0.18 , L-741626 + QP 1.51 ± 0.14 ; $p = 0.6061$) in the DL GPe. **b**, Summary statistics of absolute values of oIPSCs (paired t-test; L-741626 906.53 ± 78.22 pA, L-741626 + QP 563.84 ± 101.32 pA; $p = 0.0067$) and PPRs (paired t-test; L-741626 1.74 ± 0.26 , L-741626 + QP 1.76 ± 0.18 ; $p = 0.8967$) in the VM GPe. **c**, Summary statistics of absolute values of oIPSCs (paired t-test; Baseline 556.40 ± 82.80 pA, A-412997 332.30 ± 84.88 pA; $p = 0.0042$) and PPRs (paired t-test; Baseline 1.22 ± 0.30 , A-412997 1.12 ± 0.20 ; $p = 0.5339$) in the DL GPe. **d**, Summary statistics of absolute values of oIPSCs (paired t-test; Baseline 580.91 ± 51.23 pA, A-412997 343.99 ± 57.63 pA; $p = 0.0006$) and PPRs (paired t-test; Baseline 0.90 ± 0.12 , A-412997 0.95 ± 0.11 ; $p = 0.5108$) in the VL GPe. **e**, Summary statistics of absolute values of oIPSCs (paired t-test; Baseline 711.67 ± 65.43 pA, A-412997 492.80 ± 79.91 pA; $p = 0.0116$) and PPRs (paired t-test; Baseline 1.81 ± 0.25 , A-412997 1.81 ± 0.16 ; $p = 0.9799$) in the DM GPe. **f**, Summary statistics of absolute values of oIPSCs (paired t-test; Baseline 657.52 ± 88.38 pA, A-412997 534.09 ± 99.86 pA; $p = 0.0048$) and PPRs (paired t-test; Baseline 1.72 ± 0.15 , A-412997 1.83 ± 0.15 ; $p = 0.3998$) in the VM GPe. The data are presented as box-and-whisker plots or mean $\pm$ SEM. * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$.



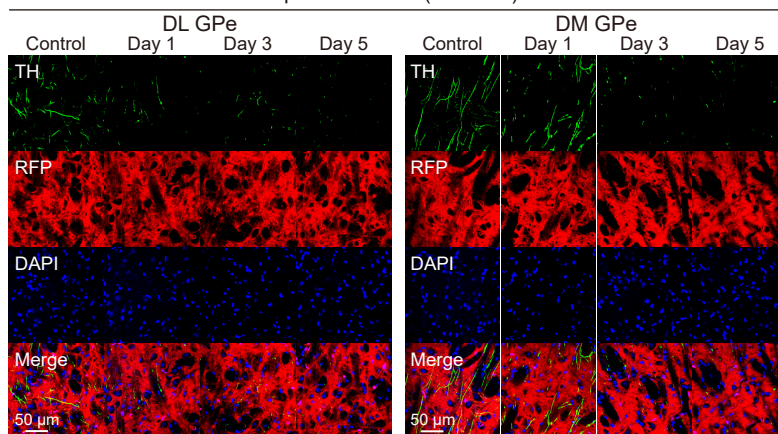
Supplementary Fig. 12 | Quantification of D2R/D4R receptor expression and lesion-induced changes in D2R expression across GPe subregions

a, Summary statistics of D2R+ area ($n = 40$ images from 9 mice for the DL and VL GPe, $n = 55$ images from 9 mice for the DM and VM GPe, one-way ANOVA with Holm-Sidak's post-hoc multiple comparisons test; DL $112.45 \pm 13.77 \mu\text{m}^2$, VL $87.86 \pm 9.29 \mu\text{m}^2$, DM $74.96 \pm 5.32 \mu\text{m}^2$, VM $107.69 \pm 9.39 \mu\text{m}^2$; $p = 0.0145$), D2R+ area colocalized with RFP+ area ($n = 42$ images from 9 mice for the DL and VL GPe, $n = 51$ images from 9 mice for the DM GPe, $n = 53$ images from 9 mice for the VM GPe, one-way ANOVA with Holm-Sidak's post-hoc multiple comparisons test; DL $16.97 \pm 2.44 \mu\text{m}^2$, VL $13.91 \pm 1.56 \mu\text{m}^2$, DM $8.25 \pm 0.90 \mu\text{m}^2$, VM $14.53 \pm 1.92 \mu\text{m}^2$; $p = 0.0045$), D2R+ area colocalized with GFP+ area ($n = 29$ images from 9 mice for the DL GPe, $n = 50$ images from 9 mice for the VL GPe, $n = 58$ images from 9 mice for the DM GPe, $n = 47$ images from 9 mice for the VM GPe, one-way ANOVA with Holm-Sidak's post-hoc multiple comparisons test; DL $23.34 \pm 5.15 \mu\text{m}^2$, VL $18.95 \pm 2.74 \mu\text{m}^2$, DM $10.67 \pm 1.88 \mu\text{m}^2$, VM $21.10 \pm 3.26 \mu\text{m}^2$; $p = 0.0158$), D2R+ area colocalized with GFP+ or RFP+ area ($n = 44$ images from 9 mice for the DL GPe, $n = 49$ images from 9 mice for the VL GPe, $n = 54$ images from 9 mice for the DM GPe, $n = 48$ images from 9 mice for the VM GPe, one-way ANOVA with Holm-Sidak's post-hoc multiple comparisons test; DL $35.39 \pm 6.05 \mu\text{m}^2$, VL $23.41 \pm 3.48 \mu\text{m}^2$, DM $19.59 \pm 3.23 \mu\text{m}^2$, VM $24.64 \pm 3.37 \mu\text{m}^2$; $p = 0.0484$), and GFP+ area ($n = 41$ images from 9 mice for the DL and VL GPe, $n = 58$ images from 9 mice for the DM GPe, $n = 55$ images from 9 mice for the VM GPe, one-way ANOVA with Holm-Sidak's post-hoc multiple comparisons test; DL $157.18 \pm 14.11 \mu\text{m}^2$, VL $221.81 \pm 21.86 \mu\text{m}^2$, DM $163.14 \pm 19.12 \mu\text{m}^2$, VM $168.39 \pm 22.32 \mu\text{m}^2$; $p = 0.1310$). **b**, Summary statistics of D4R+ fluorescence volume ($n = 25$ images from 6 mice for the DL GPe, $n = 26$ images from 6 mice for the VL and DM GPe, $n = 22$ images from 6 mice for the VM GPe, one-way ANOVA with Holm-Sidak's post-hoc multiple comparisons test; DL $13.31 \pm 1.24 \mu\text{m}^3$, VL $30.54 \pm 2.84 \mu\text{m}^3$, DM $27.58 \pm 2.35 \mu\text{m}^3$, VM $16.02 \pm 2.44 \mu\text{m}^3$; $p < 0.0001$) and number (DL 272.12 ± 27.81 , VL 522.65 ± 56.36 , DM 545.46 ± 39.83 , VM 369.73 ± 54.66 ; $p < 0.0001$). **c**, Summary statistics of GABA_AR+ fluorescence volume ($n = 25$ images from 6 mice for the DL GPe, $n = 26$ images from 6 mice for the VL and DM GPe, $n = 22$ images from 6 mice for the VM GPe, one-way ANOVA with Holm-Sidak's post-hoc multiple comparisons test; DL $555.15 \pm 34.07 \mu\text{m}^3$, VL $517.80 \pm 48.72 \mu\text{m}^3$, DM $555.41 \pm 40.83 \mu\text{m}^3$, VM $508.84 \pm 50.05 \mu\text{m}^3$; $p = 0.8188$) and number (DL 2526.36 ± 189.974 , VL 2823.69 ± 185.72 , DM 2547.92 ± 218.66 , VM 2868.23 ± 291.28 ; $p = 0.5833$). **d**, Summary statistics of D2R+ area ($n = 56$ images from 11 mice for the DL GPe, $n = 58$ images from 11 mice for the VL GPe, $n = 62$ images from 11 mice for the DM and VM GPe, one-

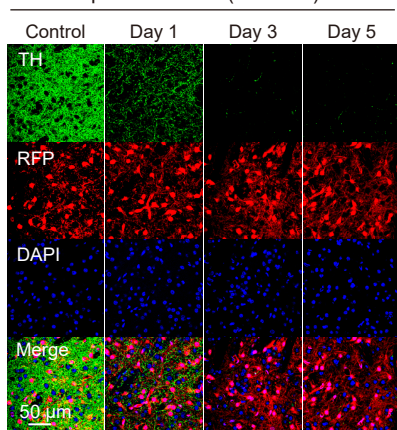
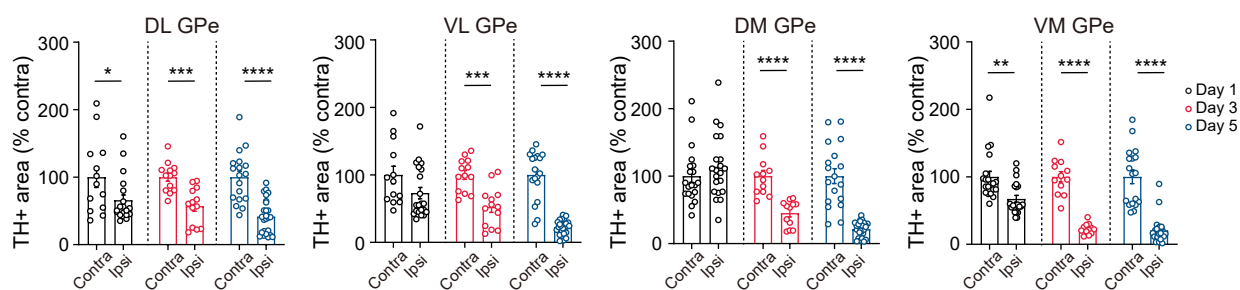
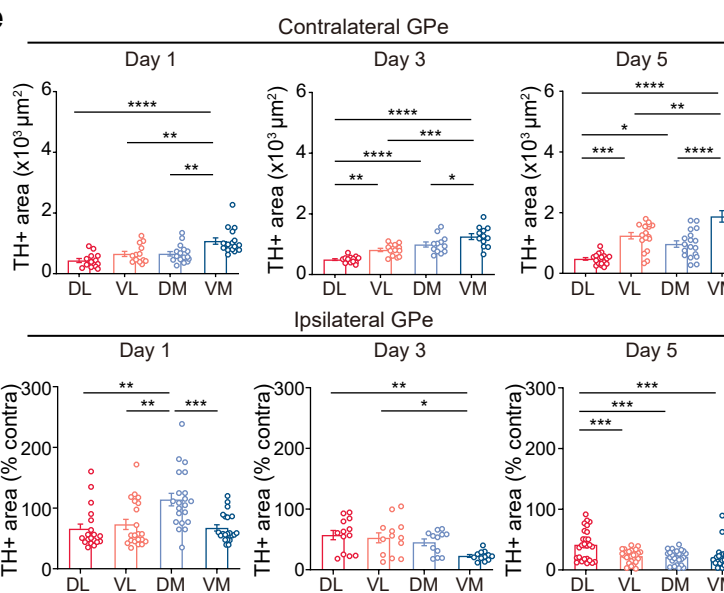
way ANOVA with Holm-Sidak's post-hoc multiple comparisons test; DL $126.07 \pm 9.83 \mu\text{m}^2$, VL $75.70 \pm 5.75 \mu\text{m}^2$, DM $60.33 \pm 6.46 \mu\text{m}^2$, VM $118.35 \pm 9.76 \mu\text{m}^2$; $p < 0.0001$), D2R+ area colocalized with RFP+ area (DL $16.11 \pm 1.46 \mu\text{m}^2$, VL $10.71 \pm 1.33 \mu\text{m}^2$, DM $7.06 \pm 0.59 \mu\text{m}^2$, VM $16.35 \pm 1.67 \mu\text{m}^2$; $p < 0.0001$), D2R+ area colocalized with GFP+ area (DL $25.07 \pm 3.41 \mu\text{m}^2$, VL $17.85 \pm 2.87 \mu\text{m}^2$, DM $8.83 \pm 1.22 \mu\text{m}^2$, VM $15.10 \pm 2.40 \mu\text{m}^2$; $p = 0.0002$), and D2R+ area colocalized with GFP+ or RFP+ area (DL $30.47 \pm 3.63 \mu\text{m}^2$, VL $20.58 \pm 3.00 \mu\text{m}^2$, DM $11.65 \pm 1.31 \mu\text{m}^2$, VM $25.28 \pm 2.97 \mu\text{m}^2$; $p < 0.0001$) between GPe subregions in the contralateral hemisphere. **e**, Summary statistics of D2R+ area (one-way ANOVA with Holm-Sidak's post-hoc multiple comparisons test; DL $102.93 \pm 12.78 \mu\text{m}^2$, VL $96.14 \pm 12.97 \mu\text{m}^2$, DM $98.58 \pm 13.25 \mu\text{m}^2$, VM $105.17 \pm 13.03 \mu\text{m}^2$; $p = 0.9606$), D2R+ area colocalized with RFP+ area (DL $19.78 \pm 3.28 \mu\text{m}^2$, VL $16.25 \pm 2.57 \mu\text{m}^2$, DM $14.31 \pm 2.48 \mu\text{m}^2$, VM $23.33 \pm 3.61 \mu\text{m}^2$; $p = 0.1589$), D2R+ area colocalized with GFP+ area (DL $6.32 \pm 1.19 \mu\text{m}^2$, VL $5.15 \pm 0.79 \mu\text{m}^2$, DM $4.99 \pm 0.75 \mu\text{m}^2$, VM $5.88 \pm 1.13 \mu\text{m}^2$; $p = 0.7599$), and D2R+ area colocalized with GFP+ or RFP+ area (DL $25.41 \pm 3.48 \mu\text{m}^2$, VL $17.94 \pm 2.47 \mu\text{m}^2$, DM $19.67 \pm 2.68 \mu\text{m}^2$, VM $25.52 \pm 3.43 \mu\text{m}^2$; $p = 0.1841$) between GPe subregions in the ipsilateral hemisphere. The data are presented as box-and-whisker plots. * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$, **** $p < 0.0001$.

a**b**

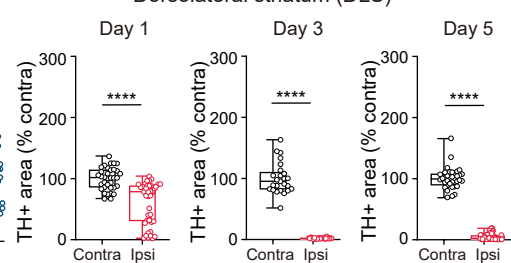
Ipsilateral GPe (6-OHDA)

**c**

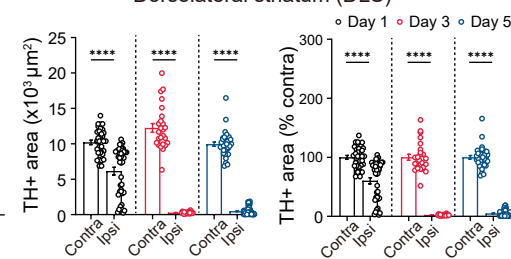
Ipsilateral DLS (6-OHDA)

**d****e****f**

Dorsolateral striatum (DLS)

