Article

# **Temporal dynamics of nucleus accumbens neurons in male mice during reward seeking**

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	The nucleus accumbens (NAc) regulates reward-motivated behavior, but the temporal dynamics of NAc neurons that enable "free-willed" animals to obtain rewards remain elusive. Here, we recorded $Ca^{2+}$ activity from individual NAc

temporal dynamics of NAc neurons that enable "free-willed" animals to obtain rewards remain elusive. Here, we recorded  $Ca^{2+}$  activity from individual NAc neurons when mice performed self-paced lever-presses for sucrose. NAc neurons exhibited three temporally-sequenced clusters, defined by times at which they exhibited increased  $Ca^{2+}$  activity: approximately 0, -2.5 or -5 sec relative to the lever-pressing. Dopamine D1 receptor (D1)-expressing neurons and D2-neurons formed the majority of the -5-sec versus -2.5-sec clusters, respectively, while both neuronal subtypes were represented in the 0-sec cluster. We found that pre-press activity patterns of D1- or D2-neurons could predict subsequent lever-presses. Inhibiting D1-neurons at -5 sec or D2neurons at -2.5 sec, but not at other timepoints, reduced sucrose-motivated lever-pressing. We propose that the time-specific activity of D1- and D2neurons mediate key temporal features of the NAc through which reward motivation initiates reward-seeking behavior.

Volitional reward-motivated behavior is not the mere act of taking a reward; it emerges through a sequence of preluding cognitive and other behavioral events. These events include processes like goal-engaging, action-initiating, distraction-blocking, and other cognitive/ behavioral components, which operate collectively and sequentially to commit the animal towards making an operant response for a reward<sup>1-3</sup>. Neural underpinnings contributing to these pre-operant events remain largely unknown.

The nucleus accumbens (NAc) has long been recognized for its involvement in reward-motivated behaviors, specifically linking motivation to reward-taking<sup>4,5</sup>. Comprising >90% of the neuronal population in the NAc, principal medium spiny neurons (MSNs) are largely divided into two subpopulations, dopamine D1 receptorexpressing MSNs (D1-MSNs) and D2-MSNs, which are differentially involved in reward-motivated behavior<sup>6-13</sup>. Due to these cell-typebased differences and other heterogeneous features, NAc MSNs are thought to form distinct ensembles, each contributing to specific aspects of reward-motivated behavior<sup>14-17</sup>. Using in vivo recordings, rodent studies demonstrate that some NAc MSNs exhibit increased activity upon reward delivery and consumption, while some others preferentially respond to predictive cues preceding reward delivery<sup>18,19</sup>, suggesting an ensemble-based organization of NAc MSNs across different temporal phases of motivational responses. Relevant to the pre-operant phase, elevated activities are observed in a population of NAc MSNs before a reward-conditioned task, while NAc lesions decrease the likelihood of rats to initiate operant

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Through GCaMP6m-mediated Ca<sup>2+</sup> imaging, we observed that, during established sucrose SA, NAc neurons organized into three temporally distinct clusters, exhibiting activity increases at -0, --2.5, or --5 s relative to the time of the lever-press. We show that the -5- and -2.5-s clusters comprised preferentially D1- versus D2-neurons, respectively, while both D1- and D2-neurons constituted the 0-s cluster. In addition, the activity patterns of D1-neurons at --5 s and D2neurons at --2.5 s provided heightened prediction accuracy for subsequent lever-presses. Optogenetic inhibition of D1-neurons at -5 s or D2-neurons at -2.5 s, but not at other timepoints, reduced subsequent lever-pressing for sucrose. Together, these findings offer insight into the sequential activity changes of NAc D1- and D2-neurons that link reward motivation to behavioral output.

# Results

## Three clusters of NAc neurons

To detect the temporal dynamics of individual NAc neurons in freely moving mice, we stereotaxically injected GCaMP6m-expressing AAV9 into the NAc and installed a GRIN lens above the injection site (Fig.1A, B). While the medial shell of the NAc was targeted, portions of the NAc core were also likely included in the sampling and viral manipulations due to the small size of the mouse NAc (Fig. S1A, B). Six weeks later, we trained these mice with an overnight (12-h; see Methods) sucrose SA session, followed by an 11 d SA procedure (1 h/session/ d), during which the mice were allowed to move freely and lever-press for a sucrose solution (10%) (Fig. 1C, D). During the first 20 min of selected SA sessions, we recorded GCaMP6m-mediated Ca<sup>2+</sup> signals continuously through a miniaturized fluorescence microscope (Miniscope)<sup>22</sup>, and extracted Ca<sup>2+</sup> transients from individual NAc neurons (Fig. 1E–G).

