782 single: p=1.0). *=p<0.05, **=p<0.01, ***=p<0.001. For all box plot figures, middle lines indicate the
783 median, lower and upper edges of the box indicate quartiles below and above the median, and upper
784 and lower whiskers indicate the points furthest from the median whose value did not exceed 1.5 times
785 the first-to-third quartile range above the third quartile or below the first quartile.
786
787 **Figure 7: Interneurons Regulate MSN Activity and Movement State.**
788 **(A)** MSN population fluorescence aligned to all PV calcium event onsets (orange) versus MSN calcium
789 event onsets (blue) from all PV-Cre animals. MSN population peak fluorescence was significantly
790 reduced in the 500ms following a PV calcium event (PV post-event: rank-sum test, two-sided,
791 ranksum=2.43e+12 n_{PV}=237528 event-neurons, n_{MSN}=20289773 event-neurons, across all 6 PV
792 animals and 18 sessions, p=1.48e-06), in comparison to a MSN calcium event (blue). Plots are mean
793 ±SEM. **(B)** Same as (A) but for Chat-Cre animals. MSN peak population fluorescence was significantly
794 elevated in the 500ms following a CHI calcium event (green: Chat-Cre post-event: two-sided, rank-
795 sum test, ranksum=1.73e+12, p=2.53e-09, n_{MSN}=22116844 event-neurons, n_{CHI}=153680 event-
796 neurons from 10 sessions in 6 animals), compared to an MSN event (blue). **(C)** Change in coincident
797 MSN activity (MSN co-activity) following a MSN calcium event (blue), a PV calcium event (orange), or
798 a CHI calcium event (green) from all animals and normalized to event onset for all three types (t=0).
799 Plots are mean ±SEM. A magnified inset demonstrating the change in MSN co-activity probability in
800 the 100ms following a MSN, PV or CHI calcium event is shown to the right. Following a CHI calcium
801 event, there is an increase in MSN co-activity, whereas following a PV calcium event, there is a
802 reduction in MSN co-activity relative to the change in MSN-triggered co-activity (Pairwise two-sided z-
803 tests, PV-MSN vs CHI-MSN, z=-40.8, p=0; PV-MSN vs MSN-MSN, z=-47, p=0; CHI-MSN vs MSN-
804 MSN, z=20.4, p=0. Bonferroni corrected post-hoc for multiple comparisons; raw proportions: MSN:
805 3.52e-03, PV:2.30e-03, CHI:5.91e-03,n_{CHI}=38189238, n_{CHI}=38189238 event-pairs, n_{MSN}=9644946557
806 event-pairs, n_{PV}=48285061 event-pairs, across all 12 animals and 28 sessions). **(D)** A time series
807 showing MSN-MSN event co-activity during laser stimulation of PV cells (orange) and CHIs (green)
808 during laser stimulation in PV-Chrimson mice (n=4 PV-Chrimson mice and n=4 Chat-Chrimson mice).
809 For reference, the change in MSN-MSN co-activity around random MSN events from all time periods
810 outside of optogenetic stimulation for all PV-Chrimson and Chat-Chrimson mice is shown in blue. Plots
811 are mean ±SEM. **(E)** Population line plots quantifying the change in the MSN-MSN co-activity upon
812 optogenetic stimulation of PVs or CHIs in PV-Chrimson and Chat-Chrimson mice. Opto-stim induced
813 co-activity was compared to the endogenous rate of MSN-MSN co-activity from the non-opto
814 stimulation periods of the imaging session, indicated by the dashed blue line. Error bars and center
815 are mean ± SEM. During optogenetic stimulation of CHIs MSN-MSN co-activity increased, whereas
816 during optogenetic stimulation of PVs, MSN-MSN co-activity decreased, relative to the endogenous
817 MSN-MSN co-activity rate (Pairwise two-sided z-tests, n_{CHI}=2078751 event-pairs, n_{MSN}=694475807
818 event-pairs, n_{PV}=682922 event-pairs; CHI-MSN vs PV-MSN z=78.7, p=0; MSN-MSN vs MSN-PV, z=-
819 228, p=0; MSN-MSN vs CHI-MSN, z=19.2,p=0, n=4 PV-Chrimson mice and n=4 Chat-Chrimson mice,
820 Bonferroni corrected post-hoc for multiple comparisons). *=p<0.05, **=p<0.01, ***=p<0.001. **(F)**
821 Change in movement speed after peaks in MSN-MSN co-activity events (see supplemental methods),
822 binned into 500ms windows for analysis. Error bars and center are mean ± SEM. Peaks in MSN co-
823 activity were followed by decreases in speed similar to that observed following CHI events, and CHI
824 optogenetic stimulation (Friedman test, main effect of time, n=2249 peaks in coactivity, $X^2(8)$=520, p<
825 0.001; Tukey's HSD post-hoc, (vs 0-0.5 s) 0.5-1 seconds, p=0.030, 1.00-1.50 seconds, p=9.30e-07,
826 1.50-4.50 seconds, all p=8.97e-08; mean ranks: 5.81, 5.54, 5.35, 5.04, 4.84, 4.72, 4.62, 4.52, and
827 4.56).
828
829 ## Online Methods
830
831 ### Animal Surgery
832 All animal procedures were approved by the Boston University Institutional Animal Care and Use
833 Committee. Combined experiments included data from mice expressing Cre recombinase in either
834 choline acetyltransferase expressing cells (Chat-Cre: n=14; GM24Gsat) or parvalbumin (Pvalb)

