Parallel Movement-suppressing Striatal Output Pathways

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Author contributions
QC conceived the study. QC and XD conducted the electrophysiological measurements. QC, IYMC, and AP performed the behavioral studies. QC, XD, BLB, DG, and AN performed histological analysis. VL and BL performed the rabies tracing. UC and YK performed the two-photon tomography. DH and AN assisted with data analyses. QC and CSC wrote the manuscript. CSC designed, directed, and supervised the project. All authors reviewed and edited the manuscript.

Abstract (152 words)

The classic basal ganglia circuit model asserts a complete segregation of the two striatal output pathways. Empirical data argue that, in addition to indirect-pathway striatal projection neurons (iSPNs), direct-pathway striatal projection neurons (dSPNs) innervate the external globus pallidus (GPe). However, the functions of the latter were not known. In this study, we interrogated the organization principles of striatopallidal projections and how they are involved in full-body movement in mice (both males and females). In contrast to the canonical motor-promoting role of dSPNs in the dorsomedial striatum (^{DMS}dSPNs), optogenetic stimulation of dSPNs in the dorsolateral striatum (^{DLS}dSPNs) suppressed locomotion. Circuit analyses revealed that dSPNs selectively target Npas1^{+} neurons in the GPe. In a chronic 6-hydroxydopamine lesion model of Parkinson's disease, the dSPN-Npas1^{+} projection was dramatically strengthened. As ^{DLS}dSPN-Npas1^{+} projection suppresses movement, the enhancement of this projection represents a circuit mechanism for the hypokinetic symptoms of Parkinson's disease that has not been previously considered.

Significance statement (102 words)

In the classic basal ganglia model, the striatum is described as a divergent structure—it controls motor and adaptive functions through two segregated, opponent output streams. However, the experimental results that show the projection from direct-pathway neurons to the external pallidum have been largely ignored. Here, we showed that this striatopallidal sub-pathway targets a select subset of neurons in the external pallidum and is motor-suppressing. We found that this sub-pathway undergoes plastic changes in a Parkinson's disease model. In particular, our results suggest that the increase in strength of this sub-pathway contributes to the slowness or reduced movements observed in Parkinson's disease.

Introduction (286 words)

The basal ganglia are a group of subcortical nuclei that are critically involved in action control. As the input station of the basal ganglia macrocircuit, the dorsal striatum (dStr) is capable of supporting a wide repertoire of innate behaviors, such as feeding, grooming, and locomotion (Albin et al., 1995; Mink, 1996; Graybiel, 2008; Redgrave et

al., 2010; Turner and Desmurget, 2010; Costa, 2011; Gerfen and Surmeier, 2011; Kravitz et al., 2012; Markowitz et al., 2018; Park et al., 2020; Weglage et al., 2020). While theories about action selection and suppression have been proposed, the precise cellular and circuit mechanisms involved remain to be determined. The classic circuit model asserts a complete segregation of the two striatal output pathways. On the other hand, empirical data argue that, in addition to indirect-pathway striatal projection neurons (iSPNs), direct-pathway striatal projection neurons (dSPNs) innervate the external globus pallidus (GPe). However, we only have limited information about the properties of the dSPN-GPe pathway. Previous investigations strongly suggest that the dSPN-GPe pathway shapes motor output (Cazorla et al., 2014). As the GPe contains a heterogenous population of neurons (Hernandez et al., 2015; Hegeman et al., 2016; Saunders et al., 2018; Abecassis et al., 2020; Cherian et al., 2020), the identity of neurons that receive dSPN input remains elusive. As we have established PV^+ neurons and $Npas1^+$ neurons in the GPe have distinct circuit and functional roles (Cherian et al., 2020; Pamukcu et al., 2020), we hypothesized that dSPNs regulate motor output by targeting a select subset of these neurons. Here, using transgenic and molecular tools, we dissected the cellular and spatial organization of the striatopallidal system; using *in vivo* optogenetics and machine-learning approaches, we studied the behavioral relevance of the striatopallidal subcircuits.

Methods (3673 words)

Mice

All experiments detailed are in accord with the Northwestern University Animal Care and Use Committee, the Institutional Animal Care and Use Committee at the University of California, San Diego, and are in compliance with the NIH Guide for the Care and Use of Laboratory Animals. *Adora2a*^{Cre} and *Drd1a*^{Cre} were obtained from MMRRC (Gong et al., 2007). *Drd1a*^{tdTomato} (Ade et al., 2011), *Pvalb*^{tdTomato} (Kaiser et al., 2016), *Pvalb*^{Cre} (Hippenmeyer et al., 2005), *R26*$^{LSL\text{-}tdTomato}$ (Madisen et al., 2010), *R26*$^{FSF\text{-}LSL\text{-}tdTomato}$ (Madisen et al., 2015), and *Tac1*^{Cre} (Harris et al., 2014) were obtained from Jackson Laboratory. *Npas1*$^{Cre\text{-}2A\text{-}tdTomato}$ (hereafter referred to as *Npas1*^{Cre}) was generated in-house (Hernandez et al., 2015). Mice for all experiments were maintained on a C57BL/6J (Jax 000664) background. Mice were group-housed in standard cages on a 12-hr light-dark cycle. Both male and female mice were used in this study. To minimize the potential alteration of the phenotypes in mice carrying the transgene alleles, only hemizygous or heterozygous mice were used.

Virus and tracer injections

Stereotaxic injections were performed as previously described (Cui et al., 2016). In brief, mice were anesthetized
60 with isoflurane and immobilized on a stereotaxic frame (David Kopf Instruments). A small craniotomy (~1 mm diameter) was made with a dental drill (Osada) for injection into a specific brain region. Virus or tracer was injected using a calibrated glass micropipette (VWR) at a rate of 0.3–0.5 µl/min. The micropipette was left *in situ* for 5–10 min post-injection to maximize tissue retention of virus or tracer and decrease capillary spread upon pipette withdrawal.

65 For optogenetic stimulation of direct-pathway striatal projection neurons (dSPNs) or indirect-pathway striatal projection neurons (iSPNs) in dorsomedial striatum (DMS) or dorsolateral striatum (DLS) used for *ex vivo* experiments, a total 360 nl of EF1α-CreOn-hChR2(H134R)-eYFP adeno-associated virus (AAV) was injected unilaterally into the DMS (in mm: 0.9 rostral, 1.4 lateral, 3.4 and 3.0 ventral from bregma) or the DLS (in mm: 0.7 rostral, 2.3 lateral, 3.4 and 3.0 ventral from bregma) of *Drd1a*^{Cre} or *Adora2a*^{Cre} mice. For *in vivo* optogenetic
70 stimulation of SPN soma or terminal fields, EF1α-CreOn-hChR2(H134R)-eYFP AAV was injected bilaterally into the DMS or DLS (540–720 nl per hemisphere). For control mice, EF1α-CreOn-eYFP AAV was injected into the same region with the same viral volume. To suppress neurotransmitter release from PV^{+} or Npas1^{+} GPe neurons, 135 nl of a tetanus toxin light chain-expressing (EF1α-CreOn-TeTLC-2A-eGFP) AAV was injected bilaterally into the external globus pallidus (GPe; in mm: 0.3 caudal, 2.0 lateral, 4.1 ventral from bregma) of *Pvalb*^{Cre} and *Npas1*^{Cre} mice,
75 respectively. To visualize the projection targets of dSPNs or iSPNs, hSyn-Flex-mRuby2-T2A-Synaptophysin-eGFP AAV (360 nl) was unilaterally injected into the DLS or DMS of *Drd1a*^{Cre}, *Tac1*^{Cre}, or *Adora2a*^{Cre} mice.

To determine whole-brain projections to the GPe, 90 nl of Cre-expressing lentivirus (LVretro-Cre) (Knowland et al., 2017) was mixed with cholera-toxin B subunit (CTb) conjugated to Alexa 488 (Thermo Fisher Scientific) at 1:1 ratio and was injected into the GPe (in mm: 0.2–0.25 caudal, 2.1–2.2 lateral, 4.1 ventral from bregma) of *R26*$^{LSL-}$
80 ^{tdTomato} mice. For rabies-based retrograde tracing, 200 nl of CreOn-mRuby2-TVA-RVG AAV (Shin et al., 2018) was first injected unilaterally into the GPe (in mm: 0.35 caudal and 2.0 lateral from bregma, 3.5 ventral from dura) of *Pvalb*^{Cre} and *Npas1*^{Cre} mice followed by EnvA-RVΔG-eGFP into the GPe three weeks later. To determine if single striatal neurons innervate both GPe and substantia nigra pars reticulata (SNr), 90 nl of CTb 488 and 180 nl of Alexa 647-conjugated CTb (CTb 647; Thermo Fisher Scientific) were injected into the GPe (in mm: 0.2–0.25 caudal, 2.1–

85 2.2 lateral, 4.1 ventral from bregma) and the SNr (in mm: 2.65 caudal, 1.5 lateral, 4.65 ventral from bregma, and 3.0 caudal, 1.44 lateral, 4.5 ventral from bregma), respectively, of *Drd1a*^{tdTomato} mice or *Tac1*^{Cre} mice for examining the colocalization of two CTbs with tdTomato or Cre. Alternatively, a CreOn-Flp canine virus (CAV) and CTb 647 were injected into the SNr together with hSyn-CreOn-FlpOn-ChR2-eYFP AAV into the dStr of *Drd1a*^{Cre} mice.

The locations of the targeted injections were visually inspected under epifluorescence microscopy in *ex*
90 *vivo* slices or histologically verified *post hoc*. AAVs, LV, CAV, and rabies virus were used for this study. AAVs and LVs were injected into mice (postnatal day 28–35, and postnatal day 55, respectively) at a final titer of 10^{12}–10^{13} genome copies/ml, using the same standard procedures as stereotaxic injections (see above). CTbs were injected into mice at postnatal day 55–70. Recordings and immunohistological analyses were performed 28–40 days postoperatively. Fiber optic implantations were performed 21–35 days after viral injection. Fluorescence *in situ*
95 hybridization was performed 1–2 weeks after the injection of rabies virus.

Chronic 6-OHDA lesion

Unilateral lesion of the nigrostriatal system was produced by 6-hydroxydopamine HCl (6-OHDA) injection into the medial forebrain bundle (MFB) at postnatal day 28–35, as described previously (Cui et al., 2016). In brief, 6-OHDA
100 (2.5–3 μg/μl) was dissolved in 0.9% (wt/vol) NaCl with 0.1% (wt/vol) ascorbic acid. Using identical procedures to those for stereotaxic injection of virus and tracer, 1 μl of 6-OHDA was injected into the MFB at (in mm) 0.70 caudal, 1.10 lateral, and 4.95 ventral from bregma. The extent of dopamine depletion was assessed using the cylinder test to quantify impairment in forelimb usage. Behavioral tests were carried out at 3–5 weeks after 6-OHDA lesion. Contacts made by each forepaw on the wall of a clear glass cylinder (9 cm diameter) during spontaneous
105 exploratory behavior were counted during a five-minute period. The asymmetry of the forelimb usage was defined as independent contralateral paw placement relative to that of the ipsilateral (to the injection) paw against the walls of the chamber during rearing and vertical or lateral explorations. Mice with less than 20% contralateral paw touches were deemed with severe dopamine loss and were used for subsequent experiments. Electrophysiological experiments or immunohistological analyses were performed 4–6 weeks after 6-OHDA
110 injection.

Fiber implantation and behavior testing

Surgical procedures were the same as those for stereotaxic injections (see above). Fiber optic cannulae (250 μm core diameter, 0.66 NA) (Prizmatix) were bilaterally implanted into the target regions: the DMS (in mm: 0.9 rostral, 1.4 lateral, 3.0 ventral from bregma), the DLS (in mm: 0.7 rostral, 2.3 lateral, 3.0 ventral from bregma), the GPe (in mm: 0.3 caudal, 2.1 lateral, 3.7 ventral from bregma), or the SNr (in mm: 2.7 caudal, 1.4 lateral, 4.4 ventral from bregma). The fiber optic cannulae had a maximal output power of 12–18 mW measured at the tip. Implants were secured to the skull with dental cement (Parkell). Mice were allowed to recover for 1–2 weeks before behavioral testing.

Motor behavior induced by optogenetic stimulation was assessed in an open field. Behavioral testing was performed between 3:00 P.M. and 8:00 P.M. On the first day, the mice were allowed to freely explore the open field area (28 cm × 28 cm) for 25 min. On the second day, the implanted fiber-optic cannulae were connected to a 470 nm LED (Prizmatix). Five minutes after the mouse was placed in the open field arena, light stimulus trains (5 ms pulses at 10 Hz for 10 s) were delivered every min. A total of 20 stimulus trains were given to each mouse. Mice were videotaped with an overhead camera. The central position of each mouse was tracked with ETHOVISION (Noldus). Data for distance traveled over time were extracted. The locations of the targeted implantations were histologically verified *post hoc*. The assessment of TeTLC silencing on motor behavior was identical to that on the first day.

Behavioral tracking and classification

DeepLabCut (https://github.com/DeepLabCut/) (Mathis et al., 2018; Nath et al., 2019) was used for tracking body parts of mice in an open field arena. Eight body parts including the nose, ears, body center, side laterals (hip-joints), tail base, and tail end were labeled in top-down view videos. To create the training dataset, 1,674 distinct frames from 50 video recordings of open field behavior were manually annotated. We used MobileNetV2-1-based network (Mathis et al., 2019; Sandler et al., 2019) with default parameters. The network was trained and refined for five rounds using default multi-step learning rates. Each round consists of 240,000–1,000,000 iterations, and the default multi-step learning rates were used. This trained network has a test error of 1.13 pixels and a training error of 4.82 pixels. Predictions of X-Y coordinates were processed using a median filter with a rolling window of five frames before further analysis. This network was then used to analyze all videos in this study.

To categorize motor behavior, DeepLabCut tracking data were first calibrated; the pixel-to-cm conversion for each video was determined by comparing the width of the arena in pixels to the actual width of the arena (28 cm). Based on the calibrated X-Y coordinates of labeled body parts, a set of movement metrics was generated for each frame. Mouse speed was measured as the body center speed. Mouse width was measured as the euclidean distance between the side laterals, and mouse length was measured as the euclidean distance between the nose and the tail base. Locomotion was defined as frames when the body center had a speed > 0.5 cm/s; motionless was defined as frames when ears, the body center, laterals, and the tail base all had a speed ≤ 0.5 cm/s. To classify rearing, we constructed a random forest classifier in SimBA. 19,058 rearing frames from 35 video recordings of open-field behavior were extracted and manually annotated as rearing by three independent annotators. Supported and unsupported rearing behaviors were not differentiated. The start frame was defined as the frame in which the mouse lifted its forelimbs off the floor and extended its head upwards; the end frame was defined as the frame before the forelimbs made contact with the floor. The model was built with the following settings: n_estimators = 2,500, RF_criterion = entropy, RF_max_features = sqrt, RF_min_sample leaf = 2, and no oversampling or undersampling. 20% of the video frames were used for testing and the other 80% were used for training. The resulting classifier has a F1-score = 0.71, precision = 0.68, and recall = 0.74. The performance of this classifier was on par with those reported recently (Nilsson et al., 2020).The discrimination threshold was set at Pr = 0.31, and each instance of rearing has a minimum duration of 300 ms. Lastly, fine movement was defined as frames that do not fall into any of the categories mentioned above (i.e., locomotion, motionless, or rearing). Finally, example videos and the trained model are available on Github (https://github.com/saviochan/SimBA-OpenFieldArena) and Zenodo (https://zenodo.org/record/3964701#.XyB8yJ5KhPZ). The data generated by the analysis pipeline were processed using custom Python Scripts. Codes are available online (https://github.com/saviochan/Python-Scripts/tree/master/OpenFieldArena_Behavior). Twenty-five different movement metrics were tracked. Event frequency, duration, and percent time spent were logged. Fold changes were calculated by dividing the movement metric during light-period by that in pre-period. 'Light-period' corresponds to 10 s of light delivery. 'Pre-period' and 'post-period' correspond to the 10 s epoch before and after light delivery, respectively.

To assess the relationship between the measured movement metrics, a correlation matrix was constructed from binned, time-series data. Rearing-motionless switch frequency and motionless-rearing switch frequency were excluded because of the low occurrence of events. Hierarchical clustering of movement metrics

was performed in ClustVis (https://biit.cs.ut.ee/clustvis/) (Metsalu and Vilo, 2015). Twenty-five movement metrics were included in the analysis. Mice with targeted optogenetic stimulation of ^{DMS}dSPNs, ^{DMS}iSPNs, ^{DLS}dSPNs and
170 ^{DLS}iSPNs, were included. Both rows and columns were clustered using correlation distance and average linkage. Movement metrics were centered and scaled.