**g**

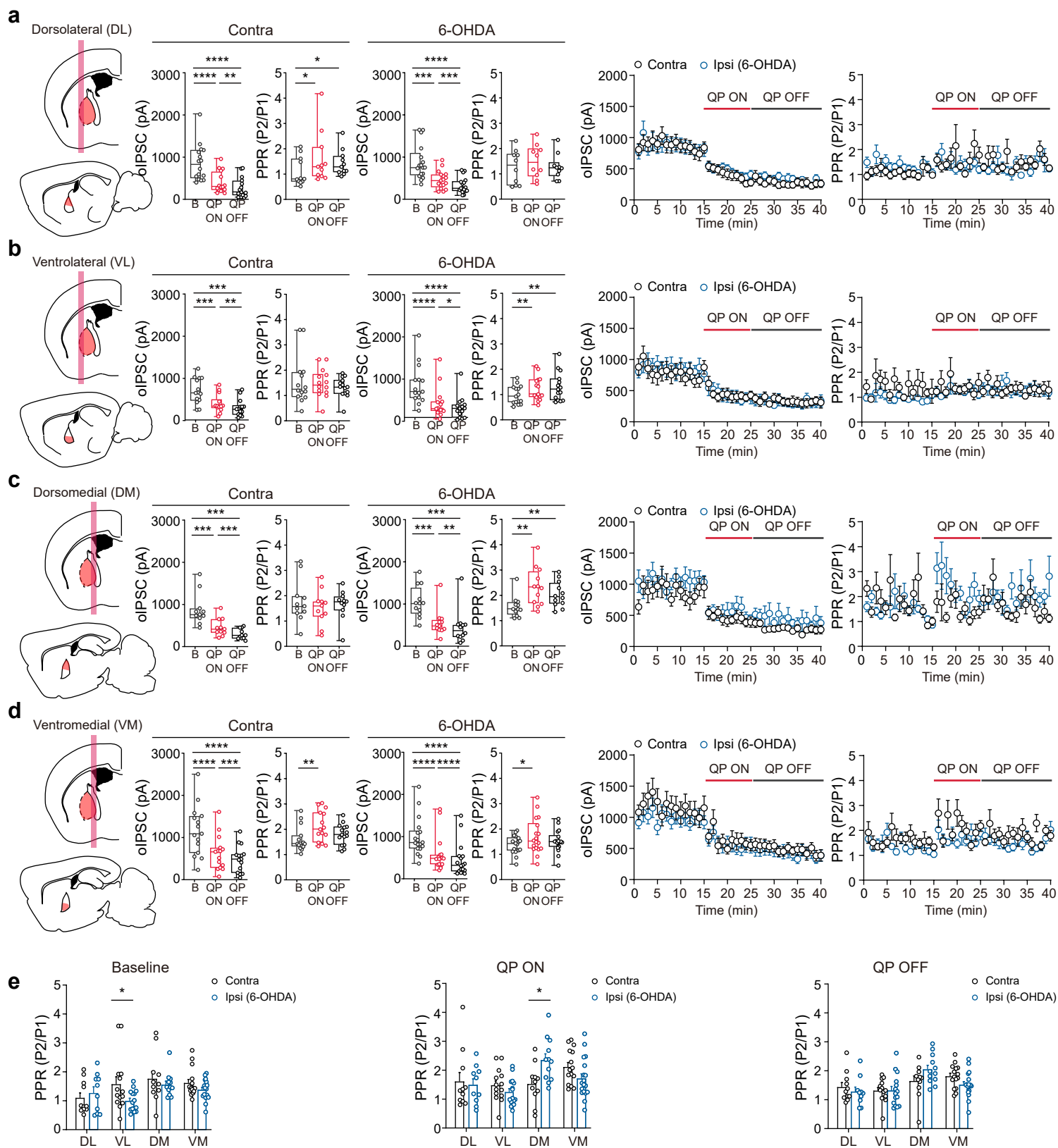
Dorsolateral striatum (DLS)



Supplementary Fig. 13 | 6-OHDA-induced degeneration of dopaminergic axons exhibits regional heterogeneity across the subregions of the GPe

a, A schematic illustration describing the unilateral injection of 6-OHDA into the MFB of Adora2A-Cre;Ai9 mice. **b**, Representative confocal images of striatopallidal axons (RFP) and TH⁺ dopaminergic axons in the GPe subregions of ipsilateral (6-OHDA) hemisphere at 1, 3, and 5 days post-6-OHDA injection. **c**, Representative confocal images of TH⁺ dopaminergic axons and iMSNs (RFP) in the DLS of ipsilateral (6-OHDA) hemispheres at 1, 3, and 5 days post-6-OHDA injection. **d**, Summary statistics of TH⁺ area normalized to the contralateral TH⁺ area in the DL GPe (n = 13-18 images from 4 mice at each time point, unpaired t-test; Day 1 Contra 100 ± 15.24%, Day 1 Ipsi 65.76 ± 7.92%, p = 0.0381; Day 3 Contra 100 ± 6.06%, Day 3 Ipsi 57.09 ± 7.59%, p = 0.0002; Day 5 Contra 100 ± 8.85%, Day 5 Ipsi 41.34 ± 4.96%, p < 0.0001), VL GPe (n = 13-26 images from 3-5 mice at each time point; Day 1 Contra 100 ± 12.90%, Day 1 Ipsi 73.06 ± 8.28%, p = 0.0743; Day 3 Contra 100 ± 6.70%, Day 3 Ipsi 52.52 ± 8.19%, p = 0.0002; Day 5 Contra 100 ± 8.43%, Day 5 Ipsi 22.62 ± 2.14%, p < 0.0001), DM GPe (n = 12-26 images from 3-5 mice at each time point; Day 1 Contra 100 ± 9.31%, Day 1 Ipsi 113.90 ± 10.31%, p = 0.3250; Day 3 Contra 100 ± 8.46%, Day 3 Ipsi 45.18 ± 5.51%, p < 0.0001; Day 5 Contra 100 ± 11.02%, Day 5 Ipsi 21.41 ± 2.15%, p < 0.0001), and VM GPe (n = 12-26 images from 3-5 mice at each time point; Day 1 Contra 100 ± 8.08%, Day 1 Ipsi 67.33 ± 5.12%, p = 0.0014; Day 3 Contra 100 ± 7.72%, Day 3 Ipsi 22.74 ± 2.28%, p < 0.0001; Day 5 Contra 100 ± 10.07%, Day 5 Ipsi 20.35 ± 3.61%, p < 0.0001). **e**, Summary statistics of TH⁺ area in the contralateral GPe (top) 1 day after 6-OHDA injection (n = 13-16 images from 4 mice per GPe subregion, one-way ANOVA; DL 433.6 ± 66.1 μm², VL 652.1 ± 84.1 μm², DM 655.5 ± 73.5 μm², VM 1074.0 ± 104.4 μm²; p < 0.0001), 3 days after 6-OHDA injection (n = 12-13 images from 3 mice per GPe subregion; DL 494 ± 29.9 μm², VL 810.7 ± 54.4 μm², DM 990.4 ± 83.8 μm², VM 1252 ± 96.6 μm²; p < 0.0001), and 5 days after 6-OHDA injection (n = 18 images from 4 mice per GPe subregion; DL 476.8 ± 42.2 μm², VL 1240 ± 104.5 μm², DM 965.8 ± 106.4 μm², VM 1877 ± 189 μm²; p < 0.0001). Summary statistics of normalized values of TH⁺ area in the ipsilateral GPe relative to the contralateral GPe (bottom) 1 day after 6-OHDA injection (n = 16 images from 4 mice per GPe subregion, one-way ANOVA; DL 65.76 ± 7.92%, VL 73.06 ± 8.28%, DM 113.89 ± 10.31%, VM 67.33 ± 5.12%; p = 0.0001), 3 days after 6-OHDA injection (n = 12-13 images from 3 mice per GPe subregion; DL 57.09 ± 7.59%, VL 52.52 ± 8.19%, DM 45.18 ± 5.51%, VM 22.73 ± 2.28%; p = 0.0027), and 5 days after 6-OHDA injection (n = 26 images from 5 mice per GPe subregion; DL 41.34 ± 4.95%, VL 22.62 ± 2.14%, DM 21.41 ± 2.15%, VM 20.35 ± 3.61%; p < 0.0001). **f**, Summary statistics of TH⁺ area normalized

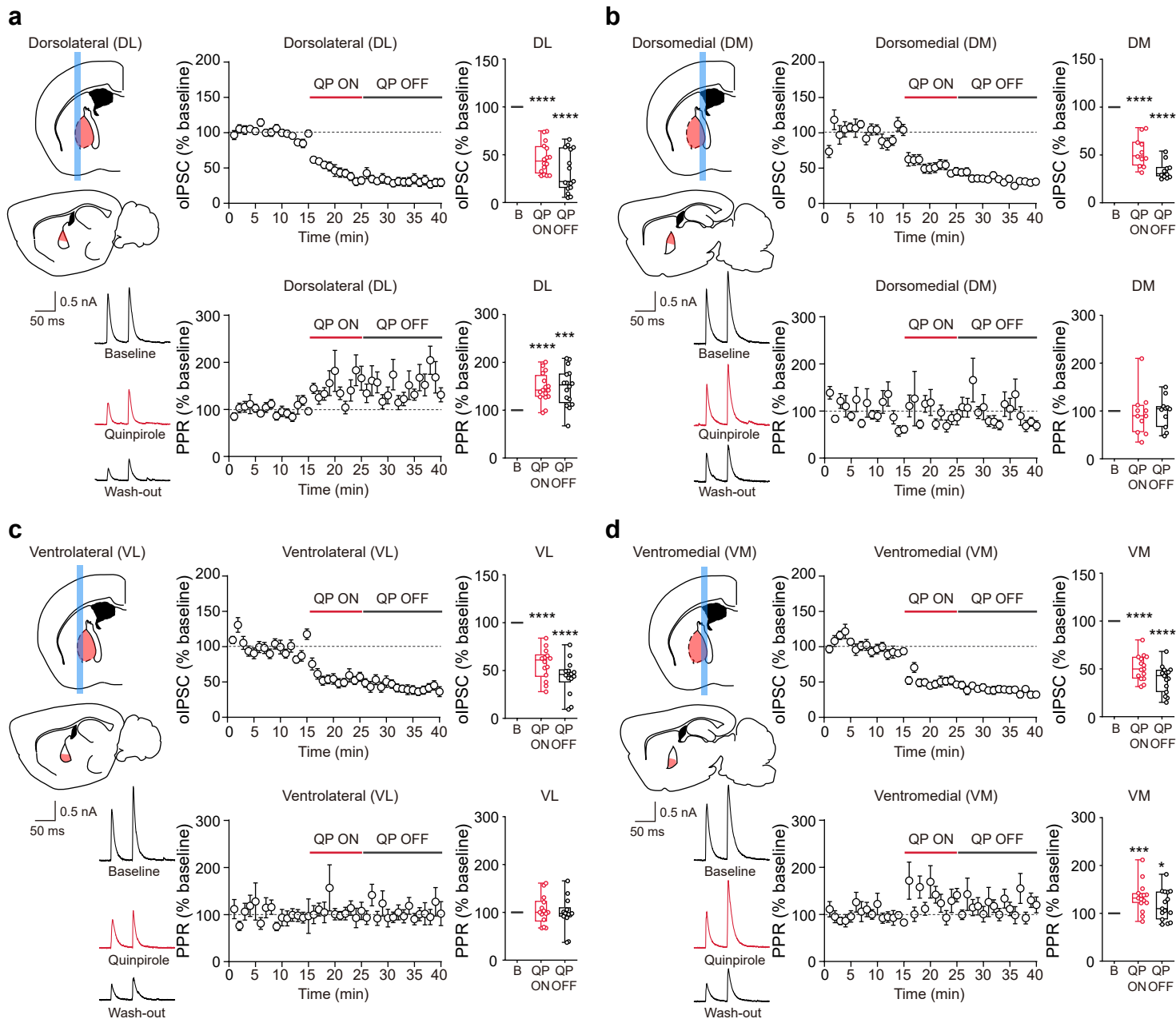
to the contralateral TH⁺ area in the DLS 1 day after 6-OHDA injection (n = 35 images from 5 mice per each hemisphere, unpaired t-test; Contra $100 \pm 3.07\%$, Ipsi $60.26 \pm 5.26\%$), 3 days after 6-OHDA injection (n = 24 images from 4 mice per each hemisphere; Contra $100 \pm 5.07\%$, Ipsi $2.25 \pm 0.21\%$), and 5 day after 6-OHDA injection (n = 36 images from 5 mice per each hemisphere; Contra $100 \pm 2.92\%$, Ipsi $4.80 \pm 0.64\%$). **g**, Summary statistics of TH⁺ area in the contralateral and ipsilateral DLS (left) (n = 24-36 images from 4-5 mice per each hemisphere at each time point, ordinary two- way ANOVA with Holm-Sidak's post-hoc multiple comparisons test; Day 1 Contra $10194.34 \pm 313.41 \mu\text{m}^2$, Day 1 Ipsi $6143 \pm 536.32 \mu\text{m}^2$, Day 3 Contra $12232.27 \pm 619.55 \mu\text{m}^2$, Day 3 Ipsi $275.46 \pm 25.24 \mu\text{m}^2$, Day 5 Contra $9950.94 \pm 290.40 \mu\text{m}^2$, Day 5 Ipsi $477.20 \pm 63.38 \mu\text{m}^2$; 6-OHDA, $p < 0.0001$, post-injection time point, $p < 0.0001$, interaction, $p < 0.0001$) and TH⁺ area of the contralateral and ipsilateral DLS normalized to the contralateral TH⁺ area (right) (n = 24- 36 images from 4-5 mice per each hemisphere at each time point, unpaired t-test; Day 1 Contra $100 \pm 3.07\%$, Day 1 Ipsi $60.26 \pm 5.26\%$, $p < 0.0001$; Day 3 Contra $100 \pm 5.07\%$, Day 3 Ipsi $2.25 \pm 0.21\%$, $p < 0.0001$; Day 5 Contra $100 \pm 2.92\%$, Day 5 Ipsi $4.80 \pm 0.64\%$, $p < 0.0001$) at 1, 3, and 5 days post-6-OHDA injection. The data are presented as box-and-whisker plots or mean $\pm$ SEM. * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$, **** $p < 0.0001$.