To quantify activity changes of individual neurons, we computed z-scores of  $Ca^{2+}$  traces (see Methods). We defined the time of leverpress as the 0-s timepoint and created a dataset that extracted z-scores of individual neurons between 10s before and 10s after each leverpress from seven wild-type mice (Fig. S1B). We first performed sequence-based sorting, which aligned neurons by the time they exhibited initial (Fig. 1H, I) or peak (Fig. S1C, D) activity increases. In a control dataset, in which neuronal activities were sampled during a randomly selected 20-s time window (trial) without lever-press, neurons were distributed evenly over time, indicating a quasi-random activity pattern of NAc neurons when mice moved freely without involving motivated sucrose-seeking (Figs. 1H and S1C). During leverpress trials on SA d 11, more neurons were detected before or around the lever-press timepoint (Figs. 11 and S1D), suggesting that select populations of NAc neurons synchronized their activities during the pre- and on-press phases.

To explore the timing of synchronized neuronal activities during the 20-s trials, we performed a timing-based sorting, which aligned neurons to a specific timepoint based on their increases in z-scores. When sorting neurons with increased activities to 0 s, we observed a 0-s neuron cluster as well as a substantial number of neurons with increased activities before 0 s (Fig. 1J), suggesting the existence of prepress neuron clusters. We thus performed K-means clustering to identify the timepoints at which NAc neurons would exhibit synchronized activity increases. This analysis revealed three neuron clusters, exhibiting increased activities at ~-5, ~-2.5, and ~0 s, respectively (Fig. 1K). We also examined clustering neurons into a smaller or larger number of clusters, but found that three clusters performed the best (Fig. S1E–G, J).

Further analysis revealed that, within each of these three clusters, some neurons exhibited increased activities with their mean z-scores >0 over a 1-s range around the cluster center timepoint, while others displayed mean z-scores <0. Based on these activity properties, we operationally defined them as "activated" versus "nonactive" neurons, respectively (Fig. S1H). Thus, activated neurons may represent a





0-s timepoint. Horizontal and oblique lines (with the same slope) are drawn to aid visualization. J Timing-based sorting of neurons with increased activities to 0 s showing the 0-s cluster as well as some neurons with increased activities during the pre-press phase. K K-means clustering detected three clusters that best described the temporal dynamics of NAc neurons during the 20-s lever-press time window. Dashed lines/arrows indicate -5, -2.5, and 0 s. L Summary of the collective z-scores of activated neurons over the 20-s lever-press time window showing three temporally distinct neuronal clusters. Dashed lines/arrows indicate -5, -2.5 and 0 s. Source data are provided in the Source Data file associated with this manuscript. Lines and shades present means and standard errors, respectively.



**Fig. 2** | **Differential contributions of D1- and D2-neurons to NAc clusters. A** Sequence-based sorting of D1-neurons with increased activities on sucrose SA d 11. Dashed lines/arrows indicate timepoints of 0, -2.5, or -5 s in this and the following panels. **B** Timing-based sorting of D1-neurons with increased activities to 0 s. **C** Sequence-based sorting of D2-neurons with increased activities on SA d 11. **D** Timing-based sorting of D2-neurons with increased activities to 0 s. **E** Timingbased sorting of D1-neurons with increased activities to 0 s. **E** Timingbased sorting of D1-neurons with increased activities to -5 s. **F** K-means clustering results show two clusters of D1-neurons. **G** Timing-based sorting of D2-neurons with increased activities to -2.5 s. **H** K-means clustering showing two clusters of D2-

neurons. **I**, **J** Collective z-scores of activated D1-neurons (**I**) or D2-neurons (**J**) in each cluster showing the temporal dynamics over the 20-s time window. Lines and shades present means and standard errors, respectively. **K** Summaries showing the mean timepoints of K-means clustering-defined clusters of D1-neurons (in s:  $-4.7 \pm 0.3$ ;  $-0.2 \pm 0.2$ ; n = 5) or D2-neurons (in s:  $-2.8 \pm 0.3$ ;  $0.3 \pm 0.2$ ; n = 6), as well as neurons from wild-type mice (in s:  $-4.6 \pm 0.4$ ;  $-2.3 \pm 0.2$ ;  $-0.4 \pm 0.4$ ; n = 7). Middle and outer lines present means and standard errors, respectively. Source data are provided in the Source Data file associated with this manuscript.

neuronal population, or a functional ensemble, that is selectively involved in constructing the pre-press temporal dynamics. To illustrate the time-dependent activity changes of the three clusters, we plotted collective z-scores (integration of number and activity intensity of neurons) of either activated neurons (Fig. 1L) or the top 50% of neurons ranked by activity (see Methods; Fig. S1I), with both showing similar temporal dynamics for each of the three clusters. Together, these clusters may represent three at least partly distinct functional ensembles that sequentially contribute to the cognitive-behavioral events during the pre- or on-press phases of sucrose-motivated behavior.

