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Reduced Vglut2/Slc17a6 gene expression levels throughout the mouse subthalamic nucleus cause cell loss and structural disorganization followed by increased motor activity and decreased sugar consumption

STN Vglut2 reduction perturbs movement and reward

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1 **Reduced *Vglut2/Slc17a6* gene expression levels throughout the mouse subthalamic**
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3 **activity and decreased sugar consumption**

4 *Abbreviated title: STN Vglut2 reduction perturbs movement and reward*

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35 The authors declare no competing interests. Sylvie Dumas is the owner of Oramacell, Paris,
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46

47 **Abstract**

48 The subthalamic nucleus (STN) plays a central role in motor, cognitive and affective
49 behavior. Deep brain stimulation (DBS) of the STN is the most common surgical intervention
50 of advanced Parkinson's disease (PD) and STN has lately gained attention as target for DBS
51 in neuropsychiatric disorders, including obsessive compulsive disorder, eating disorders and
52 addiction. Animal studies using either STN-DBS, lesioning or inactivation of STN neurons
53 have been used extensively alongside clinical studies to unravel the structural organization,
54 circuitry and function of the STN. Recent studies in rodent STN models have exposed
55 different roles for STN neurons in reward-related functions. We have previously shown that
56 the majority of STN neurons express the *Vesicular glutamate transporter 2 (Vglut2/Slc17a6)*
57 gene and that reduction of Vglut2 mRNA levels within the STN of mice (cKO) causes
58 reduced post-synaptic activity and behavioral hyperlocomotion. The cKO mice showed less
59 interest in fatty rewards, which motivated analysis of reward-response. The current results
60 demonstrate decreased sugar consumption and strong rearing behavior while biochemical
61 analyses show altered dopaminergic and peptidergic activity in the striatum. The behavioral
62 alterations were in fact correlated with opposite effects in the dorsal versus the ventral
63 striatum. Significant cell loss and disorganization of the STN structure was identified which
64 likely accounts for the observed alterations. Rare genetic variants of the human VGLUT2
65 gene exist and this study shows that reduced *Vglut2/Slc17a6* gene expression levels
66 exclusively within the STN of mice is sufficient to cause strong modifications in both the
67 STN and in the mesostriatal dopamine system.

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71 **Significance Statement**

72 The STN is the most commonly used target in deep brain stimulation of advanced
73 Parkinson's disease and it has recently been implicated in the reward circuit. VGLUT2 is the
74 main vesicular transporter of glutamate in STN neurons and rare genetic variants of the
75 VGLUT2 gene exist in human individuals. Blunting *Vglut2/Slc17a6* gene expression levels
76 throughout the extent of the mouse STN caused substantial cell loss in the STN, similar as
77 observed in pharmacological lesion models. Mice became hyperactive but showed reduced
78 sugar consumption. Opposite effects on motor versus reward behavior was correlated with
79 opposite activity of dopamine parameters in the dorsal versus the ventral striatal system. This
80 study thereby identifies an interaction between the STN and the dopamine reinforcement
81 system.

82 **Introduction**

83 The subthalamic nucleus (STN) is an excitatory structure which via extensive
84 glutamatergic projections plays a central role in motor, limbic and cognitive functions.
85 Dysregulated excitatory output from the STN can be normalized by high frequency deep brain
86 stimulation (DBS). Clinically, STN-DBS is implemented routinely for alleviation of motor
87 dysfunction in in patients suffering from advanced Parkinson's disease (PD) (Benabid et al.,
88 2009), and based on its role in limbic and cognitive functions, the STN has been proposed as
89 a putative target also in DBS approaches to treat various neuropsychiatric disorders (Williams
90 et al., 2010; Chabardès et al., 2013). In fact, STN-DBS has been tested already with positive
91 outcome in severe obsessive compulsive disorder (OCD) (Mallet et al., 2008; Blomstedt et al.,
92 2013).

93 In parallel to clinical studies of the STN, experimental animals have been used extensively
94 to unravel the structural organization and circuitry of the STN as well as functional outcome
95 upon STN intervention (Temel et al., 2005a; Baunez and Gubellini, 2010). In addition to
96 STN-DBS experiments in animals, other models implement pharmacological lesioning or
97 inactivation to disturb STN function (Temel et al., 2005a; Pratt et al., 2012). Recently, a series
98 of studies in rodent STN models have implicated the STN in the brain reward circuit
99 alongside the classical mesoaccumbal reward pathway (Breyse et al., 2015). First,
100 implementation of STN-DBS and STN-lesioning were shown to elevate the motivation for
101 food while reducing the motivation for cocaine (Baunez et al., 2002, 2005; Bezzina et al.,
102 2008; Rouaud et al., 2010). Second, the presentation of either a positive (rewarding) or
103 negative (aversive) stimulus, or to cues conditioned to either stimulus, altered the firing
104 pattern of neurons within the STN (Darbaky et al., 2005; Lardeux et al., 2009; Espinosa-
105 Parrilla et al., 2013; Breyse et al., 2015). Third, while the question of the structural
106 organization of the STN is the focus of debate between those favoring the hypothesis of the

107 STN as a tripartite structure and those favoring an STN organization without strict anatomical
108 boundaries (Temel et al., 2005b; Benarroch, 2008; Keuken et al., 2012; Alkemade and
109 Forstmann, 2014), some recent studies have focused on identifying subpopulations of STN
110 neurons. By electrophysiological profiling in rodents, distinct STN subpopulations were
111 found that adapted their responses when the rewarding substance sucrose was exchanged for
112 water (Lardeux et al., 2009, 2013) or an aversive substance, such as quinine (Breyse et al.,
113 2015).

114 Thus, by adapting to various reward-related contexts, STN neurons form a cerebral hub
115 which participates in even more aspects of motor, limbic and cognitive functions than
116 previously thought. Similar to the etiology of PD, to which aberrant STN activity is believed
117 to contribute (Rodriguez et al., 1998; Olanow and Tatton, 1999), dysfunctional STN activity
118 may therefore contribute to reward dysfunction in patients. Clinically, a putative role in
119 reward-related behavior is manifested by the recent proposals of the STN as a DBS-target for
120 treatment of addiction, eating disorders and obesity (Pelloux and Baunez, 2013; Val-Laillet et
121 al., 2015).

122 The multitude of roles ascribed to the STN further strengthens the case for solving how
123 this compact nucleus is organized to encompass such a high level of complexity. Based on the
124 excitatory nature of the STN, we recently addressed expression of the genes encoding the
125 three different Vesicular glutamate transporters (VGLUT1-3) in mice (Takamori, 2006;
126 Liguz-Leczna and Skangiel-Kramska, 2007) and could show that the vast majority of STN
127 neurons express only the *Vglut2/Slc17a6* gene (Schweizer et al., 2014). While a full knockout
128 of the *Vglut2/Slc17a6* gene was previously demonstrated as lethal (Moechars et al., 2006;
129 Wallén-Mackenzie et al., 2006), some rare genetic variants of the human VGLUT2/SLC17A6
130 gene have been identified in schizophrenia and severe alcoholism (Flatscher-Bader et al.,
131 2008; Shen et al., 2010; Comasco et al., 2014). By implementing conditional targeting of the

132 *Vglut2/Slc17a6* gene in mice using the *Paired-like homeodomain 2 (Pitx2)-Cre*-driver to
133 direct the targeting to the STN (Skidmore et al., 2008), *Vglut2* mRNA levels were reduced by
134 40% exclusively within the STN structure (Schweizer et al., 2014). This reduction was shown
135 to result in decreased post-synaptic excitatory activity in STN target neurons followed
136 through by strong behavioral hyperactivity, including decreased latency to movement
137 (Schweizer et al., 2014). Despite hyperactivity, these STN-targeted mice did not perform
138 poorer in reward-baited memory and impulsivity tests but did take longer to collect the
139 rewards. This finding led us to here address the hypothesis that the *Pitx2/Vglut2* co-expressing
140 subpopulation of STN neurons is important for regulation of both motor activity and reward-
141 related behavior.

142 **Materials and Methods**

143 *Ethical statement*

144 All mice used in the study were housed and produced as previously described (Schweizer
145 et al., 2014) in accordance with the Swedish regulation guidelines (Animal Welfare Act SFS
146 1998:56) and European Union legislation (Convention ETS123 and Directive 2010/63/EU).
147 Ethical approval was obtained from the Uppsala Animal Ethical Committee.

148 The $Vglut2^{ff;Pitx2-Cre}$ mouse line was produced by breeding $Pitx2-Cre$ male mice
149 (Skidmore et al., 2008) to floxed $Vglut2^{ff}$ females (Wallén-Mackenzie et al., 2006) to
150 generate $Vglut2^{ff/wt;Pitx2-Cre+}$ male mice which in turn were bred to $Vglut2^{ff}$ females to
151 generate cKO ($Vglut2^{ff;Pitx2-Cre+}$) and control ($Vglut2^{ff;Pitx2-Cre-}$) mice. This allows for
152 behavioral phenotyping and comparison between genotype groups due to identical genetic
153 background (Crusio, 2004). Control $Vglut2^{wt/wt;Pitx2-Cre+}$ animals were used in the tracing
154 experiment. All mice were kept on a hybrid background of C57BL/6J and Sv129.

155 *Operant self-administration of sucrose*

156 23 adult mice (13 males, of which cKO, n=7; Ctrl, n=6; 10 females, of which cKO, n=5;
157 Ctrl, n=5) were used to analyze the behavioral response to sugar in an operant self-
158 administration setup (Med Associates, USA) (Skinner, 1966; Sanchis-Segura and Spanagel,
159 2006). Source data for this experiment, summarized in Figure 2 is available at:
160 <http://goo.gl/sllH4u>. An outline of the experiment is shown in **Fig. 2A**, and an illustration of the
161 operant chamber in **Fig. 2B**. Two days prior and throughout the trial, the mice were under mild
162 food-restriction [3 grams standard rodent chow (R3; Lactamin/Lantmännen, Sweden) per
163 mouse per day] and thereafter weighed throughout the entire course of the experiment. Water
164 was accessible *ad libitum*. The mice were allowed to habituate to the novel environment for 1
165 session before begin of training and each mouse underwent one operant session per day. The
166 mice were then trained to enter their head into a feeder equipped with a food receptacle and

167 a photo beam sensor to obtain a 20 mg sucrose pellet (5TUL TestDiet). Each pellet delivery
168 was followed by a 10 s time-out period, in which head entries were registered, but no pellet
169 could be obtained. Training (acquisition of the operant task) was performed on a fixed ratio
170 (FR) 1 schedule (1 pellet / head entry, maximum 30 pellets). While a house-light was
171 continuously on, a cue-light was only lit upon head entry into the feeder giving sugar, which also
172 led to the presentation of a sound cue (*Fig. 2B, left*). Head entry into an inactive feeder did not
173 result in cue or sugar presentation (*Fig. 2B, right*). During the timeout period, no cue-light or
174 sound cue was presented. FR1 training was followed by 3 days of testing on FR1 and then on
175 FR5 to assess consummatory behavior. Before advancing the mice to an FR5 schedule (1
176 pellet / 5 head entries), they were given one training day at FR2 to adjust to a task requiring
177 multiple head entries. The mice were assessed in an FR5 schedule for 5 days, after which
178 motivation to work for the sugar pellets was measured on a progressive ratio (PR) schedule
179 during which the amount of head entries required to obtain a pellet was successively increased
180 by 3 per successful action. After this followed extinction, reinstatement and reversal of active
181 and inactive feeders to assess for task learning and cognitive flexibility.

182 During all trial days, the mice were left in the self-administration chambers until 30 sugar
183 pellets were obtained (FR1, FR2, reinstatement and reversal) or until trial time ended
184 (FR5, PR and extinction). Trial time was limited to 30 minutes for FR1, FR2,
185 reinstatement, extinction and reversal; to 40 minutes for FR5; to 90 minutes for PR, the
186 maximum time possible for all animals to complete the PR task during the light-cycle of the
187 day. Statistical analysis was performed in GraphPad Prism 6 using repeated measures
188 analysis of variance (ANOVA) and Bonferroni post-hoc test (GraphPad Software, USA).
189 A p-value equal to or less than 0.05 was considered significant (* $p \leq 0.05$, ** $p \leq 0.01$,
190 *** $p \leq 0.001$, **** $p \leq 0.0001$).

191

192 *Analysis of rearing behavior*

193 31 adult mice (cKO n=14, Ctrl n=17) were each placed in the center of a square plexiglas
194 arena (55x55x22cm) and allowed to freely explore for 15 minutes. The mice were video-
195 recorded; behavioral parameters were scored manually by an observer blind to the genotype
196 of the mouse and the duration of each rearing type was analyzed using AniTracker Software.
197 Rearing behavior was subdivided into three different types: Wall rearing, defined as an
198 upright position with the fore-paws touching a vertical surface (*Fig. 4A, left*); seated rearing
199 defined by a half-standing position using the tail for support (*Fig. 4B, left*); and free rearing,
200 in which the mouse supports its weight freely on its hind legs without using its tail or fore
201 paws (*Fig. 4C, left*), similar as previously described by (Waddington et al., 2001). Data was
202 analyzed using Mann-Whitney U-test (GraphPad Prism, GraphPad Software, USA). A p-value
203 equal to or less than 0.05 was considered significant (*p≤0.05, **p≤0.01, ***p≤0.001,
204 ****p≤0.0001).