Supplementary Fig. 14 | Absolute values of oIPSCs and PPRs reflecting reorganized, region-specific dopaminergic modulation in the GPe under 6-OHDA-lesioned conditions

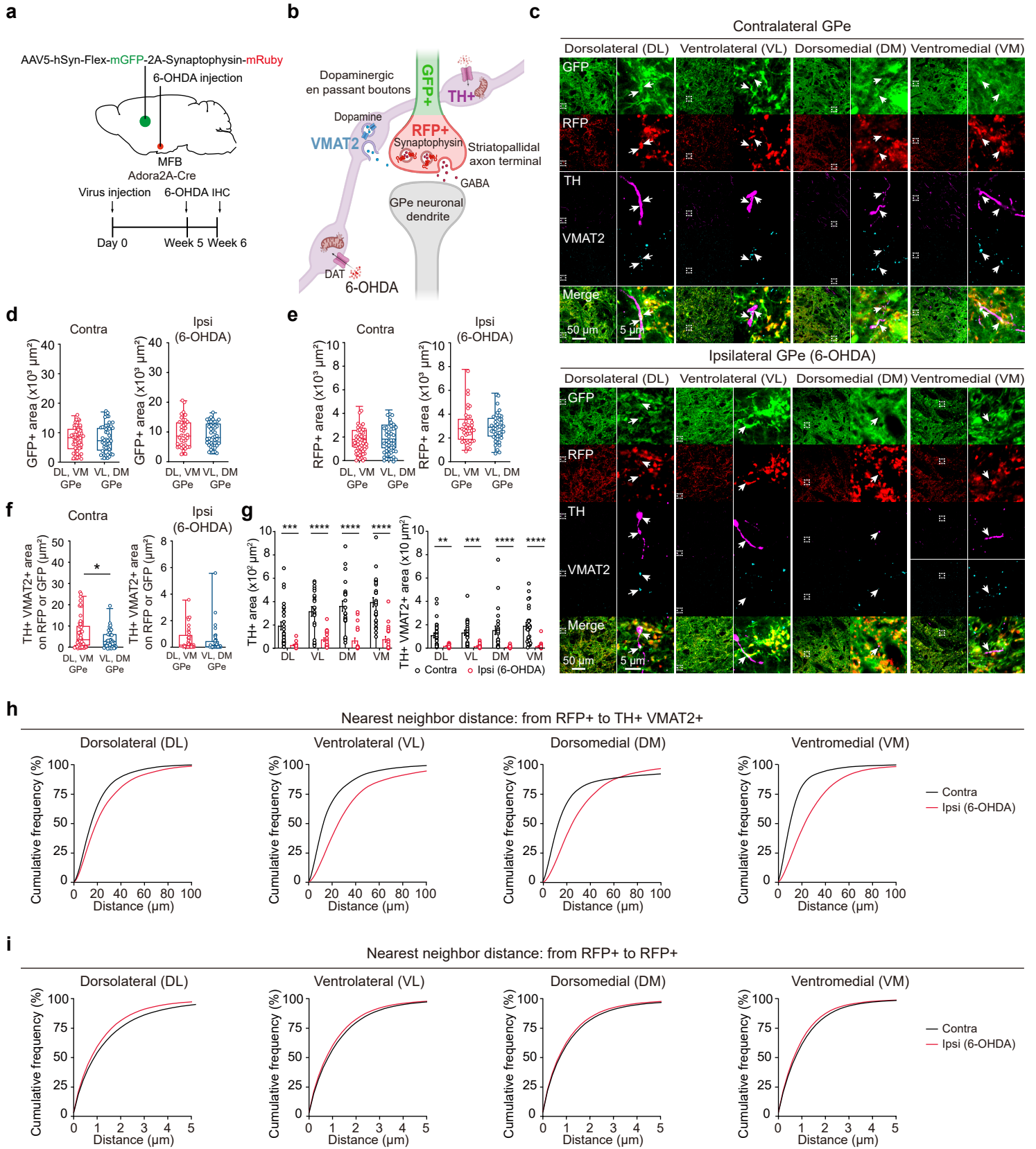
a-d, Schematic illustrations of the GPe subregions (left), summary statistics of absolute values of oIPSCs and PPRs (center), and absolute values of oIPSC amplitude and PPR plots (right) during bath application of quinpirole (10 μ M) in the DA-depleted condition. Ipsilateral (6-OHDA) data are indicated in blue, while contralateral data are shown in black. The red bars and labels indicate the quinpirole application state. **a**, Summary statistics of absolute values of oIPSCs (contra, repeated measures one-way ANOVA with Holm-Sidak's post-hoc multiple comparisons test; Baseline 876.87 ± 108.11 pA, QP ON 406.22 ± 62.82 pA, QP OFF 276.75 ± 58.29 pA; $p < 0.0001$; ipsi, repeated measures one-way ANOVA with Holm-Sidak's post-hoc multiple comparisons test; Baseline 870.82 ± 99.83 pA, QP ON 455.10 ± 51.52 pA, QP OFF 328.77 ± 45.72 pA; $p < 0.0001$) and PPRs (contra, Baseline 1.10 ± 0.17 , QP ON 1.61 ± 0.31 , QP OFF 1.43 ± 0.15 ; $p = 0.0321$; ipsi, Baseline 1.27 ± 0.21 , QP ON 1.49 ± 0.21 , QP OFF 1.28 ± 0.16 ; $p = 0.3099$) in the contralateral and ipsilateral hemisphere of the DL GPe. **b**, Summary statistics of absolute values of oIPSCs (contra, Baseline 702.61 ± 81.06 pA, QP ON 396.63 ± 56.53 pA, QP OFF 301.20 ± 53.29 pA; $p < 0.0001$; ipsi, Baseline 858.28 ± 119.34 pA, QP ON 433.06 ± 93.66 pA, QP OFF 318.08 ± 69.31 pA; $p < 0.0001$) and PPRs (contra, Baseline 1.57 ± 0.26 , QP ON 1.48 ± 0.15 , QP OFF 1.31 ± 0.10 ; $p = 0.3128$; ipsi, Baseline 0.99 ± 0.09 , QP ON 1.24 ± 0.12 , QP OFF 1.32 ± 0.14 ; $p = 0.0003$) in the contralateral and ipsilateral hemisphere of the VL GPe. **c**, Summary statistics of absolute values of oIPSCs (contra, Baseline 870.76 ± 113.61 pA, QP ON 454.96 ± 62.72 pA, QP OFF 292.78 ± 36.78 pA; $p < 0.0001$; ipsi, Baseline 1040.57 ± 106.96 pA, QP ON 545.23 ± 90.58 pA, QP OFF 437.34 ± 114.92 pA; $p = 0.0002$) and PPRs (contra, Baseline 1.76 ± 0.25 , QP ON 1.52 ± 0.20 , QP OFF 1.64 ± 0.17 ; $p = 0.5647$; ipsi, Baseline 1.56 ± 0.12 , QP ON 2.35 ± 0.22 , QP OFF 2.05 ± 0.15 ; $p = 0.0012$) in the contralateral and ipsilateral hemisphere of the DM GPe. **d**, Summary statistics of absolute values of oIPSCs (contra, Baseline 1161.38 ± 152.39 pA, QP ON 628.71 ± 104.54 pA, QP OFF 487.10 ± 80.68 pA; $p < 0.0001$; ipsi, Baseline 990.17 ± 106.12 pA, QP ON 579.78 ± 94.93 pA, QP OFF 437.18 ± 91.19 pA; $p < 0.0001$) and PPRs (contra, Baseline 1.61 ± 0.13 , QP ON 2.11 ± 0.15 , QP OFF 1.81 ± 0.11 ; $p = 0.0038$; ipsi, Baseline 1.38 ± 0.08 , QP ON 1.71 ± 0.16 , QP OFF 1.52 ± 0.10 ; $p = 0.0270$) in the contralateral and ipsilateral hemisphere of the VM GPe. **e**, Summary statistics of absolute values of PPRs during baseline (left) (ordinary two-way ANOVA with Holm-Sidak's post-hoc multiple comparisons test; Contra DL 1.10 ± 0.17 , Ipsi DL 1.27 ± 0.21 , Contra VL 1.57 ± 0.26 , Ipsi VL 0.99 ± 0.09 , Contra DM 1.76 ± 0.25 , Ipsi DM 1.56 ± 0.12 , Contra VM 1.61 ± 0.13 , Ipsi VM 1.38 ± 0.08 ; GPe subregion, $p = 0.0364$, 6-OHDA, $p =$

0.0777, interaction, $p = 0.2013$), QP ON state (center) (Contra DL 1.61 ± 0.31 , Ipsi DL 1.49 ± 0.21 , Contra VL 1.48 ± 0.15 , Ipsi VL 1.24 ± 0.12 , Contra DM 1.52 ± 0.20 , Ipsi DM 2.35 ± 0.22 , Contra VM 2.11 ± 0.16 , Ipsi VM 1.71 ± 0.16 ; GPe subregion, $p = 0.0042$, 6-OHDA, $p = 0.8891$, interaction, $p = 0.0089$), and QP OFF state (right) (Contra DL 1.43 ± 0.16 , Ipsi DL 1.28 ± 0.16 , Contra VL 1.31 ± 0.11 , Ipsi VL 1.32 ± 0.14 , Contra DM 1.64 ± 0.17 , Ipsi DM 2.04 ± 0.15 , Contra VM 1.81 ± 0.11 , Ipsi VM 1.52 ± 0.10 ; GPe subregion, $p = 0.0003$, 6-OHDA, $p = 0.9157$, interaction, $p = 0.0688$) in the contralateral and ipsilateral hemisphere of the GPe subregions in the DA-depleted condition. The data are presented as box-and-whisker plots or mean $\pm$ SEM. * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$, **** $p < 0.0001$.



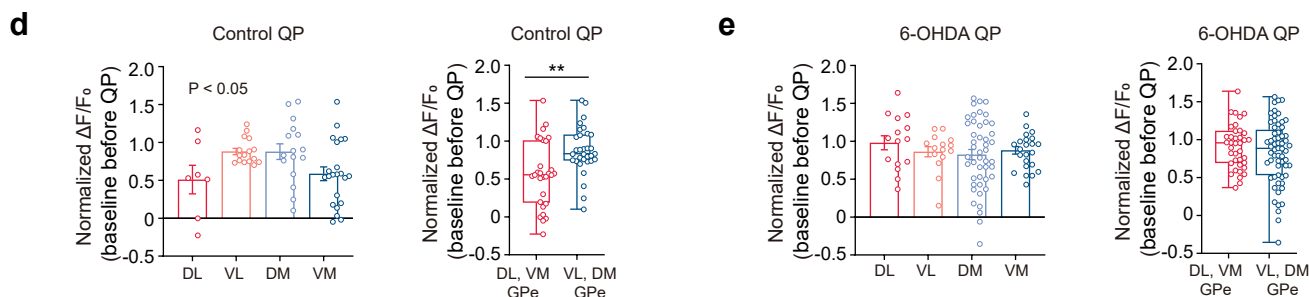
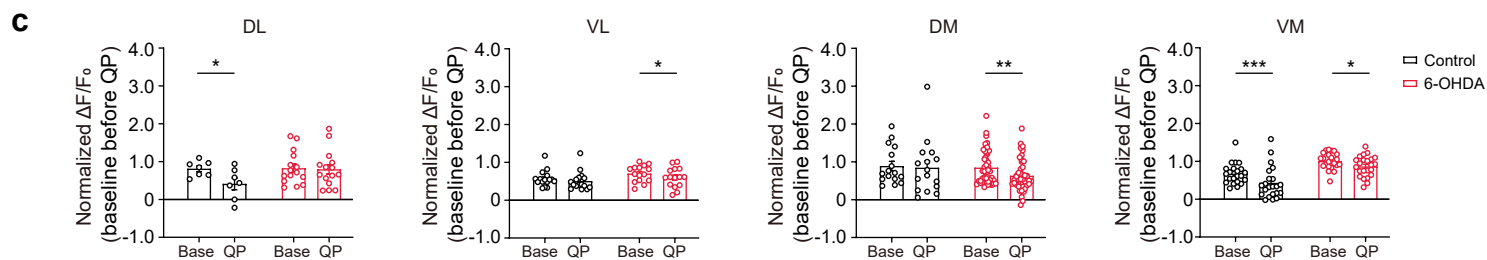
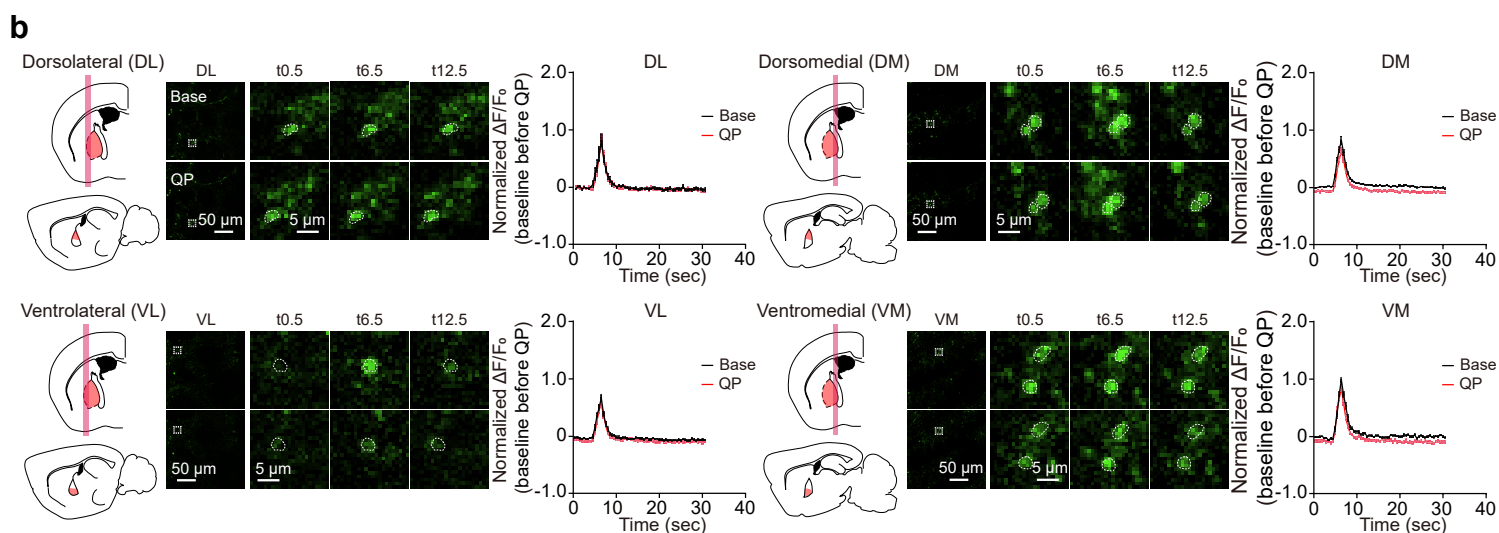
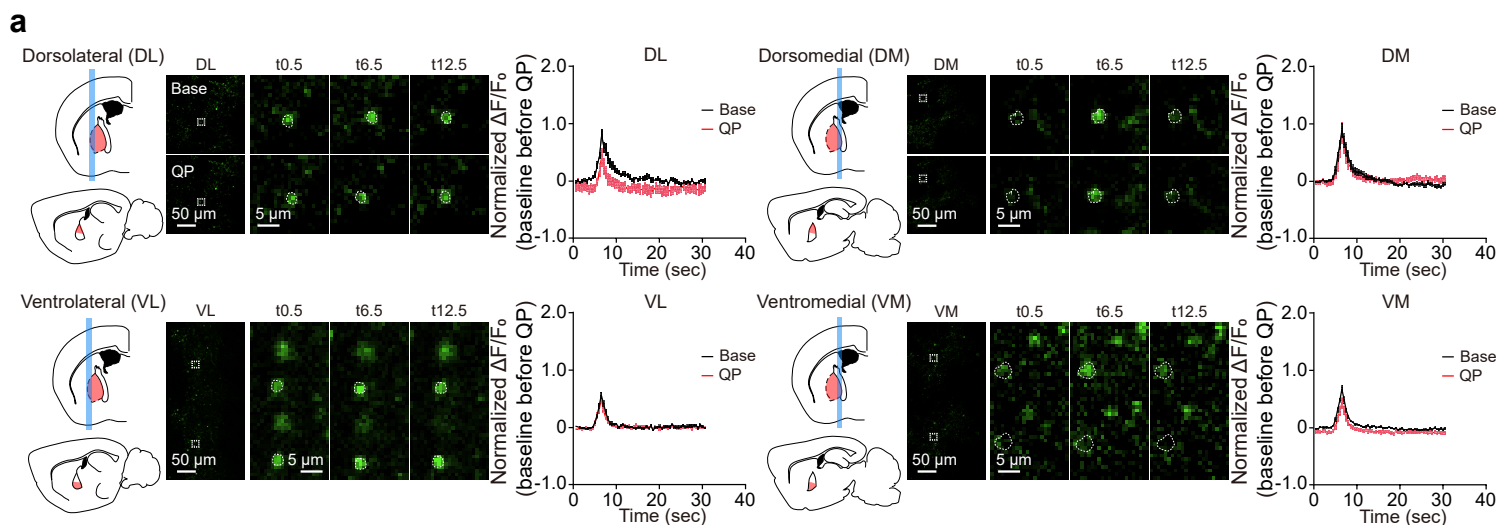
Supplementary Fig. 15 | Striatopallidal synaptic transmission in the contralateral hemisphere of 6-OHDA-lesioned mice recapitulates region-specific dopaminergic modulation in the subregions of the GPe