Fluorescence *in situ* hybridization

Brains were rapidly extracted and flash-frozen with isopentane chilled with dry ice in 70% ethanol. Coronal brain
175 sections (25 μm) containing the dStr and the GPe were prepared on a cryostat (Leica). Brain sections were mounted directly onto glass slides and stored at −80 °C until further processed. Fluorescence *in situ* hybridization was conducted using commercial probes (Advanced Cell Diagnostics). Slides were fixed in 4% PFA for 15 min at 4 °C and subsequently dehydrated for 5–10 min with a series of ethanol at room temperature. Sections were then incubated with a protease pretreat-IV solution for 30 min, and washed with PBS, before being incubated with
180 probes for 2 h at 40 °C. After washes, the signal was amplified by incubating tissue sections in amplification buffers at 40 °C. After the final rinse, DAPI solution was applied to the sections. Slides were coverslipped and visualized with a confocal microscope (Olympus).

Immunolabeling

185 Mice aged postnatal day 55–80 were anesthetized deeply with a ketamine-xylazine mixture and perfused transcardially first with 0.01 M phosphate-buffered saline (PBS) followed by fixative containing 4% (wt/vol) paraformaldehyde in PBS, pH 7.4. Brain tissue was then postfixed in the same fixative for 1–2 h at 4 ºC. Tissue blocks containing the dStr and the GPe were sectioned using a vibrating microtome (Leica Instrument) at a thickness of 60 μm. Floating sections were blocked with 10% (vol/vol) normal goat or donkey serum (Gibco) and
190 0.1% (vol/vol) Triton X-100 in PBS for 30–60 min at room temperature and subsequently incubated with primary antibodies (**Table 1**) in the same solution for ~24 h at 4 ºC. After washes in PBS, the sections were incubated with Alexa-conjugated IgG secondary antibodies at 1:500 (Life Technologies) for 2 h at room temperature. The sections were then washed, mounted, and coverslipped. Immunoreactivity was examined on a laser-scanning confocal microscope with a 10× 0.45 numerical aperture (NA) air objective and a 60× 1.35 NA oil-immersion objective
195 (Olympus).

Fiber density and synaptic contact quantifications

To measure fiber density of dSPNs in the dStr, GPe, and SNr, *Drd1a*^{Cre} mice were injected with EF1α-CreOn-hChR2(H134R)-eYFP AAV into the dStr. 60 μm-thick sections from lateral, intermediate, and medial levels (approximately 2.5 mm, 2.1 mm, 1.7 mm lateral from bregma) were sampled. eYFP fluorescence was enhanced with an antibody (**Table 1**). 10× images of YFP fluorescence in the dStr, GPe, and SNr were captured with a confocal microscope. Fiber density was estimated based on YFP fluorescence. Briefly, a region that encompasses the entirety of the dStr, GPe, or SNr with YFP fluorescence was selected. Lower and upper threshold values were set using a thresholding function in Fiji (Schindelin et al., 2012). Integrated density was then measured.

To visualize dSPN terminals within the GPe, the same tissue sections as those used for fiber density analysis were used. These sections were co-stained with antibodies for gephyrin and vesicular GABA transporter (VGAT) (**Table 1**). In each section, three z-stacks spanning across the entire rostrocaudal axis of the GPe were imaged with a confocal microscope (Olympus) using a 60× objective with a 2× digital zoom. Five consecutive optical sections (1 μm interval) were captured for each z-stack. Quantification of putative synaptic contacts was performed with Fiji. The spatial relationship between labeled structures was examined across all three orthogonal planes. Synaptic contacts were deemed to be *bona fide* only if YFP^{+} fibers were in close apposition with gephyrin^{+} or VGAT^{+} structures in all *x*-(≤ 0.2 μm), *y*-(≤ 0.2 μm), and *z*-(≤ 1 μm) planes.

To compare density of terminals from dSPNs and iSPNs, tissue sections from *Drd1a*^{Cre}, *Tac1*^{Cre}, or *Adora2a*^{Cre} mice injected with hSyn-Flex-mRuby2-T2A-Synaptophysin-eGFP AAV into the DLS or DMS were used. GFP fluorescence was enhanced with an antibody (**Table 1**). 60× z-stack images of GFP fluorescence in the GPe were captured with a confocal microscope. Two regions of interest (ROIs) from dorsorostral and ventrocaudal territories of the GPe were imaged for each section. Integrated density from maximal projection image of ten optical planes was quantified using the same thresholding function as used for fiber density analysis.

Serial two-photon tomography

Serial two-photon tomography was used to map inputs to the GPe from the entire brain. Imaging and analysis were performed as previously described (Kim et al., 2017; Abecassis et al., 2020). Two weeks after LVretro-Cre and CTb-488 injection, mouse brains were fixed as described above. Brains were then transferred to PBS and

stored at 4 °C until imaged. Brains were embedded in 4% agarose in 0.05 M phosphate buffer and cross-linked in
225 0.2% sodium borohydrate solution (in PBS, pH 9.0–9.5). Each brain was imaged with a high-speed two-photon microscope with an integrated vibratome (TissueVision) at 1 μm at both *x*–*y* resolution with 280 *z*-sections in every 50 μm. A 910 nm two-photon laser (Coherent Technologies) was used for CTb488 and tdTomato excitation. A dichroic mirror (Chroma) and band-pass filters (Semrock) were used to separate green and red fluorescence signals. Emission signals were detected by GaAsP photomultiplier tubes (Hamamatsu). An automated, whole-
230 brain cell counting and registration of the detected signal on a reference brain was applied as described before (Kim et al., 2017). The number of tdTomato neurons from each brain region was charted. The relative size of the input to the GPe was calculated by normalizing the total number of tdTomato neurons in the entire brain of each sample.

235 **Visualized recording in *ex vivo* brain slices**

Mice aged postnatal day 55–75 were anesthetized with a ketamine-xylazine mixture and perfused transcardially with ice-cold artificial cerebrospinal fluid (aCSF) containing (in mM): 125 NaCl, 2.5 KCl, 1.25 NaH_2PO4, 2.0 $CaCl_2$, 1.0 $MgCl_2$, 25 $NaHCO_3$, and 12.5 glucose, bubbled continuously with carbogen (95% O_2 and 5% CO_2). The brains were rapidly removed, glued to the stage of a vibrating microtome (Leica Instrument), and immersed in ice-cold
240 aCSF. Parasagittal (for DLS-GPe) or sagittal (for DMS-GPe) *ex vivo* slices containing the dStr and the GPe were cut at a thickness of 240 μm and transferred to a holding chamber, where they were submerged in aCSF at 35 ºC for 30 min, and returned to room temperature before recording.

Ex vivo slices were then transferred to a small volume (~0.5 ml) Delrin recording chamber that was mounted on a fixed-stage, upright microscope (Olympus). Neurons were visualized using differential interference
245 contrast optics (Olympus), illuminated at 735 nm (Thorlabs), imaged with a 60× 1.0 NA water-immersion objective (Olympus) and a CCD camera (QImaging). PV^+, PV^-, $Npas1^+$, and $Npas1^-$ GPe neurons were identified by the presence or absence of somatic tdTomato fluorescence examined under epifluorescence microscopy with a daylight (6,500 K) LED (Thorlabs) and an appropriate filter cube (Semrock) from *Pvalb*^{tdTomato} and *Npas1*^{Cre} transgenic mice.

250 Recordings were made at room temperature (20–22 ºC) with patch electrodes fabricated from capillary glass (Sutter Instruments) pulled on a Flaming-Brown puller (Sutter Instruments) and fire-polished with a

microforge (Narishige) immediately before use. Pipette resistance was typically ~3–5 MΩ. Internal solution for voltage-clamp recordings of inhibitory postsynaptic currents contained (in mM): 120 CsCl, 10 Na_2phosphocreatine, 5 HEPES, 5 tetraethylammonium-Cl, 2 Mg_2ATP, 1 QX314-Cl, 0.5 Na_3GTP, 0.5 $CaCl_2$, 0.25 EGTA, and 0.2% (wt/vol) biocytin, pH adjusted to 7.25–7.30 with CsOH. This internal solution had an osmolarity of ~290 mOsm. Somatic whole-cell patch-clamp recordings were obtained with an amplifier (Molecular Devices). The signal for voltage-clamp recordings was filtered at 1 kHz and digitized at 10 kHz with a digitizer (Molecular Devices). Stimulus generation and data acquisition were performed using pClamp (Molecular Devices).

For optogenetic experiments, blue (peak at ~450 nm) excitation wavelength from two daylight (6,500 K) LEDs (Thorlabs) was delivered to the tissue slice bidirectionally from both the 60× water immersion objective and the 0.9 NA air condenser with the aid of 520 nm dichroic beamsplitters (Semrock). The field of illumination that centered around the recorded cells was ~500 μm in diameter. The duration for all light pulses was 2 ms. All recordings were made in the presence of R-CPP (10 μM) and NBQX (5 μM) to prevent the confounding effects of incidental stimulation of glutamatergic inputs. CGP55845 (1 μM) was also included to prevent $GABA_B$ receptor-mediated modulation. In a subset of experiments, 2–4 mM Sr^{2+} was used to replace Ca^{2+} to measure quantal events (Bekkers and Clements, 1999; Xu-Friedman and Regehr, 1999, 2000; McGarry and Carter, 2017).

Off-line data analyses were performed with ClampFit (Molecular Devices) and MiniAnalysis (Synaptosoft). Paired-pulse ratios were calculated by dividing the second inhibitory postsynaptic current ($IPSC_2$) amplitude by the $IPSC_1$ amplitude (Kim and Alger, 2001). For strontium-based quantal analysis, quantal events within 300 ms after the striatal stimulation were quantified.

Drugs

R-baclofen, *R*-CPP, LY341495, and NBQX disodium salt, were obtained from Tocris. CGP55845, QX314-Cl, and SR95531 were obtained from Abcam. Na_3GTP and tetrodotoxin were from Roche and Alomone Laboratories, respectively. Other reagents not listed above were from Sigma-Aldrich. Drugs were dissolved as stock solutions in either water or DMSO and aliquoted and frozen at −30 ºC prior to use. Each drug was diluted to the appropriate concentrations by adding to the perfusate immediately before the experiment. The final concentration of DMSO in the perfusate was < 0.1%.

280 **Statistical analyses**

General graphing and statistical analyses were performed with MATLAB (MathWorks), Prism (GraphPad), JASP (https://jasp-stats.org) and the R environment (https://www.r-project.org). Custom analysis codes are available on GitHub (https://github.com/chanlab). Sample size (*n* value) is defined by the number of observations (i.e., ROIs, synaptic contacts, neurons, sections, or mice). When percentages are presented, *n* values represent only positive
285 observations. No statistical method was used to predetermine sample size. Data in the main text are presented as median values ± median absolute deviations (MADs) (Leys et al., 2013) as measures of central tendency and statistical dispersion, respectively. Box plots are used for graphic representation of population data unless stated otherwise (Krzywinski and Altman, 2014; Streit and Gehlenborg, 2014; Nuzzo, 2016). The central line represents the median, the box edges represent the interquartile ranges, and the whiskers represent 10–90th percentiles.
290 Normal distributions of data were not assumed. Individual data points were visualized for small sizes or to emphasize variability in the datasets. Non-parametric statistics were used throughout. Comparisons for unrelated samples were performed using a Mann–Whitney *U* test. The Wilcoxon signed rank test was used for pairwise comparisons for related samples. The Fisher's exact test was used for categorical data. The Spearman exact test was used for evaluating correlation between variables. Unless < 0.0001 or > 0.99, exact *P* values (two-tailed) are
295 reported in the text. To avoid arbitrary cutoffs and visual clutter, levels of significance are not included in the figures.

Results (3846 words)

300 **dSPNs send terminating axons to the GPe**

To examine the organization of the striatopallidal projection, two retrograde tracers, namely a Cre-expressing lentivirus (LVretro-Cre) (Knowland et al., 2017; Abecassis et al., 2020) and CTb 488 were co-injected into the GPe of a Cre-reporter (*R26*$^{\text{LSL-tdTomato}}$) mouse. As expected, tdTomato^{+} and CTb 488^{+} neurons were readily observed in the dStr, thus confirming that dStr neurons project to the GPe (**Figure 1a**) and critically, cross-validating the utility
305 of the retrograde labeling strategy. Using serial two-photon tomography, whole-brain inputs to the GPe were mapped (Kim et al., 2017; Abecassis et al., 2020). As shown in **Figure 1a**, the dStr provides the largest input to the GPe. The number of input neurons (i.e., tdTomato^{+}) from the dStr was at least an order of magnitude larger than

that from other brain regions charted, constituting ~80% (79.0 ± 3.1%) of total neurons (n = 45,223 neurons, 8 mice) that projected to the GPe. This observation is consistent with the earlier finding that GABAergic synapses amount to over 80% of all synapses in the GPe (Kita, 2007).

To study the innervation of the GPe by dSPNs and iSPNs, *Drd1a*^{Cre} and *Adora2a*^{Cre} mice (Gerfen et al., 2013) were used, respectively. The arborization patterns and marker expression of the axons produced by Cre-expressing dStr neurons confirmed the validity of these two transgenic lines (**Figure 2a** & **b**). Moreover, *ex vivo* recordings showed that dopamine D2 receptors selectively regulate striatopallidal GABA release from iSPN (*Adora2a*^{Cre}) but not dSPN (*Drd1a*^{Cre}) input (**Figure 2c** & **d**). To determine the innervation density of SPN subtypes, we used a Cre-inducible adeno-associated virus (AAV) that tagged transduced neurons and their axonal terminals with mRuby2 and GFP, respectively (Knowland et al., 2017; Faget et al., 2018). As expected, GFP$^+$ puncta produced by SPNs were abundant in the GPe (**Figure 1b**). These GFP$^+$ puncta correspond to GABAergic terminals, as demonstrated by their immunoreactivity for vesicular GABA transporter (VGAT) and gephyrin (**Figure 1b**). The abundance of GFP$^+$ puncta was thus used as a measure of innervation density. The density of GFP$^+$ puncta formed by iSPNs were about seven-fold higher than that formed by dSPNs (*Adora2a*^{Cre} = 5.2 ± 1.5 × 10^7 a.u., n = 12 ROIs; *Drd1a*^{Cre} = 0.7 ± 0.3 × 10^7 a.u., n = 10 ROIs; $P < 0.0001$) (**Figure 1b**).

To study whether single dSPNs innervate both the GPe and substantia nigra pars reticulata (SNr), two different retrograde tracers (i.e., CTb 488 and CTb 647) were injected into the GPe and SNr, respectively. Using *Drd1a*^{tdTomato} mice to identify all dSPNs (Ade et al., 2011), we found that CTb 488 and CTb 647 signals were detected in the same tdTomato$^+$ neurons within the dStr (**Figure 1c**). Using an intersectional approach (with *Drd1a*^{Cre} mice and a Flp-expressing retrograde virus) to confer an unparalleled spatial and genetic specificity, we observed axonal collateralization in the GPe from SNr-projecting, *Drd1a*$^{Cre+}$ dStr neurons (**Figure 1d**). These findings confirmed the earlier observations from single-cell tracing studies that show SNr-projecting dStr neurons (i.e. dSPNs) arborize within the GPe (Kawaguchi et al., 1990; Wu et al., 2000; Levesque and Parent, 2005; Fujiyama et al., 2011).

Although the results obtained from *Drd1a*^{Cre} and *Drd1a*^{tdTomato} mice were consistent with each other, as they are both bacterial artificial chromosome transgenic mice and were derived from the single parent construct (Gerfen et al., 2013), *Tac1*^{Cre} knock-in mice were employed to confirm the inferences drawn from *Drd1a*^{Cre} and *Drd1a*^{tdTomato} mice. Using the same synapse-tagging approach and CTb-based tracing mentioned above, we corroborated these findings (GFP$^+$ puncta density = 1.0 ± 0.5 × 10^7 a.u., n = 12 ROIs).

dSPNs from discrete spatial domains project to the GPe

The dStr is divided into molecularly, synaptically, and functionally distinct subregions (Smith et al., 2004; Darvas and Palmiter, 2009, 2010; Nambu, 2011; Hintiryan et al., 2016; Hooks et al., 2018; Poulin et al., 2018; Martin et al., 2019; Alegre-Cortés et al., 2020; Ortiz et al., 2020). The dorsomedial striatum (DMS) and dorsolateral striatum (DLS) are thought to be involved in regulating goal-directed and habitual behavior, respectively (Yin and Knowlton, 2006; Balleine and O'Doherty, 2010; Redgrave et al., 2010; Cox and Witten, 2019). Although the role of DMS in locomotion is consistently observed across studies (Kravitz et al., 2010; Durieux et al., 2012; Cui et al., 2013; Freeze et al., 2013; Cazorla et al., 2014), the findings are counterintuitive, as this region of the dStr receives primarily non-motor cortical input (McGeorge and Faull, 1989; Flaherty and Graybiel, 1994; Znamenskiy and Zador, 2013; Oh et al., 2014; Hintiryan et al., 2016; Hunnicutt et al., 2016; Hooks et al., 2018; Chon et al., 2019). On the other hand, while the DLS receives inputs from premotor and motor regions, recent studies argue that it is not involved in locomotion but is required for gradual motor skill acquisition (Yin and Knowlton, 2006; Nambu, 2011; Durieux et al., 2012; Rothwell et al., 2014; O'Hare et al., 2016; Malvaez and Wassum, 2018). As different approaches are used across studies, we sought to examine the role of SPNs from the two spatial domains in controlling motor behavior using a systematic approach.