205 *Dopamine receptors and transporters binding assay*

206 Brains of cKO and control mice (cKO, n=7; Ctrl, n=7) were rapidly removed from the
207 skull upon cervical dislocation, cryosectioned and processed for DA receptor and transporter
208 autoradiography, as previously described (Mahmoudi et al., 2014; Schweizer et al., 2014).
209 For DA D1 receptor (D1R) binding, the [³H]SCH23390 ligand was used. For the DA D2
210 receptor (D2R) and D3 receptor (D3R) subtypes, [¹²⁵I]iodosulpride and [¹²⁵I]7-OH-PIPAT
211 ligands were used, respectively. [¹²⁵I]RTI-121 binding was used to measure dopamine
212 transporter (DAT) density. Mann-Whitney U-test was performed for statistical analysis. A p-
213 value equal to or less than 0.05 was considered significant (*p≤0.05, **p≤0.01, ***p≤0.001).
214 All values are given as mean ± S.E.M., if not otherwise stated.

215

216 *Matrix-assisted laser desorption/ionization imaging mass spectrometry*

217 Brains of cKO and control mice were cryosectioned at 12 μm and sections encompassing
218 the striatum and GP/EP were thaw-mounted with Pertex (HistoLab Products AB, Sweden) on
219 MALDI imaging compatible conductive glass slides (Bruker Daltonics, Germany). The slides
220 were dried in a vacuum desiccator for 20 minutes and then stored at -20°C . Before analysis,
221 the sections were thawed in a desiccator for 30 minutes and then washed 10 seconds in i) 70%
222 ethanol, ii) 95% ethanol, iii) 95% ethanol (Solveco Chemicals AB, Sweden) and iv) 30-
223 seconds in an acid wash (95% ethanol and 5% glacial acetic acid) (Merck, Sweden). The
224 washing steps and matrix deposition has earlier been developed for rat brain sections
225 (Groseclose et al., 2007; Andersson et al., 2008).

226 Matrix was deposited by a piezoelectric-based Chemical Ink-jet Printer (ChIP-1000,
227 Shimadzu Co, Japan) to apply approximately 100 picoliter-sized drops of matrix in a grid
228 across the tissue sections at a resolution of 200 micrometers (25 mg/ml DHB in 50%
229 methanol, 10% ammonium acetate, 0.3% trifluoroacetic acid in water; 5 drops per pass and 25
230 passes).

231 The MALDI imaging mass spectrometry was performed on an Ultraflex II MALDI
232 TOF/TOF (Bruker Daltonics, Germany) in reflector mode. External calibration was
233 performed with a standard peptide mix (Peptide Standard Calibration II, Bruker Daltonics).
234 Baseline correction (Convex Hull) was performed for each individual spectrum and was
235 exported as dat-files using FlexAnalysis (Bruker Daltonics). Spectra of the mass range from
236 m/z 440 to 8660 were acquired from each matrix spot consisted of 600 laser shots per spot in
237 20 steps random pattern. Total ion current normalization was performed on each individual
238 spectrum and data quality assessed as previously described (Karlsson et al., 2014). A total of
239 5400 peaks with a signal-to-noise ratio >3 were selected and peak borders were defined by
240 binning analysis using mass spectrometry peak binning software pbin. The peak area was

241 calculated for each peak using an in-house developed R script. Data is expressed as average
242 peak area for 40-50 mass spectra collected from the NAc of each mouse (761 spectra in total
243 collected from the NAc of cKO, n=6 and Ctrl, n=3 mice). To specify the anatomical
244 localization of peptides, photomicrographs of matrix deposits were co-registered with
245 histological staining of the same sections. After MS acquisition the matrix was removed with
246 95% ethanol and the mouse brain sections were stained with toluidine blue (Göteborgs
247 Termometerfabrik AB, Sweden). FlexImaging 2.0 was used for visualization of peptide
248 distribution. F-test analysis of variance revealed unequal variance between groups and the
249 data was log-scaled for further analysis using Student's T-test (two-tailed, alpha 0.05, the null
250 hypothesis was rejected at $P < 0.05$).

251 *In situ hybridization analyses*

252 Radioactive *in situ* hybridization was performed as described in (Schweizer et al., 2014)
253 using antisense oligonucleotide probes for detection of Vglut2 mRNA (two independent
254 probes, one composed of a mix of 3 oligonucleotides (NM_080853.3: bases 13-47 (exon1);
255 bases 872-908 (exon 1,2); bases 3220-3254 (exon 12)) and a second probe specific for exon 5
256 (bases: 1432-1464)) mRNA, respectively, and Pdyn (NM_018863.4 : 1078-1112; 1694-1727;
257 2309-2342). Images (Fujifilm BioImaging Analyzer BAS-5000, exposure time 1 month)
258 corresponding to hybridized sections were exposed on film for mRNA expression analysis at
259 a 25 μ m resolution. For cellular mRNA expression analysis, slides were dipped in NTB
260 emulsion, revealed after an exposition of 6 weeks and sections counterstained with toluidine
261 blue. For fluorescent detection, sections were incubated with HRP-conjugated anti-DIG
262 antibody at 1/1000. Signal detection was by the TSA™ Kit (Perkin Elmer) using Biotin-
263 tyramide at dilution 1:75 followed by incubation with Neutravidin Oregon Green conjugate at
264 1:750. HRP-activity was stopped by incubation of sections in 0,1M glycine followed by a 3%
265 H₂O₂ treatment. Fluorescein epitopes were then detected with HRP conjugated anti-

266 Fluorescein antibody at 1:1000 dilution and revealed with TSA™ Kit (Perkin Elmer) using
267 Cy3 tyramide at 1:200. All slides were scanned on a x40 resolution NanoZoomer 2.0-HT
268 (Hamamatsu, Japan). Cell size measurement, silver grain (mRNA expression) and cell
269 counting were performed using the ndp.view software (Hamamatsu, Japan). Histograms and
270 scatter plots were produced with MATLAB plotting tools (The Mathworks, USA).

271 *Analysis of projection patterns*

272 *Vglut2*^{wt/wt;Pitx2-Cre+} mice (n=6) older than 8 weeks received 5 mg/kg carprofen prior to
273 being anesthetized with isoflurane (0.5-2%). Bilateral stereotactic injections of AAV-
274 DJ.Ef1a.DIO.ChR2(H134R).EYFP.IRES (1 x 10¹² vector genome/mL, UNC Vector Core
275 Facility, USA) were carried out at AP, -1.9 from bregma, ML, ±1.7 from midline. In each
276 hemisphere, 250 nl were injected at DV, -4.75 and -4.25 with a NanoFil syringe with 35-
277 gauge needle (World Precision Instruments, USA) at a rate of 100 nl/min. The needle was left
278 in place for 10 minutes after the second injection and afterwards slowly removed. Injected
279 mice were kept in their home cage for at least 5 weeks to allow EYFP detection in synaptic
280 terminals. Afterwards, the injected mice were anesthetized with isoflurane and decapitated.
281 The brain was removed and kept for 24 h in 4% formaldehyde solution. Coronal sections of
282 100 µm were prepared on a VT1200 Vibratome (Leica Microsystems, Germany) and mounted
283 in 90% Glycerol. Images were taken on a Leica CTR 6000 microscope and analyzed with
284 LAS AF lite (Leica Biosystems, Germany).

285 *Histological analysis of STN structure*

286 3D reconstruction was obtained with MATLAB 3D plotting tools (The Mathworks, USA).
287 16 and 27 images of KO and WT sections respectively were used to draw contours of the
288 STN. These images were previously adjusted so that adjacent sections fit the best to the real
289 spatial position. We applied 3D cubic spline interpolation for missing sections and standard
290 ‘box’ smoothing. Different transparency, light shedding and shading options enabled
291 visualization of 3D shape of the STN.

292 **Results**

293 *Vglut2 and Pitx2 mRNAs overlap and are both distributed over the entire STN*

294 The STN in both primates and rodents have been suggested to constitute a tripartite
295 structure composed of a dorsal motor aspect with efferent projections to the globus pallidus
296 *interna* (GPi; in mice known as the entopeduncular nucleus, EP) and *externa* (GPe; in mice
297 commonly referred to only as globus pallidus, GP); a ventral aspect which via projections to
298 the substantia nigra *pars reticulata* (SNr) regulates associative behavior; and a medial aspect
299 which communicates with the limbic system via the ventral pallidum (VP) (Kita and Kitai,
300 1987; Groenewegen and Berendse, 1990; Benarroch, 2008; Alkemade and Forstmann, 2014).
301 While this model is based on projection patterns and functional outcome, no genetic marker
302 has been identified that distinguishes between these three aspects of the STN.

303 The *Vglut2/Slc17a6* gene encoding the synaptic protein VGLUT2 is strongly expressed
304 (mRNA) within the cytoplasm of neurons located in the STN in both rodents and primates
305 (Hisano, 2003; Barroso-Chinea et al., 2007; Rico et al., 2010) and represent the major
306 glutamatergic population within the STN in mice (Schweizer et al., 2014). For this reason, we
307 wished to assess the distribution pattern of the *Vglut2/Slc17a6*-expressing neurons within the
308 mouse STN to analyze if these distribute differently within the dorsal, ventral and medial
309 aspects of the STN. High-resolution radioactive *Vglut2* mRNA-selective *in situ* hybridization
310 analysis was performed to enable visualization and subsequent quantification of *Vglut2*
311 mRNA. *Vglut2* mRNA, detected as silver grains, was readily visible across the entire extent
312 of the STN (**Fig. 1A left**). While *Vglut2* mRNA was present throughout all aspects of the
313 STN, the level of expression was visibly higher in the medial and ventral parts. While most
314 cells contained *Vglut2* mRNA, cells of different sizes appeared throughout the STN (**Fig. 1A,**
315 **right**).

316 Further, because the *Pitx2* gene has been shown to be highly expressed in the STN (Martin
317 et al., 2004), we next used double fluorescent *in situ* hybridization to analyze the distribution
318 also of *Pitx2* mRNA, as well as the overlap between *Vglut2* and *Pitx2* mRNA on a cellular
319 level. Throughout all aspects of the STN, a near-100% overlap between these two mRNAs
320 was observed (**Fig. 1B**). The distribution pattern of both *Vglut2* and *Pitx2* mRNA was
321 important to establish since we, as discussed above, use a *Pitx2-Cre* transgenic mouse line
322 (Skidmore et al., 2008) as a tool to enable targeted deletion of *Vglut2/Slc17a6* expression
323 within the STN (Schweizer et al., 2014). However, we had not previously addressed the
324 possibility of subregional targeting within this structure. Our previous analysis showed that
325 the *Vglut2*^{ff;Pitx2-Cre+} conditional knockout (cKO) mice and their control littermates
326 (*Vglut2*^{ff;Pitx2-Cre-}) as expected had similar levels of *Pitx2* mRNA in the STN. However,
327 *Vglut2/Slc17a6* expression levels were blunted in the cKO STN so that the amount of low-
328 level expression cells were increased at the expense of high-level expression cells, leaving a
329 40% decrease in *Vglut2* mRNA (Schweizer et al., 2014).

330 Having now assured that *Pitx2* and *Vglut2/Slc17a6* expressions were overlapping and
331 distributed all over the STN, we next quantified the amount of *Vglut2* mRNA by counting the
332 number of silver grains in 550 STN neurons of cKO and 792 of the control mice, respectively.
333 About 12% of all the counted STN neurons in the control mice lacked any detectable *Vglut2*
334 mRNA, while the remaining approximately 88% of STN neurons showed of wide range of
335 *Vglut2* mRNA expression levels (**Fig. 1C**). The number of cells expressing no detectable
336 *Vglut2* mRNA at all was more than double throughout the STN structure in the cKO
337 compared to control (28% vs 12%). Further, the number of low level *Vglut2* mRNA levels (1-
338 10 silver grains/cell) was higher in the cKO than control STN while more control than cKO
339 STN cells showed higher *Vglut2* mRNA levels (11 or more silver grains/cell).

340 These histological analyses show that in the mouse, Pitx2 and Vglut2 mRNAs are highly
341 overlapping (near-100%) throughout the extent of the STN and thus do not represent any
342 specific aspect of the STN. Moreover, in control mice, as much as almost 90% of all STN
343 neurons express the *Vglut2/Slc17a6* gene while the majority of cKO neurons in the STN
344 contain no or low levels of Vglut2 mRNA. Thus, the current results demonstrate that
345 *Vglut2/Slc17a6* expression levels are severely blunted throughout the entire STN structure of
346 the *Vglut2^{fl/f};Pitx2-Cre⁺* (cKO) mice.