835 expressing cells (PV-Cre mice: n=14; B6;129P2-Pvalb$^{tm1(cre)Arbr}$/J), 8–12 week old at the start of the
836 experiments. Both male and female mice were used in this study and breeders were obtained
837 commercially (Chat-Cre: Mutant Mouse Resource Center, Davis, CA; and PV-cre: Jackson
838 Laboratory, Maine). One cohort of mice was used for imaging studies without optogenetic laser
839 illumination (n=6 Chat-Cre mice, and n=6 PV-Cre mice). Mice first underwent surgery for implantation
840 of a sterilized custom imaging window with an attached guide cannula that was assembled before
841 surgery. The window/guide assembly consisted of a stainless steel imaging cannula (OD: 0.317 cm,
842 ID: 0.236 cm, height, 2 mm diameter), fitted with a circular coverslip (size 0; OD: 3mm) adhered using
843 a UV-curable optical adhesive (Norland Products). The guide cannula (26 gauge; C135GS4; Plastics,
844 Roanoke, VA) was fixed at a 45° angle and terminated flush to the base of the imaging window. To
845 access dorsal striatum, the overlying cortical tissue was carefully aspirated away to expose the corpus
846 callosum as an anatomical guide. The white matter was carefully thinned until the underlying striatal
847 tissue could be visualized via a surgical microscope. The imaging window was then lowered in place
848 and centered over the dorsal striatum (AP: +0.5, ML:1.8 mm, DV: -1.6 from brain surface). During the
849 same surgery, a custom aluminum head-plate was attached to the skull, anterior to the imaging
850 cannula. Upon complete recovery (14-21 days after surgery), animals were injected with a 1µL cocktail
851 containing 500 nL AAV9-Syn-GCaMP6f.WPRE.SV40 (titer: 6.6 e12 GC/ml) and 500 nL AAV9-CAG-
852 flex- tdTomato.WPRE.SV40 virus (titer: 5.1e12 GC/ml) through the attached guide cannula. Virus was
853 delivered via a 10uL syringe (701N; Hamilton Company, Reno, NV) controlled by a microinfusion
854 pump (UltraMicroPump3-4; World Precision Instruments, Sarasota, FL) fitted with a 33 gauge infusion
855 cannula (C135IS4; Plastics, Roanoke, VA).
856
857 A second cohort of mice was used for the behavioral and network analysis during optogenetic
858 experiments (n=16 combined: n=4 for each group analysis; PV-Cre mice expressing Chrimson-
859 tDTomato, Control PV-Cre mice expressing tDTomato without Chrimson; Chat-Cre mice expressing
860 Chrimson-tDTomato, and Control Chat-Cre mice expressing tdTomato without Chrimson). These
861 animals were prepared similar to the description above, except that virus infusion for tdTomato or
862 Chrimson-tdTomato was performed in a separate procedure 10 days prior to window implantation.
863 Mice were infused with either AAV9-CAG-flex- tdTomato (opto-controls), or AAV9-Syn-flex-Chrimson-
864 tdTomato (opto-group). To ensure the expression of Chrimson or tdTomato maximally within the
865 imaging hemisphere, a total volume of 3µL's was delivered at two depths (1.5 µL: AP: +0.5, ML:1.8
866 mm, DV: -3.5; and 1.5 µL: AP: +0.5, ML:1.8 mm, DV: -2.3). Injections were delivered via pressure
867 ejection (10-15 psi, 15-20 ms pulses delivered at 0.5Hz) through a glass pipette (diameter: 1.2 mm)
868 pulled to a sharp point and then broken at the tip to a final inner diameter of ~20µm. The pipette was
869 lowered over 3 min and allowed to remain in place for 3 min before infusion began. The injection
870 occurred at a rate of 100 nl/min and 10 min passed before raising the pipette to the second location.
871 At the conclusion of the second infusion, an additional 10 min delay was introduced before the pipette
872 was slowly withdrawn over 2-3 minutes. AAV9-Syn-flex-Chrimson was obtained from the University of
873 North Carolina Vector Core: WPRE.SV40 virus (titer: 5.9e12 GC/ml). Following the window
874 implantation surgery, and after complete recovery (14-21 days after surgery), 500 nL AAV9-Syn-
875 GCaMP6f.WPRE.SV40 (titer: 6.6 e12 GC/ml) was infused through the attached guide cannula as
876 described earlier.
877
878 **Animal Habituation**
879 Following surgery and virus infusion (typically about 21-28 days), mice were first handled for several
880 days before being head fixed to the treadmill/imaging apparatus. Mice were then habituated to running
881 on the spherical treadmill while head fixed for two weeks, 3-4 days per week, at the same time of day
882 as subsequent recording sessions. Each animal received at least 6 habituation sessions prior to the
883 first recording day. The cohort of mice used in the optogenetic studies underwent the same handling
884 and habituation protocol, but with 4-5 additional sessions. Habituation was performed in the dark with
885 the same light illumination intensity as it would be for recording sessions. Habituation sessions were
886 the same duration as an imaging session.
887

Data Acquisition

Image acquisition with sCMOS cameras:

Animals were positioned underneath the microscope, and imaged while freely running on the spherical treadmill. Image acquisition was performed via custom microscope equipped with a scientific CMOS (sCMOS) camera (ORCA-Flash4.0 LT Digital CMOS camera C11440-42U; Hamamatsu, Boston, MA). GCaMP6f fluorescence excitation was accomplished with a 5W LED (LZ1-00B200, 460 nm; LedEngin, San Jose CA). tdTomato fluorescence excitation was accomplished with a 1000mA LED (LXML-PX02-0000, 567 nm; Lumileds, San Jose CA). The custom microscope included a Leica N Plan 10X 0.25 PH1 microscope objective lens, a dual band excitation filter (FF01-468/553-25), a dichroic mirror (FF493/574-Di01-25x36), and a dual band emission filter (FF01-512/630-25; Semrock, Rochester, NY), and a commercial SLR lens focused to infinity as the tube lens (Nikon Zoom-NIKKOR 80-200mm f/4 AI-s). The camera when coupled to a 10X objective lens yields an imaging field of view of 1.343 × 1.343 mm with each pixel corresponding to 1.312 × 1.312 μm.

A custom MATLAB script was used to trigger frame capture and to synchronize image acquisition with movement. TTL trigger pulses were delivered to the camera using a common I/O interface (USB-6259; National Instruments, Austin, TX). Image acquisition was performed using HC Image Live (HC Image Live; Hamamatsu; Boston, MA). The time interval between image frame capture was 47.0 ± 0.2 ms (~21.3Hz, mean ±standard deviation, n=28 sessions). For each image frame, exposure time was fixed at 20 ms. Image data were stored as multi-page tagged image file format (mpTIFF's). For a recording session of 10 mins, approximately 24 GigaBytes of image data were stored, spreading across 6 mpTiFF video files. The acquisition software was configured to buffer all frames in computer RAM to optimize speed. At the conclusion of the GCaMP6f imaging session, we imaged tdTomato fluorescence for ~10 seconds (50 frames at 20ms or 200ms exposure per frame) to identify GCaMP expressing interneurons.

Optogenetic laser equipment and protocol:

A 635 nm 200mW red diode laser (Shanghai Laser Optics and Century Co.) was coupled to the imaging scope via an optical fiber (BFL48-200, Thor Labs, Newton, NJ) with the fiber tip focused to illuminate the entire imaging window from above. Laser illumination was under TTL control using the image acquisition software HC Image Live (HC Image Live; Hamamatsu; Boston, MA). Briefly, a 15ms pulse was initiated 10ms after "camera readout" concluded, and another image frame capture could not begin until a minimum of 5ms had passed since the laser illumination TTL pulse ended. The average sampling rate across optogenetic sessions was slower (63.4 +/- 0.4 ms/sample (+/- SEM) for the Chrimson and control sessions) due to the requirements of a 15ms laser pulse in the imaging loop.