We first examined the anatomical organization of the striatal projections from the DMS and DLS. To study the dSPN and iSPN projections to the GPe, axonal terminals from dSPNs or iSPNs were selectively tagged using the synapse tagging approach (with synaptophysin-eGFP) described above. As expected from earlier observations (Hedreen and DeLong, 1991; Deniau et al., 1996; Romanelli et al., 2005; Nambu, 2011; Bertino et al., 2020), both dSPNs and iSPNs from the DMS and DLS projected to downstream targets in a topographical manner (not shown). The innervation density of iSPN projection from the DMS and DLS, as measured by the abundance of GFP^+ puncta, were statistically indistinguishable (*Adora2a*^{Cre}: DMS = $5.2 \pm 0.7 \times 10^7$ a.u., n = 6 ROIs; DLS = $5.1 \pm 1.7 \times 10^7$ a.u., n = 6 ROIs; P = 0.94) (**Figure 2d** & **e**). The dSPN projection estimated with *Drd1a*^{Cre} was organized similarly (*Drd1a*^{Cre}: DMS = $0.7 \pm 0.2 \times 10^7$ a.u., n = 4 ROIs; DLS = $0.7 \pm 0.2 \times 10^7$ a.u., n = 6 ROIs; P = 0.91) (**Figure 2d** & **e**). Using *Tac1*^{Cre} to estimate the dSPN projection to the GPe, we found a stronger projection from the DMS than DLS (*Tac1*^{Cre}: DMS = $1.4 \pm 0.5 \times 10^7$ a.u., n = 6 ROIs; DLS = $0.7 \pm 0.3 \times 10^7$ a.u., n = 6 ROIs; P = 0.041) (**Figure 2d** & **e**). We do not currently

have an explanation for the difference observed between *Drd1a*^{Cre} and *Tac1*^{Cre} mice; it is possible that these two lines have differences in the striosome-matrix bias.

365

^{DLS}dSPNs are motor-suppressing

To study the roles of SPN subtypes from the DMS and DLS in motor regulation, we first selectively stimulated ^{DMS}dSPNs and ^{DMS}iSPNs using ChR2, an excitatory opsin (Boyden et al., 2005), as a proof of concept. Consistent with the findings from prior studies (Kravitz et al., 2010; Durieux et al., 2012; Freeze et al., 2013), stimulation of
370 ^{DMS}dSPNs and ^{DMS}iSPNs led to the canonical movement promotion and suppression, respectively, as measured by the change in average speed in an open-field (^{DMS}dSPNs = +0.71 ± 0.28 fold, n = 9 mice, P = 0.0039; ^{DMS}iSPNs = –0.43 ± 0.05 fold, n = 11 mice, P = 0.00098). On the contrary, optogenetic stimulation of ^{DLS}dSPNs and ^{DLS}iSPNs suppressed and promoted movement, respectively (^{DLS}dSPNs = –0.34 ± 0.24 fold, n = 13 mice, P = 0.0017; ^{DLS}iSPNs = +0.38 ± 0.31 fold, n = 15 mice, P = 0.00061). The motor effects were different from their corresponding eYFP
375 controls (not shown), arguing that the findings were not artifacts of light delivery (Owen et al., 2019). By interrogating with optogenetic approaches, here we conclude that striatal spatial subdomains exhibit divergent locomotor regulation.

To survey the full range of motor behaviors, a machine learning approach was used to track body kinematics and movement dynamics (Cherian et al., 2020). These data are summarized in a heatmap format
380 (**Figure 3a**). By performing a hierarchical clustering of movement metrics, we showed that the optogenetic stimulation of ^{DMS}dSPNs and ^{DMS}iSPNs induced congruent changes in motor behaviors across all mice examined—mice with targeted optogenetic stimulation of ^{DMS}dSPNs and ^{DMS}iSPNs fell into distinct clusters. On the contrary, mice with targeted optogenetic stimulation of ^{DLS}dSPNs and ^{DLS}iSPNs were intermixed with the two main clusters formed by mice that were targeted for optogenetic stimulation of ^{DMS}dSPNs and ^{DMS}iSPNs. The different motor
385 patterns induced by selective stimulation of specific SPNs can be readily observed when 'motionless', 'fine movement', 'rearing', and 'locomotion' are charted (**Figure 3b** & **c**).

In particular, the data from ^{DMS}dSPNs and ^{DMS}iSPNs are the most intuitive. Consistent with the well-established roles of ^{DMS}dSPNs and ^{DMS}iSPNs, optogenetic stimulation of ^{DMS}dSPNs and ^{DMS}iSPNs led to coordinated changes in motionless and locomotion. On the contrary, the changes induced by optogenetic
390 stimulation of ^{DLS}dSPNs and ^{DLS}iSPNs resulted in less marked or coherent changes in motionless and locomotion;

the changes in net motor output as measured with the distance traveled were primarily driven by the changes in movement speed. In addition, fine movement was increased with ^{DLS}dSPNs stimulation while decreased with ^{DLS}iSPNs stimulation. The differences in the movement dynamics induced with optogenetic stimulation of SPN subtypes can be found in **Table 2**. Lastly, the uniqueness of each SPN population in the induced motor behavior is more clearly illustrated in the correlation matrix and principal component analysis of movement metrics (**Figure 3d** & **e**).

In summary, these findings are consistent with the idea that the striatum is involved in controlling complex body kinematics and a wide repertoire of innate complex behaviors (Turner and Anderson, 1997; Turner et al., 1998; Graybiel, 2008; Desmurget and Turner, 2010; Redgrave et al., 2010; Jin et al., 2014; Rueda-Orozco and Robbe, 2015; Ahmari, 2016; Barbera et al., 2016; Klaus et al., 2017; Markowitz et al., 2018; Fobbs et al., 2020; Park et al., 2020; Weglage et al., 2020).

^{DLS}dSPN-mediated motor suppression involves the GPe

Given the similar anatomical arrangements between the DMS and DLS, these results were not expected. To understand the circuit basis that accounts for ^{DLS}dSPN-mediated movement suppression, we first optogenetically stimulated terminals of ^{DLS}dSPNs in their main projection target, i.e., the SNr. Consistent with the motor effect of ^{DLS}dSPNs, optogenetic stimulation of their terminals in the lateral SNr led to movement suppression (–0.42 ± 0.14 fold, n = 7 mice, P = 0.016). As expected, this effect was opposite to the movement promotion induced with stimulation of ^{DMS}dSPN terminals in the medial SNr (+0.68 ± 0.32 fold, n = 6 mice, P = 0.031). Similar to the findings with stimulation of ^{DLS}dSPNs and their terminals in the lateral SNr, optogenetic stimulation of their terminals within the GPe produced motor suppression (–0.34 ± 0.21 fold, n = 16 mice, P = 0.00021) (**Figure 4d**). The effect was different (P = 0.0046) from mice in which no ChR2 (i.e., eYFP only) was expressed (+0.01 ± 0.07 fold, n = 6 mice, P > 0.99). The fold changes were indistinguishable between stimulation of soma and their terminals in the GPe (P = 0.88) (**Figure 4e**).

As action potentials propagate (both orthodromically and antidromically), it can be difficult to pinpoint the precise effector loci with ChR2-mediated stimulation. To unequivocally demonstrate the involvement of the GPe in mediating the downstream effects of ^{DLS}dSPNs, tetanus toxin light chain (TeTLC) was expressed selectively in PV^{+} neurons or Npas1^{+} neurons to silence their neurotransmitter release (Yamamoto et al., 2003; Murray et al.,

2011; Xu and Sudhof, 2013; Cui et al., 2016) (**Figure 4a**, **c**, & **e**). Consistent with the motor-suppressing role of
420 Npas1$^+$ neurons (Glajch et al., 2016; Pamukcu et al., 2020), silencing of Npas1$^+$ neurons with TeTLC increased locomotion compared to mice that only expressed eYFP in Npas1$^+$ neurons (control = 57.4 ± 1.0 m, *n* = 8 mice; TeTLC = 77.1 ± 8.6 m, *n* = 11 mice; *P* = 0.0050) (**Figure 4b**). In mice with Npas1$^+$ neurons silenced, stimulation of ^{DLS}dSPN axons in the GPe did not result in the expected movement suppression (–0.06 ± 0.09 fold, *n* = 10 mice, *P* = 0.32) (**Figure 4d** & **e**). In contrast, silencing of PV$^+$ neurons led to movement suppression when ^{DLS}dSPN axons
425 were stimulated (–0.20 ± 0.12 fold, *n* = 11 mice, *P* = 0.0068); this effect was statistically indistinguishable from that without PV$^+$ neuron silencing (*n* = 16 mice, *P* = 0.080) (**Figure 4d** & **e**).

^{DLS}dSPNs strongly target Npas1$^+$ neurons

The *in vivo* behavioral experiments indicate that Npas1$^+$ neurons mediated the movement-suppressing effect of
430 ^{DLS}dSPNs, suggesting that ^{DLS}dSPNs selectively target Npas1$^+$ neurons. To determine the connectivity pattern of striatopallidal projections, we first used rabies-mediated tracing (Hunt et al., 2018; Shin et al., 2018). Among all SPNs that were retrogradely labeled from PV$^+$ neurons, a larger fraction were positive for *Drd2* mRNA than for *Drd1a* mRNA (*Drd1a* = 40.7 ± 3.1%, *Drd2* = 59.3 ± 3.1%, *n* = 5 mice) (**Figure 5a** & **c**). In contrast, among all SPNs that were retrogradely labeled from Npas1$^+$ neurons, around two-thirds were positive for *Drd1a* mRNA (*Drd1a* =
435 66.4 ± 0.6%, *Drd2* = 33.6 ± 0.6%, *n* = 5 mice) (**Figure 5a** & **c**); this connectivity pattern was different from the relative abundance of *Drd1a*- or *Drd2*-expressing SPNs that project to the PV$^+$ neurons (*P* < 0.0001).

The anatomical data showed a biased connectivity pattern where PV$^+$ neurons and Npas1$^+$ neurons are preferentially innervated by iSPNs and dSPNs, respectively. However, we were precluded from interrogating the spatial organization of the striatopallidal subcircuits with rabies-tracing, as the GPe is relatively small. Instead, we
440 performed *ex vivo* patch-clamp recordings in identified GPe neurons. The size of optogenetically evoked inhibitory postsynaptic currents (IPSCs) was used as a measure of connection strength. The strength of ^{DLS}dSPN input to PV$^+$ neurons was smaller than that to Npas1$^+$ neurons. This difference was consistently observed across a large range of stimulus intensities (5.1–56.7 mW/mm^2) ($IPSC_{max}$: PV$^+$ = 38.5 ± 29.3 pA, *n* = 8 neurons; Npas1$^+$ = 213.8 ± 122.0 pA, *n* = 28 neurons; *P* = 0.00011) (**Figure 5b** & **c**). These electrophysiological and anatomical data collectively
445 argue that ^{DLS}dSPNs targeted Npas1$^+$ neurons over PV$^+$ neurons.

Our rabies-tracing data suggest that iSPNs preferentially innervate PV$^+$ neurons. Here we asked whether ^{DLS}iSPNs differentially target PV$^+$ neurons versus Npas1$^+$ neurons. As shown in **Figure 5b** & **c**, PV$^+$ neurons received stronger iSPN input compared to Npas1$^+$ neurons; this difference was observed across a wide range of stimulus intensities (2.4–56.7 mW/mm^2) tested (IPSCs$_{max}$: PV$^+$ = 1,740.7 ± 627.7 pA, *n* = 12 neurons; Npas1$^+$ = 76.9 ± 60.9 pA, *n* = 20 neurons; *P* < 0.0001). Among all individual DLS inputs examined, ^{DLS}iSPN-PV$^+$ input was the strongest. In summary, our data altogether indicate that ^{DLS}iSPNs preferentially target PV$^+$ neurons. A full description of the input-output relationship for distinct DLS inputs is summarized in **Table 3**.

Consistent with the differences in ^{DLS}dSPN input between PV$^+$ neurons and Npas1$^+$ neurons, optogenetic stimulation of ^{DLS}dSPNs only modestly decreased the firing of PV$^+$ neurons, but strongly suppressed the firing of Npas1$^+$ neurons (PV$^+$ = –0.19 ± 0.21 fold, *n* = 9 neurons, *P* = 0.027; Npas1$^+$ = –0.73 ± 0.23 fold, *n* = 11 neurons, *P* = 0.00098) (**Figure 5d**); the effects were different between PV$^+$ neurons and Npas1$^+$ neurons (*P* = 0.020). On the other hand, although there was a big difference in the strength of the ^{DLS}iSPN input between PV$^+$ neurons and Npas1$^+$ neurons, we did not observe a difference (*P* = 0.083) in the fold change of firing between PV$^+$ neurons and Npas1$^+$ neurons from ^{DLS}iSPN stimulation (PV$^+$ = –0.93 ± 0.06 fold, *n* = 9 neurons, *P* = 0.0039; Npas1$^+$ = –0.55 ± 0.27 fold, *n* = 11 neurons, *P* = 0.0020) (**Figure 5d**). Given the higher input resistance of Npas1$^+$ neurons (Hernandez et al., 2015), it is not surprising to see that a weak ^{DLS}iSPN input to Npas1$^+$ neurons suppressed firing disproportionally. The GABAergic nature of the ^{DLS}dSPN input was confirmed in a subset of Npas1$^+$ neurons. Similarly, in all PV$^+$ neurons tested (*n* = 5 neurons), the application of SR95531 completely blocked the ^{DLS}iSPN IPSCs, confirming the GABAergic nature of the synapse (**Figure 6f**).

DMS and DLS inputs share a similar organization

So far, we have shown that ^{DLS}dSPNs and ^{DLS}iSPNs preferentially innervate Npas1$^+$ neurons and PV$^+$ neurons, respectively. While there are subtle spatial distributions of neuron subtypes in the GPe (Mastro et al., 2014; Abdi et al., 2015; Hernandez et al., 2015; Abecassis et al., 2020), their relationship with striatopallidal projections was not known. To this end, we asked whether ^{DMS}dSPNs have different connectivity with PV$^+$ neurons and Npas1$^+$ neurons compared to ^{DLS}dSPN input. Similar to ^{DLS}dSPNs that preferentially target Npas1$^+$ neurons, ^{DMS}dSPNs provided a stronger input to Npas1$^+$ neurons compared to PV$^+$ neurons, regardless of the stimulus intensity examined (**Figure 6e**). In addition, ^{DMS}iSPNs had a stronger input to PV$^+$ neurons than Npas1$^+$ neurons (**Figure 6e**). DMS inputs shared

a similar organization with DLS inputs (**Figure 6e**). A complete description of the input-output relationship for
475 distinct DMS inputs is listed in **Table 4**.

To ascertain selective recruitment of striatal input from unique spatial domain, all data so far were obtained from somatic stimulation of SPNs (either within the DMS or DLS). Although the slicing angle was chosen to maintain maximal dStr-GPe connectivity, some axons were inevitably severed. To ensure our observations were not confounded by axonal preservation, we recorded synaptic responses with full-field stimulation of SPN
480 terminals in the GPe. As shown in **Figure 6e**, this approach yielded results that were highly concordant with that obtained from somatic stimulation. The spatial specificity of the stimulation was confirmed with sequential applications of tetrodotoxin (TTX, a voltage-gated sodium channel blocker) and 4-aminopyridine (4-AP, a voltage-gated potassium channel blocker) (Petreanu et al., 2009). Although IPSCs were abolished with TTX for both somatic (i.e., intrastriatal) and axonal (i.e., intrapallidal) stimulation, subsequent co-application of TTX with 4-AP
485 selectively restored the IPSCs with terminal stimulation. These results thus confirmed that somatic stimulation, but not terminal stimulation, involved conducting events (**Figure 6g**). In sum, dSPNs from both DLS and DMS preferentially target Npas1^{+} neurons; whereas iSPNs from both spatial domains preferentially target PV^{+} neurons.