a-d, Schematic illustrations of the GPe subregions of the contralateral hemisphere (top left), representative recording traces (bottom left), oIPSC amplitude (top center) and PPR plots (bottom center) normalized to baseline during bath application of quinpirole (10 μ M), and summary statistics of normalized oIPSCs (top right) and PPRs (bottom right). **a**, Summary statistics of normalized oIPSCs ($n = 10$ cells from 9 mice, one sample t-test; Baseline 100%, QP ON $44.34 \pm 5.09\%$, QP OFF $26.77 \pm 6.32\%$) and PPRs (Baseline 100%, QP ON $139.90 \pm 9.38\%$, QP OFF $147 \pm 14.87\%$) in the DL GPe. **b**, Summary statistics of normalized oIPSCs ($n = 11$ cells from 11 mice, one sample t-test; Baseline 100%, QP ON $53.38 \pm 4.65\%$, QP OFF $34.37 \pm 2.79\%$) and PPRs (Baseline 100%, QP ON $95.11 \pm 13.94\%$, QP OFF $97.97 \pm 9.61\%$) in the DM GPe. **c**, Summary statistics of normalized oIPSCs ($n = 9$ cells from 9 mice, one sample t-test; Baseline 100%, QP ON $51.45 \pm 4.93\%$, QP OFF $37.66 \pm 5.80\%$) and PPRs (Baseline 100%, QP ON $108.90 \pm 12.28\%$, QP OFF $99.99 \pm 14.06\%$) in the VL GPe. **d**, Summary statistics of normalized oIPSCs ($n = 15$ cells from 12 mice, one sample t-test; Baseline 100%, QP ON $51.44 \pm 3.43\%$, QP OFF $39.53 \pm 3.71\%$) and PPRs (Baseline 100%, QP ON $134 \pm 8.13\%$, QP OFF $117.30 \pm 8.07\%$) in the VM GPe. The data are presented as box-and-whisker plots. * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$, **** $p < 0.0001$.



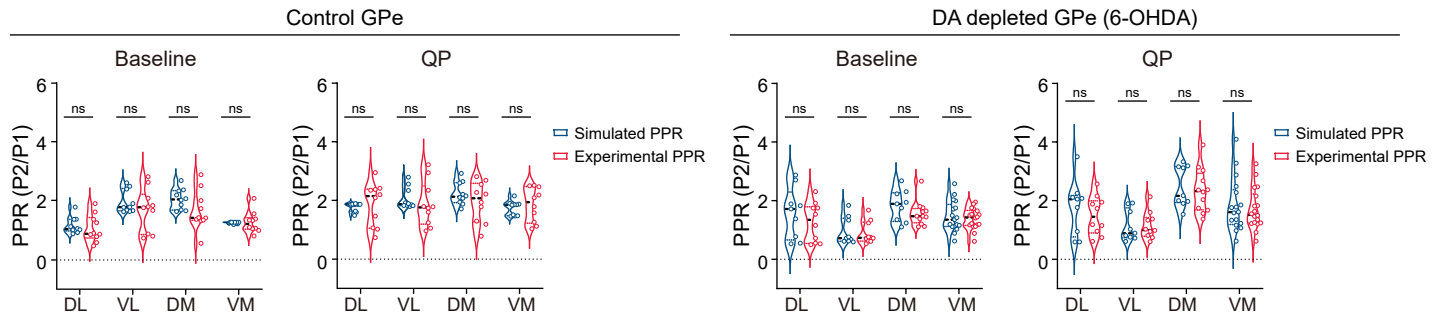
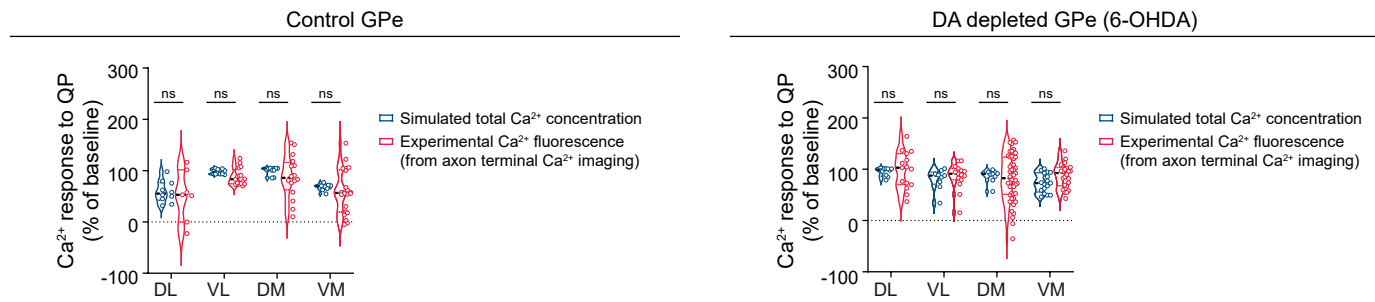
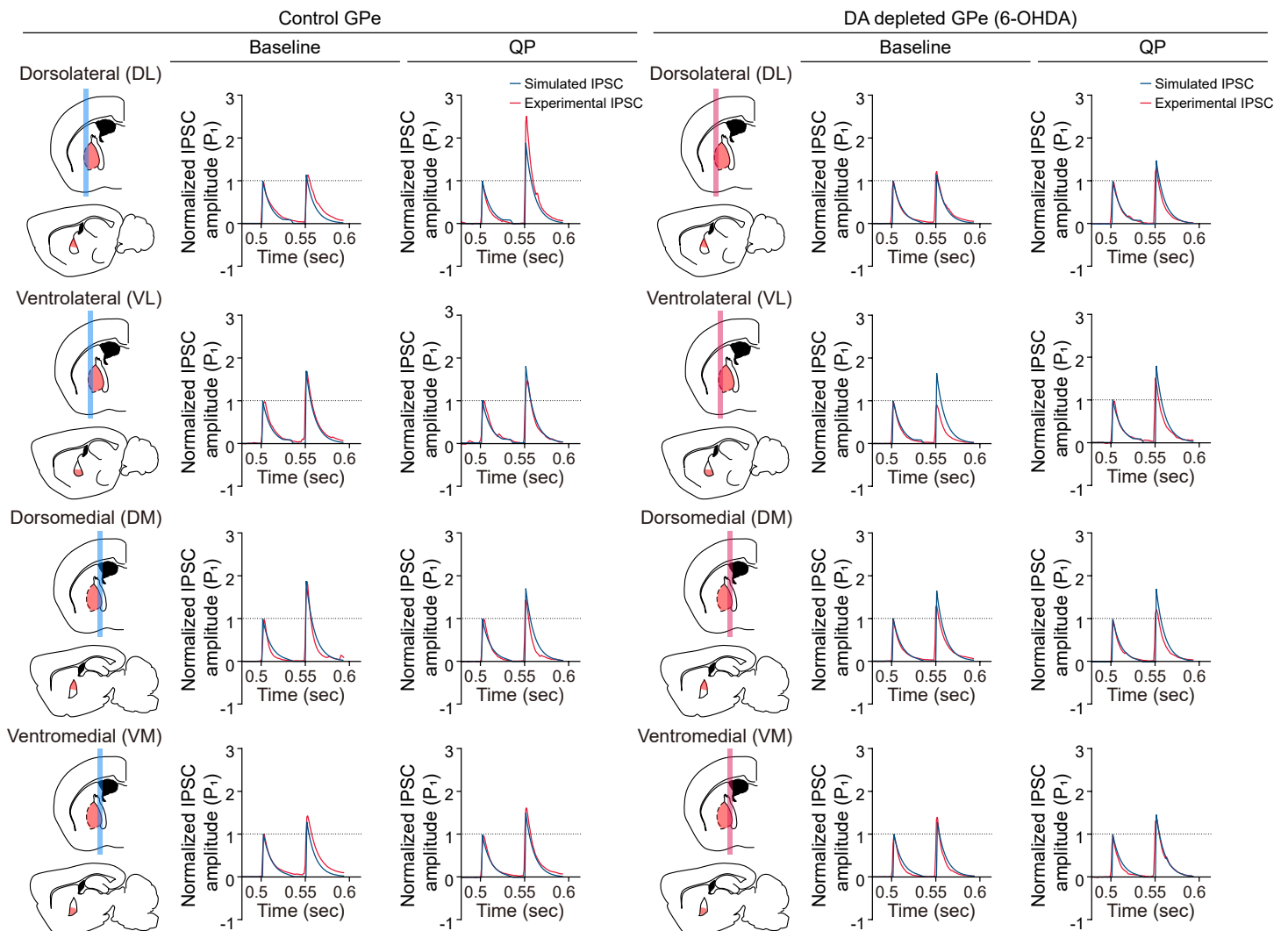
Supplementary Fig. 16 | No significant differences in striatopallidal axons and axon terminals were observed between the GPe subgroups after DA depletion

a, A schematic illustration depicting the injection of AAV5-hSyn-Flex-mGFP-2A-Synaptophysin- mRuby virus into the striatum of Adora2A-Cre mice, along with the unilateral injection of 6- OHDA into the MFB. **b**, A schematic illustration depicting fluorescently labeled striatopallidal axons (GFP), axon terminals (RFP), dopaminergic axons (TH), and vesicular monoamine transporter 2 (VMAT2) with 6-OHDA injection. **c**, Representative enhanced confocal images of striatopallidal axon terminals and potential dopaminergic boutons (TH+ VMAT2+) in the GPe subregions of the contralateral and ipsilateral (6-OHDA) hemispheres. **d**, Summary statistics of virally expressed GFP+ area in the GPe subgroups of the contralateral (left) (n = 46 images from 7 mice per GPe subgroup, unpaired t-test; DL-VM GPe $7755.1 \pm 543.2 \mu\text{m}^2$, VL-DM GPe $7922 \pm 677.9 \mu\text{m}^2$) and ipsilateral hemispheres (right) (DL-VM GPe $9384.3 \pm 766.8 \mu\text{m}^2$, VL-DM GPe $8864.2 \pm 588.1 \mu\text{m}^2$). **e**, Summary statistics of virally expressed RFP+ area in the GPe subgroups of the contralateral (left) (n = 46 images from 7 mice per GPe subgroup, unpaired t-test; DL-VM GPe $1934.5 \pm 136.1 \mu\text{m}^2$, VL-DM GPe $2005.9 \pm 170.4 \mu\text{m}^2$) and ipsilateral hemispheres (right) (DL-VM GPe $3017.2 \pm 235.8 \mu\text{m}^2$, VL-DM GPe $2912.4 \pm 171.8 \mu\text{m}^2$). **f**, Summary statistics of VMAT2+ area colocalized with TH+ area on striatopallidal axons (RFP+ or GFP+) in the GPe subgroups of the contralateral (left) (n = 46 images from 7 mice per GPe subgroup, unpaired t-test; DL-VM GPe $6.4 \pm 0.9 \mu\text{m}^2$, VL-DM GPe $3.9 \pm 0.6 \mu\text{m}^2$) and ipsilateral hemispheres (right) (DL- VM GPe $0.6 \pm 0.1 \mu\text{m}^2$, VL-DM GPe $0.4 \pm 0.1 \mu\text{m}^2$). **g**, Summary statistics of TH+ area (left) (ordinary two-way ANOVA with Holm-Sidak's post-hoc multiple comparisons test; Contra DL $190.1 \pm 34.3 \mu\text{m}^2$, Ipsi DL $25.4 \pm 5.6 \mu\text{m}^2$, Contra VL $314 \pm 40.8 \mu\text{m}^2$, Ipsi VL $73.2 \pm 14.7 \mu\text{m}^2$, Contra DM $360.2 \pm 44.4 \mu\text{m}^2$, Ipsi DM $64.5 \pm 21.2 \mu\text{m}^2$, Contra VM $393.2 \pm 38.7 \mu\text{m}^2$, Ipsi VM $75.4 \pm 23.9 \mu\text{m}^2$; GPe subregion, $p = 0.0009$, 6-OHDA, $p < 0.0001$, interaction, $p = 0.0911$) and VMAT2+ area colocalized with TH+ area (right) (Contra DL $11 \pm 2.1 \mu\text{m}^2$, Ipsi DL $1.7 \pm 0.4 \mu\text{m}^2$, Contra VL $13.2 \pm 2.3 \mu\text{m}^2$, Ipsi VL $1.6 \pm 0.4 \mu\text{m}^2$, Contra DM $15.3 \pm 3.5 \mu\text{m}^2$, Ipsi DM $0.7 \pm 0.2 \mu\text{m}^2$, Contra VM $19 \pm 3.1 \mu\text{m}^2$, Ipsi VM $1.5 \pm 0.7 \mu\text{m}^2$; GPe subregion, $p = 0.3448$, 6-OHDA, $p < 0.0001$, interaction, $p = 0.2763$) in the GPe subregions of the contralateral and ipsilateral hemispheres. **h,i**, Cumulative plots of the nearest neighbor distances from striatopallidal axon terminals (RFP+) to potential dopaminergic boutons (TH+ VMAT2+) or to other striatopallidal axon terminals (RFP+) in the GPe subregions of the contralateral and ipsilateral hemispheres. The data are presented as box-and-whisker plots or mean $\pm$ SEM. * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$, **** $p < 0.0001$.