Prior to each imaging session, laser output was adjusted to 10mW at the height of the imaging cannula window using a light meter calibrated for 635nm wavelength (PM100D, Thor Labs, Newton, NJ). Optogenetic recording sessions were identical to other imaging sessions described earlier, but with 13-23 laser stimulation trials. Laser trials occurred randomly within a session, but each trial was separated by 40±15 seconds. A laser trial consisted of 100 light pulses, 15ms per pulse, delivered between imaging exposures (at ~15 Hz). All four groups of animals underwent two recording sessions with 3-7 days between sessions.

Movement data acquisition:

The spherical treadmill was constructed following the design of Dombeck et al.[51]. Briefly, the treadmill consisted of a 3D printed plastic housing and a Styrofoam ball supported with air. Movement was monitored using two computer USB mouse sensors affixed to the plastic housing at the equator of the Styrofoam ball. Each sensor was mounted 3-4mm away from the surface of the ball, and 78 degrees apart. The x- and y-surface displacement measured by each sensor was acquired using a separate computer running a Linux OS (minimal CentOS 6). A simple multi-threaded python script was used to send packaged <dx,dy> data at 100Hz to the image acquisition computer via a RS232 serial link. Packaged motion data were received on the imaging computer using a MATLAB script, and

synchronized to each acquired frame. Because of a delay in initiating movement sensor data capture, we excluded the first 5 seconds of the motion data (following interpolation) and imaging data (following event identification) from the beginning of every recording session in the subsequent analysis.

ROI Calcium Trace Processing and Calcium Event Characterization

Image pre-processing: contrast enhancement, motion correction and baseline subtraction:
Image frames underwent several pre-processing steps prior to trace extraction[52]. Briefly, we first applied homomorphic filtering to each image frame to enhance contrast, and then performed motion correction using cross-correlation between a given image frame and a reference frame. The reference frame was updated by sequential addition of each corrected frame. Baseline subtraction was performed using a two-step process. We first identified the minimum fluorescence for each pixel across the first 2047 frames of each recording session (~96 seconds), and spatially convolved the minimum fluorescence throughout the whole image field to determine the background value for each pixel. We then subtracted this value from each frame. In the second step, we subtracted the average intensity of pixels with the lowest dynamic range within the first 2047 frames of the recording sessions from all pixels within a frame, and set the lower pixel value boundary to 0. Each frame was then converted to a uint8 file format.

Region of Interest (ROI) identification and ROI ΔF/F trace extraction:
Several semi-automatic algorithms have been developed for ROI identification[52-54]. However, we found that these algorithms were not sufficiently robust in identifying all neurons in the striatum. Thus, we manually selected ROIs based on morphology using a circle with a radius of 6 pixels (7.8 microns), from single frame representations of the recording session. To identify the PV or CHI cells, we first processed the tdTomato video as that described in image pre-processing above, but without background subtraction. We further smoothed each image with a spatial filter (a square spatial Gaussian filter of width 5 pixels and a standard deviation of 0.8). Images were then thresholded to reveal the brightest 5% pixels that correspond to PV and CHI cells.

ROI Fluorescence was calculated as the average intensity across all pixels in the circle. In instances when a small number of pixels overlapped between two ROIs, the overlapping pixels were only assigned to one of the labeled ROIs. We interpolated fluorescence time series, so that consecutive data were 0.0469 seconds apart, using MATLAB function: interp1(*, 'pchip')). ΔF/F was calculated as the fluorescence at each time point minus the mean, and then divided by the mean.

Calcium event identification:
Two types of calcium events were detected. One type we considered "transient", with a fast rise and decay, and others we considered "slow", with a delayed rise and long decay. Each cell was first assigned to one of these two categories through manual inspection. We found 1.9% of neurons had both transient and slow calcium event characteristics. These neurons were excluded from further analyses. To identify individual calcium events, ΔF/F calcium traces were first smoothed using a moving average of 21 points, scaled by a value of 1.05. We then detrended the ΔF/F calcium traces by subtracting a local minimum value for each time point, defined as the minimum value within a radius of 500 data points of the smoothed trace, similar to Jia et al[55]. For "transient" calcium events, we identified all points with fluorescence exceeding 3 standard deviations above the mean computed from the non-event portion of the trace. We iteratively performed this step, where the points above threshold were excluded from future iterations. Consecutive points above this threshold were then grouped as a putative event, plus one data point before the onset. If the addition of the single data point resulted in two overlapping putative events, they were grouped into one event. Calcium events overlapping with the start or the end of a recording session were discarded. Finally, only events with maximum amplitudes exceeding 5 standard deviations of the baseline were considered a calcium event.

For "slow" calcium events, we further smoothed "detrended ΔF/F" with the MATLAB function

994 "sgolayfilt", with an order 3 polynomial, and 101 data points. We then identified all points using the
995 same methods as described for transient calcium events, except using a threshold of 2 standard
996 deviations above the mean.
997
998 Laser induced calcium events, manually identified as those coincident with laser onset have durations
999 between the transient and the slow calcium events. For these events, we first high-pass filtered the
1000 ΔF/F calcium traces at ~2e-05 Hz (MATLAB commands "butter" with arguments 2 and 0.0005, and
1001 then "filtfilt" for zero-phase filtering). We then identified all points using the same methods as
1002 described for transient calcium events, using a threshold of 2 standard deviations above the mean.
1003
1004 After removal of the first five seconds of the fluorescence traces due to motion artifact as described
1005 previously, events continuous with the beginning of the shortened session were not considered for
1006 further analysis.
1007
1008 *Calcium event property calculation:*
1009 To characterize calcium events from each cell type, we first subtracted the baseline, calculated as the
1010 mean of the 20 data points before each event onset from the event time series. To estimate area
1011 under the curve for transient calcium events, we further smoothed these events with a 21 point moving
1012 average filter before baseline subtraction. Rise time was calculated as the time from calcium event
1013 onset, the first data point of a calcium event, to the peak. To compute area under the curve, peak
1014 widths, and calcium event amplitude, we added one extra data point to each event after event
1015 termination. To compare calcium event properties between high- versus low-speed time periods,
1016 calcium events were first averaged for each ROI, and then compared across all neurons. ROIs that did
1017 not have an event in either low or high-speed time period were excluded from the respective statistical
1018 testing.
1019
1020 *Deconvolution of calcium traces:*
1021 Deconvolution occurred by labeling the rising phase of a calcium event, including the event maximum
1022 as ones (active regions), and the rest zeroes. Deconvolved calcium traces were used in Figures 2H,
1023 4D-E, 5A-C, and 7C-F.
1024
1025 **Movement Data Analysis**
1026 *Linear velocity calculation:*
1027 We first calibrated the spherical treadmill by pinning the two sides of the ball at the equator for
1028 physical distance, or at the top and the bottom for rotation. Linear velocity in perpendicular X and Y
1029 directions is calculated as:
1030