The dSPN-GPe innervation is selectively strengthened in a chronic PD model

490 Both circuit model and experimental data converge on the idea that an increased striatopallidal input contributes to the aberrant activity in the GPe in PD (Albin et al., 1989; Wichmann and DeLong, 2003; Walters et al., 2007; Ballion et al., 2009; Kita and Kita, 2011a, b; Lemos et al., 2016; Ryan et al., 2018; McIver et al., 2019). Our previous study demonstrated that total striatal input in unidentified GPe neurons increased following chronic 6-OHDA lesion (Cui et al., 2016). However, the alterations of individual striatopallidal subcircuit (i.e. dSPN-PV^{+}, dSPN-Npas1^{+}, iSPN-
495 PV^{+}, iSPN-Npas1^{+}) were unknown. We therefore examined the alterations in the input-output relationship of these subcircuits in the chronic 6-OHDA lesion model of PD. ^{DLS}dSPN-Npas1^{+} input was dramatically strengthened across all the stimulus intensities tested (IPSCs$_{max}$: Npas1$^{+}_{naïve}$ = 213.8 ± 122.0 pA, n = 28 neurons; Npas1$^{+}_{6\text{-}OHDA}$ = 815.8 ± 530.5 pA, n = 15 neurons; P = 0.0017) (**Figure 6d** & **e**). In contrast, ^{DLS}dSPN-PV^{+} input was not consistently altered across all stimulus intensities tested (IPSCs$_{max}$: PV$^{+}_{naïve}$ = 38.5 ± 29.3 pA, n = 8 neurons; PV$^{+}_{6\text{-}OHDA}$ = 81.0 ±
500 76.7 pA, n = 13 neurons; P = 0.14) (**Figure 6d** & **e**). To our surprise, given a predicted increase in iSPN input with the classic circuit model (Albin et al., 1989; Wichmann and DeLong, 2003), neither ^{DLS}iSPN-PV^{+} input nor ^{DLS}iSPN-

Npas1$^+$ input was altered regardless of the stimulus location or stimulus intensity examined (IPSCs$_{max}$: PV$^+_{naïve}$ = 1,740.7 ± 627.7 pA, n = 12 neurons; PV$^+_{6\text{-OHDA}}$ = 1,682.0 ± 820.4 pA, n = 18 neurons; P = 0.75; Npas1$^+_{naïve}$ = 76.9 ± 60.9 pA, n = 20 neurons; Npas1$^+_{6\text{-OHDA}}$ = 39.2 ± 22.2 pA, n = 11 neurons; P = 0.36) (**Figure 6e**). DMS inputs were similarly altered in the chronic 6-OHDA lesioned mice. ^{DMS}dSPN-Npas1$^+$ input was strengthened while no consistent change was detected for ^{DMS}iSPN-PV$^+$ input and ^{DMS}iSPN-Npas1$^+$ input (**Figure 6e**). As in naïve mice, our findings from 6-OHDA lesioned mice were consistent across the dStr subregions examined; dSPN inputs were biased toward Npas1$^+$ neurons while iSPN inputs were biased toward PV$^+$ neurons following chronic 6-OHDA lesion (**Figure 6e**). A full description of the input-output relationship for distinct striatal inputs is summarized in **Table 3** & **4**.

We hypothesize that the selective increase in the connection strength of the dSPN-Npas1$^+$ input is a result of increased innervation. To test this idea, we measured the density of axons produced by dSPNs in naïve and 6-OHDA lesioned mice. To visualize dSPN axons, Cre-inducible ChR2-eYFP was expressed in *Drd1a*^{Cre} mice. We observed a dramatic increase in the dSPN axonal density in the GPe following 6-OHDA lesion (+2.64 ± 0.88 fold; $n_{naïve}$ = 7 sections, 4 mice; $n_{6\text{-OHDA}}$ = 12 sections, 6 mice; P = 0.00048) (**Figure 6a** & **c**), whereas only modest increases were observed in the dStr (+0.50 ± 0.22 fold; $n_{naïve}$ = 12 sections, 4 mice; $n_{6\text{-OHDA}}$ = 18 sections, 6 mice; P = 0.0050) and SNr (+0.57 ± 0.60 fold; $n_{naïve}$ = 4 sections, 4 mice; $n_{6\text{-OHDA}}$ = 6 sections, 6 mice; P = 0.48). The fold increase in the GPe was much higher than that in the dStr and SNr (GPe vs. dStr, P = 0.0087; GPe vs. SNr, P = 0.0087) (**Figure 6c**). As axonal density in the GPe reflects a sum of axonal arborizations and passage axons, synaptic contacts were then quantified as an additional measure of innervation. Synaptic contacts were identified based on the close spatial relationship between eYFP$^+$ structures and VGAT$^+$ or gephyrin$^+$ elements (**Figure 6b**). The density of eYFP$^+$-VGAT$^+$ puncta in the GPe was greatly increased following 6-OHDA lesion (naïve = 3.9 ± 2.1 × 10^4 count/mm^3, n = 6 sections, 3 mice; 6-OHDA = 11.9 ± 3.0 × 10^4 count/mm^3, n = 10 sections, 5 mice; P = 0.0096); additionally, a similar increase in the density of eYFP$^+$-gephyrin$^+$ puncta was found under the same conditions (naïve = 4.1 ± 1.5 × 10^4 count/mm^3, n = 6 sections, 3 mice; 6-OHDA = 19.3 ± 3.0 × 10^4 count/mm^3, n = 8 sections, 4 mice; P = 0.0020) (**Figure 6c**). As dSPN-Npas1$^+$ input is the major input of dSPN projection, the increase in synaptic contacts from dSPNs explains the strengthening of the dSPN-Npas1$^+$ input measured with *ex vivo* electrophysiology following chronic 6-OHDA lesion. In contrast, we did not find any alterations in release probability for the dSPN-Npas1$^+$ input following 6-OHDA lesion, as indicated by the unaltered paired-pulse ratio (naïve = 1.1 ±

530 0.1, n = 10 neurons; 6-OHDA = 1.3 ± 0.2, n = 11 neurons; P = 0.20). In addition, no alterations in quantal amplitudes were observed following chronic 6-OHDA lesion (naïve = 86.1 ± 24.5 pA, n = 13 neurons; 6-OHDA = 92.8 ± 29.2 pA, n = 22 neurons; P = 0.39).

535 **Discussion** (1332 words)

The anatomical projection from dSPNs to the GPe has been described for decades, but its postsynaptic targets and functions were largely unknown. In this study, we showed that dSPNs strongly targeted Npas1$^+$ GPe neurons, whereas iSPNs strongly targeted PV$^+$ GPe neurons. In contrast to the prediction from the classic circuit model, ^{DLS}dSPNs suppressed movements. This suppression was mediated through Npas1$^+$ neurons. In a chronic 6-OHDA
540 lesioned mouse model of PD, dSPN-Npas1$^+$ input was dramatically strengthened through an increase in the number of synaptic contacts.

iSPN-PV$^+$ input is the principal component of the striatopallidal system

Here, we demonstrated that iSPN-PV$^+$ input was the strongest connection among all striatopallidal inputs
545 examined, namely, dSPN-PV$^+$, dSPN-Npas1$^+$, iSPN-PV$^+$, and iSPN-Npas1$^+$. Considering that PV$^+$ neurons and Npas1$^+$ neurons constitute 50% and 30% of all GPe neurons, respectively (Abdi et al., 2015; Dodson et al., 2015; Hernandez et al., 2015; Abecassis et al., 2020), iSPN-PV$^+$ input should be regarded as the principal striatopallidal input.

Our finding that iSPN-PV$^+$ input is stronger than iSPN-Npas1$^+$ input is consistent with earlier anatomical
550 studies showing that iSPNs form more synaptic contacts with PV$^+$ neurons compared to PV$^-$ neurons (Yuan et al., 2017).In addition, it is in line with recent electrophysiological studies that iSPNs strongly target Nkx2.1$^+$ neurons (which are dominated by PV$^+$ neurons) while providing minimal input to Foxp2$^+$ neurons (which are a subset of Npas1$^+$ neurons) (Yuan et al., 2017; Aristieta et al., 2020; Ketzef and Silberberg, 2020). Furthermore, we showed that the selective targeting of iSPN input to PV$^+$ neurons was topographically conserved between the DMS and the
555 DLS.

At a circuit level, stimulation of iSPNs strongly suppresses firing of PV$^+$ neurons, thus disinhibiting the targets of PV$^+$ neurons, i.e., the STN and substantia nigra (Mastro et al., 2014; Hernandez et al., 2015; Saunders et

al., 2016; Oh et al., 2017; Abecassis et al., 2020). As activity of PV$^+$ neurons promotes movement (Pamukcu et al., 2020), the selective targeting of PV$^+$ neurons by iSPNs is in agreement with the movement suppressing role of ^{DMS}iSPNs (Kravitz et al., 2010; Durieux et al., 2012). On the contrary, we found stimulation of ^{DLS}iSPNs promoted movement; this cannot be explained by the targeting properties of ^{DLS}iSPNs. Further investigations are needed to determine the circuit mechanisms involved. In the present study, we did not find any alterations in the iSPN-PV$^+$ input in the parkinsonian state. Given that iSPN-PV$^+$ input is the principal striatopallidal input, this result is at odds with our previous observation that total striatopallidal input increases following chronic 6-OHDA lesion (Cui et al., 2016). As our prior study employed electrical stimulation, it is likely that subtle differences in the size and the waveform of the induced currents with optogenetic stimulation interfere with presynaptic regulation of release processes.

The dSPN-Npas1$^+$ input is functionally unique

Previous studies showed that dSPNs provide roughly half the number of boutons compared to iSPNs in the GPe (Kawaguchi et al., 1990; Fujiyama et al., 2011). Here, we found the relative number of boutons formed by iSPNs was seven times higher than that formed by dSPNs. Importantly, we demonstrated that Npas1$^+$ neurons are the principal target of dSPNs from both the DMS and DLS. This is in contrast with the earlier observation that the receptors for substance P (a neuropeptide that can be released by dSPNs) are selectively expressed in PV$^+$ neurons (Mizutani et al., 2017). These findings altogether suggest a target-specific innervation with transmitters released from a single cell type, i.e., GABA and substance P released from dSPNs preferentially inhibit Npas1$^+$ neurons and excite PV$^+$ neurons, respectively. Segregation of neurotransmitter release has also been found in other systems (Zhang et al., 2015; Lee et al., 2016; Granger et al., 2020). Given that Npas1$^+$ neurons and PV$^+$ neurons have opposite effects on motor control (Cherian et al., 2020; Pamukcu et al., 2020), the inhibition of Npas1$^+$ neurons by GABA and excitation of PV$^+$ neurons by substance P should work in concert to reinforce the same behavioral outcomes.

The highly selective targeting of dSPNs to Npas1$^+$ neurons can have important functional implications. Here, we demonstrated that stimulation of ^{DLS}dSPNs or their terminals in the GPe suppressed movement. Our silencing experiment confirms that this effect is mediated by Npas1$^+$ neurons, but not PV$^+$ neurons. However, the motor-suppressing effect of ^{DLS}dSPNs (mediated through inhibitory input to Npas1$^+$ neurons) contradicts the

motor-promoting effect that we found with silencing or inhibition of Npas1^{+} neurons (this study; Pamukcu et al., 2020). The movement-suppressing effect exerted by ^{DLS}dSPNs is opposite to the movement-promoting effect produced by ^{DMS}dSPNs shown in this and other studies (Kravitz et al., 2010; Durieux et al., 2012; Freeze et al., 2013). Opposing regulation by ^{DMS}dSPNs and ^{DLS}dSPNs has also been found recently in regulating action sequence (Garr and Delamater, 2020). The dichotomous actions of ^{DMS}dSPNs and ^{DLS}dSPNs cannot be explained by their cell-targeting properties as they both strongly targeted Npas1^{+} neurons (over PV^{+} neurons) in their corresponding topographical territories within the GPe. It is possible that the effect of ^{DMS}dSPNs is predominantly mediated through the SNr rather than the GPe, as the DMS only innervates a small portion of the GPe.

We do not currently have a mechanistic explanation for the contradictory effects between stimulation of ^{DLS}dSPNs and inhibition or silencing of Npas1^{+} neurons. First, our observations were limited to gain-of-function experiments (i.e., ChR2-mediated stimulation). Further work is needed to examine the effects with inhibition or silencing of ^{DLS}dSPNs. Second, it is possible that chronic silencing induces confounding cellular and circuit changes. Third, recent studies established the existence of two subclasses of Npas1^{+} neurons, i.e., Npas1^{+}-Foxp2^{+} neurons and Npas1^{+}-Nkx2.1^{+} (aka Npr3^{+}) neurons that display distinct axonal projection patterns (Hernandez et al., 2015; Glajch et al., 2016; Saunders et al., 2018; Evans et al., 2019; Abecassis et al., 2020; Cherian et al., 2020; Pamukcu et al., 2020). It is possible that ^{DLS}dSPN input has differential impacts on these two neuron subclasses and their downstream targets. Lastly, the effect with stimulation of Npas1^{+} neurons can be an aggregated effect of suppressing multiple targets. As the basal ganglia is topographically organized, including the ^{DLS}dSPN projection, which only innervate the lateral to intermediate regions of the GPe (Hedreen and DeLong, 1991; Deniau et al., 1996; Romanelli et al., 2005; Nambu, 2011; Bertino et al., 2020), the circuitry mediating the downstream effects of ^{DLS}dSPNs should differ from that of the entirety of the Npas1^{+} neuron population.

In this study, we provided both anatomical and functional evidence that dSPN input to the GPe was strengthened following chronic 6-OHDA lesion. These observations were unexpected, as activity of dopamine D2 receptors is known to positively regulate the density of dSPN innervation to the GPe (Cazorla et al., 2014). On the other hand, as iSPN activity promotes dSPN-GPe innervation, it is likely that the observed increase in dSPN-GPe innervation following chronic 6-OHDA lesion is a consequence of increased iSPN activity *in vivo*. This argument is in agreement with the observation that the activity of iSPNs (or presumably iSPNs) are enhanced in animal models of PD (Calabresi et al., 1993; Schwarting and Huston, 1996; Kish et al., 1999; Pang et al., 2001; Tseng et al., 2001;

Mallet et al., 2006; Kita and Kita, 2011a, b; Kovaleski et al., 2020). As stimulation of ^{DLS}dSPN-Npas1^{+} input suppresses movement, the increase in this input following chronic 6-OHDA lesion constitutes a novel mechanism underlying hypokinetic symptoms in this disease state.

Parallel motor-suppressing striatal output pathways

The existence of parallel motor-suppressing striatopallidal pathways, i.e., ^{DMS}iSPN-PV^{+} and ^{DLS}dSPN-Npas1^{+}, suggests a complex movement regulation by the dStr. Although stimulation of either pathway similarly decreased average speed, the two pathways tune movement behavior in different patterns. Recent studies revealed that distinct behaviors are multiplexed by the same spatially compact clusters while different clusters encode different speed information (Barbera et al., 2016; Fobbs et al., 2020). As the DMS and the DLS are involved in distinct functions (goal-directed behavior and habitual behavior, respectively), it is conceivable that each functional subdomain is equipped with both motor-suppressing and motor-promoting elements for the proper movement execution.

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Figure Legends

Figure 1. dSPNs send terminating axons to the GPe.

920 **a**. *Top left*, a confocal micrograph showing retrogradely-labeled spiny projection neurons (SPNs) in the dorsal striatum (dStr) from a Cre-reporter (*R26*$^{LSL\text{-}tdTomato}$) mouse. A Cre-expressing lentivirus and CTb 488 were injected into the GPe. tdTomato^{+} and CTb 488^{+} neurons (in white circles) were visible. *Bottom left*, unbiased quantification of GPe-projecting neurons across the entire brain. Each marker represents a mouse (*n* = 8 mice). The arrow points to the data (red) from the dStr. *Right*, representative two-photon images from coronal sections showing GPe-
925 projecting neurons were found in the dStr, central amygdala (CeA), parafascicular nucleus (PF), and subthalamic nucleus (STN). Inset in the first image indicates the location of the injection site. Scale bar in the third image applies to the bottom three images.

b. *Left*, high-magnification images showing that terminals (eGFP^{+}, white) from iSPNs or dSPNs were abundant in the GPe. CreOn-mRuby2-T2A-Synaptophysin-eGFP adeno-associated virus (AAV) was injected into the dStr of
930 *Adora2a*^{Cre} (*top*), *Drd1a*^{Cre} (*middle*), and *Tac1*^{Cre} (*bottom*) mice to visualize SPN terminals. Maximal projections from ten optical sections are shown. *Inset*, mRuby2^{+} dSPNs in the dStr. *Top & middle right*, immunohistological analyses showing that eGFP^{+} boutons (green) were in proximity with vesicular GABA transporter (VGAT) and gephyrin (magenta), as shown in white in three orthogonal planes. *Bottom right*, quantification of eGFP^{+} bouton density in the GPe from *Adora2a*^{Cre} (*n* = 12 ROIs), *Drd1a*^{Cre} (*n* = 10 ROIs), and *Tac1*^{Cre} (*n* = 12 ROIs) mice.