347 *Normal reward-associated learning, memory and cognitive flexibility but lower sugar*
348 *consumption when Vglut2/Slc17a6 expression is blunted within the STN*

349 Hyperactive individuals, mice as well as humans, can be lean without having any kind of
350 deficiency in food consumption. Therefore, the slightly smaller size of the hyperactive cKO
351 mice did not appear abnormal at first, but since a lower rate in collecting high-fat food
352 pellets in the baited radial arm maze and in the delay discounting test was measured
353 (Schweizer et al., 2014), a more thorough analysis of feeding behavior was motivated.

354 Generally, decreased consumption of fatty food might reflect a decreased eating overall
355 or a lack of consumption of palatable eatables specifically, the latter which could reflect a
356 deficiency in the mesostriatal reinforcement system (Everitt and Robbins, 2005), also known
357 as the brain reward system. To differentiate between these two possibilities, voluntary
358 consumption of high-sucrose food, another palatable eatable, was assessed in an operant self-
359 administration paradigm (Skinner, 1966) under mild food-restriction (**Fig. 2A**, schematic
360 presentation of the entire experiment; **2B**, illustration of the operant chamber). The results of this
361 analysis showed that no difference between control and cKO groups could be observed in task
362 acquisition (training) as both groups learned equally well to collect the maximum of 30 pellets
363 and decreased the time for task completion during training (change over time: $p < 0.0001$;
364 $F = 13.16$ $Df = 3$) (**Fig. 2C**). Both groups were able to reliably collect 30 pellets on three

365 consecutive days on the FR1 schedule (*Fig. 2D, left and middle*). However, the time to
366 complete the FR1 task was significantly increased for cKO mice compared to controls
367 (variation between genotypes: $p < 0.0001$; $F = 23.58$; $Df = 1$) (*Fig. 2E, left*). Furthermore, the
368 control mice continued to increase the number of head entries during time-out over the trial
369 while the number of head entries of cKO mice declined (time x genotype: $p = 0.00113$;
370 $F = 5.024$; $Df = 2$) (*Fig. 2D, right*). During FR5, the control mice showed a higher number of
371 head entries than cKO mice when a pellet could be obtained (time x genotype: $p = 0.0336$;
372 $F = 2.802$, $Df = 4$; variation between genotypes: $p = 0.0076$; $F = 9.476$; $Df = 1$) (*Fig. 2E, left*), thus
373 leading to a higher consumption of sugar pellets (time x genotype: $p = 0.0336$; $F = 2.802$; $Df = 4$;
374 variation between genotypes: $p = 0.0076$; $F = 9.476$; $Df = 1$) (*Fig. 2E, middle*). In addition, cKO
375 mice displayed decreased seeking for sugar during time-out in the FR5 paradigm (variation
376 between genotypes: $p = 0.0175$; $F = 7.012$; $Df = 1$) (*Fig. 2E, right*).

377 While FR5 is used to measure sugar consumption rate, the PR paradigm has been
378 described as a measure for the motivational aspect of consumption (Sanchis-Segura and
379 Spanagel, 2006). During PR, the number of head entries when the feeder was active (time x
380 genotype: $p = 0.3776$; $F = 0.9992$; $Df = 2$) or during time-out (time x genotype: $p = 0.1506$;
381 $F = 1.986$; $Df = 2$) was similar between cKO and controls (*Fig. 2F*). A breaking point was not
382 observed in either group. During the extinction phase, both groups decreased their number of
383 head entries at a similar pace (change over time: $p < 0.0001$; $F = 45.24$; $Df = 4$; variation
384 between genotypes: $p = 0.9457$; $F = 0.0049$; $Df = 1$) (*Fig. 2H, left*). Head entries during time-out
385 decreased as well (time x genotype: $p = 0.0085$; $F = 4.105$; $Df = 4$; change over time: $p =$
386 < 0.0001 ; $F = 130.2$; $Df = 4$; variation between genotypes: $p = 0.2763$; $F = 1.365$; $Df = 1$) with head
387 entries in cKO only significantly lower on the first day (Post-hoc test with Bonferroni
388 correction, $p < 0.01$; $t = 3.736$) but not the other days (*Fig. 2H, right*). Upon reinstatement of
389 the operant task, control and cKO groups showed no difference in the level of activity at the

390 active feeder ($p>0.05$) and were also equally able to switch sides upon reversal of the active
391 and inactive feeders (time x genotype: $p=0.0015$; $F=4.005$; $Df=6$; change over time: $p=0.0014$;
392 $F=7.172$; $Df=2$) (**Fig. 2I**). Throughout the experiment, activity on the inactive feeder was low
393 in both the control and cKO groups (*source data Figure 2-1*).

394 Analysis of operant sugar consumption behavior thus demonstrates that while the cKO
395 mice displayed normal reward-related learning, motivation, memory and ability for task-
396 switching, their consummatory rate of sugar eatables was significantly reduced.

397 *Lower weight but normal re-feeding after food restriction*

398 During the whole self-administration regime, mice were weighed daily to control for body
399 weight fluctuations. This procedure showed that the cKO mice weighed less than controls
400 throughout the trial but that cKO and control mice followed the same overall shifting in
401 weights between days (time x genotype: $p=0.0011$; $F=2.860$; $Df=12$) (**Fig. 3A**). Upon
402 completion of the self-administration task, all mice were allowed to feed freely in their home
403 cage environment (re-feeding). Despite weight difference, both control and cKO mice
404 consumed similar amounts of standard rodent chow during re-feeding (time x genotype:
405 $p=0.6323$; $F=0.6911$; $Df=5$) (**Fig. 3B**).

406 As the cKO mice consumed normal amounts of standard chow during re-feeding after the
407 operant task, the results suggest that the observed effect on sugar consumption is specific to
408 sweet food and that the leaner shape of the cKO mice prior to food-restriction rather reflects
409 their hyperactivity than a deficiency in standard chow feeding.

410 *Significant increase in seated and free rearing corroborates elevated motor activity*

411 *Vglut2^{ff};Pitx2-Cre⁺* cKO mice are both vertically and horizontally hyperactive (Schweizer et
412 al., 2014). By showing that they consume less sugar, we wished to know more about their
413 motor behavior. Rearing behavior differs from locomotion as it does not serve to move the
414 mouse forward, but instead signifies a sensing of the environment, commonly interpreted as

415 an exploratory behavior. Further, rearing displayed in a repetitive format is commonly
416 interpreted as a form of stereotypy in rodent models of various neuropsychiatric disorders
417 (Kim et al., 2016). It has also been shown that the presentation of rearing behavior in mice
418 can appear in different ways depending on body posture and the positioning of the paws and
419 tail (Waddington et al., 2001). To explore the type of rearing accentuated in the *Vglut2^{ff};Pitx2-
420 Cre⁺* cKO mice, we analyzed it in detail by sub-categorizing rearing into the three different
421 subtypes; wall rearing (**Fig. 4A, left**), seated rearing (**Fig. 4B, left**), and free rearing (**Fig. 4C,
422 left**), as previously described (Waddington et al., 2001). By quantifying the duration of each
423 of the types of rearing, no significant difference in wall rearing was found between control
424 and cKO mice (variation between genotypes: $p=0.2577$; $F=1.441$; $Df=1$) (**Fig. 4A, right**). In
425 contrast, both seated rearing (interaction: $p=0.0127$; $F=5.625$; $Df=2$) (**Fig. 4B, right**) and free
426 rearing ($p=0.0081$; $F=6.366$; $Df=2$) (**Fig. 4C, right**), the two more complex forms of rearing,
427 were significantly over-represented in the *Vglut2^{ff};Pitx2-Cre⁺* cKO group of mice (**Fig. 4**).

428 Summarizing the behavioral findings, the results demonstrate that mice lacking normal
429 expression levels of the *Vglut2/Slc17a6* gene in the STN display severely elevated motor
430 activity, including advanced subtypes of rearing barely detected in control mice, and blunted
431 reward consumption. These findings suggest an over-activity of the motor system at the
432 expense of the reward system, a finding which next motivated analysis of the mesostriatal
433 dopamine (DA) system.

434 *Significant alterations in DA receptor and DA transporter capacity*

435 DA neurotransmission in the dorsal striatum, mediated by the nigrostriatal DA neurons
436 located in the substantia nigra *pars compacta* (SNc), is strongly correlated with locomotion
437 and rearing, while DA transmission in the nucleus accumbens (NAc), the ventral aspect of the
438 striatum, is primarily mediated by DA neurons of the ventral tegmental area (VTA) and is
439 triggered by palatable food and drugs of abuse (Björklund and Dunnett, 2007). The reduced

440 interest in palatable food rewards alongside the elevated motor behavior thus suggested an
441 opposing circuitry effect by the targeted deletion of the *Vglut2/Slc17a6* gene in the STN on
442 dorsal and ventral striatal DA signaling. Indeed, in our previous analyses, we showed that the
443 nigrostriatal DA system is over-active with increased levels of DA release and reduced DA
444 clearance due to reduced levels of the DA transporter (DAT) in the DStr, while no alteration
445 in terms of DA receptor availability was detected (Schweizer et al., 2014).

446 Having now unraveled an effect of the *Vglut2*-targeting of the STN on consumption of
447 natural rewards, we focused on addressing a possible contribution of the NAc. The levels of
448 DA receptors are important for the hedonic impact of drugs of abuse and palatable food
449 (Volkow et al., 1999; Wenzel and Cheer, 2014). We therefore implemented receptor
450 autoradiography of [³H]SCH23390, [¹²⁵I]iodosulpride and [¹²⁵I]7-OH-PIPAT bindings
451 (Mahmoudi et al., 2014) to measure the density of DA receptor D1R, D2R and D3R subtypes,
452 respectively (**Fig. 5A**). No difference between control and cKO mice was detected for D1R in
453 either the core or shell subregions of the NAc (NAcC and NAcSh, respectively) (**Fig. 5B**).
454 However, for both D2R and D3R, ligand binding was altered in the NAcSh. D2R binding was
455 elevated above control levels in the cKO brain while D3R ligand binding was decreased (**Fig.**
456 **5C and D**). In addition, D2R binding was also above control levels in the cKO NAcC (**Fig.**
457 **5D**). Next, we assessed DAT capacity using [¹²⁵I]RTI-121 binding. [¹²⁵I]RTI-121 binding
458 was significantly increased in the NAcSh (**Fig. 5E**).

459 These findings point to different, and even opposite, modifications in the dorsal versus
460 the ventral striatal DA systems upon the targeted deletion of *Vglut2* in the STN such that
461 the NAcSh of the cKO mice have altered D2R and D3R availability as well as increased DAT
462 capacity, as opposed to unaltered receptor state and decreased DAT capacity in the dorsal
463 striatum (Schweizer et al., 2014). The higher activity of the dorsal over the ventral striatal DA
464 system likely accounts for the observed strengthening of motor behavior and weakening of

465 the natural reward-related behavior, and with focus on the reward system, the NAc was
466 therefore analyzed in more detail.

467 *Altered levels of dynorphin neuropeptide, but not gene expression, in the NAc*

468 To enable analysis of the molecular constitution within the neurons of the NAc and to
469 assay for peptide alterations within this region of $Vglut2^{ff;Pitx2-Cre+}$ cKO and control mice, we
470 implemented Matrix-assisted laser desorption/ionization analysis (MALDI) imaging as
471 previously described (Hanrieder et al., 2011; Ljungdahl et al., 2011) (**Fig. 6A** schematic
472 illustration of the procedure). The unknown peptides with mass to charge ratio (m/z) 1835 and
473 m/z 1393 were used to visualize white matter fiber tracts and the striatum, respectively,
474 serving as landmarks for the localization of the NAc (**Fig. 6B**).

475 The majority of over hundred detected peptides detected in the MALDI imaging were not
476 differentially expressed in cKO and control animals. However, 19 peaks were significantly
477 downregulated and 48 upregulated in the cKO mice. Among these upregulated peptides, the
478 strong changes in the family of dynorphin (Dyn) neuropeptides were most striking. Ion
479 images for the Dyn peptides DynA and alpha-neoendorphine (aNeo) revealed visibly elevated
480 Dyn levels in the NAc (**Fig. 6B**). Ion images obtained from cKO mice exhibited 25 to 50%
481 higher levels of Dyn and aNeo peptides compared to control mice. These alterations were
482 mainly localized to the NAc (**Fig. 6C**). Dyn peptides including DynB (9-13; $p=0.0290$), DynB
483 (1-6; $p=0.0087$), DynB (2-13; $p=0.0334$), aNeo ($p=0.0196$ for first and $p=0.0352$ for second
484 isotope), aNeo (2-10; $p=0.0289$), and DynA ($p=0.0021$) were upregulated in the NAc of the
485 cKO compared to the control brains (**Fig 6D**). The Dyn neuropeptides are products generated
486 by prohormone convertase cleavage of the prodynorphin (Pdyn) propeptide (Berman et al.,
487 2000; Yakovleva et al., 2006; Orduna and Beaudry, 2016), and while Dyn peptides can
488 represent either afferent or local projections, expression of the *Pdyn* gene was next analyzed
489 at mRNA level by in situ hybridization in the NAc. No difference in expression between

490 control and cKO could be detected, suggesting that the regulation of the Pdyn peptide
491 products does not occur at mRNA but at the peptide level (**Fig. 6F**).