1031 $$X = \frac{L - R\cos\theta}{\cos(\frac{\pi}{2} - \theta)}$$

1032

1033 $$Y = R$$

1034
1035 Where L is the vertical reading from the left sensor, R is the vertical reading from the right sensor, and
1036 θ is the angle between the sensors (78 degrees). X or Y values exceeding 100 cm/s were excluded.
1037 Then, X and Y values were interpolated at 21.3Hz as fluorescence signals, and linear velocity D was
1038 computed as:
1039

1040 $$D = (X^2 + Y^2)^{\frac{1}{2}}$$

1041
1042 *Rotational velocity calculation and directional preference:*
1043 To compute rotational velocity, lateral readings from both computer sensors were first converted to
1044 radians/sec, and then averaged. Readings corresponding to angular velocities exceeding a magnitude

1045 of 15 radians/s were excluded. Readings were then converted to angular displacement, interpolated at
1046 21.3Hz, and then converted to rotational velocity.
1047
1048 *Identification of sustained periods of movement with high and low linear velocity:*
1049 We identified periods of high versus low linear velocity similarly to Barbera et al.[12]. Briefly, we first
1050 smoothed linear velocity traces using a 1.5Hz low-pass filter (MATLAB commands "butter" and then
1051 "filtfilt" for zero-phase filtering). Periods of high speed movement were identified as the time periods
1052 with linear velocity exceeding 5 cm/s for more than 2 seconds (43 data points). Similarly, periods of
1053 low speed movement were those where linear velocity remained below 1 cm/s for more than 2
1054 seconds. Periods overlapping with the beginning or end of the session were excluded.
1055
1056 *Movement onset, offset and peak velocity identification:*
1057 To identify movement onset, offset, and peak velocity, we used the unsmoothed linear velocity trace.
1058 To identify movement onsets, we first identified acceleration transition points as those when linear
1059 velocity rose to above 5cm/s. A movement onset was then defined as the second data point prior to
1060 the transition points where velocity remained $\leq$ 5cm/s for at least ~500ms (10 data points) before, and
1061 exceeded 40 cm/s at some point within ~1000ms (20 data points) after. To identify movement offsets,
1062 we first identified deceleration transition points as those when linear velocity decreased to below
1063 5cm/s. Movement offset was defined as the point before the deceleration transition point where
1064 velocity exceeded 15 cm/s within ~500ms before, and also remained $\leq$ 5cm/s for at least ~500ms after
1065 the transition point. Peak velocity was identified as local maximum using the MATLAB function
1066 "findpeaks", which were then thresholded at 55 cm/s. To identify rotational onsets, we identified the
1067 acceleration transition point when absolute rotational velocity increased to above 0.5 radians/s. A
1068 rotation onset was then identified as the second data point prior to the transition point where velocity
1069 remained $\leq$ 0.5 radians/s for at least ~500ms before, and also exceeded 2 radians/s within ~1000ms
1070 after. Movement onsets and offsets that extended beyond the length of the session were truncated to
1071 the beginning and end of the session.
1072
1073 **Relationship between calcium activity and movement**
1074
1075 *Movement triggered calcium fluorescence:*
1076 Population movement-triggered fluorescence was computed on $\Delta F/F$ values from each neuron over
1077 100 time points (Figures S4 and S7), or 200 time points (Figures 2D and 2F), on either side of each
1078 movement event (*onset, offset and peak velocity).* All recording sessions from all mice were used.
1079 Error bar plots were plotted neuron-wise, and the value for each neuron is the mean of the 40 data
1080 points before or after each movement event. These neuron-wise averages and statistics were
1081 computed after first identifying and averaging windows of 50 time points on either side of each event
1082 for each neuron.
1083
1084 To compare the timing of maxima in fluorescence around velocity peaks, we examined a window of
1085 100 time points before and after each velocity peak. We constructed a mixed effects model, averaging
1086 fluorescence values over a 6 second window for each neuron, grouped in 1-second bins, beginning 2
1087 seconds before each velocity peak. Models were fitted using maximum likelihood, MATLAB function
1088 "fitlme", and p-values were determined using the residual degrees of freedom. The full mixed-effects
1089 model appeared as, in Wilkinson notation:
1090
1091 Fluorescence ~ 1 + Time*Cell_type + (1 | Event_ID) + (1 | Cell_ID) + (1 | Mouse)
1092
1093 Where, "Time" refers to the time bin, "Cell_type" to the genotype of the respective cell. Random
1094 intercepts were included for each mouse ("Mouse"), for each individual cell ("Cell_ID"), and for each
1095 peak-velocity event ("Event_ID"). In these models, we identified the time period of maximum
1096 fluorescence by finding the bin with the highest expected value. After identifying a significant
1097 interaction term between Time and Cell_type, we broke up this model by cell type. P-values were

1098 corrected using the Benjamini-Hochberg procedure after pooling all p-values across all time bin
1099 comparisons to baseline in all models (15 total comparisons) [56].
1100
1101 To determine whether or not a neuron was significantly positively, or negatively, modulated by speed
1102 or rotation, we used one-tailed rank-sum tests to compare the fluorescence values of the 40 data
1103 points before versus after an identified movement onset, using a p-value threshold of 0.025. Neurons
1104 were then assigned to one of the four categories: speed-only, rotation-only, conjunctive, and neither.
1105
1106 To assess the proportion of neurons positively modulated in the 500ms before movement onset
1107 (Figure S2H), we analyzed each neuron's average fluorescence during baseline time points (-950 to -
1108 500 ms before movement onset) to the pre-movement period (-450ms to movement onset) using one-
1109 sided rank-sum tests with p-value cutoffs of 0.025. To quantify the time difference between PV and
1110 MSN fluorescence increases at movement onset, we identified the first time point in the movement
1111 onset window when averaged ΔF/F trace of all PV cells or MSNs of that session exceeded a ΔF/F of
1112 0.02. This represents a moderate increase in ΔF/F from baseline. The latency between PV cells and
1113 MSNs responses were then calculated across all sessions where this criterion was met (n=13
1114 sessions in total).
1115
1116 For proximity tests (Figure S9B-C), we first computed the proportion of neurons within 100um of a
1117 neuron that belongs to a certain category. We then compared the proportions surrounding neurons of
1118 a given category to proportions surrounding all other neurons. These two sets of proportions were
1119 compared neuron-wise. Neurons without any neighbors were excluded from analysis, and only MSNs
1120 were used for this analysis.
1121
1122 *<u>Neuron pair-wise asymmetric correlation analysis</u>*:
1123 An asymmetric correlation coefficient from neuron A to B was calculated as described previously using
1124 deconvolved calcium traces[12,33] using the equation:
1125