935 **c**. *Left*, a low-magnification micrograph from a sagittal brain section demonstrating the target of retrograde tracers CTb 488 and CTb 647 into the GPe and SNr, respectively. The *Drd1a*^{tdTomato} allele was used to decipher the identity of SPNs. *Right*, representative high-magnification images illustrating CTb 488 and CTb 647 were detected in the same tdTom^{+} neurons in the dStr. White circles denote colocalization.

d. A low-magnification micrograph from a sagittal brain section showing the expression of eYFP in the dStr as well
940 as its projection targets including the GPe, GPi, and SNr following injections of CreOn-Flp canine adenovirus (CAV) into the SNr in combination with CreOn-FlpOn-ChR2-eYFP AAV into the dStr of a *Drd1a*^{Cre} mouse. CTb 647 was co-injected with CreOn-Flp CAV to visualize the injection site. Inset shows the eYFP^{+} axons in the GPe.

Abbreviations: BLA, basolateral amygdalar nucleus; BSTa, bed nuclei of the stria terminalis, anterior division; cc, corpus callosum; CeA, central amygdala; CLA, claustrum; cpd, cerebral peduncle; Ctx, cortex; DR, dorsal raphe
945 nucleus; dStr, dorsal striatum; fr, fasciculus retroflexus; GPe, external globus pallidus; GPi, internal globus pallidus;

GU, gustatory areas; MOp, primary motor area; MOs, secondary motor area; MRN, midbrain reticular nucleus; opt, optic tract; PAG, periaqueductal gray; PF, parafascicular nucleus; PO, posterior complex of the thalamus; PPN, pedunculopontine nucleus; PRNc, pontine reticular nucleus, caudal part; PRNr, pontine reticular nucleus, rostral part; SCm, superior colliculus, motor related; SI, substantia innominata; SNc, substantia nigra pars compacta; SNr, substantia nigra pars reticulata; SSp-bfd, primary somatosensory area, barrel field; SSp-ll, primary somatosensory area, lower limb; SSp-m, primary somatosensory area, mouth; SSp-n, primary somatosensory area, nose; SSp-tr, primary somatosensory area, trunk; SSp-ul, primary somatosensory area, upper limb; SSs, supplemental somatosensory area; STN, subthalamic nucleus; VAL, ventral anterior-lateral complex of the thalamus; VISC, visceral area; VM, ventromedial thalamic nucleus; VPM, ventral posteromedial thalamic nucleus; Th, thalamus; ZI, zona incerta.

Figure 2. dSPN and iSPN inputs to GPe have unique properties.

a. *Left*, confocal micrographs of two neighboring brain sections showing the iSPN projection to the GPe. The dStr of an *Adora2a*^{Cre} mouse was transduced with a CreOn-ChR2-eYFP AAV. The association of enkephalin (*top*) and substance P (*bottom*) with eYFP-labeled axonal fibers in the GPe was assessed with immunofluorescence labeling. *Right*, high-magnification images showing the spatial relationship between enkephalin (magenta, *top*) and substance P (magenta, *bottom*) with iSPN axons (green) in the GPe. Rectangular images show orthogonal projections. Crosshairs indicate the projected planes.

b. *Left*, confocal micrographs of two neighboring brain sections showing the dSPN projection to the GPe. The dStr of a *Drd1a*^{Cre} mouse was transduced with a CreOn-ChR2-eYFP AAV. The association of enkephalin (*top*) and substance P (*bottom*) with eYFP-labeled axonal fibers in the GPe was assessed with immunofluorescence labeling. *Right*, high-magnification images showing the spatial relationship between enkephalin (magenta, *top*) and substance P (magenta, *bottom*) with dSPN axons (green).

c. *Top*, representative voltage-clamp recordings showing striatopallidal (dStr-GPe) inhibitory postsynaptic currents (IPSCs) in control (gray) condition and in the presence of quinpirole (10 μM, black). IPSCs were evoked with optogenetics; light was delivered in the dStr. *Drd1a*^{Cre} and *Adora2a*^{Cre} mice were used to examine the properties of dSPN and iSPN inputs, respectively. dSPN-GPe IPSCs (*top*) and iSPN-GPe IPSCs (*middle* and *bottom*) are shown. The bottom recording was from an identified PV^{+} neuron. *Bottom*, the relative iSPN-GPe IPSC amplitude was

plotted vs. time (n = 12 neurons). The horizontal black line denotes the timing of quinpirole application.

975 **d**. *Top*, box plots summarizing the effect of quinpirole on dStr-GPe IPSC amplitude. All recorded neurons for dSPN or iSPN input (dSPN input = 6 neurons, iSPN input = 16 neurons) are shown on the *left*. Plots on the *right* show iSPN input broken down by neuron types (PV^+ = 4 neurons, $Npas1^-$ = 7 neurons, $Npas1^+$ = 5 neurons). *Bottom*, quantification of $eGFP^+$ bouton density in the GPe shown in **e** (DMS: *Adora2a*^{Cre} = 6 ROIs, *Drd1a*^{Cre} = 4 ROIs, *Tac1*^{Cre} = 6 ROIs, DLS: *Adora2a*^{Cre} = 6 ROIs, *Drd1a*^{Cre} = 6 ROIs, *Tac1*^{Cre} = 6 ROIs).

980 **e**. Representative high-magnification images showing SPN terminals ($eGFP^+$, white) in the GPe. CreOn-mRuby2-T2A-Synaptophysin-eGFP AAV was injected into the dStr subregions of *Adora2a*^{Cre}, *Drd1a*^{Cre} and *Tac1*^{Cre} mice. Terminals from iSPNs (*Adora2a*^{Cre}) or dSPNs (*Drd1a*^{Cre} & *Tac1*^{Cre}) from the dorsomedial striatum (DMS) (*left*) or dorsolateral striatum (DLS) (*right*) were abundant in the GPe. Images from medial and intermediate levels of the GPe are shown for terminals from the DMS and DLS, respectively. Maximal intensity from ten optical sections is

985 shown for each example.

Figure 3. Optogenetic stimulation of SPN subtypes produces unique changes in movement metrics.

a. *Left*, a heatmap summarizing motor responses of mice to optogenetic stimulation of ^{DLS}dSPNs (red), ^{DMS}dSPNs (blue), ^{DLS}iSPNs (green), ^{DMS}iSPNs (purple). Twenty-five movement metrics were measured to fully capture the

990 behavioral structures. Each of the 25 rows represents the fold change of movement metrics. Warm colors (red) represent positive changes; cool colors (blue) represent negative changes. Rows and columns were sorted using hierarchical clustering. Dendrograms are divided into two main arms; metrics on the upper arm are positively correlated with 'total frequency', while metrics on the lower arm are negatively correlated with 'total frequency'. Each column is a mouse; 48 mice were used in this and all subsequent analyses in **b**–**e** (^{DLS}dSPNs = 13 mice,

995 ^{DMS}dSPNs = 9 mice, ^{DLS}iSPNs = 15 mice, ^{DMS}iSPNs = 11 mice). *Right*, a heatmap summarizing motor responses of mice to optogenetic stimulation of genetically-defined neurons in the GPe. The neurons of interest are $Foxp2^+$ (pink), $Kcng4^+$ (purple), $Npas1^+$ (green), PV^+ (orange). The plot was reproduced from Cherian et al. (Cherian et al., 2020).

b. Mean changes in the event frequency of motionless, fine movement, rearing, and locomotion upon optogenetic

000 stimulation (blue horizontal lines) of ^{DMS}dSPNs, ^{DLS}dSPNs, ^{DMS}iSPNs, and ^{DLS}iSPNs.

c. Slopegraphs showing the time spent for motionless, fine movement, and locomotion in mice and the effect with optogenetic stimulation of selective neuron types. Each connected line represents a mouse.

d. A correlation matrix constructed using data from *Adora2a*^{Cre} and *Drd1a*^{Cre} mice transduced with CreOn-ChR2-eYFP AAV. Eighteen parameters were included in this matrix. Blue colors indicate positive correlations, whereas brown colors indicate negative correlations. *Inset*, Principal component analysis plots showing the distribution of ^{DMS}dSPNs (blue), ^{DLS}dSPNs (red), ^{DMS}iSPNs (purple), and ^{DLS}iSPNs (green). Fold changes of twenty three movement metrics with optogenetic stimulation were used in this analysis.

e. A correlation matrix constructed from fold changes in movement metrics following optogenetic stimulation of ^{DMS}dSPNs, ^{DLS}dSPNs, ^{DMS}iSPNs, and ^{DLS}iSPNs. Blue colors indicate positive correlations, brown colors indicate negative correlations.

Figure 4. ^{DLS}dSPNs-mediated motor suppression requires Npas1^{+} neurons.

a. A low-magnification micrograph showing the expression of eGFP in Npas1^{+} neurons and their axonal projections following a targeted injection of a tetanus toxin light chain (TeTLC)-expressing AAV (CreOn-eGFP-2A-TeTLC) in the GPe of a *Npas1*^{Cre} mouse.

b. The validity of the silencing mediated by TeTLC was demonstrated by the increased locomotor activity in an open-field arena (control = 8 mice, TeTLC = 11 mice). *Npas1*^{Cre} mice transduced with CreOn-eYFP AAV were used as the control.

c. The transduction specificity in Npas1 neurons was assessed by eGFP expression patterns. Somatic eGFP expression was exclusively observed in the GPe. Consistent with specific transduction of Npas1^{+} neurons, axonal expression of eGFP was abundant in Ctx, dStr, TRN, and SNc, but not in STN or SNr.

d. *Left*, time course of normalized distance pre, during, and after stimulation of ^{DLS}dSPN terminals in the GPe, with no neurons silenced (ctrl, *n* = 16 mice), with PV^{+} neurons silenced (*n* = 11 mice), and with Npas1^{+} neurons silenced (*n* = 10 mice) using CreOn-TeTLC-eGFP AAV (*top* to *bottom*). Black lines indicate the mean value. Top and bottom ends of the gray shaded area represent standard error of mean. Blue bars denote the period of blue light stimulation. *Middle*, speed during light-period was plotted against speed during pre-period for the respective groups to the left. Data from *Drd1a*^{Cre} mice receiving CreOn-eYFP AAV injection and stimulation identical to ChR2 group were also included in the top plot (*n* = 6 mice). *Right*, movement tracks during pre-period and light-period

are shown. For each group, data from six mice (ten trials each) were pooled for illustration.

e. *Left*, summary of changes in speed for experimental groups in **d**. Experimental setup is summarized at bottom of the box plots. Effects with stimulation of ^{DLS}dSPN soma (*n* = 13 mice) and ^{DMS}dSPN terminals (*n* = 6 mice) in the GPe were also included for comparison. *Inset*, immunohistology reveals the selective expression of TeTLC (as indicated by eGFP expression) in Npas1$^+$ neurons from *Npas1*^{Cre} mice injected with CreOn-TeTLC-eGFP AAV into the GPe.

Figure 5. dSPNs strongly innervate Npas1$^+$ neurons.

a. *Top*, low-magnification images showing GPe starter cells (*left,* white) and striatal input cells (*right,* green) in coronal brain sections from *Npas1*^{Cre} (*left*) or *Pvalb*^{Cre} (*right*) mice injected with hSyn-DIO-mRuby2-TVA-RVG AAV and rabies virus expressing eGFP sequentially into the GPe. *Bottom*, representative high-magnification images showing that striatal input cells (eGFP$^+$, green) from *Pvalb*^{Cre} (*left*) or *Npas1*^{Cre} (*right*) mice were positive for *Drd1a* (yellow) or *Drd2* (magenta) mRNA.

b. *Left*, representative traces showing IPSCs recorded in PV$^+$ or Npas1$^+$ neurons with optogenetic stimulation of dSPNs (*top*) or iSPNs (*bottom*) in the DLS. Traces from five stimulus intensities (2.4–56.7 mW/mm^2) are shown. *Right*, input-output relationship for corresponding inputs. A full list of median values, sample sizes, and statistical comparisons at different stimulus intensities for discrete inputs is shown in **Table 3**. Response rate for each input is shown in **Table 5**.

c. Summary of anatomical (see **a**; *Pvalb*^{Cre} = 5 mice, *Npas1*^{Cre} = 5 mice) and functional (see **b**; dSPN-PV$^+$ = 8 neurons, dSPN-Npas1$^+$ = 28 neurons, iSPN-PV$^+$ = 12 neurons, iSPN-Npas1$^+$ = 20 neurons) connectivity for discrete dStr-GPe inputs. The IPSC amplitudes at maximal stimulus intensity are plotted.

d. *Top*, representative raster plots showing that stimulation (10 Hz for 2s) of iSPNs or dSPNs in the DLS strongly suppressed firing of PV$^+$ or Npas1$^+$ neurons, respectively. Blue bars indicate the period of blue light stimulation. *Bottom*, summary of changes in baseline activity with stimulation of discrete dStr-GPe inputs (dSPN-PV$^+$ = 9 neurons, dSPN-Npas1$^+$ = 11 neurons, iSPN-PV$^+$ = 9 neurons, iSPN-Npas1$^+$ = 11 neurons).

Figure 6. dSPN inputs are selectively strengthened following chronic 6-OHDA lesion.

a. Confocal micrographs showing the innervation of dSPN axons in the GPe from naïve (*left*) and 6-OHDA lesioned

(*right*) mice. To visualize dSPN axons, *Drd1a*^{Cre} mice were transduced with CreOn-ChR2-eYFP AAV. Intermediate (*top*) and medial (*bottom*) levels are shown.

b. Representative high-magnification images showing dSPN bouton density in the GPe from naïve (*left*) and 6-OHDA lesioned (*right*) mice. dSPN boutons were represented by VGAT^{+} (magenta) and syp-eGFP^{+} (green) puncta. CreOn-mRuby2-T2A-Synaptophysin-eGFP AAV was injected into the dStr of *Drd1a*^{Cre} mice for the visualization of dSPN terminals. Breakout panels show orthogonal xz-projection (*bottom*) and yz-projection (*right*). Crosshairs indicate the pixel of interest. The colocalization of the signals is shown as white.

c. Quantification of the data shown in **a** and **b**: axonal density (naïve = 4 mice, 6-OHDA = 6 mice), eYFP^{+}-VGAT^{+} puncta density (naïve = 6 sections, 6-OHDA = 10 sections), and eYFP^{+}-gephyrin^{+} puncta density (naïve = 6 sections, 6-OHDA = 8 sections).

d. Representative voltage-clamp recordings showing IPSCs arose from dSPNs in PV^{+} neurons (*top*) and Npas1^{+} neurons (*bottom*). A range of stimulus intensities (2.4–56.7 mW/mm^{2}) were tested. Note the increase in IPSC amplitude in 6-OHDA mice (red, *right*) compared to that from naïve (black, *left*).

e. Connection strengths from dSPNs (*left*) and iSPNs (*right*) to PV^{+} neurons and Npas1^{+} neurons across two DLS (*top*) and DMS domains (*bottom*) were assessed with both somatic (i.e, intrastriatal, dStr) and terminal (i.e., intrapallidal, GPe) stimulation. Results are summarized as box plots. See **Table 3** & **4** for a full listing of IPSC amplitudes and sample sizes.

f. GABA$_{A}$ receptor dependency of the IPSCs were tested with a GABA$_{A}$ receptor antagonist, SR95531 (10 μM). Each marker represents a cell (dSPN-Npas1^{+} = 4 neurons, iSPN-PV^{+} = 5 neurons).

g. The spatial specificity of the optogenetic stimulation was assessed with the applications of tetrodotoxin (TTX 1 μM, light green) and its co-application with 4-aminopyridine (4-AP 100 μM, dark green). Each marker represents a cell (dSPN-Npas1^{+}: dStr stim = 5 neurons, GPe stim = 5 neurons, iSPN-PV^{+}: dStr stim = 7 neurons, GPe stim = 3 neurons).