492 Taken together with the results from the DA receptor and DAT binding shown above,
493 these findings reveal that the targeted reduction of Vglut2 within the STN had a strong impact
494 on the mesostriatal DA reward system, and we sought to explore this correlation further.

495 *Pitx2-Cre-expressing STN neurons show unique projection patterns to EP/GP and SNr*

496 The STN has been reported to send a multitude of efferents to the basal ganglia and their
497 associated structures, including the GPi/EP, GPe/GP, SNr, VP, pedunculopontine nucleus
498 (PPN), SNc and basolateral amygdala (BLA) (Kita and Kitai, 1987; Parent and Hazrati, 1995;
499 Parent et al., 2000; Sato et al., 2000; Benarroch, 2008; Degos et al., 2008; Watabe-Uchida et
500 al., 2012; Hachem-Delaunay et al., 2015). However, to our knowledge, no direct innervation
501 from the STN to either the NAc or DStr has so far been identified. While we already
502 confirmed a strongly reduced glutamatergic activity by implementing patch-clamp recordings
503 both upon electrical and optogenetic stimulations in post-synaptic neurons in the main STN
504 target areas EP and SNr (Schweizer et al., 2014), we now aimed to establish if there is a
505 projection from *Pitx2/Vglut2* co-expressing STN neurons directly to the NAc, which could
506 explain the strong effects observed in this region of the cKO mice. To selectively trace the
507 efferent projections and thereby pin-point their target areas, an adeno-associated virus (AAV)
508 carrying a Cre-dependent DNA construct of the *Channelrhodopsin-2* (ChR2) gene and the
509 gene encoding the Enhanced yellow fluorescent protein reporter (EYFP) was stereotactically
510 injected bilaterally into the STN of control *Vglut2^{wt/wt};Pitx2-Cre⁺* mice (**Fig. 7A-B**). Virus was
511 injected in two different dorsal-ventral stereotactic STN coordinates to ensure expression
512 throughout the length of the STN (**Fig. 7C**). Histological analysis revealed absence of EYFP
513 in structures surrounding the STN, while ample EYFP-positive cell bodies were detected
514 throughout the extent of the STN, confirming both successful expression of the *ChR2-EYFP*

515 construct exclusively in the *Pitx2-Cre*-expressing neurons and the observation described
516 above that *Pitx2/Vglut2* co-expressing cells are distributed uniformly over this structure (**Fig.**
517 **7D**). The EP, GP and SNr were verified as targets of the *Pitx2-Cre*-expressing STN neurons
518 by EYFP localized to fibers throughout these areas (**Fig. 7E-G**). However, no EYFP-positive
519 innervation at all could be detected in either the NAc or in the DStr (**Fig. 7H**). Further, EYFP
520 could not be detected in any of the other target areas described for the STN in different
521 species, i.e. the SNc, VP, BLA and PPN (**Fig. 7H**).

522 The results of these tracing studies thereby show that the alterations observed on the DA
523 parameters in the NAc are most likely mediated via the already established target areas of the
524 *Pitx2/Vglut2* co-expressing neurons, i.e. EP, GP or SNr, and not via a direct projection from
525 the STN to the NAc. To further explore how the *Vglut2*-targeting of the STN might have
526 caused the striatal alterations observed, we next sought to explore if the targeted blunting of
527 *Vglut2/Slc17a6* gene expression might have caused any alterations in the structure of the STN
528 that might contribute to the dopaminergic phenotype observed.

529 *Cell loss as well as altered structural size and shape of the STN*

530 A previous study of dopamine-glutamate co-releasing neurons in the midbrain has shown
531 that expression of the *Vglut2/Slc17a6* gene is important for maintaining cell density (Fortin et
532 al., 2012). During visual inspection of cryosectioned brains, we had detected a difference in
533 the shape of the STN between cKO and control mice and for this reason we decided to
534 quantify cell density and to also measure the size and shape of the STN. Toluidine blue-
535 contrast staining of the serially sectioned control and cKO mice used to quantify *Vglut2*
536 mRNA described above enabled quantification of cell number and cell size (area) in the same
537 material. This analysis revealed a reduction in total number of cells by 39% in the cKO
538 compared to control. Further, more STN neurons in the cKO than control mice had larger cell
539 area (201-350 μm^2), leading to right-sided shift in the histogram presenting cell area as a

540 function of % of total cells (**Fig. 8A**). It was also evident that within the STN of cKO mice,
541 there are neurons of a larger size range (351-500 μm^2) than observed at all in the control STN.

542 We next analyzed if the overall structure of the STN in the cKO mice had been altered as a
543 consequence of this cell loss. For this task, 2D and 3D reconstruction analyses were
544 performed in parallel. For 2D analysis, anatomical outlines of the STN were made on each
545 section microscope photograph and linear measurements were made at the widest part of the
546 STN and the adjacent cerebral peduncle (**Fig. 8B-C**). These analyses revealed that the STN
547 was slimmer in the cKO than in the control animals while the cerebral peduncle was wider,
548 thus pointing to shrinkage of the STN in the cKO. The STN outlines were subsequently used
549 to establish 3D overlay pictures of cKO and control STN both from coronal and sagittal view,
550 both of which readily exposed the smaller size of the STN in the cKO mice (**Fig. 8D**).

551 Further, the ventral and dorsomedial aspects of the STN were exposed as the regions most
552 affected by the reduction in STN size and this led to a change in the overall shape of the STN
553 which appeared visibly narrower ventrally and dorsomedially (**Fig. 8D**). 3D-quantification
554 confirmed a 14% smaller diameter as well as a 38% reduction in volume in the cKO STN.

555 These results demonstrate that the targeted deletion of the *Vglut2/Slc17a6* gene in the STN
556 causes substantial loss of neurons, primarily those of small cell area, which in turn likely has
557 caused the alteration in the size as well as shape of the entire STN structure. This substantial
558 alteration likely contributes to the motor and reward behavioral alterations observed. Further,
559 the results obtained pinpoint *Vglut2/Slc17a6* gene expression levels as crucial for the
560 structure and function of the STN.

561 **Discussion**

562 The STN has gained wide attention based on its pivotal role in motor, limbic and cognitive
563 functions and therapies based on electrical brain stimulation of the STN show a steady
564 increase as a treatment of advanced PD and a range of neuropsychiatric disorders (Chabardès
565 et al., 2013). Aberrant excitation from the STN not only contributes to the core symptoms of
566 PD, i.e bradykinesia, rigidity, tremor and axial instability, but excessive excitation from the
567 STN has also been proposed to also contribute to the degeneration of midbrain DA neurons
568 and may thus play a role in the etiology of this disease (Rodriguez et al., 1998; Olanow and
569 Tatton, 1999; Menegas et al., 2015).

570 While the so called tripartite model of the STN dominates the current way of correlating
571 the anatomy of the STN with its many functional roles, this model has recently been
572 challenged (Keuken et al., 2012; Alkemade and Forstmann, 2014; Lambert et al., 2015).
573 Interestingly, no molecular markers have been identified that could be used to delineate
574 putative anatomical borders between the three main subdivisions of the STN; this lack of
575 subdivision-selective markers contributes, in our mind, to the difficulty in firmly confirming
576 or dismissing the tripartite model. Both *Vglut2* and *Pitx2* mRNAs localize within the mouse
577 STN (Martin et al., 2004; Schweizer et al., 2014) but the current study shows that they are
578 both distributed throughout the entire STN structure; neither *Vglut2* or *Pitx2* can thus serve as
579 a selective marker for any specific aspect within the STN. We further conclude that while we
580 already previously referred to the *Pitx2/Vglut2* co-expressing neurons as a subpopulation of
581 the STN (Schweizer et al., 2014), the demonstration that *Pitx2* and *Vglut2* mRNA overlap in
582 almost 90% of all STN neurons now pin-points that the *Pitx2/Vglut2* subpopulation represent
583 the vast majority of the STN.

584 Given this broad distribution of *Vglut2* and *Pitx2* mRNAs throughout the STN, and the
585 reduction of *Vglut2* mRNA levels throughout the STN structure of the *Vglut2^{ffj;Pitx2-Cre+}* cKO

586 mice, a strong behavioral phenotype might not be surprising. The surprise, if any, rather lays
587 in the seemingly opposing effects observed on motor and reward-related behavior. While
588 motorically hyperactive both vertically and horizontally, the cKO mice consume less sugar
589 than control mice. Previous studies in rats selected for their low (LRA) or high (HRA) rearing
590 activity have shown that HRA rats display elevated locomotor activity and collect rewards in
591 the baited radial arms maze faster than LRA rats, but as they also make more working
592 memory errors, these results suggested that higher reward consumption in hyperactive rodents
593 is correlated with working memory failure (Görisch and Schwarting, 2006). While the
594 *Vglut2^{fl/f;Pitx2-Cre+}* cKO mice previously were shown to be strongly hyperactive both in terms of
595 locomotion and rearing, they did not make more errors in the baited radial arm maze; neither
596 reference or working memory errors were elevated in the cKO mice (Schweizer et al., 2014;
597 Pupe et al., 2015). However, consistently throughout our natural reward-related tests, i.e. the
598 baited radial arm and delay discounting tests as well as the sugar self-administration presented
599 here, the *Vglut2^{fl/f;Pitx2-Cre+}* cKO mice consumed less than controls.

600 Based on these observed behavioral alterations, we argue that the motoric hyperactivity
601 overrides the interest in palatable food. In efforts to unravel the biochemical correlates of such
602 a behavioral phenotype, we identified a series of modifications that support this argument.
603 First, a strong correlation between DA signaling in the NAcSh and reward-related behaviors is
604 already well established (Everitt and Robbins, 2005) and dysfunction of the mesostriatal DA
605 system is strongly implicated in disorders with a reward-related component, including
606 addiction (Volkow et al., 2009), anorexia nervosa (Kontis and Theochari, 2012) and over-
607 eating (Wang et al., 2001; Stice et al., 2008). By now demonstrating that the targeting of
608 *Vglut2/Slc17a6* gene has caused an increase in the DA activity in the DStr (mainly motor) but
609 decreased it in the NAc (mainly reward), opposite behavioral outcome mediated by these two
610 systems might indeed be achieved. The selective lack of interest in palatable food, while

611 showing normal levels of regular chow consumption, is likely correlated to the biochemical
612 alterations in the NAc. Increased DAT capacity suggests faster clearance of DA while the
613 elevated levels of Dyn peptides might represent a biochemical indication for a dysphoric
614 state in these animals.

615 Microinjection of the selective κ opioid receptor agonist DAMGO in the NAc of
616 experimental animals has previously been shown to produce conditioned place aversion
617 (Bals-Kubik et al., 1993), while an antagonist of these receptors causes an anti-depressant
618 effect (Shirayama and Chaki, 2006). The Dyn neuropeptides are mainly present in D1R-
619 expressing cells of the NAcSh (Al-Hasani et al., 2015); although we did not observe D1R
620 upregulation, the observed reduction in binding to D3R, which can oppose D1R activity,
621 could have relieved D1R intracellular signaling to increase Dyn levels in the NAc (Schwartz
622 et al., 1998). Thus, while elevated motor activity might be explained by the observed
623 reduction of glutamatergic post-synaptic activity in the EP and SNr alongside the reduced DAT
624 clearance in the DStr observed in the *Vglut2^{ff;Pitx2-Cre+}* cKO mice, the current findings of
625 elevated DAT levels in the NAcSh as well as increased levels of both D2R and Dyn
626 neuropeptides likely provide a biochemical correlate of the deficiency in the reward-collecting
627 behavior demonstrated by the *Vglut2^{ff;Pitx2-Cre+}* cKO mice. Further, by unraveling the severe
628 impact on the size and shape of the STN structure itself, we propose that slimming of the ventral
629 (presumably associative) and part of the medial (limbic) aspects of the STN due might cause the
630 reduced dopaminergic activity in the NAc. Similar slimming of the STN structure has been
631 observed upon ibotenic acid-induced STN lesioning in which a substantial amount of STN cells
632 are lost (Baunez et al., 1995, 2002), while targeted deletion of the *Vglut2/Slc17a6* gene in the
633 midbrain has been shown before to lead to reduced cell density (Fortin et al., 2012).