Supplementary Fig. 17 | Presynaptic Ca²⁺ dynamics may contribute to region-specific dopaminergic modulation in the GPe

a,b, Schematic illustrations of the GPe subregions of the contralateral hemisphere (left) and transients of GCaMP6f fluorescence (dF/F_0) evoked by 20 Hz stimulation at axonal boutons of the striatopallidal presynaptic axon terminals before and after QP application (black traces, basal condition; red traces, 10 μ M QP). Inset images: calcium images of an axonal bouton before ($t = 0.5$ s, left), during ($t = 6.5$ s, center) and after stimulation ($t = 12.5$ s, right) in the GPe subregions of the contralateral and ipsilateral hemispheres. **c**, Summary statistics of GCaMP6f fluorescence (dF/F_0) normalized to the baseline before QP application in the DL GPe ($n = 7$ ROIs for the contra and $n = 15$ ROIs for the ipsi from 5 mice, repeated measures two-way ANOVA with Holm-Sidak's post-hoc multiple comparisons test; Contra Base 0.81 ± 0.07 , Contra QP 0.41 ± 0.15 , Ipsi Base 0.82 ± 0.11 , Ipsi QP 0.79 ± 0.12 ; QP treatment, $p = 0.0147$, 6-OHDA, $p = 0.2747$, interaction, $p = 0.0326$), VL GPe ($n = 16$ ROIs for the contra and $n = 15$ ROIs for the ipsi from 5 mice, repeated measures two-way ANOVA with Holm-Sidak's post-hoc multiple comparisons test; Contra Base 0.57 ± 0.05 , Contra QP 0.51 ± 0.06 , Ipsi Base 0.70 ± 0.05 , Ipsi QP 0.59 ± 0.06 ; QP treatment, $p = 0.0086$, 6-OHDA, $p = 0.1647$, interaction, $p = 0.4746$), DM GPe ($n = 16$ ROIs for the contra and $n = 46$ ROIs for the ipsi from 5 mice, repeated measures two-way ANOVA with Holm-Sidak's post-hoc multiple comparisons test; Contra Base 0.89 ± 0.12 , Contra QP 0.84 ± 0.18 , Ipsi Base 0.85 ± 0.06 , Ipsi QP 0.63 ± 0.06 ; QP treatment, $p = 0.0573$, 6-OHDA, $p = 0.3042$, interaction, $p = 0.2097$), and VM GPe ($n = 22$ ROIs for the contra and $n = 23$ ROIs for the ipsi from 5 mice, repeated measures two-way ANOVA with Holm-Sidak's post-hoc multiple comparisons test; Contra Base 0.67 ± 0.06 , Contra QP 0.43 ± 0.09 , Ipsi Base 1.00 ± 0.04 , Ipsi QP 0.86 ± 0.05 ; QP treatment, $p < 0.0001$, 6-OHDA, $p < 0.0001$, interaction, $p < 0.0001$). **d**, Summary statistics of GCaMP6f fluorescence (dF/F_0) normalized to the baseline before QP application, comparing GPe subregions (left) (one-way ANOVA; DL 0.51 ± 0.19 , VL 0.88 ± 0.42 , DM 0.88 ± 0.10 , VM 0.59 ± 0.09 , $p = 0.0219$) and GPe subgroups (right) (unpaired t-test; DL/VM GPe 0.57 ± 0.08 , VL/DM GPe 0.88 ± 0.05 , $p = 0.0020$) in the contralateral hemispheres. **e**, Summary statistics of GCaMP6f fluorescence (dF/F_0) normalized to the baseline before QP application, comparing GPe subregions (left) (one-way ANOVA; DL 0.98 ± 0.09 , VL 0.86 ± 0.06 , DM 0.82 ± 0.06 , VM 0.86 ± 0.04 , $p = 0.5821$) and GPe subgroups (right) (unpaired t-test; DL/VM GPe 0.91 ± 0.04 , VL/DM GPe 0.83 ± 0.05 , $p = 0.3284$) in the ipsilateral hemispheres. The data are presented as box-and-whisker plots or mean $\pm$ SEM. * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$.

a**b****c**

Supplementary Fig. 18 | Validation of the computational model through comparison with experimental PPRs and Ca²⁺ responses across GPe subregions

a,b, Summary statistics comparing simulated and experimental values of PPRs and Ca²⁺ responses under control and DA-depleted conditions across GPe subregions. **a**, Summary statistics comparing simulated and experimental values of PPRs in the contralateral (left) (ordinary two-way ANOVA with Holm-Sidak's post-hoc multiple comparisons test; baseline simulated PPRs in the DL GPe 1.17 ± 0.09 , baseline experimental PPRs in the DL GPe 1.07 ± 0.15 , baseline simulated PPRs in the VL GPe 1.98 ± 0.12 , baseline experimental PPRs in the VL GPe 1.72 ± 0.23 , baseline simulated PPRs in the DM GPe 2.07 ± 0.11 , baseline experimental PPRs in the DM GPe 1.67 ± 0.21 , baseline simulated PPRs in the VM GPe 1.27 ± 0.01 , baseline experimental PPRs in the VM GPe 1.29 ± 0.12 ; data type, $p = 0.0780$, GPe subregions, $p < 0.0001$, interaction, $p = 0.4973$; QP simulated PPRs in the DL GPe 1.78 ± 0.05 , QP experimental PPRs in the DL GPe 1.87 ± 0.23 , QP simulated PPRs in the VL GPe 2.06 ± 0.12 , QP experimental PPRs in the VL GPe 1.87 ± 0.24 , QP simulated PPRs in the DM GPe 2.22 ± 0.12 , QP experimental PPRs in the DM GPe 1.95 ± 0.22 , QP simulated PPRs in the VM GPe 1.74 ± 0.08 , QP experimental PPRs in the VM GPe 1.85 ± 0.18 ; data type, $p = 0.5791$, GPe subregions, $p = 0.2917$, interaction, $p = 0.5771$) and ipsilateral hemisphere (right) (baseline simulated PPRs in the DL GPe 1.58 ± 0.29 , baseline experimental PPRs in the DL GPe 1.27 ± 0.21 , baseline simulated PPRs in the VL GPe 0.96 ± 0.16 , baseline experimental PPRs in the VL GPe 0.89 ± 0.12 , baseline simulated PPRs in the DM GPe 1.83 ± 0.18 , baseline experimental PPRs in the DM GPe 1.56 ± 0.12 , baseline simulated PPRs in the VM GPe 1.46 ± 0.13 , baseline experimental PPRs in the VM GPe 1.38 ± 0.08 ; data type, $p = 0.1059$, GPe subregions, $p = 0.0002$, interaction, $p = 0.8013$; QP simulated PPRs in the DL GPe 1.77 ± 0.31 , QP experimental PPRs in the DL GPe 1.50 ± 0.21 , QP simulated PPRs in the VL GPe 1.14 ± 0.18 , QP experimental PPRs in the VL GPe 1.15 ± 0.15 , QP simulated PPRs in the DM GPe 2.49 ± 0.23 , QP experimental PPRs in the DM GPe 2.35 ± 0.22 , QP simulated PPRs in the VM GPe 1.84 ± 0.22 , QP experimental PPRs in the VM GPe 1.71 ± 0.16 ; data type, $p = 0.4026$, GPe subregions, $p < 0.0001$, interaction, $p = 0.9466$). **b**, Summary statistics comparing simulated and experimental values of Ca²⁺ responses to the QP application in the contralateral (left) (ordinary two-way ANOVA with Holm-Sidak's post-hoc multiple comparisons test; simulated Ca²⁺ responses in the DL GPe 58.76 ± 6.57 , experimental Ca²⁺ responses in the DL GPe 50.94 ± 18.84 , simulated Ca²⁺ responses in the VL GPe 97.96 ± 1.58 , experimental Ca²⁺ responses in the VL GPe 88.06 ± 4.16 , simulated Ca²⁺ responses in the DM GPe 99.99 ± 2.39 , experimental Ca²⁺ responses in the DM GPe 87.87 ± 10.30 , simulated Ca²⁺ responses in the VM GPe 67.97 ± 1.93 , experimental Ca²⁺ responses

in the VM GPe 58.66 ± 9.10 ; data type, $p = 0.1344$, GPe subregions, $p < 0.0001$, interaction, $p = 0.9967$) and ipsilateral hemisphere (right) (simulated Ca^{2+} responses in the DL GPe 94.35 ± 2.80 , experimental Ca^{2+} responses in the DL GPe 98.09 ± 9.26 , simulated Ca^{2+} responses in the VL GPe 80.59 ± 6.84 , experimental Ca^{2+} responses in the VL GPe 86.22 ± 6.67 , simulated Ca^{2+} responses in the DM GPe 86.74 ± 4.24 , experimental Ca^{2+} responses in the DM GPe 82.45 ± 6.75 , simulated Ca^{2+} responses in the VM GPe 73.29 ± 4.48 , experimental Ca^{2+} responses in the VM GPe 88.07 ± 5.01 ; data type, $p = 0.4311$, GPe subregions, $p = 0.3411$, interaction, $p = 0.6871$). **c**, Schematic illustrations of the GPe subregions (left), representative paired overlays of simulated and experimental IPSCs during baseline (center), and QP application (right) under control and DA-depleted conditions in the GPe subregions. The scale of representative traces was normalized to the first amplitude. The data are presented as violin plots with individual data points. The solid lines indicate the median, and dashed lines indicate the 25th and 75th percentiles.

Table S1. oIPSC kinetics in striatopallidal synaptic transmission within the GPe

	PV+	FoxP2+	PV-/FoxP2-
Baseline PPR (P2/P1)	1.63 ± 0.06	1.1 ± 0.15	1.6 ± 0.09
Time of Peak (ms)	7.14 ± 0.27	11.52 ± 0.86	7.94 ± 0.57
Half-width (ms)	9.23 ± 0.75	18.18 ± 1.75	11.5 ± 1.27
Rise slope (dV/dt)	373.59 ± 49.91	94.2 ± 27.51	311.05 ± 40.1
Decay slope (dV/dt)	-31.42 ± 4.08	-10.7 ± 2.49	-24.1 ± 2.9

Table S2. Pairwise regional distinctiveness comparisons with Holm and FDR corrections

Region A	Region B	Uncorrected p-value	Holm–Bonferroni corrected p-value	Benjamini–Hochberg FDR-adjusted q-value
DL	VL	0.00009999	0.00059994	0.00011999
DL	DM	0.00029997	0.00059994	0.00029997
DL	VM	0.00009999	0.00059994	0.00011999
VL	DM	0.00009999	0.00059994	0.00011999
VL	VM	0.00009999	0.00059994	0.00011999
DM	VM	0.00009999	0.00059994	0.00011999

P-values are derived from a one-sided permutation test (10,000 iterations). Significance was assessed after correcting for multiple comparisons across all pairs using Holm-Bonferroni and Benjamini-Hochberg methods.

Table S3. Summary of parameter bounds for parameter optimization

Parameter	Bounds
K_c	$(1e^{-9}, 1e^{-5}) \text{ M}^{92,94,100}$
τ_{rec}	$(0, 2) \text{ s}^{48,101}$
τ_{Ca}	$(0.02, 0.5) \text{ s}^{93,95,101}$
$[\text{Ca}]_{\text{influx}}$	$(1e^{-7}, 100e^{-5}) \text{ M}^{100-102}$

Table S4. Goodness-of-fit metrics (MSE and RMSE) for simulated versus experimental PPRs across regions and conditions

Region	Group	Condition	MSE	RMSE
DL	Control	Baseline	0.0796514	0.28222579
DL	Control	QP	0.02712165	0.16468653
VL	Control	Baseline	0.20275093	0.45027872
VL	Control	QP	0.1569112	0.39612018
DM	Control	Baseline	0.26924825	0.51889136
DM	Control	QP	0.20432699	0.45202544
VM	Control	Baseline	0.0011156	0.03340056
VM	Control	QP	0.06525461	0.25544982
DL	6-OHDA	Baseline	0.76080167	0.87223946
DL	6-OHDA	QP	0.84769364	0.9207028
VL	6-OHDA	Baseline	0.19506254	0.44165885
VL	6-OHDA	QP	0.24444782	0.49441665
DM	6-OHDA	Baseline	0.32439537	0.56955717
DM	6-OHDA	QP	0.45101633	0.67157749
VM	6-OHDA	Baseline	0.25767622	0.50761819
VM	6-OHDA	QP	0.78876258	0.88812306