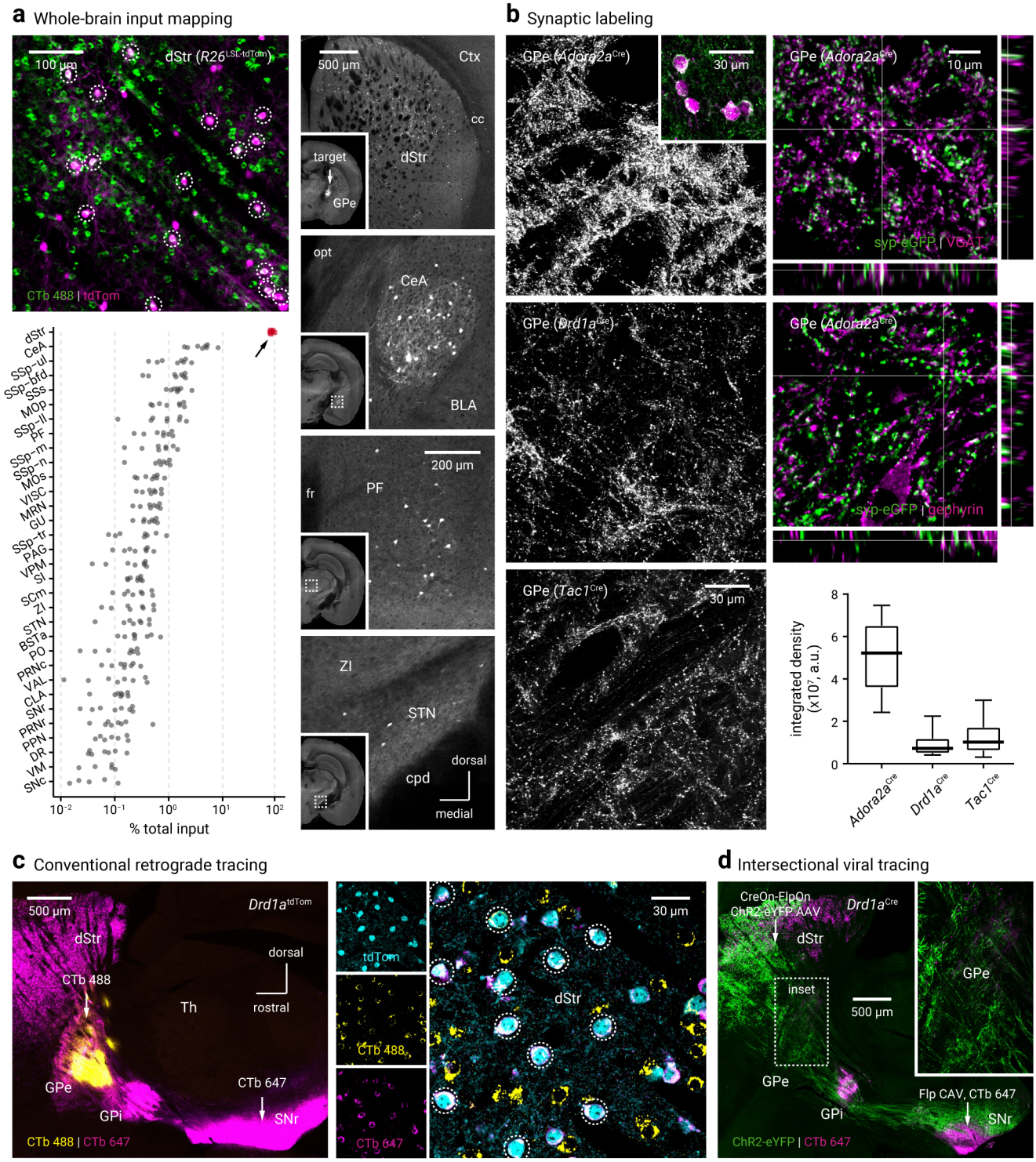
a Whole-brain input mapping
dStr (R26LSL-tdTom)
100 µm
CTb 488 | tdTom
dStr
CeA
SSp-ul
SSp-bfd
SSs
MOp
SSp-ll
PF
SSp-m
SSp-n
MOs
VISC
MRN
GU
SSp-tr
PAG
VPM
SI
SCm
ZI
STN
BSTa
PO
PRNc
VAL
CLA
SNr
PRNr
PPN
DR
VM
SNc
% total input
500 µm
Ctx
cc
dStr
target
GPe
opt
CeA
BLA
200 µm
fr
PF
ZI
STN
dorsal
cpd
medial
b Synaptic labeling
GPe (Adora2aCre)
30 µm
10 µm
syp-eGFP | VGAT
GPe (Drd1aCre)
syp-eGFP | gephyrin
GPe (Tac1Cre)
integrated density (x10^7, a.u.)
Adora2aCre
Drd1aCre
Tac1Cre
c Conventional retrograde tracing
500 µm
Drd1atdTom
dStr
dorsal
CTb 488
Th
rostral
GPe
CTb 647
GPi
SNr
CTb 488 | CTb 647
tdTom
CTb 488
CTb 647
30 µm
d Intersectional viral tracing
CreOn-FlpOn ChR2-eYFP AAV
Drd1aCre
dStr
inset
500 µm
GPe
GPi
Flp CAV, CTb 647
SNr
ChR2-eYFP | CTb 647

Figure 1

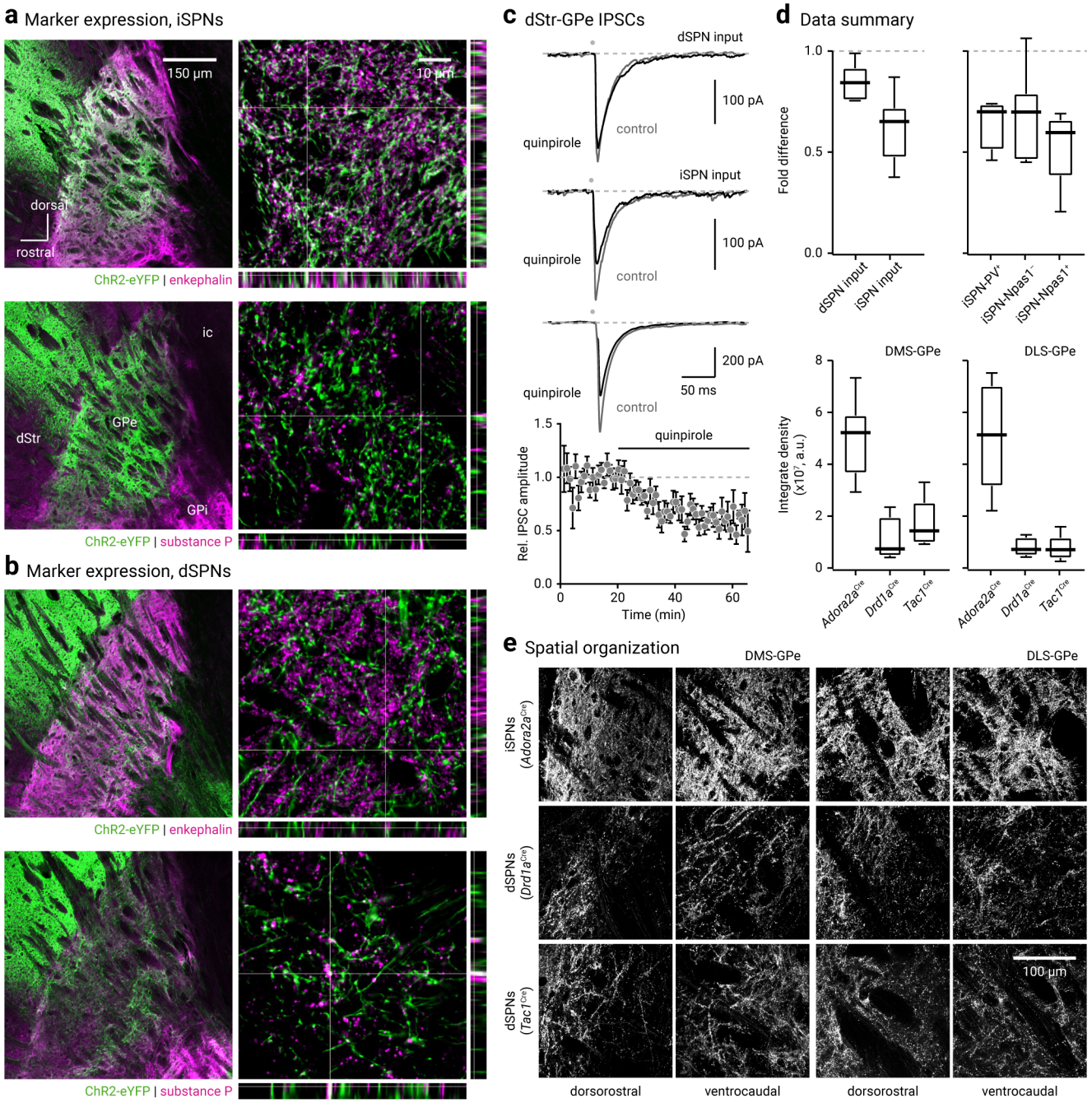
a Marker expression, iSPNs
150 µm
10 µm
dorsal
rostral
ChR2-eYFP | enkephalin
ic
GPe
dStr
GPi
ChR2-eYFP | substance P
b Marker expression, dSPNs
ChR2-eYFP | enkephalin
ChR2-eYFP | substance P
c dStr-GPe IPSCs
dSPN input
100 pA
control
quinpirole
iSPN input
100 pA
control
quinpirole
200 pA
50 ms
control
quinpirole
quinpirole
Rel. IPSC amplitude
Time (min)
d Data summary
Fold difference
dSPN input
iSPN input
iSPN-PV+
iSPN-Npas1-
iSPN-Npas1+
DMS-GPe
DLS-GPe
Integrate density (x10^7, a.u.)
Adora2a^Cre
Drd1a^Cre
Tac1^Cre
e Spatial organization
DMS-GPe
DLS-GPe
iSPNs (Adora2a^Cre)
dSPNs (Drd1a^Cre)
dSPNs (Tac1^Cre)
100 µm
dorsorostral
ventrocaudal
dorsorostral
ventrocaudal

Figure 2

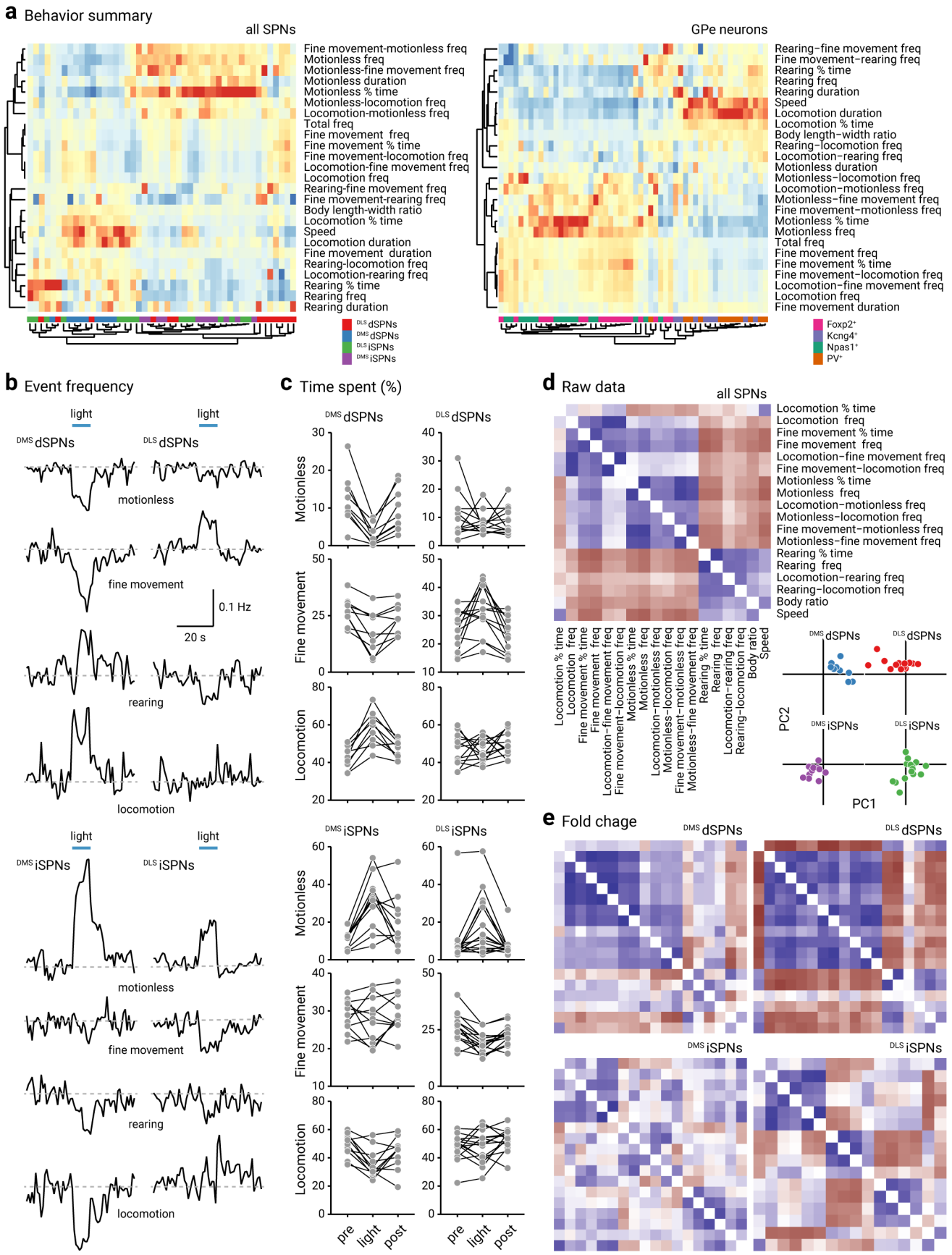
a Behavior summary
all SPNs
Fine movement-motionless freq
Motionless freq
Motionless-fine movement freq
Motionless duration
Motionless % time
Motionless-locomotion freq
Locomotion-motionless freq
Total freq
Fine movement freq
Fine movement % time
Fine movement-locomotion freq
Locomotion-fine movement freq
Locomotion freq
Rearing-fine movement freq
Fine movement-rearing freq
Body length-width ratio
Locomotion % time
Speed
Locomotion duration
Fine movement duration
Rearing-locomotion freq
Locomotion-rearing freq
Rearing % time
Rearing freq
Rearing duration
DLS dSPNs
DMS dSPNs
DLS iSPNs
DMS iSPNs
GPe neurons
Rearing-fine movement freq
Fine movement-rearing freq
Rearing % time
Rearing freq
Rearing duration
Speed
Locomotion duration
Locomotion % time
Body length-width ratio
Rearing-locomotion freq
Locomotion-rearing freq
Motionless duration
Motionless-locomotion freq
Locomotion-motionless freq
Motionless-fine movement freq
Fine movement-motionless freq
Motionless % time
Motionless freq
Total freq
Fine movement freq
Fine movement % time
Fine movement-locomotion freq
Locomotion-fine movement freq
Locomotion freq
Fine movement duration
Foxp2+
Kcng4+
Npas1+
PV+
b Event frequency
light
DMS dSPNs
DLS dSPNs
motionless
fine movement
0.1 Hz
20 s
rearing
locomotion
DMS iSPNs
DLS iSPNs
c Time spent (%)
Motionless
Fine movement
Locomotion
pre
light
post
d Raw data
all SPNs
Locomotion % time
Locomotion freq
Fine movement % time
Fine movement freq
Locomotion-fine movement freq
Fine movement-locomotion freq
Motionless % time
Motionless freq
Locomotion-motionless freq
Motionless-locomotion freq
Fine movement-motionless freq
Motionless-fine movement freq
Rearing % time
Rearing freq
Locomotion-rearing freq
Rearing-locomotion freq
Body ratio
Speed
PC1
PC2
e Fold chage