634 In the *Vglut2^{ff;Pitx2-Cre+}* cKO mice, expression of the *Vglut2/Slc17a6* gene is targeted from
635 early embryogenesis and onwards. Having now verified that reduced *Vglut2* mRNA levels

636 occur throughout the STN structure, and also shown that the STN suffers from cell loss and
637 structural modifications, this genetic intervention resembles to some extent a pharmacological
638 lesion model of the STN. Indeed, pharmacological lesioning, as well as inactivation, of the
639 STN increases motoric activity and have also been shown more recently to affect motivated
640 behavior, including consumption of palatable food (Baunez et al., 2002, 2005; Bezzina et al.,
641 2008; Rouaud et al., 2010). While pharmacological lesioning and inactivation of the STN, as
642 well as STN-DBS, in experimental animals show similar beneficial effects on motor behavior
643 as STN-DBS in humans (Baunez and Gubellini, 2010), the results have been more variable
644 and difficult to interpret in terms of motivated and reward-related behavior; this is likely due
645 to the use of different experimental paradigms and to the metabolic states of animals (e.g.
646 food-restriction) analyzed in the reported studies (Uslaner et al., 2007; Pratt et al., 2012).

647 Importantly, the *Vglut2/Slc17a6* “genetic lesion model” (represented by the *Vglut2<sup>fl/fl;Pitx2-
648 Cre+</sup>* cKO mice) has a developmental onset which sets it aside from current pharmacological
649 lesion models. In the *Vglut2^{fl/fl;Pitx2-Cre+}* cKO mice, there is a significant reduction in
650 number of the STN neurons in the adult animal, which in turn likely has caused the alteration
651 in STN shape. However, addressing dysfunction in developmental processes, such as defects
652 in proliferation or premature cell death, is beyond the scope of the present study. Further,
653 STN neurons may not differentiate or migrate in a normal manner and they may not even
654 form functional connections in the absence of normal levels of *Vglut2/Slc17a6* gene
655 expression.

656 The impact of a developmentally-induced “genetic lesion” likely has a substantial effect of
657 overall circuitry. Therefore, identifying the exact nature of the correlation between the
658 reduced *Vglut2/Slc17a6* gene expression levels, the altered shape of the STN and the observed
659 effects on the DA system is not straight-forward. While we can conclude that there is no direct
660 innervation of either the ventral or dorsal striatum by the *Pitx2/Vglut2* co-expressing STN

661 neurons that might be directly affected by the targeted deletion of *Vglut2/Slc17a6*, we have
662 established that both the EP and SNr are innervated by these STN neurons, and that the
663 glutamatergic input into these targets is reduced in the *Vglut2^{ff};Pitx2-Cre⁺* cKO mice. The EP is
664 the main projection target in the STN motor loop while the SNr also mediates associative
665 functions (Benarroch, 2008), and we therefore hypothesize that the observed alterations in
666 reward-related behavior might be connected more specifically to the STN-SNr pathway. While
667 STN neurons generally are excitatory in nature, high-frequency stimulation of the STN leads to a
668 reduced drive for burst firing in the SNr (Shen and Johnson, 2008) and can through
669 endocannabinoid mechanisms attenuate the GABAergic innervation of the SNc through the SNr
670 (Freestone et al., 2015). The reduction in glutamatergic transmission in the STN of the
671 *Vglut2^{ff};Pitx2-Cre⁺* cKO could therefore have led to a developmental alteration in the
672 excitation/inhibition balance within the STN-SNr-SNc axis, presumably via the structurally
673 disturbed ventral and part of the medial aspects of the STN.

674 Developmental effects might make it difficult to pinpoint additional circuitry components
675 in the STN-EP/GP/SNr-striatum-loop unraveled here. However, targeting the *Vglut2/Slc17a6*
676 gene bears a physiological relevance that is not matched by toxin-induced models. Null
677 mutations of the *Vglut2/Slc17a6* gene in mice are lethal directly after birth due to disturbance
678 of the pre-Bötzinger respiratory central pattern generator (Wallén-Mackenzie et al., 2006) and
679 the same is likely true for humans. However, some rare genetic variants of the human
680 VGLUT2/SLC17A6 gene have been identified in schizophrenia and severe alcoholism
681 (Flatscher-Bader et al., 2008; Shen et al., 2010; Comasco et al., 2014). In the *Vglut2^{ff};Pitx2-Cre⁺*
682 cKO mice, expression levels of the *Vglut2/Slc17a6* gene are merely blunted, but not
683 eliminated, and may therefore expose effects that are of relevance to human conditions.
684 Indeed, we show that the blunting of *Vglut2/Slc17a6* gene expression levels selectively within
685 the STN of mice cause opposite biochemical modifications in the dorsal and ventral striatal

686 DA systems followed through by behavioral hyperactivity and decreased interest in palatable
687 food, possibly due to a dysphoric state. We tentatively propose that genetic variants of the
688 human VGLUT2/SLC17A6 gene might be correlated with similar modifications. Further, by
689 demonstrating an association between reduced Vglut2 mRNA levels in the STN and reduced
690 STN size in mice, brain imaging analysis of STN size in human individuals might serve a
691 purpose in future clinical investigations of human brain disorders implicating the STN, and
692 where STN-based therapies are implemented already, such as PD and OCD, as well as for
693 addiction, eating disorders and obesity, disorders proposed to benefit from STN-based
694 therapy.
695

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927 **Figure Legends**

928 **Figure 1: Strong overlap of Vglut2 and Pitx2 in the STN and reduction of Vglut2 mRNA**
929 **in cKO mice.**

930 **A:** Representative examples of cell morphology and distribution. Overview of the STN (left)
931 as well as close-up images of the dorsal (right top), ventral (right center) and medial (right
932 bottom); cells are stained blue, small dots represent silver grains bound to Vglut2 mRNA. **B:**
933 double fluorescent *in situ* hybridization for Vglut2 (red) and Pitx2 (green) as well as nuclear
934 stain with DAPI (blue) in the dorsal (top), ventral (center) and medial (bottom) STN. **C:** High
935 resolution *in situ* hybridization analysis of Vglut2 mRNA-based silver grain intensity showed
936 a generally lowered expression of Vglut2 in the STN of cKO mice.

937 cKO: conditional knock-out; STN: subthalamic nucleus.

938 **Figure 2: Decreased consumption of sugar in STN-VGLUT2 cKO mice.**

939 **A:** Schematic self-administration (SA) schedule. Black lines indicate the number of days
940 during which each paradigm was carried out. **B:** Operant SA was carried out in modular SA
941 boxes with two feeders, of which one was delivering pellets upon head entry (south, green =
942 active), while the other was not (north, red = inactive). Yellow: house light, black bars: head
943 entry holes measuring exploration with no feeder attached. When a mouse made a head entry
944 at the active feeder, a sugar reward was delivered, and simultaneously, a light and a sound cue
945 were presented to confirm the choice (left), while a head entry at the inactive feeder produced
946 neither reward delivery, nor a light or sound cue (right). **C:** During task learning, both Ctrl
947 (white circles) and cKOs (filled circles) decreased time to obtain the maximum of 30 sugar
948 pellets. **D:** During FR1, the time to consume 30 pellets was significantly higher for cKOs
949 (filled circles) compared to Ctrl (white circles) (left panel). All mice were able to obtain the
950 maximum of 30 pellets during the FR1 protocol (middle panel). The amount of head entries
951 during the inactive time (timeout) decreased in cKOs, while Ctrl increased (right). **E:** During

952 FR5, head entries during active time (left), the amount of pellets obtained (middle) and head
953 entries during inactive time (right) were lower for cKOs compared to Ctrl. **F:** During
954 progressive ratio (PR), no difference was seen in head entries during the active (left) or the
955 inactive time (timeout, right) between Ctrl and cKO mice. **G:** Cognitive ability testing.
956 During reinstatement, the mice were presented to the original task after an extinction period
957 (left). During reversal, the positions of the active and inactive feeders were switched (right).
958 **H:** To allow testing of the retention of the task (reinstatement), both cKO and Ctrl groups
959 were put through extinction. For 5 consecutive days, the active feeder delivered both light and
960 sound cues, but no sugar pellets. For both groups, the amount of head entries strongly
961 decreased during both the active time (left) and during timeout (right). **I:** No differences
962 between Ctrl and cKO mice were seen during reinstatement or reversal.

963 Statistical analysis of the SA data was performed using repeated-measures ANOVA followed
964 by a post-hoc test with Bonferroni correction. #/* $p \leq 0.05$; ##/** $p \leq 0.01$; ###/*** $p \leq 0.001$,
965 ####/**** $p \leq 0.0001$. cKO: conditional knock-out; Ctrl: control; d: day; Extinct. Extinction;
966 FR: fixed ratio; Hab.: habituation; minutes: minutes; PR: progressive ratio; Rev.: reversal; RI:
967 reinstatement; s: seconds.

968 **Figure 3: The average weight of STN-VGLUT2 cKO mice is decreased, while home cage**
969 **food consumption is unaltered.**

970 **A:** Ctrl mice (white circles) had a higher body weight than cKO (filled circles) over the
971 course of the experiment. **B:** Refeeding after SA was not significantly different between Ctrl
972 and cKOs.

973 Statistical analysis of weight and food intake data were analyzed using repeated measures
974 ANOVA followed by a post-hoc test with Bonferroni correction. * $p \leq 0.05$; ** $p \leq 0.001$. cKO:
975 conditional knock-out; Ctrl: control; g: gram; h: hours; SA: self-administration.

976

977 **Figure 4: Increased seated and free rearing in STN-VGLUT2 cKO mice.**

978 Three different rearing types were observed in STN-VGLUT2 cKO mice: wall rearing, where
979 the mouse takes support against a vertical surface (A, left),; seated rearing, where the mouse
980 supports itself on the tail base (B, left),, and free rearing, where the mouse stretches its hind
981 legs and uses no other support (C, left),. All rearing types were scored in an open field arena.
982 Both groups were habituated to the environment (# marks the change over time), cKOs show
983 increased seated (B) and free (C) rearing throughout the session (□ marks the difference
984 between genotypes and * marks the difference at a certain time point between genotypes).
985 Rearing data was analyzed by repeated measures ANOVA and post-hoc test with Bonferroni
986 correction. * $p \leq 0.05$; ** $p \leq 0.001$; *** $p \leq 0.0001$. cKO: conditional knock-out; Ctrl: control.

987 **Figure 5: The availability of dopamine receptor D2 and D3 as well as DAT binding sites**
988 **in the ventral striatum is regulated by Vglut2 reduction in the STN.**

989 **A:** Representative examples of serial coronal striatal sections analyzed for DAT, D1R, D2R
990 and D3R (from top to bottom). **B:** Comparison of specific binding capacity levels expressed
991 as percent of control for DAT-specific [125I] RTI binding, D1R-specific [3H] SCH23390,
992 D2R-specific [125I] Iodosulpride and D3R-specific [125I]-7-OH-PIPAT binding in Ctrl and
993 cKO mice. DAT binding was unaltered in the NAcC and upregulated in the NAcSh of cKO
994 mice (left). The amount of D1 receptor binding sites (middle left) in both NAcC and NAcSh
995 remained unaltered, whereas more D2 receptor binding sites were measured in both NAcC
996 and NAcSh (middle right) and less D3 receptor binding sites were available in NAcSh (right).
997 Data analyzed by Mann-Whitney U-test. * $p \leq 0.05$. cKO: conditional knock-out; Ctrl: control;
998 NAcC, nucleus accumbens core; NAcSh: nucleus accumbens shell; STN: subthalamic nucleus.

999 **Figure 6: Elevated levels of dynorphin peptides in the NAc of STN-VGLUT2 cKO mice.**

1000 **A:** MALDI analysis was performed on cryosections at the level of the DStr and NAc. Each
1001 slice was coated with droplets of matrix for ionization of the peptide fragments and analyzed

1002 in MALDI-TOF. **B:** A brightfield (BF) picture of the cresyl violet-stained section analyzed
1003 for aNeo was used to determine the localization of DStr and NAc (black outlines).
1004 Representative examples of aNeo (depicted in red) in cKO. Overlays with peptide fragment
1005 m/z 1835 and m/z 1393 (middle and right, depicted in green) visualized the fiber bundles used
1006 as landmarks for the anatomical localization of the NAc. **C:** Representative examples of slices
1007 used for MALDI imaging in controls (left) and cKOs (right). aNeo and DynA peptide levels
1008 were significantly elevated in cKOs and showed a more restricted localization to the NAc. **D:**
1009 Fluorescence intensity of different peptides measured by MALDI imaging, shown as percent
1010 of control (fold change, see table). **E:** Example peaks of DynA (top) and aNeo (bottom) from
1011 MALDI analysis. **F:** Oligo in situ hybridization analysis of Dyn expression in the forebrain of
1012 Ctrl (left) and cKO (right) mice.

1013 cKO: conditional knock-out. aNeo: alpha-neo-endorphin; cKO: conditional knock-out; Ctrl:
1014 control; DynA: dynorphin A; DynB: dynorphin B; FC: fold change; m/z: mass to charge ratio;
1015 numbers in brackets indicate, which amino acids constitute each peptide fragment. * $p \leq 0.05$
1016 and ** $p \leq 0.01$; error given as S.E.M.