1126 $$r_{A \to B} = \frac{n_{A \cap B}}{n_A}$$

1127
1128 That is, the number of events in the deconvolved traces in neuron A that overlapped with events in
1129 neuron B were divided by the total number of events in neuron A. Pair-wise correlation between
1130 neurons A and B was then calculated as the averaged correlation coefficients in both directions, A to B
1131 and B to A.
1132
1133 To compute baseline correlation coefficients, the deconvolved traces were randomly shifted circularly
1134 and uniformly over the entire length as discussed by Barbera et al.[12]. This process was repeated 5000
1135 times for each neuron pair, and the correlation coefficients of these shifted traces were used to
1136 determine significance using one-sided p-values of <0.05 (Figure 4). Correlations with deconvolved
1137 traces with no events were labeled as NaN, and they were considered not significant. The random
1138 values in the plots (Figure 4D-E) are the mean shuffled correlation coefficients for each neuron pair.
1139
1140 To compare the proportions of neuron pairs with significant correlations that were spatially close (<100
1141 um) or spatially far (≥750 and <1500 um), we constructed a generalized linear model:
1142
1143 Is_significant ~ 1 + Cell_pair_type*Distance
1144
1145 where "Is_significant" is a random variable corresponding to whether or not the particular pair is
1146 significantly correlated, "Cell_pair_type" is a categorical variable corresponding to "MSN-CHI", "MSN-
1147 MSN", or "MSN-PV", and "Distance" is an indicator variable that equals 1 if the pair is spatially far. We
1148 used a binomial distribution with an identity link function. To compare differences between the time
1149 periods, we compared the interaction terms for all three pair-types.

1150
1151 For Figure 4A, we used the complete-linkage clustering function of MATLAB (linkage(*,'complete'),
1152 followed by cluster(*, 'cutoff', [distance cutoff], 'criterion', 'distance'), where [distance cutoff] was
1153 equivalent to 100 um). We statistically compared within-cluster and outside of cluster groups by
1154 treating each directional measure of asymmetric correlation as independent, and computed the rank-
1155 sum between the directional within-cluster and out-of-cluster groups. In this case, a correlation
1156 coefficient from A→B, where B has no events, has a correlation coefficient of 0, and in the opposite
1157 case (from B to A), of NaN.
1158
1159 For Figure 5A, the number of neuron pairs with significant correlations divided by the average number
1160 of neuron pairs with significant correlations in all bins, were plotted over their anatomical distance. The
1161 distance between pairs of neurons centroid(A) – centroid(B) or centroid(B) – centroid(A), was
1162 assigned randomly.
1163
1164 *Neuron pair-wise Pearson's correlation analysis*:
1165 Because of the sparseness of calcium events during periods of low speed movement, we used
1166 Pearson's correlation (Figure 4B and 4C). During each motor bout, the correlation coefficients were
1167 determined between each MSN pairs, and then averaged across all motor bouts for each session.
1168 Shuffled traces (1000 times) were created by concatenating ΔF/F values from high or low velocity time
1169 periods, for each ROI, and circularly shifting each concatenated trace by a random, uniformly-
1170 distributed value, over the length of the trace. Then, the shuffled traces were broken into segments
1171 equal to the length of the original high speed or low speed segments. Correlation values for each pair
1172 during high and low time periods were averaged over all 1000 repetitions.
1173
1174 *Correlation of MSNs subsets with distinct CHI populations:*
1175 To examine whether the same set of MSNs was correlated with CHIs that were positively or negatively
1176 modulated by movement (Figure S7G), we analyzed sessions with at least 1 positively movement-
1177 modulated CHI and 1 negatively movement-modulated CHI (n=8 sessions). To test whether the
1178 MSNs correlated with the positively modulated CHIs and the MSNs correlated with negatively
1179 modulated CHIs belong to different communities, we calculated the Jaccard index of the two sets of
1180 MSNs as follows:
1181

1182
$$Jaccard\ Index = \frac{MSN_{+} \cap MSN_{-}}{MSN_{+} \cup MSN_{-}}$$

1183
1184 In this equation, "MSN_+" represents the set of MSNs correlated with at least one positively modulated
1185 CHI using the pair-wise asymmetric correlation analysis, and "MSN_-" represents the set of MSNs
1186 correlated with at least one negatively modulated CHI. To test whether the MSNs correlated with these
1187 two types of CHIs were non-overlapping, we performed a permutation test (Figure S7G). Briefly, we
1188 first identified MSNs that exhibit significant correlation with any CHI. We then performed a
1189 bootstrapping procedure 5000 times without replacement. For each CHI, we randomly assignedfrom
1190 this pool of MSNs a number of MSNs equal to the number correlated with the given CHI. Then, a
1191 Jaccard Index was computed for each iteration.
1192
1193 *Neuron-triggered fluorescence analysis:*
1194 Neuron-triggered fluorescence was determined using deconvolved calcium traces (Figure 7A, B).
1195 In these analyses, triggering events are the time point immediate before calcium event onset. Unless
1196 otherwise noted, triggering events within 50 time points of the beginning or 51 time points of the end of
1197 the trace were not included for analysis. We centered fluorescence values for each MSN around each
1198 triggering event, and compared changes in ΔF/F values during the 10 data points (~500ms) after each
1199 event using a rank-sum test (ROI-event-wise). Standard error of the mean across the entire ~5 second
1200 interval was calculated with Welford's algorithm [57].

1201

1202 *Neuron-triggered speed and rotation:*

1203 To analyze changes in velocity following an event in a given cell type, we constructed a mixed-effects
1204 model using the MATLAB function “fitlme” on the normalized data (data was normalized for each cell
1205 type to the data point coincident with event onset, by subtracting and then dividing). In Wilkinson-
1206 notation the model was:

1207

1208 Velocity ~ 1 + Time*Cell_type + (1|Mouse) + (1|Cell_ID)

1209

1210 “Time” is a categorical variable corresponding to time bin. “Cell_type” corresponds to PV, MSN, or
1211 CHI in Figure 2H, or positively or negatively modulated cells in Figures S4H and S7H. We accounted
1212 for variance in intercept introduced by each mouse (“Mouse”) and each individual cell (“Cell_ID”). We
1213 broke up the model by cell type in order to test the effect of time by removing all terms relating to cell
1214 type, and created smaller models. P-values were corrected for the collections of p-values obtained
1215 from each of the smaller models using the Benjamini-Hochberg procedure.