Figure 3

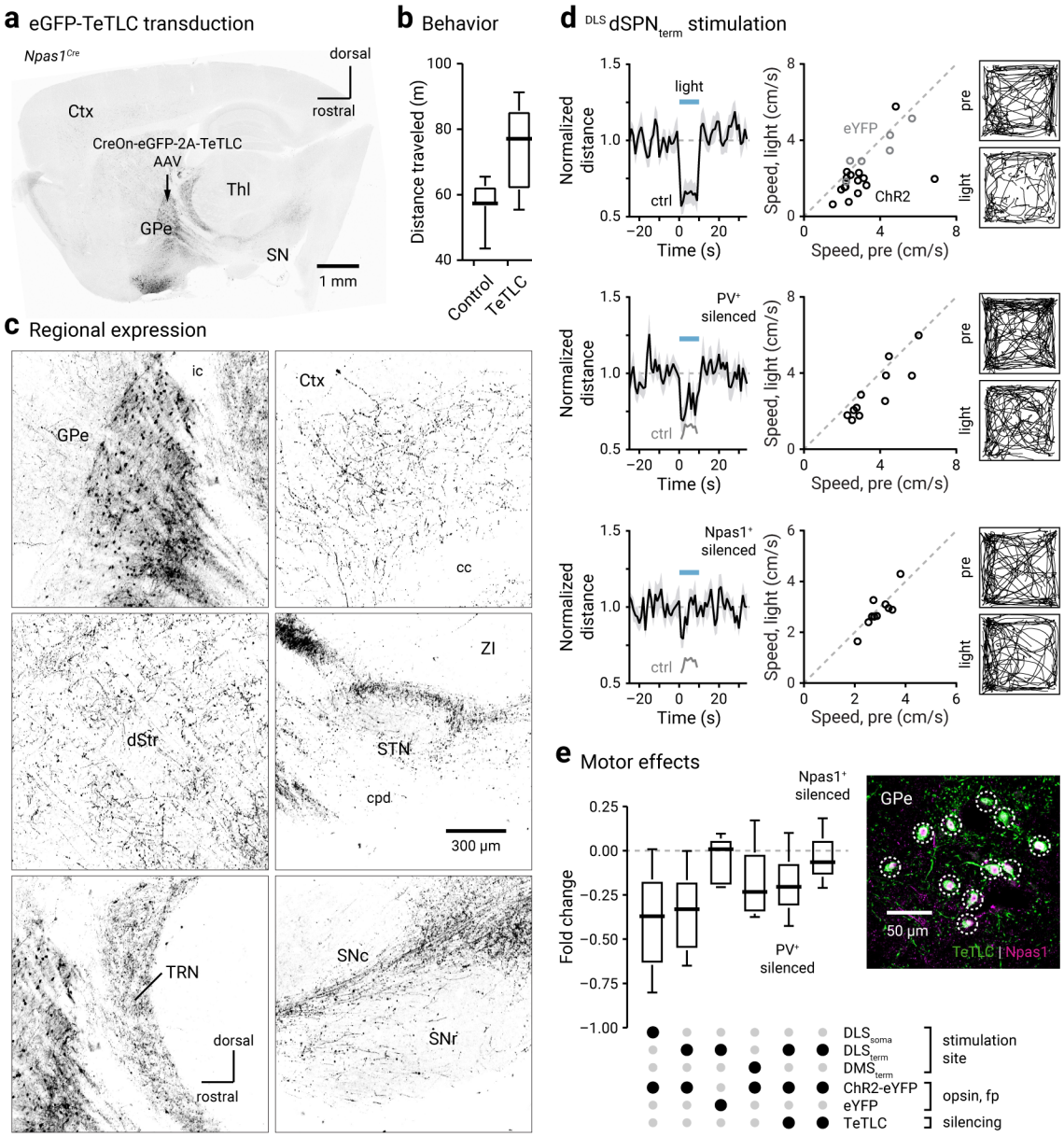
a eGFP-TeTLC transduction
Npas1Cre
dorsal
rostral
Ctx
CreOn-eGFP-2A-TeTLC
AAV
Thl
GPe
SN
1 mm
b Behavior
Distance traveled (m)
100
80
60
40
Control
TeTLC
c Regional expression
ic
GPe
Ctx
cc
dStr
ZI
STN
cpd
300 µm
TRN
dorsal
rostral
SNc
SNr
d DLS dSPNterm stimulation
light
ctrl
Normalized distance
Time (s)
Speed, light (cm/s)
Speed, pre (cm/s)
eYFP
ChR2
pre
light
PV+ silenced
Npas1+ silenced
e Motor effects
Fold change
Npas1+ silenced
PV+ silenced
GPe
50 µm
TeTLC | Npas1+
DLSsoma
DLSterm
DMSterm
ChR2-eYFP
eYFP
TeTLC
stimulation site
opsin, fp
silencing

Figure 4

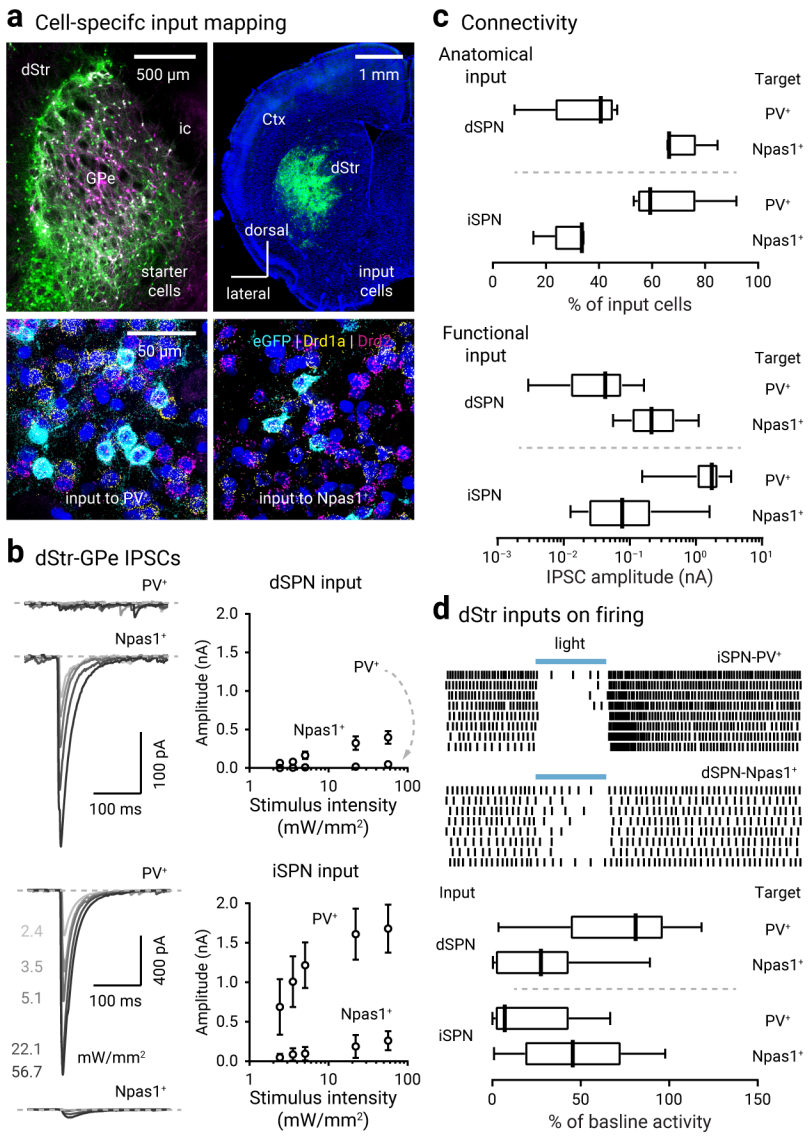
a Cell-specifc input mapping
dStr
500 µm
ic
GPe
starter cells
1 mm
Ctx
dStr
dorsal
lateral
input cells
50 µm
input to PV+
eGFP | Drd1a | Drd2
input to Npas1+
b dStr-GPe IPSCs
PV+
Npas1+
100 pA
100 ms
dSPN input
Amplitude (nA)
Stimulus intensity (mW/mm2)
2.4
3.5
5.1
22.1
56.7
mW/mm2
400 pA
iSPN input
c Connectivity
Anatomical input
Target
dSPN
iSPN
% of input cells
Functional input
IPSC amplitude (nA)
d dStr inputs on firing
light
iSPN-PV+
dSPN-Npas1+
Input
% of basline activity

Figure 5

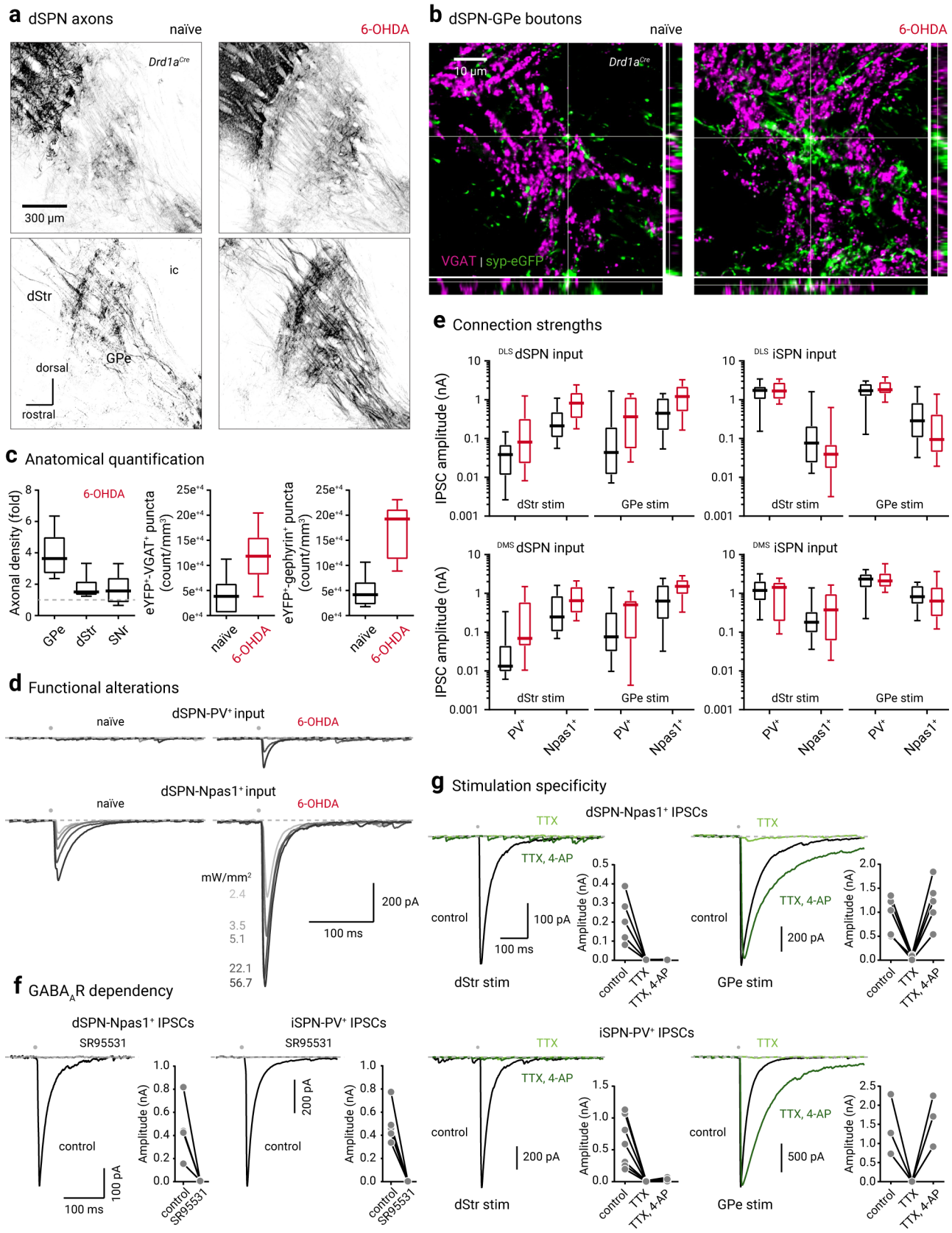
a dSPN axons
naïve
6-OHDA
Drd1a^Cre
300 µm
ic
dStr
GPe
dorsal
rostral
b dSPN-GPe boutons
naïve
6-OHDA
10 µm
Drd1a^Cre
VGAT | syp-eGFP
c Anatomical quantification
6-OHDA
Axonal density (fold)
GPe
dStr
SNr
eYFP+-VGAT+ puncta (count/mm3)
eYFP+-gephyrin+ puncta (count/mm3)
naïve
6-OHDA
d Functional alterations
naïve
dSPN-PV+ input
6-OHDA
naïve
dSPN-Npas1+ input
6-OHDA
mW/mm2
2.4
3.5
5.1
22.1
56.7
200 pA
100 ms
e Connection strengths
DLS dSPN input
DLS iSPN input
DMS dSPN input
DMS iSPN input
IPSC amplitude (nA)
dStr stim
GPe stim
PV+
Npas1+
f GABAAR dependency
dSPN-Npas1+ IPSCs
SR95531
control
100 pA
100 ms
Amplitude (nA)
control
SR95531
iSPN-PV+ IPSCs
SR95531
200 pA
control
Amplitude (nA)
control
SR95531
g Stimulation specificity
dSPN-Npas1+ IPSCs
TTX
TTX, 4-AP
control
100 pA
100 ms
dStr stim
Amplitude (nA)
control
TTX
TTX, 4-AP
TTX
TTX, 4-AP
control
200 pA
GPe stim
Amplitude (nA)
control
TTX
TTX, 4-AP
iSPN-PV+ IPSCs
TTX
TTX, 4-AP
control
200 pA
dStr stim
Amplitude (nA)
control
TTX
TTX, 4-AP
TTX
TTX, 4-AP
control
500 pA
GPe stim
Amplitude (nA)
control
TTX
TTX, 4-AP

Figure 6

Table 1. Primary antibodies used in this study.

Antigen	Host species [a]	Clonality	Source	Catalog #	Working concentration	Dilution
Cre	Gp	Polyclonal	Synaptic Systems	257004		1:2,000
RFP	Rb	Polyclonal	Clontech	632496	1 μg/ml	1:500
Enkephalin	Rb	Polyclonal	Immunostar	20065		1:200
Gephyrin	Ms	Monoclonal	Synaptic Systems	147011	2 μg/ml	1:500
GFP	Ck	Polyclonal	Abcam	ab13970	10 μg/ml	1:1,000
Npas1	Gp	Polyclonal	Chan Laboratory (Hernandez et al., 2015)			1:5,000
Substance P	Rt	Monoclonal	Abcam	ab7340		1:200
Substance P	Gp	Polyclonal	Abcam	ab10353		1:200
tdTomato	Rt	Monoclonal	Kerafast	EST203	3.5 μg/ml	1:500
VGAT	Gp	Polyclonal	Synaptic Systems	131004		1:500

Notes:
[a] Abbreviations: chicken (Ck), guinea pig (Gp), mouse (Ms), rabbit (Rb), and rat (Rt).

Table 2. Summary of optogenetic effects on behavior metrics.

	^{DMS}dSPNs, ChR2 (n = 9)				^{DMS}iSPNs, ChR2 (n = 11)			
	Pre	Light	Fold change	*P* value [c]	Pre	Light	Fold change	*P* value
Speed (cm/s)	2.43 ± 0.60	4.12 ± 0.56	1.90 ± 0.25	**0.0039**	2.47 ± 0.43	1.23 ± 0.19	0.52 ± 0.09	**0.00098**
Body length-width ratio	2.34 ± 0.13	2.75 ± 0.15	1.14 ± 0.11	**0.0039**	2.32 ± 0.19	2.16 ± 0.12	0.97 ± 0.04	0.083
Total frequency [a]	35.33 ± 3.43	24.30 ± 8.03	0.76 ± 0.16	**0.0039**	36.40 ± 3.30	38.70 ± 2.70	1.12 ± 0.09	0.31
Locomotion frequency	13.20 ± 0.66	11.70 ± 2.63	0.91 ± 0.18	0.20	14.60 ± 0.80	13.30 ± 0.55	0.90 ± 0.04	**0.0098**
Fine movement frequency	15.44 ± 2.24	10.10 ± 4.57	0.82 ± 0.14	**0.0039**	15.00 ± 0.75	15.70 ± 1.70	1.04 ± 0.08	0.81
Rearing frequency	1.40 ± 0.70	1.10 ± 0.70	0.97 ± 0.32	0.97	1.10 ± 0.30	0.30 ± 0.20	0.29 ± 0.11	**0.00098**
Motionless frequency	5.40 ± 1.60	1.50 ± 1.10	0.33 ± 0.14	**0.0039**	5.00 ± 1.29	10.50 ± 1.75	1.88 ± 0.34	**0.00098**
Locomotion % time	42.80 ± 3.70	59.90 ± 6.10	1.37 ± 0.12	**0.0039**	49.60 ± 4.90	32.50 ± 4.80	0.66 ± 0.10	**0.0029**
Fine movement % time	26.78 ± 3.92	16.80 ± 7.87	0.79 ± 0.13	**0.0039**	28.93 ± 3.07	27.90 ± 5.60	1.03 ± 0.08	0.64
Rearing % time	15.70 ± 6.70	13.40 ± 8.40	1.11 ± 0.57	0.65	12.60 ± 5.90	3.70 ± 3.40	0.39 ± 0.18	**0.00098**
Motionless % time	10.20 ± 2.60	1.80 ± 1.65	0.18 ± 0.10	**0.0039**	12.50 ± 1.00	32.30 ± 5.40	2.84 ± 0.34	**0.00098**
Locomotion duration [b]	0.34 ± 0.03	0.60 ± 0.14	1.70 ± 0.41	**0.0039**	0.34 ± 0.05	0.34 ± 0.07	0.95 ± 0.23	0.21
Fine movement duration	0.18 ± 0.01	0.16 ± 0.01	0.93 ± 0.07	**0.027**	0.18 ± 0.01	0.17 ± 0.01	0.94 ± 0.05	**0.019**
Rearing duration	1.16 ± 0.07	1.01 ± 0.30	0.84 ± 0.29	0.82	0.96 ± 0.11	0.88 ± 0.35	1.28 ± 0.56	0.43
Motionless duration	0.20 ± 0.13	0.11 ± 0.01	0.61 ± 0.08	**0.0039**	0.19 ± 0.03	0.30 ± 0.07	1.67 ± 0.32	**0.0020**
Locomotion-fine movement frequency	10.70 ± 9.73	9.30 ± 8.33	1.01 ± 0.24	0.50	11.79 ± 11.24	9.10 ± 8.38	0.72 ± 0.13	**0.0020**
Locomotion-rearing frequency	1.50 ± 0.28	1.58 ± 0.18	1.14 ± 0.13	0.31	1.43 ± 0.32	1.00 ± 0.00	0.57 ± 0.29	**0.031**
Locomotion-motionless frequency	2.00 ± 0.43	1.20 ± 0.20	0.77 ± 0.06	**0.0039**	2.09 ± 0.42	2.89 ± 0.51	1.38 ± 0.35	**0.0088**
Fine movement-locomotion frequency	10.22 ± 0.63	9.20 ± 3.24	1.02 ± 0.30	0.48	11.70 ± 0.77	9.40 ± 2.65	0.80 ± 0.12	**0.0020**
Fine movement-rearing frequency	1.00 ± 0.17	1.00 ± 0.00	0.86 ± 0.46	0.44	1.00 ± 0.00	0.00 ± 0.00	0.00 ± 0.00	> 0.99
Fine movement-motionless frequency	3.67 ± 1.13	2.00 ± 0.90	0.45 ± 0.11	**0.0039**	4.13 ± 0.75	6.75 ± 1.00	1.56 ± 0.36	**0.00098**
Rearing-locomotion frequency	1.67 ± 0.33	1.43 ± 0.29	1.07 ± 0.18	0.81	1.50 ± 0.13	1.00 ± 0.00	0.67 ± 0.17	**0.0078**
Rearing-fine movement frequency	1.00 ± 0.00	1.00 ± 0.00	1.00 ± 0.14	0.63	1.00 ± 0.33	1.00 ± 0.00	1.00 ± 0.33	> 0.99
Motionless-locomotion frequency	2.17 ± 0.37	1.40 ± 0.40	0.71 ± 0.07	**0.0078**	2.17 ± 0.29	2.60 ± 0.35	1.42 ± 0.27	**0.0059**
Motionless-fine movement frequency	4.13 ± 1.03	1.75 ± 0.75	0.43 ± 0.11	**0.0039**	4.67 ± 1.17	6.29 ± 1.17	1.67 ± 0.35	**0.00098**