Table S5. All values and statistics for Figures 1 to 8

FIGURE		DESCRIPTION	VALUE	N NUMBER	STATISTICS	P VALUE	POST TEST	POST TEST P VALUE	
1	A	Schematic illustration	N/A	N/A	N/A	N/A	N/A	N/A	
	B	Representative fluorescence images (M1 cortex, GPe)	N/A	15 slices / 4 mice	N/A	N/A	N/A	N/A	
		Representative fluorescence images (DLS)	N/A	22 slices / 4 mice	N/A	N/A	N/A	N/A	
	C	Representative immunostaining images	N/A	N/A	N/A	N/A	N/A	N/A	
	D	RFP+ area (DL)	19920 ± 1618 μm2	18 images / 3 mice	Ordinary one-way ANOVA Group effect, F(3, 68) = 1.086	0.3612	Post hoc Holm-Sidak's test		
		RFP+ area (VL)	18920 ± 1507 μm2	18 images / 3 mice			Dorsolateral vs. Ventrolateral	0.8719	
		RFP+ area (DM)	22350 ± 1271 μm2	18 images / 3 mice			Dorsolateral vs. Dorsomedial	0.6966	
		RFP+ area (VM)	21650 ± 1603 μm2	18 images / 3 mice			Dorsolateral vs. Ventromedial	0.8038	
	E	TH+ area (Lateral)	632.7 ± 84.3 μm2	36 images / 6 mice	t(70) = 3.339 (Unpaired t-test)	0.0013	N/A	N/A	
		TH+ area (Medial)	1190 ± 144.1 μm2	36 images / 6 mice					
		TH+ area (Dorsal)	570.8 ± 98.9 μm2	36 images / 6 mice	t(70) = 4.251 (Unpaired t-test)	< 0.0001	N/A	N/A	
		TH+ area (Ventral)	1252 ± 1216.1 μm2	36 images / 6 mice					
	F	TH+ area (DL)	280 ± 36.6 μm2	18 images / 3 mice	Ordinary two-way ANOVA DV axis effect, F(1, 68) = 21.23 LM axis effect, F(1, 68) = 14.22 Interaction, F(1, 68) = 14.22	< 0.0001 0.0003 0.8713	Post hoc Holm-Sidak's test		
		TH+ area (VL)	985.4 ± 115.4 μm2	18 images / 3 mice			Dorsal:Lateral vs. Dorsal:Medial	0.0208	
		TH+ area (DM)	861.7 ± 170.2 μm2	18 images / 3 mice			Dorsal:Lateral vs. Ventral:Lateral	0.0061	
		TH+ area (VM)	1519 ± 209.3 μm2	18 images / 3 mice			Dorsal:Lateral vs. Ventral:Medial	<0.0001	
	G	representative fluorescence images (DL, VL, DM, VM GPe)	N/A	N/A	N/A	N/A	N/A	N/A	
		H	Peak fluorescence changes (DL GPe)	N/A	9 slices / 4 mice	N/A	N/A	N/A	N/A
			Peak fluorescence changes (VL GPe)	N/A	10 slices / 4 mice	N/A	N/A	N/A	N/A
			Peak fluorescence changes (DM GPe)	N/A	6 slices / 4 mice	N/A	N/A	N/A	N/A
Peak fluorescence changes (VM GPe)	N/A		10 slices / 4 mice	N/A	N/A	N/A	N/A		
I	Peak fluorescence changes (DL GPe)	0.00378 ± 0.00231	9 slices / 4 mice	Ordinary one-way ANOVA Group effect, F(3, 31) = 0.4654	0.3875	Post hoc Holm-Sidak's test			
	Peak fluorescence changes (VL GPe)	0.00748 ± 0.00374	10 slices / 4 mice			Dorsolateral vs. Ventrolateral	0.861		
	Peak fluorescence changes (DM GPe)	0.00766 ± 0.00378	6 slices / 4 mice			Dorsolateral vs. Dorsomedial	0.861		
	Peak fluorescence changes (VM GPe)	0.01287 ± 0.00458	10 slices / 4 mice			Dorsolateral vs. Ventromedial	0.4333		
2	A	Schematic illustration	N/A	N/A	N/A	N/A	N/A	N/A	
	B	Baseline (Normalized oIPSC)	100%	40 cells/ 26 mice	N/A	N/A	N/A	N/A	
		QP ON (Normalized oIPSC)	50.60 ± 2.17%	40 cells/ 26 mice	t(39) = 23.37 (one sample t-test)	< 0.0001			
		QP OFF (Normalized oIPSC)	38.99 ± 2.77%	40 cells/ 26 mice	t(39) = 14.05 (one sample t-test)	< 0.0001			
	C	Baseline (PPR)	1.44 ± 0.10	40 cells/ 26 mice	Repeated measures one-way ANOVA QP treatment effect, F (2, 78) = 13.68 Individual effect, F (39, 78) = 5.943	< 0.0001 < 0.0001	Post hoc Holm-Sidak's test	N/A	
		QP ON (PPR)	1.89 ± 0.11	40 cells/ 26 mice			Baseline vs. QP ON	<0.0001	
		QP OFF (PPR)	1.69 ± 0.09	40 cells/ 26 mice			Baseline vs. QP OFF	0.0087	
	D	Baseline (Normalized PPR)	100%	40 cells/ 26 mice	N/A	N/A	N/A	N/A	
		QP ON (Normalized PPR)	143.10 ± 8.88%	40 cells/ 26 mice	t(39) = 4.854 (one sample t-test)	< 0.0001			
		QP OFF (Normalized PPR)	129.80 ± 7.73%	40 cells/ 26 mice	t(39) = 3.852 (one sample t-test)	0.0004			
	E	DL, VM GPe subgroup (Normalized PPR)	165.1 ± 13.66%	20 cells/ 17 mice	t(19) = 2.167 (Unpaired t-test)	0.0112	N/A	N/A	
		VL, DM GPe subgroup (Normalized PPR)	121.1 ± 9.28%	20 cells/ 16 mice					
		Baseline (Normalized oIPSC)	100%	10 cells/ 9 mice					N/A
	F	QP ON (Normalized oIPSC)	54.38 ± 4.60%	10 cells/ 9 mice	t(9) = 9.929 (one sample t-test)	< 0.0001			
		QP OFF (Normalized oIPSC)	39.33 ± 4.79%	10 cells/ 9 mice	t(9) = 12.67 (one sample t-test)	< 0.0001			
		Baseline (Normalized PPR)	100%	10 cells/ 9 mice	N/A	N/A	N/A	N/A	
	G	QP ON (Normalized PPR)	184 ± 23.37%	10 cells/ 9 mice	t(9) = 3.593 (one sample t-test)	0.0058			
		QP OFF (Normalized PPR)	154.10 ± 14.71%	10 cells/ 9 mice	t(9) = 3.680 (one sample t-test)	0.0051			
		H	Baseline (Normalized oIPSC)	100%	10 cells/ 8 mice	N/A	N/A	N/A	N/A
	QP ON (Normalized oIPSC)		45.29 ± 4.53%	10 cells/ 8 mice	t(9) = 12.07 (one sample t-test)	< 0.0001			
QP OFF (Normalized oIPSC)	34.79 ± 5.23%		10 cells/ 8 mice	t(9) = 12.48 (one sample t-test)	< 0.0001				
I	Baseline (Normalized PPR)	100%	10 cells/ 8 mice	N/A	N/A	N/A	N/A		
	QP ON (Normalized PPR)	126.30 ± 15.15%	10 cells/ 8 mice	t(9) = 1.736 (one sample t-test)	0.1166				
	QP OFF (Normalized PPR)	135.30 ± 22.82%	10 cells/ 8 mice	t(9) = 1.545 (one sample t-test)	0.1567				
J	Baseline (Normalized oIPSC)	100%	10 cells/ 8 mice	N/A	N/A	N/A	N/A		
	QP ON (Normalized oIPSC)	47.49 ± 4.07%	10 cells/ 8 mice	t(9) = 12.90 (one sample t-test)	< 0.0001				
	QP OFF (Normalized oIPSC)	35.84 ± 5.35%	10 cells/ 8 mice	t(9) = 11.98 (one sample t-test)	< 0.0001				
K	Baseline (Normalized PPR)	100%	10 cells/ 8 mice	N/A	N/A	N/A	N/A		
	QP ON (Normalized PPR)	115.90 ± 11.32%	10 cells/ 8 mice	t(9) = 1.406 (one sample t-test)	0.1934				
	QP OFF (Normalized PPR)	112.20 ± 10.24%	10 cells/ 8 mice	t(9) = 1.187 (one sample t-test)	0.2657				
L	Baseline (Normalized oIPSC)	100%	10 cells/ 8 mice	N/A	N/A	N/A	N/A		
	QP ON (Normalized oIPSC)	55.24 ± 3.85%	10 cells/ 8 mice	t(9) = 9.929 (one sample t-test)	< 0.0001				
	QP OFF (Normalized oIPSC)	45.99 ± 6.78%	10 cells/ 8 mice	t(9) = 12.67 (one sample t-test)	< 0.0001				
M	Baseline (Normalized PPR)	100%	10 cells/ 8 mice	N/A	N/A	N/A	N/A		
	QP ON (Normalized PPR)	146.30 ± 12.77%	10 cells/ 8 mice	t(9) = 3.624 (one sample t-test)	0.0055				
	QP OFF (Normalized PPR)	117.50 ± 8.48%	10 cells/ 8 mice	t(9) = 2.061 (one sample t-test)	0.0694				
N	Sr ²⁺ (Amplitude)	44.48 ± 6.68 pA	8 cells/ 6 mice	t(7) = 3.070 (Paired t-test)	0.0181	N/A	N/A		
	Sr ²⁺ + OP (Amplitude)	37.54 ± 5.32 pA	8 cells/ 6 mice						

3	B	Sr ²⁺ (Frequency)	42.80 ± 9.12 Hz	8 cells/ 6 mice	t(7) = 2.929 (Paired t-test)	0.0221	N/A	N/A
			Sr ²⁺ + QP (Frequency)	31.80 ± 8.30 Hz				
		Sr ²⁺ (Amplitude)	52.31 ± 6.07 pA	16 cells/ 15 mice	t(15) = 2.729 (Paired t-test)	0.0155	N/A	N/A
			Sr ²⁺ + QP (Amplitude)	47.91 ± 6.03 pA				
		Sr ²⁺ (Frequency)	41.03 ± 4.74 Hz	16 cells/ 15 mice	t(15) = 0.5001 (Paired t-test)	0.6242	N/A	N/A
			Sr ²⁺ + QP (Frequency)	40.26 ± 4.35 Hz				
		Sr ²⁺ (Amplitude)	52.84 ± 8.51 pA	7 cells/ 7 mice	t(6) = 3.421 (Paired t-test)	0.0141	N/A	N/A
			Sr ²⁺ + QP (Amplitude)	45.05 ± 6.83 pA				
		Sr ²⁺ (Frequency)	46.85 ± 7.95 Hz	7 cells/ 7 mice	t(6) = 1.054 (Paired t-test)	0.3325	N/A	N/A
			Sr ²⁺ + QP (Frequency)	43.29 ± 8.96 Hz				
		Sr ²⁺ (Amplitude)	42.62 ± 3.15 pA	9 cells/ 8 mice	t(8) = 5.311 (Paired t-test)	0.0007	N/A	N/A
			Sr ²⁺ + QP (Amplitude)	32.38 ± 2.64 pA				
		Sr ²⁺ (Frequency)	54.32 ± 5.36 Hz	9 cells/ 8 mice	t(8) = 5.031 (Paired t-test)	0.001	N/A	N/A
			Sr ²⁺ + QP (Frequency)	28.63 ± 2.38 Hz				
		Cumulative plots		N/A	N/A	N/A	N/A	N/A
		DL, VM GPe subgroup (Quantal amplitude)	84.10 ± 3.37%	17 cells/ 14 mice	t(38) = 1.469 (Unpaired t-test)	0.15	N/A	N/A
			VL, DM GPe subgroup (Quantal amplitude)	90.06 ± 2.44%				
		DL, VM GPe subgroup (Quantal frequency)	67.32 ± 7.59%	17 cells/ 14 mice	t(38) = 3.802 (Unpaired t-test)	0.0005	N/A	N/A
			VL, DM GPe subgroup (Quantal frequency)	97.57 ± 3.93%				
		Schematic illustration		N/A	N/A	N/A	N/A	N/A
		L741626 (Normalized oIPSC)	100%	7 cells/ 5 mice	N/A	N/A	N/A	N/A
			L741626 + QP (Normalized oIPSC)	56.04 ± 5.73%				
		L741626 (Normalized PPR)	100%	7 cells/ 5 mice	N/A	N/A	N/A	N/A
			L741626 + QP (Normalized PPR)	111.70 ± 12.13%				
		Schematic illustration		N/A	N/A	N/A	N/A	N/A
		L741626 (Normalized oIPSC)	100%	7 cells/ 4 mice	N/A	N/A	N/A	N/A
			L741626 + QP (Normalized oIPSC)	61.37 ± 8.55%				
		L741626 (Normalized PPR)	100%	7 cells/ 4 mice	N/A	N/A	N/A	N/A
			L741626 + QP (Normalized PPR)	106.8 ± 8.90%				
4	A	Schematic illustration		N/A	N/A	N/A	N/A	N/A
		Schematic illustration		N/A	N/A	N/A	N/A	N/A
		Representative immunostaining images		N/A	N/A	N/A	N/A	N/A
		D	D2R+ area (DL,VM GPe)	109.70 ± 7.91 μm ²	95 images/ 9 mice	t(188) = 3.133 (Unpaired t-test)	0.002	N/A
			D2R+ area (VL,DM GPe)	80.39 ± 4.99 μm ²	95 images/ 9 mice			
			D2R+RFP+ area (DL,VM GPe)	15.61 ± 1.52 μm ²	95 images/ 9 mice	t(186) = 2.705 (Unpaired t-test)	0.0075	N/A
			D2R+RFP+ area (VL,DM GPe)	10.80 ± 0.90 μm ²	93 images/ 9 mice			
			D2R+GFP+ area (DL,VM GPe)	21.96 ± 2.80 μm ²	76 images/ 9 mice	t(182) = 2.426 (Unpaired t-test)	0.0163	N/A
			D2R+GFP+ area (VL,DM GPe)	14.51 ± 1.66 μm ²	108 images/ 9 mice			
			D2R+GFP+ or D2R+RFP+ area (DL,VM GPe)	29.78 ± 3.41 μm ²	92 images/ 9 mice	t(193) = 2.052 (Unpaired t-test)	0.0415	N/A
			D2R+GFP+ or D2R+RFP+ area (VL,DM GPe)	21.41 ± 2.36 μm ²	103 images/ 9 mice			
		E	GFP+ area (DL,VM GPe)	163.60 ± 14.08 μm ²	96 images/ 9 mice	t(193) = 1.173 (Unpaired t-test)	0.2423	N/A
			GFP+ area (VL,DM GPe)	187.40 ± 14.62 μm ²	99 images/ 9 mice			
		Cumulative plots (DL,VM GPe)		0.9783 ± 0.0064 μm	92 images/ 9 mice	N/A	N/A	N/A
		Cumulative plots (VL,DM GPe)		1.2309 ± 0.0104 μm	103 images/ 9 mice			
		Schematic illustration		N/A	N/A	N/A	N/A	N/A
		Schematic illustration		N/A	N/A	N/A	N/A	N/A
		Representative immunostaining images		N/A	N/A	N/A	N/A	N/A
		I	D4R+ volume (DL,VM GPe)	14.58 ± 1.32 μm ³	47 images/ 6 mice	t(97) = 3.029 (Unpaired t-test)	0.0031	N/A
			D4R+ volume (VL,DM GPe)	29.06 ± 1.84 μm ³	52 images/ 6 mice			
			The number of D4R+ fluorescence (DL,VM GPe)	317.80 ± 30.08	47 images/ 6 mice	t(97) = 4.705 (Unpaired t-test)	< 0.0001	N/A
			The number of D4R+ fluorescence (VL,DM GPe)	534.10 ± 32.20	52 images/ 6 mice			
		J	GABA _A R+ volume (DL,VM GPe)	533.50 ± 29.48 μm ³	47 images/ 6 mice	t(97) = 0.07017 (Unpaired t-test)	0.9442	N/A
			GABA _A R+ volume (VL,DM GPe)	536.60 ± 31.58 μm ³	52 images/ 6 mice			
		K	The number of GABA _A R+ fluorescence (DL,VM GPe)	2686.30 ± 169.60	47 images/ 6 mice	t(97) = 0.002606 (Unpaired t-test)	0.9979	N/A
			The number of GABA _A R+ fluorescence (VL,DM GPe)	2685.80 ± 143.30	52 images/ 6 mice			
		Cumulative plots (DL,VM GPe)		1.259 ± 0.0026 μm	47 images/ 6 mice	N/A	N/A	N/A
		Cumulative plots (VL,DM GPe)		0.8895 ± 0.001964 μm	52 images/ 6 mice			
5	B	Schematic illustration		N/A	N/A	N/A	N/A	N/A
		Baseline oIPSC (0 sec)	100%	15 cells/ 13 mice	Repeated measures two-way ANOVA Pulse train effect, F (9, 126) = 31.42 QP treatment effect, F (1, 14) = 26.60 Interaction, F (9, 126) = 4.639	< 0.0001	Post hoc Holm-Sidak's test Baseline vs Scaled QP oIPSC (0 sec)	>0.9999
			81.10 ± 9.90%	15 cells/ 13 mice				
			53.63 ± 9.30%	15 cells/ 13 mice				
			40.39 ± 7.81%	15 cells/ 13 mice				
			35.77 ± 7.97%	15 cells/ 13 mice				
			32.74 ± 8.83%	15 cells/ 13 mice				
			24.38 ± 5.45%	15 cells/ 13 mice				
			26.99 ± 6.60%	15 cells/ 13 mice				
			31.73 ± 11.77%	15 cells/ 13 mice				
			25.84 ± 6.50%	15 cells/ 13 mice				
			100%	15 cells/ 13 mice				
			131.19 ± 16.00%	15 cells/ 13 mice				
			88.91 ± 11.67%	15 cells/ 13 mice				
			67.76 ± 10.01%	15 cells/ 13 mice				
			52.57 ± 7.88%	15 cells/ 13 mice				
			49.96 ± 7.89%	15 cells/ 13 mice				
			52.64 ± 12.30%	15 cells/ 13 mice				
			51.09 ± 10.98%	15 cells/ 13 mice				
			54.16 ± 11.47%	15 cells/ 13 mice				
			51.96 ± 10.14%	15 cells/ 13 mice				