1216

1217 Neuron-triggered rotation (Figure S8C) was analyzed in a similar way, using the absolute value of the
1218 rotational velocity in place of speed.

1219

1220 To determine the rate at which speed changed following a calcium event (Figure S2I), we first
1221 computed the normalized event triggered speed for each neuron. We then used the normalized speed
1222 values for each neuron between 0 and 1.5 seconds after each calcium event to construct a series of
1223 simple linear models. These models had predictors including only an intercept and the instantaneous
1224 time values, from which we obtained a slope value for each neuron. We compared slope values
1225 between the three neuron types using the following linear mixed-effects model:

1226

1227 Coefficients ~ 1 + Cell_type + (1|Mouse)

1228

1229 Here, “Coefficients” represent the slops of the simple linear models, “Mouse” and “Cell_type” are as
1230 described previously.

1231

1232 *Neuron co-activation analysis:*

1233 Co-activation was calculated using deconvolved calcium traces. We calculated the total number of co-
1234 active MSN pairs around each triggering event, defined as the data point before calcium event onset,
1235 and the total number of possible MSN pairs across all triggering events, for all neurons across all
1236 recording sessions. We then calculated the proportion of co-active pairs over all events out of total
1237 pairs over all events.

1238

1239 To compare across neuron types (Figure 7C), we averaged the two data points following each
1240 triggering event subtracted by the value at the triggering point, and the errors of the two data points
1241 were propagated. We then used the z-tests to compare between cell types. Shaded error bar plots
1242 (Figure 7C) are standard error estimates computed from: $\sqrt{\frac{p(p-1)}{n}}$, where p is the probability of the
1243 neuron pair being coactive at that time point, and n is the number of total pairs over all events. Error
1244 bar plots were centered at triggering onset.

1245

1246 To detect changes in movement speed around MSN-MSN peak co-activation (Figure 7F), we summed
1247 the deconvolved traces for all MSNs recorded in each session, and identified MSN-MSN co-activation
1248 as when the summed activity exceeded 2 standard deviations above the mean. Peak co-activation
1249 within each co-activation period is identified as the local maximum. If two local maxima of the same
1250 amplitude occurred in the same co-activation period, the first peak was used. Co-activations within
1251 100 time points of the beginning or end of a recording session were excluded.

1252
1253 *Calculation of predictor performance using regression analysis:*
1254 To estimate how each cell type predicted movement or population MSN activity (Figure 6), we built
1255 linear models, and assessed the model performance using correlations similar to the time-series
1256 forecasting cross-validation method described by Hyndman and Athanasopoulos[58], and that used by
1257 Parker et al.[11]. We used the framework of partitioning a time series into equally-sized, temporally
1258 continuous sets for training and testing models. Data of the entire session was separated into 10
1259 consecutive and equally sized segments. Linear model parameters were determined using 9
1260 segments, and then the values for the last segment were predicted using these parameters. The
1261 Pearson correlation coefficient between the predicted values and the actual values of this last
1262 segment was used to assess predictive ability. This process was repeated 10 times, and the Pearson
1263 correlation coefficients were averaged for a given predictor. To plot predicted values for both summed
1264 MSN fluorescence and speed, predictors were determined using the entire session.
1265
1266
1267 To predict linear velocity using MSN, PV, CHI cells (Figures 6D, 6H), we first binned $\Delta F/F$ traces and
1268 linear speed to 0.1 second bins. $\Delta F/F$ traces were then combined, and their average Z-scored $\Delta F/F$
1269 value was used as the predictor variable. Then, this predictor along with an intercept was tested using
1270 our modified cross-validation. To estimate the predictor performance of MSN subpopulations, a
1271 random subsample of MSNs with equal number of simultaneously recorded interneurons in the
1272 session was used. This process was repeated 5000 times, and the average value was used as the
1273 predictor performance for each recording session. For single interneurons and single MSNs, the
1274 average value across all single neurons was used as the predictor performance for each session. For
1275 sessions in which there was only 1 interneuron, the mean value over all single MSNs was used as the
1276 value of the MSN subpopulation.
1277
1278 To predict MSN population fluorescence (Figures 6B, 6F), we used summed population MSN
1279 fluorescence as the response variable. Each predictor was binned as above. To estimate the predictor
1280 performance of MSN subpopulations, random subsample of MSNs with equal number of
1281 simultaneously recorded interneurons in the session was used, and the MSN population response was
1282 calculated without the sub-sampled MSNs. This process was repeated 5000 times and the average
1283 value was used as the predictor performance. An intercept term was also included in each model.
1284 These analyses were also performed using only positively- or negatively-modulated interneurons
1285 (Figures S4I and S7I), for sessions that had at least 1 positively and 1 negatively modulated
1286 interneuron.
1287
1288 To compare predictor performance (Figure S12), we incorporated cell type into a simple, multivariate
1289 mixed-effects model:
1290
1291 Velocity ~ 1+ Fluorescence + Cell_type:Fluorescence + Velocity_lag1 + Velocity_lag2 + (1|Session) +
1292 (1+Fluorescence|Cell_ID)
1293
1294 "Cell_type" is the genotype of the predicting neuron, "Fluorescence" is the z-scored average
1295 fluorescence over 0.1 second bins, "Session" is a session ID corresponding to the fluorescence trace,
1296 and Cell_ID corresponds to each cell. Velocity is the z-scored, binned velocity, and Velocity_lag1 and
1297 Velocity_lag2 are analogous terms accounting for the autocorrelation of Velocity values. For the
1298 complete analysis, data from all 28 sessions were used, and MSNs were used as the reference cell
1299 type variable. In order to plot this analysis, the above mixed effects model was also run separately for
1300 each session with at least 1 interneuron (10 CHI sessions and 17 PV sessions), and the coefficient of
1301 the interaction term that corresponded to Cell_type:Fluorescence was plotted. Because each session
1302 was modeled separately, the (1|Session) term was excluded from these models. Each dot in this plot
1303 corresponds to a coefficient from each of these smaller models, and the lines correspond to the
1304 coefficient values from the larger model.