1017 **Figure 7: Optogenetic tracing of Vglut2-Pitx2 co-expressing neurons revealed a**
1018 **projection pattern restricted to the EP and SNr. A-C: Schematic illustrations of**
1019 **injection procedure. A:** Mice were stereotactically injected with AAV-ChR2-EYFP virus
1020 into the STN; **B:** The injection was performed bilaterally but one side at a time to infect the
1021 left- and right-hand side STN at equal levels; **C:** Two close coordinates were used for each
1022 STN to allow even spread of the virus (-4.25 and -4.75 DV). **D:** Histological results of
1023 injections. AAV-ChR2-EYFP-positive cell bodies in the STN. **E:** AAV-ChR2-EYFP-positive
1024 fibers projecting to EP (left), GP (middle) and SNr (right). Upper row: EYFP expression.
1025 Lower row: bright field photographs of the same area.

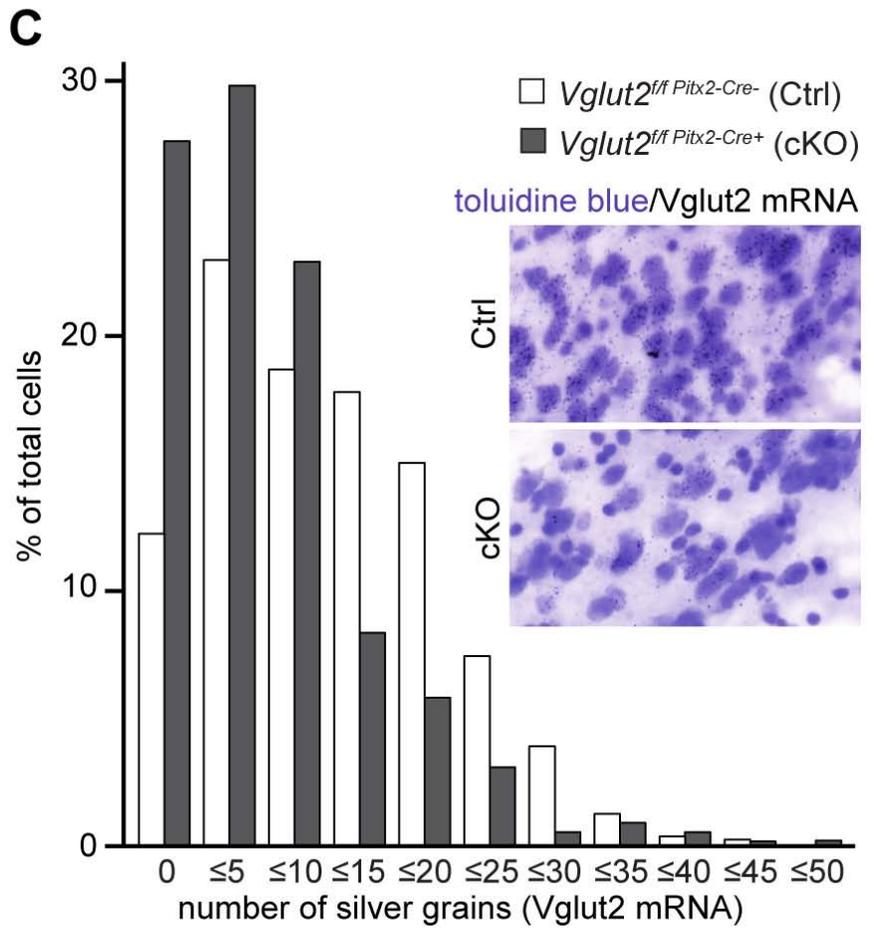
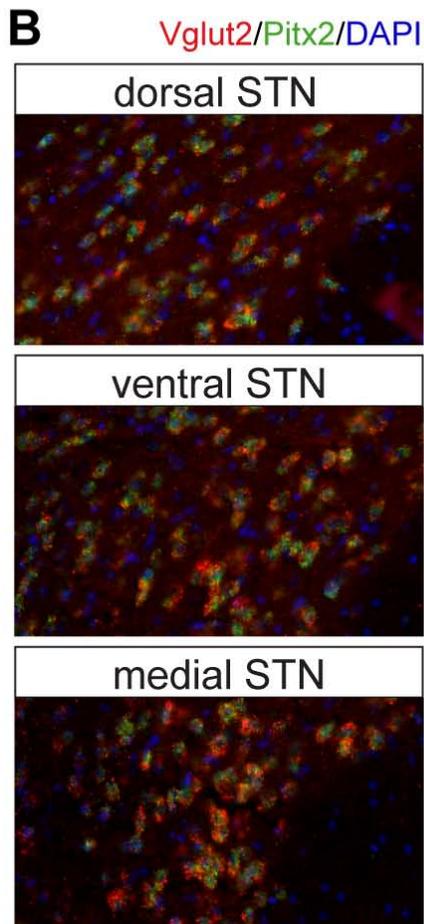
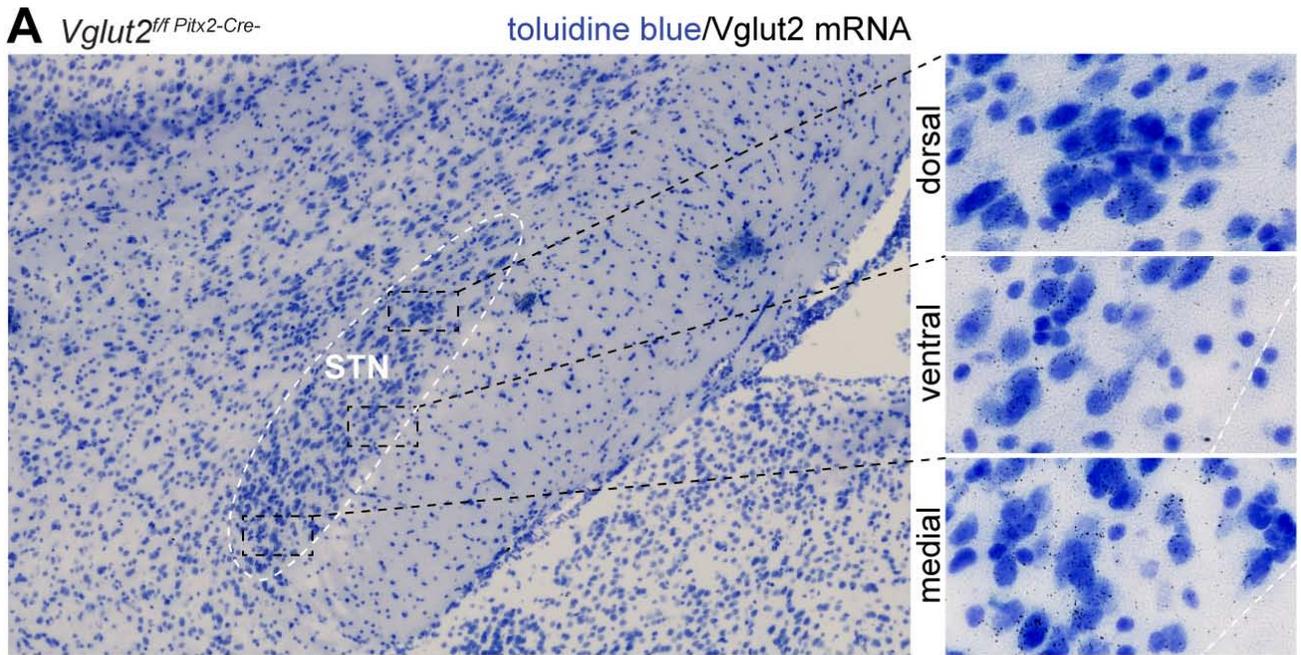
1026 EP: entopeduncular nucleus; GP: globus pallidus; SNr: substantia nigra pars reticulata; PSTN:
1027 parasubthalamic nucleus; STN: subthalamic nucleus.

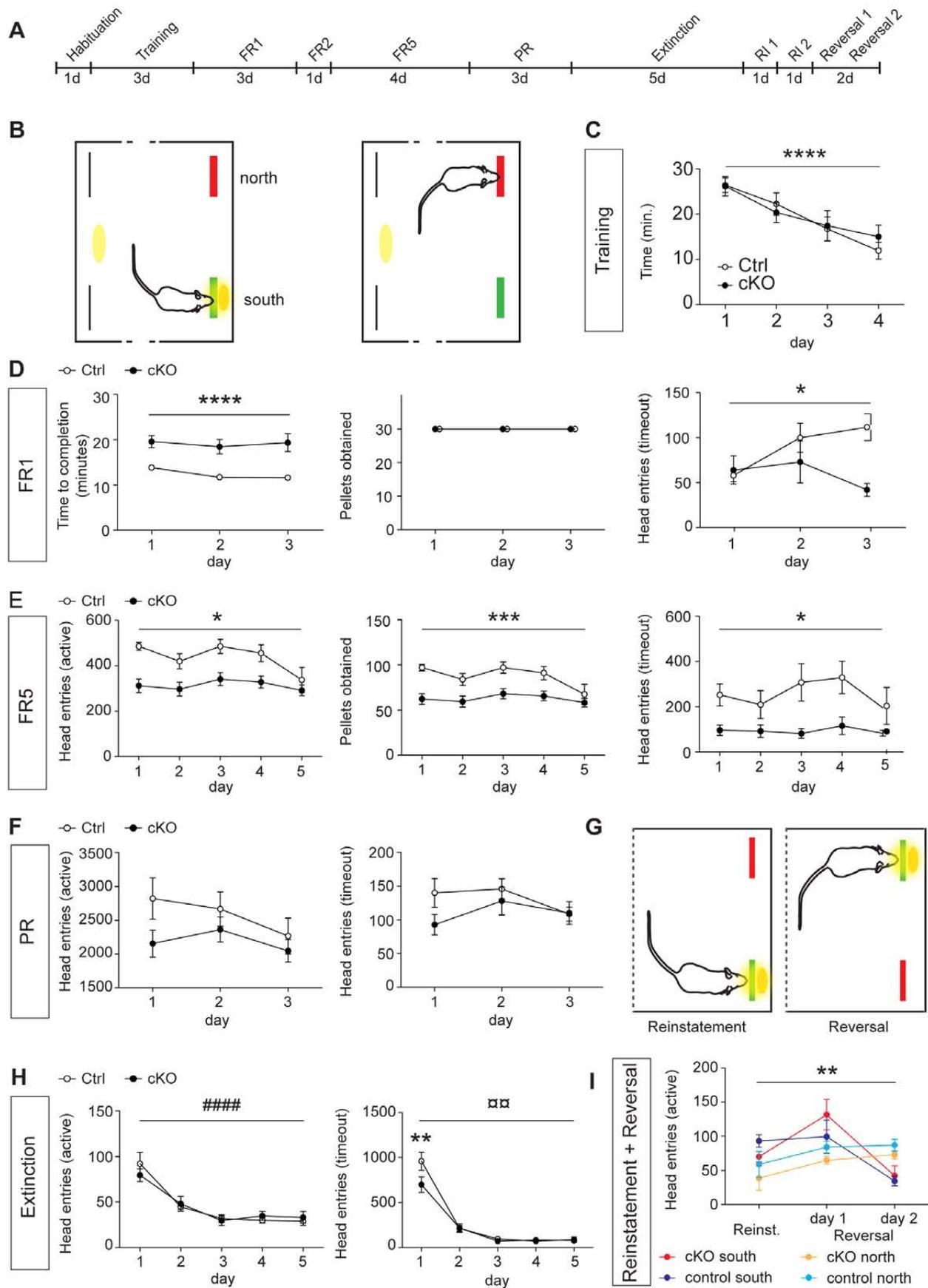
1028 **Figure 8: Vglut2 reduction leads to cell loss and reduction in size of STN.**

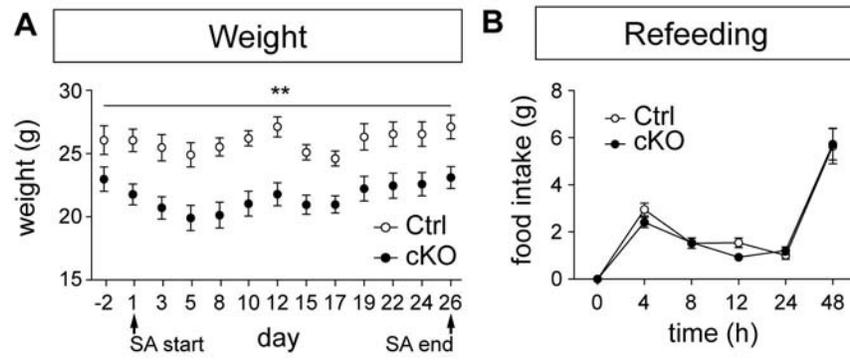
1029 **A:** Cell size is increased in cKO (black bars) mice compared to Ctrl (white bars). The cKOs
1030 show a much wider spread of cell size than Ctrl **B:** Representative pictures of STN
1031 morphology in cKOs and Ctrl. The STN of cKO mice appears slimmer compared to controls.
1032 The white outlines were used for 2D and 3D analysis of STN morphology. **C:** 2D analysis of
1033 STN morphology. The size of the STN was assessed by measuring the diameter of the STN at
1034 its widest point and comparing it to the diameter of the cp and the total diameter of both
1035 structures at the same point. **D:** Representative example of a Ctrl (left, red) and a cKO STN
1036 (middle, green), and their overlay (right). Both diameter (white dotted line) and volume of the
1037 cKO STN is reduced compared to the Ctrl.