5	C	Baseline oIPSC (P2/P1)	0.795 ± 0.089	15 cells/ 13 mice	Repeated measures two-way ANOVA		Post hoc Holm-Sidak's test	
		Baseline oIPSC (P10/P1)	0.258 ± 0.065	15 cells/ 13 mice	QP treatment effect, F (1, 14) = 23.52	0.0003	P2/P1 - P10/P1	
		QP oIPSC (P2/P1)	1.259 ± 0.149	15 cells/ 13 mice	Peak ratio effect, F (1, 14) = 48.16	< 0.0001	Baseline	<0.0001
		QP oIPSC (P10/P1)	0.520 ± 0.101	15 cells/ 13 mice	Interaction, F (1, 14) = 4.015	0.0648	QP(10uM)	<0.0001
							Baseline - QP(10uM)	
							P2/P1	<0.0001
							P10/P1	0.0026
	D	Schematic illustration	N/A	N/A	N/A	N/A	N/A	N/A
	E	Baseline oIPSC (0 sec)	100.00 ± 0.00%	15 cells/ 13 mice	Repeated measures two-way ANOVA		Post hoc Holm-Sidak's test	
		Baseline oIPSC (0.05 sec)	103.70 ± 15.91%	15 cells/ 13 mice	Pulse train effect, F (9, 126) = 18.31	< 0.0001	Baseline vs Scaled QP oIPSC (0 sec)	>0.9999
		Baseline oIPSC (0.10 sec)	82.71 ± 19.06%	15 cells/ 13 mice	QP treatment effect, F (1, 14) = 2.724	0.1211	Baseline vs Scaled QP oIPSC (0.05 sec)	0.9964
		Baseline oIPSC (0.15 sec)	57.37 ± 15.80%	15 cells/ 13 mice	Interaction, F (9, 126) = 0.8486	0.573	Baseline vs Scaled QP oIPSC (0.10 sec)	0.4109
		Baseline oIPSC (0.20 sec)	48.38 ± 15.34%	15 cells/ 13 mice			Baseline vs Scaled QP oIPSC (0.15 sec)	0.864
		Baseline oIPSC (0.25 sec)	38.92 ± 11.41%	15 cells/ 13 mice			Baseline vs Scaled QP oIPSC (0.20 sec)	0.8571
		Baseline oIPSC (0.30 sec)	30.65 ± 9.27%	15 cells/ 13 mice			Baseline vs Scaled QP oIPSC (0.25 sec)	0.0709
		Baseline oIPSC (0.35 sec)	25.47 ± 7.32%	15 cells/ 13 mice			Baseline vs Scaled QP oIPSC (0.30 sec)	0.9313
		Baseline oIPSC (0.40 sec)	21.02 ± 5.24%	15 cells/ 13 mice			Baseline vs Scaled QP oIPSC (0.35 sec)	0.9964
		Baseline oIPSC (0.45 sec)	14.89 ± 2.80%	15 cells/ 13 mice			Baseline vs Scaled QP oIPSC (0.40 sec)	0.864
		Scaled QP oIPSC (0 sec)	100.00 ± 0.00%	15 cells/ 13 mice			Baseline vs Scaled QP oIPSC (0.45 sec)	0.864
		Scaled QP oIPSC (0.05 sec)	102.28 ± 11.26%	15 cells/ 13 mice				
		Scaled QP oIPSC (0.10 sec)	96.91 ± 16.72%	15 cells/ 13 mice				
		Scaled QP oIPSC (0.15 sec)	65.95 ± 16.61%	15 cells/ 13 mice				
		Scaled QP oIPSC (0.20 sec)	57.57 ± 17.76%	15 cells/ 13 mice				
		Scaled QP oIPSC (0.25 sec)	59.08 ± 18.59%	15 cells/ 13 mice				
		Scaled QP oIPSC (0.30 sec)	35.79 ± 8.77%	15 cells/ 13 mice				
		Scaled QP oIPSC (0.35 sec)	24.76 ± 4.76%	15 cells/ 13 mice				
		Scaled QP oIPSC (0.40 sec)	29.07 ± 6.20%	15 cells/ 13 mice				
		Scaled QP oIPSC (0.45 sec)	23.18 ± 5.08%	15 cells/ 13 mice				
	F	Baseline oIPSC (P2/P1)	1.037 ± 0.159	15 cells/ 13 mice	Repeated measures two-way ANOVA		Post hoc Holm-Sidak's test	
		Baseline oIPSC (P10/P1)	0.149 ± 0.028	15 cells/ 13 mice	QP treatment effect, F (1, 14) = 0.4500	0.5132	P2/P1 - P10/P1	
		QP oIPSC (P2/P1)	1.023 ± 0.113	15 cells/ 13 mice	Peak ratio effect, F (1, 14) = 47.37	< 0.0001	Baseline	<0.0001
		QP oIPSC (P10/P1)	0.232 ± 0.051	15 cells/ 13 mice	Interaction, F (1, 14) = 1.189	0.2939	QP(10uM)	<0.0001
							Baseline - QP(10uM)	
							P2/P1	0.824
							P10/P1	0.3749
	G	Schematic illustration		N/A	N/A	N/A	N/A	N/A
	H	Baseline oIPSC (0 sec)	100.00 ± 0.00%	16 cells/ 14 mice	Repeated measures two-way ANOVA		Post hoc Holm-Sidak's test	
		Baseline oIPSC (0.05 sec)	165.43 ± 7.47%	16 cells/ 14 mice	Pulse train effect, F (9, 135) = 4.607	< 0.0001	Baseline vs Scaled QP oIPSC (0 sec)	>0.9999
		Baseline oIPSC (0.10 sec)	188.33 ± 12.19%	16 cells/ 14 mice	QP treatment effect, F (1, 15) = 0.2218	0.6445	Baseline vs Scaled QP oIPSC (0.05 sec)	0.9749
		Baseline oIPSC (0.15 sec)	190.52 ± 17.69%	16 cells/ 14 mice	Interaction, F (9, 135) = 1.125	0.3497	Baseline vs Scaled QP oIPSC (0.10 sec)	0.1195
		Baseline oIPSC (0.20 sec)	178.87 ± 21.44%	16 cells/ 14 mice			Baseline vs Scaled QP oIPSC (0.15 sec)	0.9656
		Baseline oIPSC (0.25 sec)	165.80 ± 22.42%	16 cells/ 14 mice			Baseline vs Scaled QP oIPSC (0.20 sec)	0.2537
		Baseline oIPSC (0.30 sec)	159.53 ± 23.76%	16 cells/ 14 mice			Baseline vs Scaled QP oIPSC (0.25 sec)	0.9696
		Baseline oIPSC (0.35 sec)	158.96 ± 28.00%	16 cells/ 14 mice			Baseline vs Scaled QP oIPSC (0.30 sec)	0.9749
		Baseline oIPSC (0.40 sec)	152.83 ± 30.35%	16 cells/ 14 mice			Baseline vs Scaled QP oIPSC (0.35 sec)	0.9658
		Baseline oIPSC (0.45 sec)	146.68 ± 31.74%	16 cells/ 14 mice			Baseline vs Scaled QP oIPSC (0.40 sec)	0.9749
		Scaled QP oIPSC (0 sec)	100.00 ± 0.00%	16 cells/ 14 mice			Baseline vs Scaled QP oIPSC (0.45 sec)	0.9437
		Scaled QP oIPSC (0.05 sec)	161.76 ± 10.79%	16 cells/ 14 mice				
		Scaled QP oIPSC (0.10 sec)	209.78 ± 21.78%	16 cells/ 14 mice				
		Scaled QP oIPSC (0.15 sec)	183.08 ± 21.99%	16 cells/ 14 mice				
		Scaled QP oIPSC (0.20 sec)	197.26 ± 21.36%	16 cells/ 14 mice				
		Scaled QP oIPSC (0.25 sec)	171.50 ± 22.91%	16 cells/ 14 mice				
		Scaled QP oIPSC (0.30 sec)	161.37 ± 25.07%	16 cells/ 14 mice				
		Scaled QP oIPSC (0.35 sec)	165.67 ± 27.88%	16 cells/ 14 mice				
		Scaled QP oIPSC (0.40 sec)	157.26 ± 32.40%	16 cells/ 14 mice				
		Scaled QP oIPSC (0.45 sec)	155.47 ± 33.47%	16 cells/ 14 mice				
	I	Baseline oIPSC (P2/P1)	1.654 ± 0.075	16 cells/ 14 mice	Repeated measures two-way ANOVA		Post hoc Holm-Sidak's test	
		Baseline oIPSC (P10/P1)	1.467 ± 0.317	16 cells/ 14 mice	QP treatment effect, F (1, 15) = 0.06557	0.8014	P2/P1 - P10/P1	
		QP oIPSC (P2/P1)	1.618 ± 0.108	16 cells/ 14 mice	Peak ratio effect, F (1, 15) = 0.1687	0.6871	Baseline	0.1466
		QP oIPSC (P10/P1)	1.555 ± 0.335	16 cells/ 14 mice	Interaction, F (1, 15) = 0.8001	0.3852	QP(10uM)	0.781
							Baseline - QP(10uM)	
							P2/P1	0.7151
							P10/P1	0.6229
	J	Schematic illustration		N/A	N/A	N/A	N/A	N/A
	K	Baseline oIPSC (0 sec)	100.00 ± 0.00%	17 cells/ 15 mice	Repeated measures two-way ANOVA		Post hoc Holm-Sidak's test	
		Baseline oIPSC (0.05 sec)	152.01 ± 10.32%	17 cells/ 15 mice	Pulse train effect, F (9, 144) = 19.30	< 0.0001	Baseline vs Scaled QP oIPSC (0 sec)	>0.9999
		Baseline oIPSC (0.10 sec)	167.70 ± 15.34%	17 cells/ 15 mice	QP treatment effect, F (1, 16) = 13.37	0.0021	Baseline vs Scaled QP oIPSC (0.05 sec)	0.001
		Baseline oIPSC (0.15 sec)	159.77 ± 13.98%	17 cells/ 15 mice	Interaction, F (9, 144) = 4.609	< 0.0001	Baseline vs Scaled QP oIPSC (0.10 sec)	<0.0001
		Baseline oIPSC (0.20 sec)	134.11 ± 12.43%	17 cells/ 15 mice			Baseline vs Scaled QP oIPSC (0.15 sec)	<0.0001
		Baseline oIPSC (0.25 sec)	119.70 ± 13.64%	17 cells/ 15 mice			Baseline vs Scaled QP oIPSC (0.20 sec)	<0.0001
		Baseline oIPSC (0.30 sec)	96.48 ± 12.29%	17 cells/ 15 mice			Baseline vs Scaled QP oIPSC (0.25 sec)	0.0006
		Baseline oIPSC (0.35 sec)	79.90 ± 12.00%	17 cells/ 15 mice			Baseline vs Scaled QP oIPSC (0.30 sec)	0.0274
		Baseline oIPSC (0.40 sec)	69.39 ± 13.79%	17 cells/ 15 mice			Baseline vs Scaled QP oIPSC (0.35 sec)	0.0038
		Baseline oIPSC (0.45 sec)	60.09 ± 12.49%	17 cells/ 15 mice			Baseline vs Scaled QP oIPSC (0.40 sec)	0.0027
		Scaled QP oIPSC (0 sec)	100.00 ± 0.00%	17 cells/ 15 mice			Baseline vs Scaled QP oIPSC (0.45 sec)	0.0274
		Scaled QP oIPSC (0.05 sec)	199.06 ± 13.45%	17 cells/ 15 mice				
		Scaled QP oIPSC (0.10 sec)	253.46 ± 33.42%	17 cells/ 15 mice				
		Scaled QP oIPSC (0.15 sec)	243.57 ± 37.74%	17 cells/ 15 mice				