Optogenetic activation induced changes in calcium activity and movement

Laser-triggered Changes in calcium fluorescence, calcium event probability, and neuron co-activation:
ROI identification, trace extraction, and movement data processing were largely the same as described above for nonoptogenetic sessions. One session displayed two brief (~2 and ~14 seconds) large motion artifacts during part of the recording, and we replaced the affected data points with interpolated values. Another session displayed a baseline shift toward the beginning (~50 seconds), these data were excluded from further analysis.

To examine laser induced fluorescence change in MSNs, PV cells, and CHIs (Figure S11), we aligned the ΔF/F of each cell to laser illumination period. The difference in fluorescence following laser stimulation onset (20 time points) versus the 20 time points immediately prior to laser onset was compared cell-wise.

To examine the change in calcium event probability, we used deconvolved calcium traces (Fig. S11E-F). Event probability was aligned to laser onset for each neuron, and we normalized the event probability by averaging the across all sessions the respective neuron type in the corresponding mice.

To examine changes in neuron co-activation (Figure 7D-E), we first computed MSN-MSN co-activation at the onset of MSN triggering events during non-laser time period by averaging the two time points immediately following each event onset. Events within 50 time points of the beginning of the session or the end of the session were not included. To compute the mean co-activation of MSN-MSN pairs during each laser period, all neuron pairs were combined after normalizing co-activation values by dividing by the mean co-activation during non-laser epochs. This was repeated for non-laser epochs as well, in Figure 7E. To plot MSN-triggered co-activation during non-laser period (7D), we analyzed the 50 time points on either side of the triggering event after discarding events within 100 time points of the beginning or end of a recording session. To plot the laser-triggered MSN-MSN co-activation time series, we plotted the mean and the standard error of the mean across all time points after normalizing via the previously mentioned Welford's algorithm[57].

For MSN-triggered and laser-triggered co-activation for both Chat-Chrimson and PV-Chrimson mice, we used pairwise z-tests and the sample means and sample standard errors of the means as estimates to test significance. Figure 7E was plotted event-pair wise with event-pairs included from all sessions.

Laser-triggered changes in movement velocity:
We calculated normalized movement velocity to the movement speed immediately before each laser onset, and then subtracted 1 to represent changes. To test whether or not there was a significant change in speed during laser activation, we used a linear mixed-effects model on the normalized velocity. Our models appear as follows:

Velocity ~ 1 + Time + (1|Mouse) + (1|Event_ID) + (1+TimeBin|Event_ID) + (1+Mouse|Event_ID)

"Event_ID" here corresponds to unique laser epochs. We tested for a significant main effect of time using an ANOVA on this model, and computed post-hoc t-tests for each time bin versus the time bin at time t=0. P-values were corrected within each model using the Benjamini-Hochberg procedure. We then separated data into those events occurring only in sustained low-speed time periods, and then repeated the analysis on these smaller data sets. Both Figures 3B and 3C are plotted event-wise.

Laser-triggered changes in direction:
To distinguish between vigorous directional change from small rotational velocity changes associated with balancing behavior, we set a threshold where directional changes exceeding 1 radian/second

1358 were counted as vigorous directional changes. To quantify whether there were more vigorous
1359 directional changes during laser-on time periods versus laser-off time periods, we identified all
1360 directional changes for each session, and compared the probability of such changes during each
1361 laser-on versus laser-off time period across all sessions. We compared the difference in the
1362 probabilities of directional changes during the rising and falling phases of PV or CHI calcium events
1363 (including events continuous with the beginning of the session), versus other time periods (Figure
1364 S8A,C), neuron wise.
1365
1366 *Correlations of MSN activity with laser-induced PV activation*
1367 To examine the uniformity of PVs influence on MSNs, while the population of PV interneurons was
1368 activated optogenetically, we calculated the number of MSNs that had significant asymmetric
1369 correlation coefficients during optogenetic stimulation in PV-Chrimson-TDT mice. This analysis was
1370 identically to the neuron pair-wise asymmetric correlations described above in the non-optogenetic
1371 mice. To compute significance, we randomly and circularly shifted the deconvolved MSN traces 5000
1372 times to generate a distribution of randomly shifted MSN traces. We then computed the asymmetric
1373 correlation coefficients between the randomly shifted MSN traces and laser-on time periods. To test
1374 whether or not PV optogenetic activation homogeneously affected the MSN population (Figure S4G),
1375 we randomly sampled with replacement 10000 times the binary values as to whether or not an MSN
1376 was significantly correlated with laser-on time periods. We compared the proportion of MSNs
1377 significantly correlated to zero by taking the total number of random samples with no significantly
1378 correlated values and dividing by the total number of samples (10000). We compared the proportions
1379 of MSNs to a value of one analogously.
1380
1381 **Histology and quantification:**
1382 At the end of the experiments, all mice were transcardially perfused and tissue was processed to
1383 confirm GCaMP6f as well as tdTomato expression, and cannula placement. Mice were perfused with
1384 30 mL 0.01M phosphate buffered saline (Fisher Scientific, BP2944-100, Pittsburgh, PA), followed by
1385 30 mL 4% paraformaldehyde (Sigma Aldrich, 158127, St. Louis, MO). Brains were carefully removed
1386 and post-fixed overnight in 4% paraformaldehyde before being transferred to a 30% sucrose solution.
1387 Brains were sectioned horizontally at a thickness of 40μm with a freezing microtome (CM 2000R;
1388 Leica). Tissue sections were collected throughout the striatum. A subset of sections (4-6 sections per
1389 animal) were stained with antibodies against PV (rabbit anti-PV, SWANT PV25 1:1000) or Chat (goat
1390 anti-Chat antibody, Millipore AB144P 1:500), followed by Alexa Fluor 633 goat anti-rabbit secondary
1391 antibody for PV staining (Invitrogen A11011, 1:1000) or Alexa Fluor 633 donkey anti-goat secondary
1392 antibody for Chat staining (Life Technologies, A21082 1:200). Antibodies and dilution concentrations
1393 were previously reported [59,60]. Briefly, sections were rinsed with 0.05 M Tris-HCL-buffer (Tris, pH=7.6),
1394 followed by 60 mins rinse in blocking buffer containing 5% serum and 0.2% Triton. Sections were
1395 incubated for 24 hours with primary antibody. Sections were then rinsed 3X at 10 min each in Tris-
1396 HCL and then incubated with the secondary antibody for 2 hours. Sections were rinsed again and then
1397 mounted on gelatin-coated slides using anti-fade mounting media (Vectashield H-1400).
1398
1399 Confocal images were taken on an Olympus FV1000 scanning confocal microscope using a 60X
1400 water immersion lens. All images were comprised of Z-stacks taken at 5 μm intervals throughout the
1401 40μm slices. Stacks were taken from horizontal sections as near as possible to the bottom of the
1402 imaging window and all imaging stacks were taken within 1 mm of the imaging plane. Areas were
1403 chosen to include similarly dense tdTomato cell counts across animals by an experimenter blinded to
1404 the animal strain. To confirm targeting specificity, each tdTomato+ cell was categorized as immune-
1405 positive or immune-negative for the antibody stain. We also quantified the number of immune-positive
1406 cells from each stack that were tdTomato+ to estimate the infection efficiency near the imaging
1407 window. We analyzed 2-4 non-overlapping confocal stacks from 4-6 slices per animal from a large
1408 subset of animals that made up our GCaMP imaging dataset (n=7 PV-Cre) and (n=7 Chat-Cre mice).
1409 Cell counts were pooled across slices stained for the same marker for each animal, and averaged to
1410 produce a single data point for quantification.