	^{DLS}dSPNs, ChR2 (n = 13)				^{DLS}iSPNs, ChR2 (n = 15)			
	Pre	Light	Fold change	*P* value	Pre	Light	Fold change	*P* value
Speed (cm/s)	3.04 ± 0.92	1.32 ± 0.44	0.59 ± 0.34	**0.0061**	2.75 ± 0.32	3.80 ± 0.65	1.35 ± 0.30	**0.0012**
Body length-width ratio	2.54 ± 0.14	2.46 ± 0.12	1.01 ± 0.06	0.84	2.39 ± 0.15	2.52 ± 0.11	1.06 ± 0.06	**0.035**
Total frequency	32.20 ± 6.40	37.80 ± 5.33	1.13 ± 0.15	0.057	35.20 ± 3.87	27.85 ± 3.25	0.85 ± 0.12	**0.0081**
Locomotion frequency	13.25 ± 1.42	15.53 ± 1.55	1.17 ± 0.11	**0.0024**	14.17 ± 2.28	10.22 ± 0.81	0.72 ± 0.11	**0.00085**
Fine movement frequency	13.92 ± 2.88	16.70 ± 2.10	1.18 ± 0.20	**0.017**	14.31 ± 1.61	11.15 ± 1.60	0.80 ± 0.12	**0.00085**
Rearing frequency	1.40 ± 0.32	0.70 ± 0.37	0.50 ± 0.31	**0.0081**	1.80 ± 0.45	1.17 ± 0.61	0.90 ± 0.43	0.61
Motionless frequency	3.70 ± 1.40	4.50 ± 0.75	1.16 ± 0.45	0.72	3.07 ± 0.90	5.62 ± 1.85	1.45 ± 0.55	**0.027**
Locomotion % time	48.40 ± 7.47	45.00 ± 5.00	1.03 ± 0.13	0.84	49.43 ± 4.07	49.92 ± 9.12	0.99 ± 0.16	0.92
Fine movement % time	24.83 ± 6.42	32.30 ± 8.40	1.17 ± 0.24	**0.021**	26.38 ± 4.62	18.77 ± 3.21	0.75 ± 0.08	**0.00085**
Rearing % time	17.30 ± 4.01	10.75 ± 6.55	0.78 ± 0.26	0.057	17.10 ± 7.56	11.77 ± 6.19	0.96 ± 0.53	0.36
Motionless % time	6.08 ± 3.42	6.70 ± 1.60	0.90 ± 0.51	0.49	4.79 ± 1.37	12.38 ± 8.28	2.01 ± 1.10	**0.0051**
Locomotion duration	0.38 ± 0.08	0.32 ± 0.07	0.86 ± 0.20	0.13	0.38 ± 0.05	0.51 ± 0.10	1.18 ± 0.20	**0.00031**
Fine movement duration	0.17 ± 0.01	0.18 ± 0.01	1.02 ± 0.10	0.22	0.17 ± 0.01	0.16 ± 0.01	0.91 ± 0.06	0.095
Rearing duration	1.21 ± 0.11	1.48 ± 0.28	1.10 ± 0.22	0.11	1.03 ± 0.23	0.98 ± 0.18	0.90 ± 0.32	0.22
Motionless duration	0.18 ± 0.02	0.13 ± 0.01	0.73 ± 0.14	**0.00073**	0.15 ± 0.02	0.24 ± 0.07	1.42 ± 0.43	**0.0026**
Locomotion-fine movement frequency	10.80 ± 9.72	12.58 ± 11.46	1.26 ± 0.11	**0.00098**	11.70 ± 10.96	6.46 ± 5.93	0.62 ± 0.12	**0.00043**
Locomotion-rearing frequency	1.50 ± 0.20	1.40 ± 0.40	0.97 ± 0.17	0.75	1.43 ± 0.26	1.33 ± 0.33	1.00 ± 0.25	0.81
Locomotion-motionless frequency	1.70 ± 0.27	2.14 ± 0.46	1.25 ± 0.31	0.13	2.00 ± 0.33	2.08 ± 0.50	1.08 ± 0.25	0.22
Fine movement-locomotion frequency	10.60 ± 1.15	12.90 ± 1.33	1.28 ± 0.17	**0.00024**	11.64 ± 1.94	6.38 ± 1.08	0.62 ± 0.12	**0.00037**
Fine movement-rearing frequency	1.00 ± 0.00	1.00 ± 0.00	0.88 ± 0.21	0.88	1.33 ± 0.33	1.00 ± 0.25	0.77 ± 0.23	0.07
Fine movement-motionless frequency	3.63 ± 1.10	4.00 ± 1.00	1.03 ± 0.41	0.79	2.80 ± 0.63	3.45 ± 1.31	1.42 ± 0.35	**0.035**
Rearing-locomotion frequency	1.33 ± 0.17	1.00 ± 0.00	0.89 ± 0.14	0.12	1.50 ± 0.35	1.43 ± 0.24	1.00 ± 0.25	0.78
Rearing-fine movement frequency	1.00 ± 0.00	1.00 ± 0.00	1.00 ± 0.20	0.81	1.00 ± 0.00	1.00 ± 0.00	1.00 ± 0.06	0.88
Motionless-locomotion frequency	2.15 ± 0.35	2.20 ± 0.20	1.04 ± 0.25	0.64	1.86 ± 0.36	2.00 ± 0.50	1.11 ± 0.16	0.2
Motionless-fine movement frequency	3.20 ± 0.76	4.38 ± 0.88	1.36 ± 0.68	0.3	2.75 ± 0.58	3.36 ± 1.30	1.39 ± 0.50	0.12

Notes:
[a] Unit for all frequencies is count/10 s.
[b] Unit for all durations is seconds.
[c] Wilcoxon test; two-tailed exact *P* values are shown. $P < 0.05$ are shown in bold.

Table 3. Input-output relationship of DLS inputs in naïve and 6-OHDA lesioned mice.

Input & stimulus location	Stimulus intensity (mW/mm^2)	IPSC peak amplitude (pA)								Statistical analyses [b]			
		naïve PV$^+$		naïve Npas1$^+$		6-OHDA PV$^+$		6-OHDA Npas1$^+$		naïve PV$^+$ vs naïve Npas1$^+$	naïve PV$^+$ vs 6-OHDA PV$^+$	naïve Npas1$^+$ vs 6-OHDA Npas1$^+$	6-OHDA PV$^+$ vs 6-OHDA Npas1$^+$
		Median ± MAD	*n*[a]	Median ± MAD	*n*	Median ± MAD	*n*	Median ± MAD	*n*				
dSPN, dStr	2.4	0.0 ± 0.0	4	22.7 ± 22.7	11	2.0 ± 2.0	10	324.2 ± 290.8	11	0.078	0.27	**0.0052**	**0.0046**
	3.5	2.1 ± 2.1	5	33.7 ± 33.7	12	5.6 ± 5.6	12	271.1 ± 255.5	12	0.076	0.48	**0.0044**	**0.0035**
	5.1	8.1 ± 6.2	6	79.1 ± 59.5	17	10.5 ± 10.5	13	375.5 ± 305.5	13	**0.00014**	0.62	**0.017**	**0.0050**
	22.1	7.7 ± 3.5	8	158.3 ± 125.0	18	55.4 ± 54.1	13	866.3 ± 537.5	13	**< 0.0001**	**0.037**	**0.0095**	**0.0051**
	56.7	38.5 ± 29.3	8	213.8 ± 122.0	28	81.0 ± 76.7	13	815.8 ± 530.5	15	**0.00011**	0.14	**0.0017**	**0.0015**
dSPN, GPe	2.1	15.7 ± 12.6	12	182.7 ± 170.1	20	120.0 ± 102.1	11	527.7 ± 447.2	23	**0.012**	0.051	**0.039**	**0.042**
	3.5	43.9 ± 36.3	12	448.4 ± 371.0	20	364.7 ± 310.1	11	1,208.7 ± 818.2	23	**0.0031**	**0.044**	**0.013**	**0.0075**
iSPN, dStr	2.4	295.0 ± 253.8	6	0.0 ± 0.0	13	578.9 ± 503.9	10	4.3 ± 4.3	6	**0.00085**	0.79	0.34	**0.023**
	3.5	761.7 ± 439.2	8	0.0 ± 0.0	14	819.5 ± 667.0	13	17.1 ± 17.1	7	**0.00041**	0.86	0.32	**0.0011**
	5.1	969.2 ± 546.4	10	8.6 ± 7.7	15	891.6 ± 544.2	14	12.7 ± 5.6	8	**0.00022**	0.71	0.40	**0.00028**
	22.1	1,593.1 ± 682.9	11	30.0 ± 23.1	14	1,355.1 ± 713.5	16	29.8 ± 19.2	10	**0.00052**	0.75	0.80	**< 0.0001**
	56.7	1,740.7 ± 627.7	12	76.9 ± 60.9	20	1,682.0 ± 820.4	18	39.2 ± 22.2	11	**< 0.0001**	0.75	0.36	**< 0.0001**
iSPN, GPe	2.1	1,495.6 ± 440.9	16	103.4 ± 74.6	16	1,705.2 ± 480.2	16	57.8 ± 43.9	15	**0.0034**	0.24	0.13	**< 0.0001**
	3.5	1,715.2 ± 691.9	16	288.0 ± 212.9	17	1,806.1 ± 689.2	16	94.5 ± 84.0	15	**0.0016**	0.36	0.19	**< 0.0001**

Notes:

[a] Sample size (*n*) only included cells that responded to maximal stimulus intensity.

[b] Mann-Whitney *U* test; two-tailed exact *P* values were shown. $P < 0.05$ were shown in bold.

Table 4. Input-output relationship of DMS inputs in naïve and 6-OHDA lesioned mice.

Input & stimulus location	Stimulus intensity (mW/mm^2)	IPSC peak amplitude (pA)								Statistical analyses [b]			
		naïve PV$^+$		naïve Npas1$^+$		6-OHDA PV$^+$		6-OHDA Npas1$^+$		naïve PV$^+$ vs naïve Npas1$^+$	naïve PV$^+$ vs 6-OHDA PV$^+$	naïve Npas1$^+$ vs 6-OHDA Npas1$^+$	6-OHDA PV$^+$ vs 6-OHDA Npas1$^+$
		Median ± MAD	*n*[a]	Median ± MAD	*n*	Median ± MAD	*n*	Median ± MAD	*n*				
dSPN, dStr	2.4	8.5 ± 8.5	8	16.2 ± 16.2	15	16.3 ± 16.3	14	109.5 ± 107.4	20	0.17	0.53	0.23	**0.012**
	3.5	3.8 ± 3.8	7	17.3 ± 17.3	18	37.1 ± 32.8	14	88.6 ± 84.9	21	0.18	0.22	0.068	**0.047**
	5.1	5.9 ± 4.6	12	48.7 ± 46.2	18	35.4 ± 28.7	15	144.3 ± 124.7	27	**0.021**	**0.046**	0.052	**0.0019**
	22.1	11.2 ± 7.7	14	123.0 ± 91.2	22	87.7 ± 74.2	15	498.5 ± 289.9	27	**0.00051**	**0.0079**	**0.0019**	**0.00053**
	56.7	13.3 ± 6.5	16	246.2 ± 156.7	23	69.1 ± 56.0	16	649.7 ± 396.5	27	**< 0.0001**	**0.0085**	**0.0093**	**0.00044**
dSPN, GPe	2.1	33.8 ± 28.2	17	469.5 ± 334.9	21	272.2 ± 261.7	19	1,138.4 ± 664.5	27	**0.0013**	0.17	**0.030**	**< 0.0001**
	3.5	75.7 ± 64.7	17	635.6 ± 551.0	19	507.1 ± 384.7	17	1,518.0 ± 685.4	24	**0.0048**	0.25	**0.033**	**< 0.0001**
iSPN, dStr	2.4	14.5 ± 13.2	19	23.5 ± 23.5	19	31.3 ± 29.3	11	28.5 ± 28.3	16	0.74	0.66	0.68	0.58
	3.5	11.9 ± 11.4	22	34.2 ± 31.8	20	236.5 ± 216.5	18	31.6 ± 31.6	19	0.76	**0.011**	0.88	**0.031**
	5.1	43.4 ± 39.6	22	36.6 ± 35.2	20	282.0 ± 271.5	22	62.7 ± 42.9	17	0.42	0.16	0.56	0.11
	22.1	674.9 ± 548.4	25	136.1 ± 95.6	23	1,009.3 ± 864.9	24	193.7 ± 172.0	19	**0.016**	0.41	0.35	**0.038**
	56.7	1,191.7 ± 640.5	25	179.8 ± 89.5	24	1,433.9 ± 890.2	25	376.5 ± 339.4	20	**< 0.0001**	0.51	0.52	**0.021**
iSPN, GPe	2.1	2,185.5 ± 819.1	40	625.0 ± 459.1	24	1,889.3 ± 999.3	25	506.5 ± 410.5	19	**< 0.0001**	0.84	0.78	**0.0011**
	3.5	2,340.6 ± 849.7	41	823.0 ± 442.4	25	2,098.5 ± 727.5	25	635.5 ± 417.9	17	**< 0.0001**	0.83	0.46	**0.00025**

Notes:

[a] Sample size (*n*) only included cells that responded to maximal stimulus intensity.

[b] Mann-Whitney *U* test; two-tailed exact *P* values were shown. $P < 0.05$ were shown in bold.

Table 5. Response rate to discrete dStr inputs in naïve and 6-OHDA lesioned mice.

Input	Stimulus location	Stimulus intensity (mW/mm^2)	Percentage of responders (%)								Statistical analyses [b]			
			naïve PV^+		naïve $Npas1^+$		6-OHDA PV^+		6-OHDA $Npas1^+$		naïve PV^+ vs naïve $Npas1^+$	naïve PV^+ vs 6-OHDA PV^+	naïve $Npas1^+$ vs 6-OHDA $Npas1^+$	6-OHDA PV^+ vs 6-OHDA $Npas1^+$
			%	*n*[a]	%	*n*	%	*n*	%	*n*				
^{DLS}dSPN	dStr	56.7	44.4	18	93.8	32	86.7	15	100	15	**0.00019**	**0.027**	> 0.99	0.48
	GPe	3.5	70.6	17	95.2	21	91.7	12	100	18	0.071	0.35	> 0.99	0.40
^{DLS}iSPN	dStr	56.7	92.9	14	90.9	22	100	18	68.8	16	> 0.99	0.44	0.11	**0.016**
	GPe	3.5	100	9	94.4	18	100	16	100	15	> 0.99	> 0.99	> 0.99	> 0.99
^{DMS}dSPN	dStr	56.7	76.2	21	100	24	61.5	26	100	30	**0.017**	0.35	> 0.99	**0.00015**
	GPe	3.5	94.4	18	100	21	95	20	100	28	0.46	> 0.99	> 0.99	0.42
^{DMS}iSPN	dStr	56.7	100	25	89.7	29	100	26	96.2	26	0.24	> 0.99	0.61	> 0.99
	GPe	3.5	100	41	100	25	100	25	100	19	> 0.99	> 0.99	> 0.99	> 0.99

Notes:

[a] Sample size (*n*) included all cells with or without responses.

[b] Fisher's exact test; two-tailed exact *P* values were shown. $P < 0.05$ were shown in bold.