6	L	Scaled QP oIPSC (0.20 sec)	204.30 ± 26.10%	17 cells/ 15 mice				
		Scaled QP oIPSC (0.25 sec)	168.62 ± 20.64%	17 cells/ 15 mice				
		Scaled QP oIPSC (0.30 sec)	128.56 ± 16.88%	17 cells/ 15 mice				
		Scaled QP oIPSC (0.35 sec)	120.95 ± 21.55%	17 cells/ 15 mice				
		Scaled QP oIPSC (0.40 sec)	112.36 ± 19.90%	17 cells/ 15 mice				
		Scaled QP oIPSC (0.45 sec)	90.87 ± 16.98%	17 cells/ 15 mice				
	M	Baseline oIPSC (P2/P1)	1.520 ± 0.103	17 cells/ 15 mice	Repeated measures two-way ANOVA		Post hoc Holm-Sidak's test	
		Baseline oIPSC (P10/P1)	0.601 ± 0.125	17 cells/ 15 mice	QP treatment effect, F (1, 16) = 31.09	< 0.0001	P2/P1 - P10/P1	
		QP oIPSC (P2/P1)	1.991 ± 0.135	17 cells/ 15 mice	Peak ratio effect, F (1, 16) = 28.65	< 0.0001	Baseline	<0.0001
		QP oIPSC (P10/P1)	0.909 ± 0.170	17 cells/ 15 mice	Interaction, F (1, 16) = 2.160	0.1611	QP(10uM)	<0.0001
							Baseline - QP(10uM)	
							P2/P1	<0.0001
							P10/P1	0.0012
		Baseline P10/P1 (DL)	0.2584 ± 0.0650	15 cells/ 13 mice	Ordinary one-way ANOVA		Post hoc Holm-Sidak's test	
		Baseline P10/P1 (VL)	0.1489 ± 0.0280	15 cells/ 13 mice	Group effect, F (3, 59) = 11.18	< 0.0001	DL vs. VL	0.6728
		Baseline P10/P1 (DM)	1.4670 ± 0.3174	16 cells/ 14 mice			DL vs. DM	<0.0001
		Baseline P10/P1 (VM)	0.6009 ± 0.1249	17 cells/ 15 mice			DL vs. VM	0.3219
							VL vs. DM	<0.0001
							VL vs. VM	0.2114
							DM vs. VM	0.0034
		Baseline P10/P1 (DL)	0.258 ± 0.065	15 cells/ 13 mice	Repeated measures two-way ANOVA		Post hoc Holm-Sidak's test	
		QP P10/P1 (DL)	0.520 ± 0.101	15 cells/ 13 mice	QP treatment effect, F (1, 59) = 14.14	0.0004	Baseline - QP(10uM)	
		Baseline P10/P1 (VL)	0.149 ± 0.028	15 cells/ 13 mice	GPe subregion effect, F (3, 59) = 10.00	< 0.0001	DL	0.0353
		QP P10/P1 (VL)	0.232 ± 0.051	15 cells/ 13 mice	Interaction, F (3, 59) = 1.426	0.2442	VL	0.604
		Baseline P10/P1 (DM)	1.467 ± 0.317	16 cells/ 14 mice			DM	0.604
		QP P10/P1 (DM)	1.555 ± 0.335	16 cells/ 14 mice			VM	0.0075
		Baseline P10/P1 (VM)	0.601 ± 0.125	17 cells/ 15 mice				
		QP P10/P1 (VM)	0.909 ± 0.170	17 cells/ 15 mice				
6	N	Charge ratio (DL)	1.2260 ± 0.0914	15 cells/ 13 mice	Ordinary one-way ANOVA		Post hoc Holm-Sidak's test	
		Charge ratio (VL)	0.9444 ± 0.0654	15 cells/ 13 mice	Group effect, F (3, 59) = 2.972	0.0389	DL vs. VL	0.0604
		Charge ratio (DM)	1.0430 ± 0.0767	16 cells/ 14 mice			DL vs. DM	0.2982
		Charge ratio (VM)	1.1770 ± 0.0586	17 cells/ 15 mice			DL vs. VM	0.6375
							VL vs. DM	0.5797
							VL vs. VM	0.131
							DM vs. VM	0.4675
		Charge ratio (DL,VM GPe)	1.20 ± 0.0522	32 cells/ 28 mice				
		Charge ratio (VL,DM GPe)	0.9951 ± 0.0506	31 cells/ 27 mice	t(61) = 2.815 (Unpaired t-test)	0.0066	N/A	N/A
	A	Schematic illustration	N/A	N/A	N/A	N/A	N/A	N/A
	B	Baseline (Normalized oIPSC)	100%	17 cells/ 15 mice	N/A	N/A		
		QP ON (Normalized oIPSC)	54.92 ± 4.49%	17 cells/ 15 mice	t(16) = 10.03 (one sample t-test)	< 0.0001	N/A	N/A
		QP OFF (Normalized oIPSC)	39.84 ± 4.32%	17 cells/ 15 mice	t(16) = 13.93 (one sample t-test)	< 0.0001		
		Baseline (Normalized PPR)	100%	17 cells/ 15 mice	N/A	N/A		
		QP ON (Normalized PPR)	119.25 ± 10.12%	17 cells/ 15 mice	t(16) = 1.903 (one sample t-test)	0.0752	N/A	N/A
		QP OFF (Normalized PPR)	109.88 ± 8.24%	17 cells/ 15 mice	t(16) = 1.199 (one sample t-test)	0.2478		
	C	Baseline (Normalized oIPSC)	100%	12 cells/ 12 mice	N/A	N/A		
		QP ON (Normalized oIPSC)	52.51 ± 5.44%	12 cells/ 12 mice	t(11) = 8.734 (one sample t-test)	< 0.0001	N/A	N/A
		QP OFF (Normalized oIPSC)	41.80 ± 7.14%	12 cells/ 12 mice	t(11) = 8.150 (one sample t-test)	< 0.0001		
		Baseline (Normalized PPR)	100%	12 cells/ 12 mice	N/A	N/A		
		QP ON (Normalized PPR)	153.30 ± 12.68%	12 cells/ 12 mice	t(11) = 4.208 (one sample t-test)	0.0015	N/A	N/A
		QP OFF (Normalized PPR)	136.0 ± 10.86%	12 cells/ 12 mice	t(11) = 3.312 (one sample t-test)	0.0069		
	D	Baseline (Normalized oIPSC)	100%	15 cells/ 12 mice	N/A	N/A		
		QP ON (Normalized oIPSC)	49.55 ± 5.52%	15 cells/ 12 mice	t(14) = 9.155 (one sample t-test)	< 0.0001	N/A	N/A
		QP OFF (Normalized oIPSC)	37.71 ± 5.30%	15 cells/ 12 mice	t(14) = 11.75 (one sample t-test)	< 0.0001		
		Baseline (Normalized PPR)	100%	15 cells/ 12 mice	N/A	N/A		
		QP ON (Normalized PPR)	126.90 ± 6.77%	15 cells/ 12 mice	t(14) = 3.971 (one sample t-test)	0.0014	N/A	N/A
		QP OFF (Normalized PPR)	132.75 ± 6.55%	15 cells/ 12 mice	t(14) = 4.998 (one sample t-test)	0.0002		
	E	Baseline (Normalized oIPSC)	100%	18 cells/ 16 mice	N/A	N/A		
		QP ON (Normalized oIPSC)	56.77 ± 3.77%	18 cells/ 16 mice	t(17) = 11.47 (one sample t-test)	< 0.0001	N/A	N/A
		QP OFF (Normalized oIPSC)	41.40 ± 4.70%	18 cells/ 16 mice	t(17) = 12.47 (one sample t-test)	< 0.0001		
		Baseline (Normalized PPR)	100%	18 cells/ 16 mice	N/A	N/A		
		QP ON (Normalized PPR)	122.0 ± 6.69%	18 cells/ 16 mice	t(17) = 3.293 (one sample t-test)	0.0043	N/A	N/A
		QP OFF (Normalized PPR)	111.70 ± 5.74%	18 cells/ 16 mice	t(17) = 2.046 (one sample t-test)	0.0566		
	F	QP ON: PPR DL (Contra)	147.0 ± 7.63%	16 cells/ 14 mice	t(31) = 2.166 (Unpaired t-test)	0.0381	N/A	N/A
		QP ON: PPR DL (Ipsi)	119.2 ± 10.12%	17 cells/ 15 mice				
		QP ON: PPR VL (Contra)	104.8 ± 7.95%	14 cells/ 12 mice	t(27) = 2.130 (Unpaired t-test)	0.0424	N/A	N/A
		QP ON: PPR VL (Ipsi)	126.9 ± 6.77%	15 cells/ 12 mice				
		QP ON: PPR DM (Contra)	95.11 ± 13.94%	11 cells/ 11 mice	t(21) = 3.098 (Unpaired t-test)	0.0055	N/A	N/A
		QP ON: PPR DM (Ipsi)	153.35 ± 12.68%	12 cells/ 12 mice				
	G	QP ON: PPR VM (Contra)	134.01 ± 8.13%	15 cells/ 12 mice	t(31) = 2.221 (Unpaired t-test)	0.0343	N/A	N/A
		QP ON: PPR VM (Ipsi)	113.63 ± 4.58%	18 cells/ 16 mice				
		QP OFF: PPR DL (Contra)	148.19 ± 9.91%	16 cells/ 14 mice	t(31) = 2.987 (Unpaired t-test)	0.0055	N/A	N/A
		QP OFF: PPR DL (Ipsi)	109.88 ± 8.24%	17 cells/ 15 mice				
		QP OFF: PPR VL (Contra)	98.43 ± 8.89%	14 cells/ 12 mice	t(27) = 3.137 (Unpaired t-test)	0.0041	N/A	N/A
		QP OFF: PPR VL (Ipsi)	132.75 ± 6.55%	15 cells/ 12 mice				
		QP OFF: PPR DM (Contra)	97.97 ± 9.61%	11 cells/ 11 mice	t(21) = 2.601 (Unpaired t-test)	0.0167	N/A	N/A
		QP OFF: PPR DM (Ipsi)	135.96 ± 10.86%	12 cells/ 12 mice				
		QP OFF: PPR VM (Contra)	117.35 ± 8.07%	15 cells/ 12 mice	t(31) = 0.5791 (Unpaired t-test)	0.5667	N/A	N/A
		QP OFF: PPR VM (Ipsi)	111.74 ± 5.74%	18 cells/ 16 mice				

7	A	Schematic illustration	N/A	N/A	N/A	N/A	N/A	N/A
	B	Representative immunostaining images	N/A	N/A	N/A	N/A	N/A	N/A
	C	D2R+ area (DL, VM GPe) D2R+ area (VL, DM GPe)	122.0 ± 6.91 μm2 67.76 ± 4.38 μm2	118 images/ 11 mice 120 images/ 11 mice	t(236) = 6.651 (Unpaired t-test)	< 0.0001	N/A	N/A
		D2R+RFP+ area (DL, VM GPe) D2R+RFP+ area (VL, DM GPe)	16.23 ± 1.11 μm2 8.83 ± 0.73 μm2	118 images/ 11 mice 120 images/ 11 mice	t(236) = 5.548 (Unpaired t-test)	< 0.0001	N/A	N/A
		D2R+GFP+ area (DL, VM GPe) D2R+GFP+ area (VL, DM GPe)	19.92 ± 2.11 μm2 12.29 ± 1.30 μm2	118 images/ 11 mice 120 images/ 11 mice	t(236) = 2.622 (Unpaired t-test)	0.0093	N/A	N/A
		D2R+GFP+ or D2R+RFP+ area (DL, VM GPe) D2R+GFP+ or D2R+RFP+ area (VL, DM GPe)	27.79 ± 2.34 μm2 15.97 ± 1.65 μm2	118 images/ 11 mice 120 images/ 11 mice	t(236) = 4.150 (Unpaired t-test)	< 0.0001	N/A	N/A
	D	D2R+ area (DL, VM GPe) D2R+ area (VL, DM GPe)	104.0 ± 9.10 μm2 97.36 ± 9.25 μm2	120 images/ 11 mice 120 images/ 11 mice	t(238) = 0.5151 (Unpaired t-test)	0.6068	N/A	N/A
		D2R+RFP+ area (DL, VM GPe) D2R+RFP+ area (VL, DM GPe)	21.56 ± 2.44 μm2 15.94 ± 1.85 μm2	120 images/ 11 mice 120 images/ 11 mice	t(238) = 1.825 (Unpaired t-test)	0.0687	N/A	N/A
		D2R+GFP+ area (DL, VM GPe) D2R+GFP+ area (VL, DM GPe)	6.18 ± 0.83 μm2 5.09 ± 0.55 μm2	120 images/ 11 mice 120 images/ 11 mice	t(238) = 1.082 (Unpaired t-test)	0.2801	N/A	N/A
		D2R+GFP+ or D2R+RFP+ area (DL, VM GPe) D2R+GFP+ or D2R+RFP+ area (VL, DM GPe)	25.74 ± 2.44 μm2 18.91 ± 1.83 μm2	120 images/ 11 mice 120 images/ 11 mice	t(238) = 2.230 (Unpaired t-test)	0.0263	N/A	N/A
	E	Edge-corrected Ripley's H function analysis	N/A	N/A	N/A	N/A	N/A	N/A
	F	Edge-corrected Ripley's H function analysis	N/A	N/A	N/A	N/A	N/A	N/A
	G	D2R+ area (Contra DL, VM GPe) D2R+ area (Ipsi DL, VM GPe) D2R+ area (Contra VL, DM GPe) D2R+ area (Ipsi VL, DM GPe)	122.01 ± 6.91 μm2 107.96 ± 9.16 μm2 67.76 ± 4.38 μm2 97.36 ± 9.25 μm2	118 images/ 11 mice 120 images/ 11 mice 120 images/ 11 mice 120 images/ 11 mice	Ordinary two-way ANOVA GPe subregion effect, F (1, 474) = 9.435 6-OHDA effect, F (1, 474) = 0.5357 Interaction, F (1, 474) = 9.435	0.0023 0.4646 0.0023	Post hoc Holm-Sidak's test Control - 6-OHDA DL, VM GPe VL, DM GPe	0.0994 0.0145
		D2R+RFP+ area (Contra DL, VM GPe) D2R+RFP+ area (Ipsi DL, VM GPe) D2R+RFP+ area (Contra VL, DM GPe) D2R+RFP+ area (Ipsi VL, DM GPe)	16.23 ± 1.11 μm2 21.56 ± 2.44 μm2 8.83 ± 0.73 μm2 15.94 ± 1.85 μm2	118 images/ 11 mice 120 images/ 11 mice 120 images/ 11 mice 120 images/ 11 mice	Ordinary two-way ANOVA GPe subregion effect, F (1, 474) = 9.586 6-OHDA effect, F (1, 474) = 8.747 Interaction, F (1, 474) = 0.1824	0.002 0.0032 0.6695	Post hoc Holm-Sidak's test Control - 6-OHDA DL, VM GPe VL, DM GPe	0.0729 0.0345
	H	Edge-corrected Ripley's H function analysis	N/A	N/A	N/A	N/A	N/A	N/A
8	A	Schematic illustration	N/A	N/A	N/A	N/A	N/A	N/A
	B	Schematic illustration	N/A	N/A	N/A	N/A	N/A	N/A
	C	Baseline (Ca ²⁺ channel P _{open}) QP (Ca ²⁺ channel P _{open})	0.5097 ± 0.0349 0.2664 ± 0.0405	10 models 10 models	Wilcoxon matched-pairs signed rank test Sum of positive, negative ranks: 0.000 , -55.00	0.002	N/A	N/A
		Baseline (Ca ²⁺ concentration) QP (Ca ²⁺ concentration)	0.6020 ± 0.1056 μM 0.3679 ± 0.0908 μM	10 models 10 models	Wilcoxon matched-pairs signed rank test Sum of positive, negative ranks: 0.000 , -55.00	0.002	N/A	N/A
	D	Baseline (Ca ²⁺ channel P _{open}) QP (Ca ²⁺ channel P _{open})	0.5167 ± 0.0479 0.5203 ± 0.0486	10 models 10 models	Wilcoxon matched-pairs signed rank test Sum of positive, negative ranks: 36.00 , -19.00	0.4316	N/A	N/A
		Baseline (Ca ²⁺ concentration) QP (Ca ²⁺ concentration)	0.4880 ± 0.1019 μM 0.4960 ± 0.1090 μM	10 models 10 models	Wilcoxon matched-pairs signed rank test Sum of positive, negative ranks: 38.00 , -17.00	0.3223	N/A	N/A
	E	Baseline (Ca ²⁺ channel P _{open}) QP (Ca ²⁺ channel P _{open})	0.5549 ± 0.0434 0.5390 ± 0.0389	10 models 10 models	Wilcoxon matched-pairs signed rank test Sum of positive, negative ranks: 15.00 , -40.00	0.2324	N/A	N/A
		Baseline (Ca ²⁺ concentration) QP (Ca ²⁺ concentration)	0.8195 ± 0.0764 μM 0.7952 ± 0.0680 μM	10 models 10 models	Wilcoxon matched-pairs signed rank test Sum of positive, negative ranks: 15.00 , -40.00	0.2227	N/A	N/A
	F	Baseline (Ca ²⁺ channel P _{open}) QP (Ca ²⁺ channel P _{open})	0.4178 ± 0.0614 0.2778 ± 0.0421	10 models 10 models	Wilcoxon matched-pairs signed rank test Sum of positive, negative ranks: 0.000 , -55.00	0.002	N/A	N/A
		Baseline (Ca ²⁺ concentration) QP (Ca ²⁺ concentration)	0.5936 ± 0.0883 μM 0.4043 ± 0.0636 μM	10 models 10 models	Wilcoxon matched-pairs signed rank test Sum of positive, negative ranks: 0.000 , -55.00	0.002	N/A	N/A
	G	Baseline (Ca ²⁺ channel P _{open}) QP (Ca ²⁺ channel P _{open})	0.4732 ± 0.0353 0.4407 ± 0.0354	9 models 9 models	Wilcoxon matched-pairs signed rank test Sum of positive, negative ranks: 10.00 , -35.00	0.1641	N/A	N/A
		Baseline (Ca ²⁺ concentration) QP (Ca ²⁺ concentration)	0.5746 ± 0.0812 μM 0.5404 ± 0.0736 μM	9 models 9 models	Wilcoxon matched-pairs signed rank test Sum of positive, negative ranks: 10.00 , -35.00	0.1523	N/A	N/A
	H	Baseline (Ca ²⁺ channel P _{open}) QP (Ca ²⁺ channel P _{open})	0.5309 ± 0.0280 0.4528 ± 0.0358	9 models 9 models	Wilcoxon matched-pairs signed rank test Sum of positive, negative ranks: 1.000 , -44.00	0.0078	N/A	N/A
		Baseline (Ca ²⁺ concentration) QP (Ca ²⁺ concentration)	0.6650 ± 0.0935 μM 0.5680 ± 0.0802 μM	9 models 9 models	Wilcoxon matched-pairs signed rank test Sum of positive, negative ranks: 1.000 , -44.00	0.0078	N/A	N/A
	I	Baseline (Ca ²⁺ channel P _{open}) QP (Ca ²⁺ channel P _{open})	0.4341 ± 0.0639 0.3318 ± 0.0608	9 models 9 models	Wilcoxon matched-pairs signed rank test Sum of positive, negative ranks: 0.000 , -45.00	0.0039	N/A	N/A
		Baseline (Ca ²⁺ concentration) QP (Ca ²⁺ concentration)	0.4544 ± 0.0682 μM 0.3648 ± 0.0651 μM	9 models 9 models	Wilcoxon matched-pairs signed rank test Sum of positive, negative ranks: 0.000 , -45.00	0.0039	N/A	N/A
	J	Baseline (Ca ²⁺ channel P _{open}) QP (Ca ²⁺ channel P _{open})	0.5001 ± 0.0314 0.3607 ± 0.0370	17 models 17 models	Wilcoxon matched-pairs signed rank test Sum of positive, negative ranks: 1.000 , -152.0	< 0.0001	N/A	N/A
		Baseline (Ca ²⁺ concentration) QP (Ca ²⁺ concentration)	0.6953 ± 0.0625 μM 0.5048 ± 0.0506 μM	17 models 17 models	Wilcoxon matched-pairs signed rank test Sum of positive, negative ranks: 1.000 , -152.0	< 0.0001	N/A	N/A