Statistical Tests

Sample sizes were estimated based on neuron yields from pilot studies and published anatomical descriptions of PV and CHI population densities using G*Power 3.1.9.2. We applied a two tailed Wilcoxon-Mann-Whitney test utilizing a β/α ratio=1.0, an effect size of 0.5. Additional assumptions included the expectations of 300 neurons/recording and PV and CHI density of 2.5% of all cells. Our sample sizes are also consistent with previous publications of calcium imaging in the striatum[14,38,51].

Researchers were aware of the animal strain at the time of recording but analysis was done off-line by a researcher that was unaware of cell identity. For histology experiments, areas were chosen to include similarly dense tdTomato cell counts across animals by an experimenter blinded to the animal strain.

Data recording sessions were randomized between PV and Chat animals over the course of the study. Optogenetic stimulations sessions were randomized in Chrimson and tdT control animals with several non-stimulation days occurring between the two sessions. For all calcium imaging sessions, no direct replication was performed although each animal was subjected to calcium imaging 1-3 times and data was collapsed together for analysis. For confocal images, we analyzed 2-4 non-overlapping confocal stacks from 4-6 slices which were pooled together per animal and averaged for quantification.

The detailed statistical tests were described above in related analysis. Briefly, the following statistical tests were used in this study: Chi-square tests, Wilcoxon rank-sum tests, sign-tests, Kruskal-Wallis tests, Friedman tests, Fisher tests, binomial tests, z-tests, and Pearson's correlation. When conducting non-parametric tests we did not make any assumptions of data, including normality. For z-tests, the sample sizes of the distributions were large enough that by the central limit theorem, their means were expected to follow normal distributions. If present in a sign-test, ties were removed from consideration automatically and their presence was noted in the manuscript. All values that evaluated to "NaN" were treated as missing data.

All tests were two-tailed unless noted otherwise. Post-hoc tests were conducted using the MATLAB function "multcompare" following a Kruskal-Wallis or a Friedman test. Use of this function was noted in the manuscript as "Tukey's HSD", as it utilizes for both Kruskal-Wallis and Friedman Tukey-like procedures for non-parametric data.

Data were plotted using neuron-weighted averages unless otherwise noted. Standard error of the mean was computed using the standard formula, based on the assumption of normality of the mean regardless of the shape of the underlying distribution whose mean we describe. Because non-parametric statistics are used throughout the manuscript, estimated standard errors of the mean were shown primarily as a tool for visualization. Unless otherwise noted, box plots were constructed via the MATLAB function "boxplot", and outliers were removed for visualization. Outliers were determined automatically by the "boxplot" function. They were defined as data points that were greater than the third quartile value plus 1.5 times the distance between quartile three and quartile one, or data points that were less than the first quartile value minus 1.5 times the distance between quartile three and quartile one.

Please refer to the Life Sciences Reporting Summary for a detailed description of all statistical tests used and Study Design.

Data availability statement

All raw data will be available by request.

Software availability statement:

1464 All source code and custom scripts for analysis will be made available at request.
1465
1466 **Online Methods References**
1467
1468 51 Dombeck, D. A., Khabbaz, A. N., Collman, F., Adelman, T. L. & Tank, D. W. Imaging large-
1469 scale neural activity with cellular resolution in awake, mobile mice. *Neuron* **56**, 43-57,
1470 doi:S0896-6273(07)00614-9 [pii]
1471 10.1016/j.neuron.2007.08.003 (2007).
1472 52 Mohammed, A. I. *et al.* An integrative approach for analyzing hundreds of neurons in task
1473 performing mice using wide-field calcium imaging. *Sci Rep* **6**, 20986, doi:10.1038/srep20986
1474 srep20986 [pii] (2016).
1475 53 Mukamel, E. A., Nimmerjahn, A. & Schnitzer, M. J. Automated analysis of cellular signals from
1476 large-scale calcium imaging data. *Neuron* **63**, 747-760, doi:10.1016/j.neuron.2009.08.009
1477 S0896-6273(09)00619-9 [pii] (2009).
1478 54 Pnevmatikakis, E. A. *et al.* Simultaneous Denoising, Deconvolution, and Demixing of Calcium
1479 Imaging Data. *Neuron* **89**, 285-299, doi:10.1016/j.neuron.2015.11.037
1480 S0896-6273(15)01084-3 [pii] (2016).
1481 55 Jia, H., Rochefort, N. L., Chen, X. & Konnerth, A. In vivo two-photon imaging of sensory-
1482 evoked dendritic calcium signals in cortical neurons. *Nat Protoc* **6**, 28-35,
1483 doi:10.1038/nprot.2010.169
1484 nprot.2010.169 [pii] (2011).
1485 56 Reiner, A., Yekutieli, D. & Benjamini, Y. Identifying differentially expressed genes using false
1486 discovery rate controlling procedures. *Bioinformatics* **19**, 368-375 (2003).
1487 57 Knuth, D. E. *The art of computer programming*. (Addison-Wesley, 2005).
1488 58 Hyndman, R. J. & Athanasopoulos, G. *Forecasting : principles and practice*. (OTexts, 2013).
1489 59 James, N. M., Gritton, H. J., Kopell, N., Sen, K. & Han, X. Muscarinic receptors regulate
1490 auditory and prefrontal cortical communication during auditory processing.
1491 *Neuropharmacology*, doi:S0028-3908(18)30814-1 [pii]
1492 10.1016/j.neuropharm.2018.10.027 (2018).
1493 60 Keaveney, M. K. *et al.* A MicroRNA-Based Gene-Targeting Tool for Virally Labeling
1494 Interneurons in the Rodent Cortex. *Cell Rep* **24**, 294-303, doi:S2211-1247(18)30959-8 [pii]
1495 10.1016/j.celrep.2018.06.049 (2018).
1496