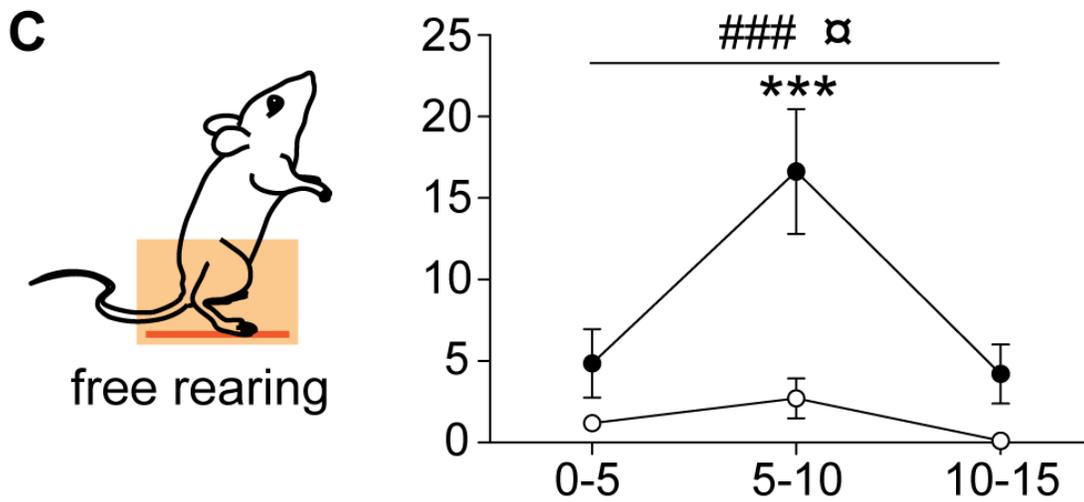
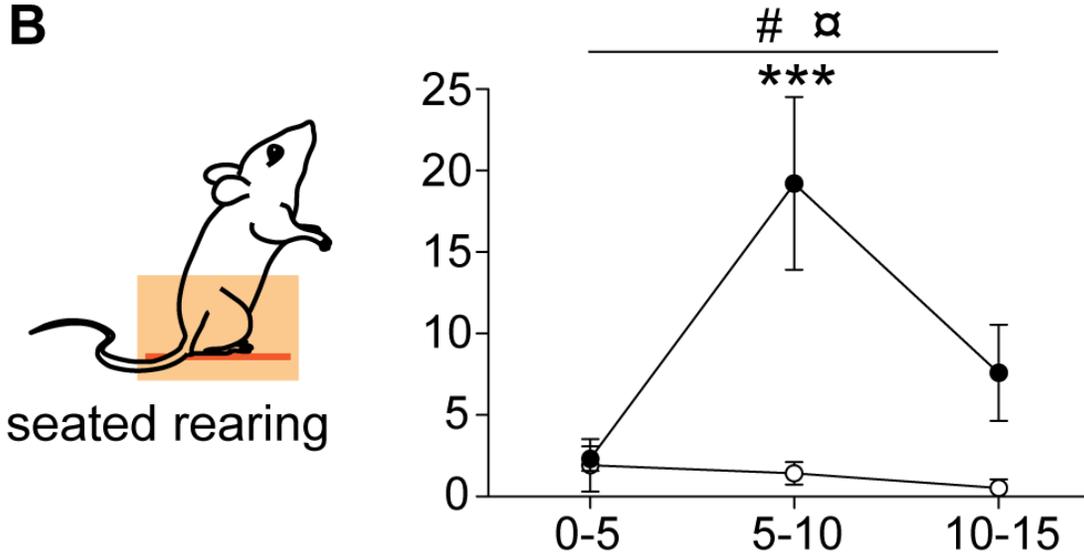
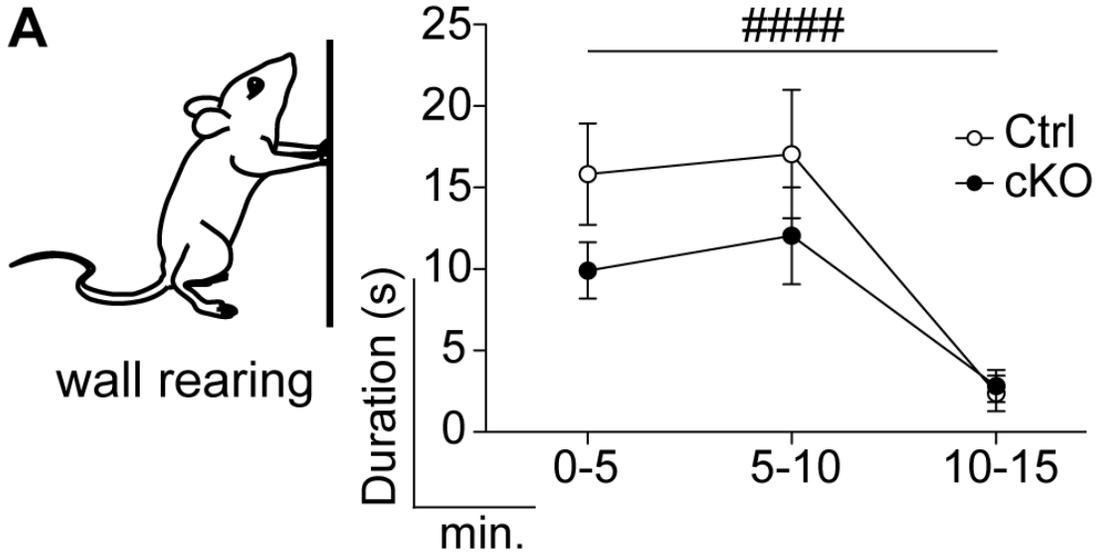
1038 3D reconstruction was obtained with MATLAB from 16 and 27 images of a cKO and a Ctrl,
1039 respectively. cKO: conditional knock-out; cp: cerebral peduncle; Ctrl: control; STN:
1040 subthalamic nucleus.

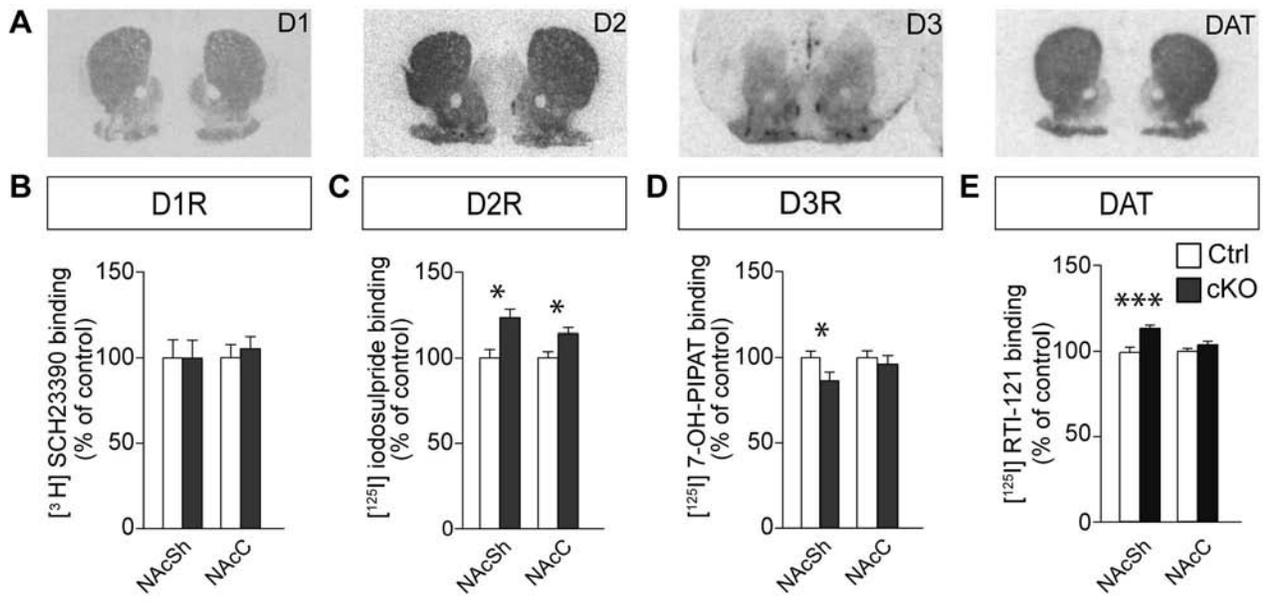
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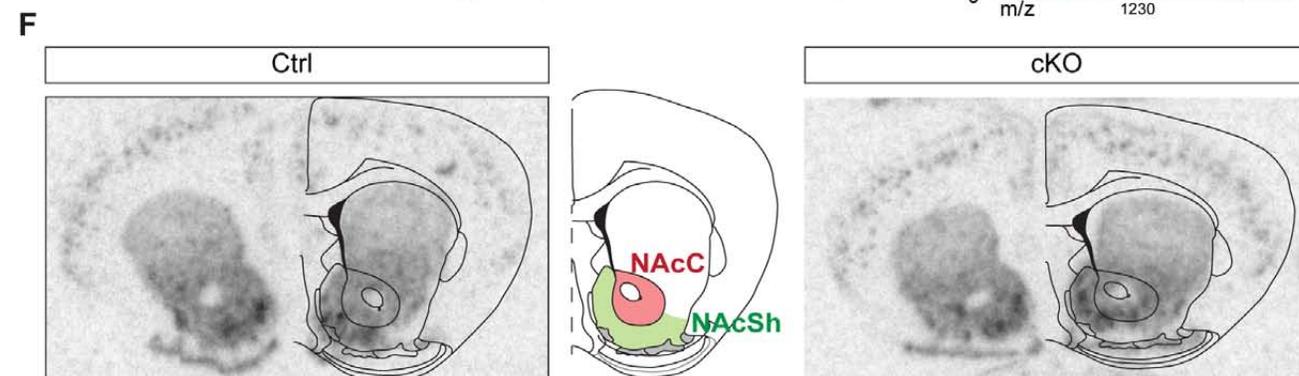
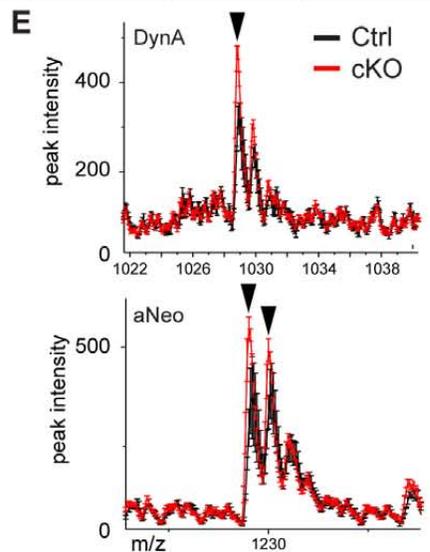
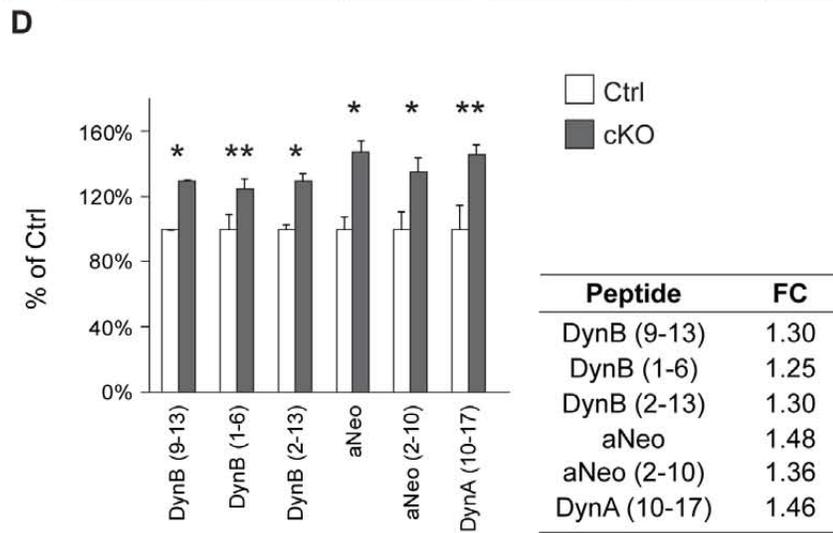
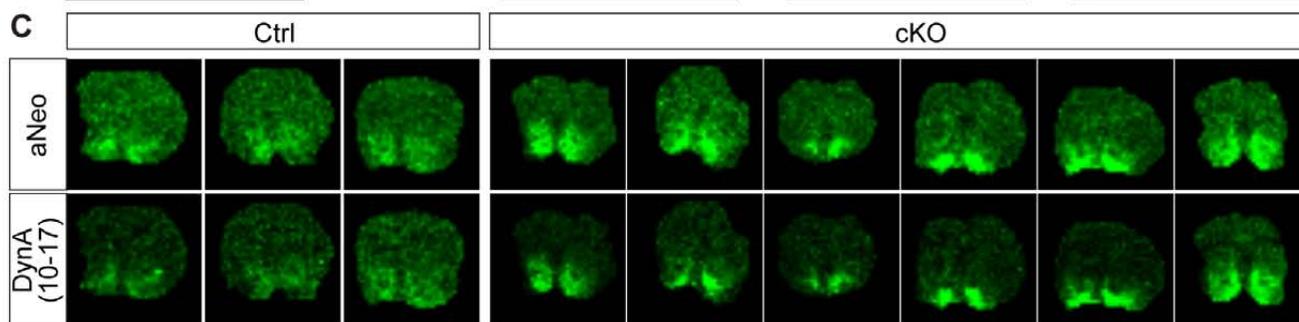
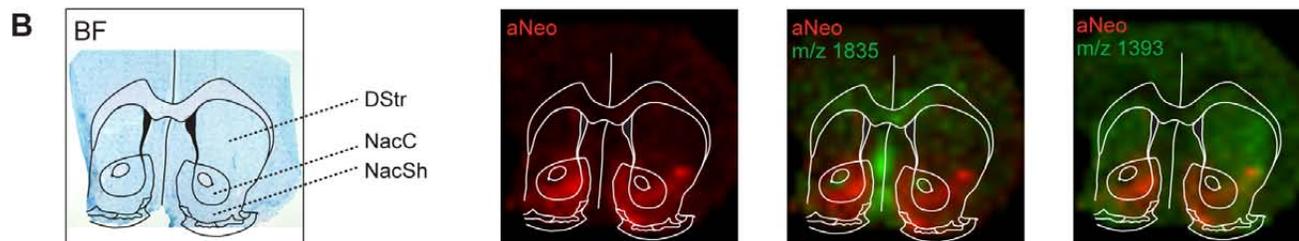
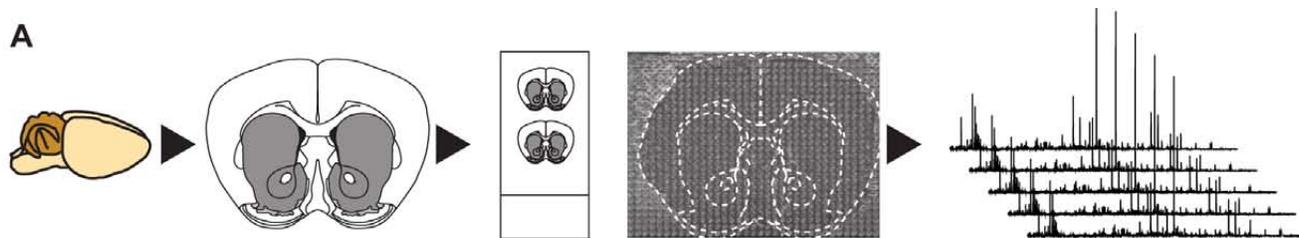


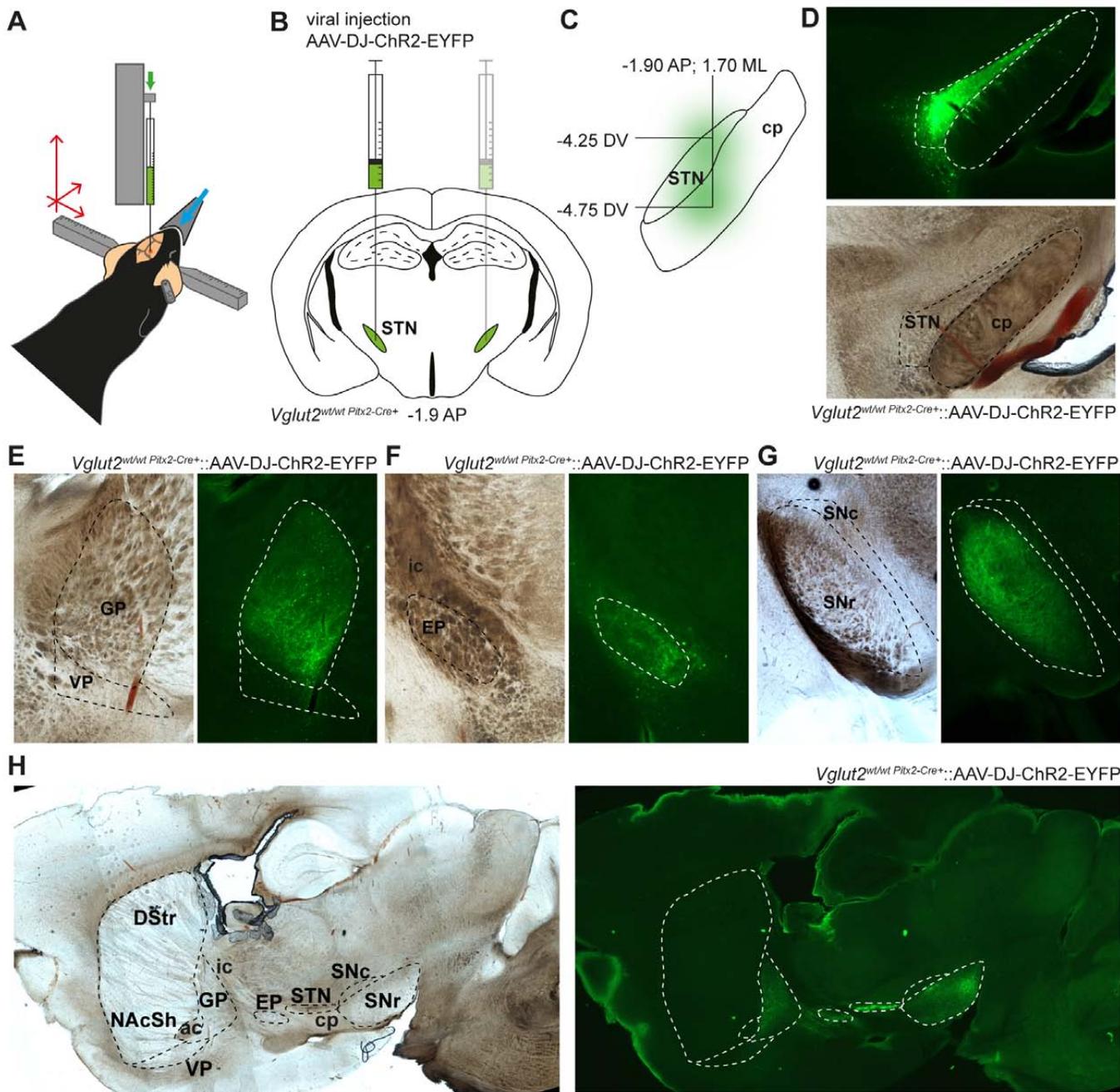


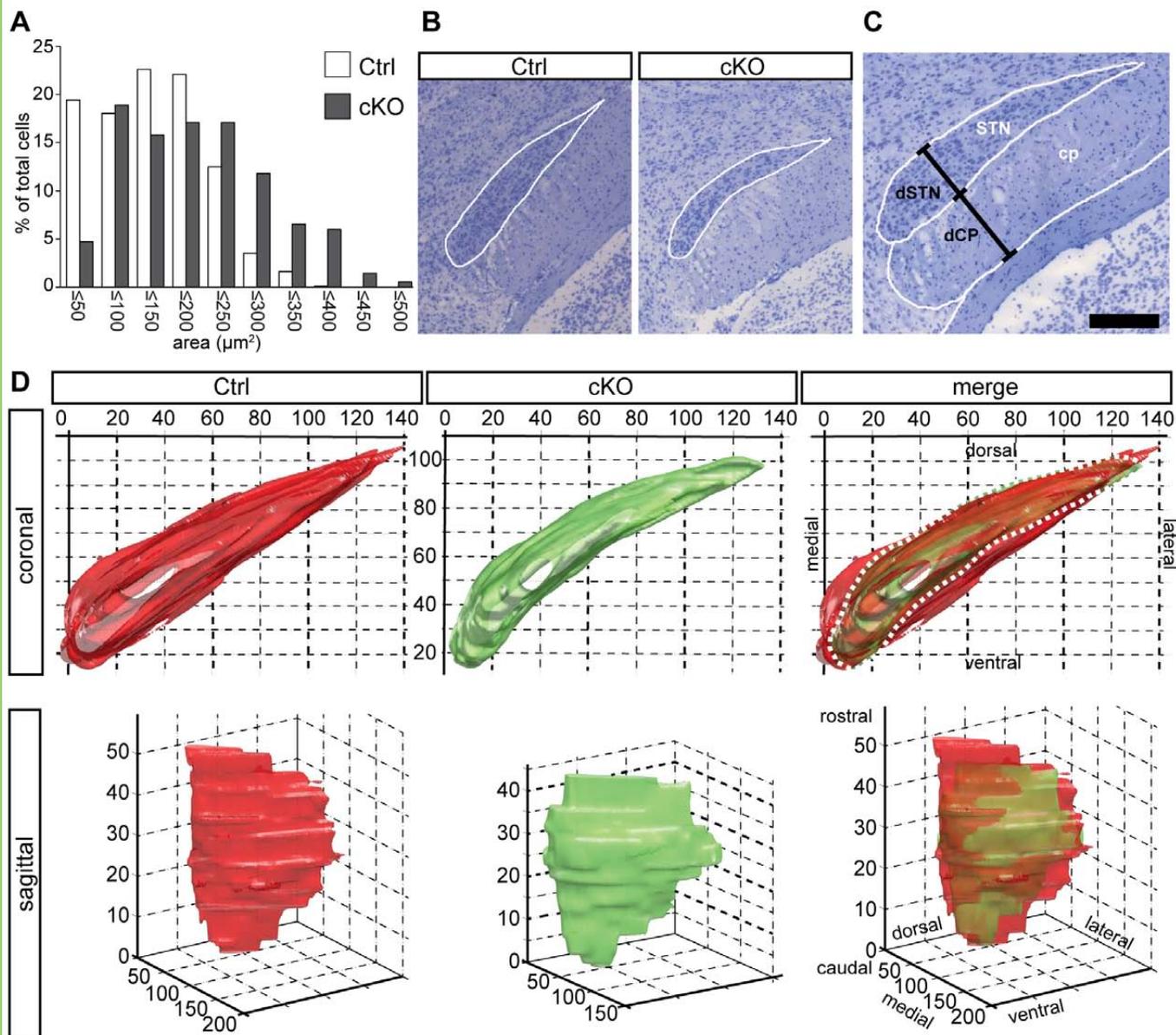




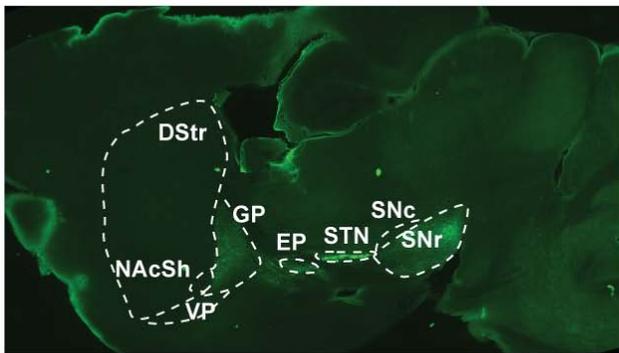




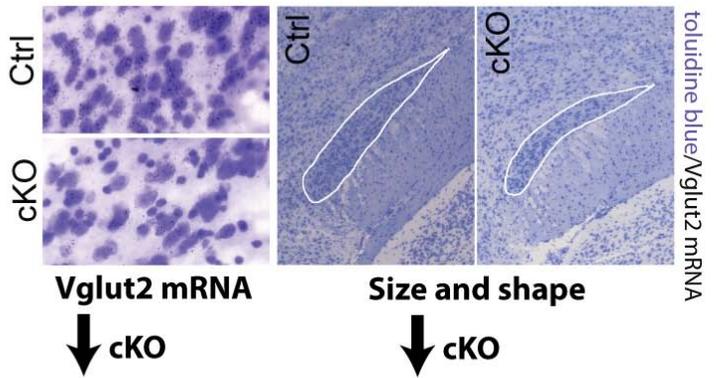




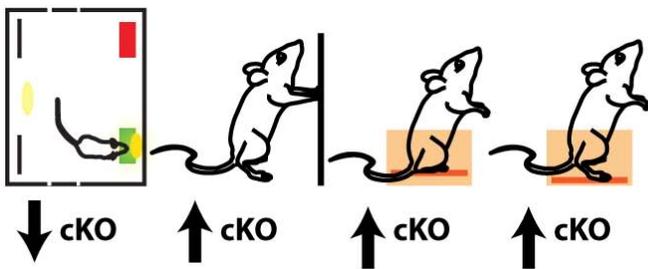
Pitx2-Cre::Chr2-EYFP



Structural alterations in STN



Behavioral alterations



Biochemical alterations in NAc