#### D1- versus D2-neurons

Representing the two major subtypes of principal neurons in the NAc, D1- and D2-MSNs may contribute differentially to the three clusters related to sucrose SA. To explore this, we injected AAV-Flex-GCaMP6m in the NAc of D1-Cre or D2-Cre mice, which resulted in GCaMP6m

later, we monitored the activities of individual neurons in these mice
 during the 11-d sucrose SA procedure (Fig. S2A–D).
 On SA d 11, sequence-based sorting revealed prominent portions

of D1-neurons exhibiting increased activities during the pre- and onpress phases (Fig. 2A). Timing-based sorting of D1-neurons to 0 s showed a 0-s cluster, as well as a substantial percentage of neurons exhibiting increased activities during the pre-press phase (Fig. 2B). Similarly, populations of D2-neurons exhibited activity increases during both the pre- and on-press phases on SA d 11, (Fig. 2C, D).

expression in D1- or D2-neurons, respectively. Approximately 6 weeks

Over the 20-s trial, we found more D1- and D2-neurons that exhibited high activity (i.e., >95% of the mean z-scores of all neurons) at ~-5 and ~2.5 s, respectively, compared to other timepoints (Fig. S2E-H). Furthermore, rather than the three neuronal clusters deduced in wild-type mice, the cluster-wise assessment of cluster stability revealed that two clusters best captured the organization of either D1-neuron or D2-neuron activities during the pre- and on-press phases (Fig. S2I, J). Based on the timing of the two pre-press clusters described in wild-type mice, we performed timing-based sorting to align D1- and D2-neurons with increased activities to either -2.5 or -5 s. We found that -5 s better aligned the pre-press activities of D1-neurons (Figs. 2E and S2K, L). K-means clustering likewise revealed that the activities of D1-neurons were described by two clusters centered at --5 and -0 s (Fig. 2F). On the other hand, timing-based sorting to -2.5 s better aligned the pre-press activities of D2-neurons compared to -5 s (Figs. 2G and S2M, N), with K-means clustering also identifying two clusters of D2-neurons centered at --2.5 and -0 s (Fig. 2H).

As observed for neurons in wild-type mice, D1- or D2-neurons were both composed of activated and nonactive portions in each cluster (Fig. S2O, P). Time-dependent changes in collective z-scores of activated neurons revealed distinct temporal dynamics of the D1- neuron versus D2-neuron clusters during the pre-press phase (Fig. 2I, J). As a further validation, we pooled all activated D1- and D2-neurons together for K-means clustering analysis. This reconstituted population of both neuronal subtypes once again revealed three clusters with temporal dynamics consistent with those seen in wild-type mice (Fig. S2Q). Importantly, the -5- and -2.5-s clusters grouped by K-means clustering from pooled neurons were enriched in D1- and D2-neurons, respectively (Fig. S2R).

The three timepoints (--5, --2.5, and -0 s) above were estimated based on neurons pooled from all mice in each group. K-means clustering of individual mice revealed between-subject variations, but the deductions remained consistent with the mean timepoints (Fig. 2K).

Taken together, our findings show that D1-neurons and D2neurons differentially contribute to the two sequential clusters during the pre-press phase, which may contribute to a sequence of cognitivebehavioral events that leads to operant responses for sucrose. Meanwhile, both D1- and D2-neurons contribute to the 0-s cluster, corresponding to the lever-press action and sucrose consumption.

#### Populational activity patterns

To test whether the pre-press neuronal activity can predict leverpressing, we performed a variant of principal component analysis (PCA)<sup>23</sup>, in which we built our PCA matrix on a trial-averaged 30-s time window, centered around lever-presses (Fig. S3A). The first two principal components (PCs) captured >30% of the variance of trialaveraged data from D1- or D2-neurons, as well as neurons in wild-type mice (Fig. S3B).

For each mouse on SA d 11, we plotted the PC1 and PC2 values over the 20-s trials with lever-pressing, using the PC plot of randomly selected 20-s trials as baseline controls. In an example D1-Cre mouse, the lever-press and baseline control PC data points appeared largely overlapping at -10 s but separated at 0 s (Figs. 3A, B and S3C, D). To quantify this separation, we identified the centroids of lever-press versus non-lever-press data points in each mouse, measured the Euclidiean distance between the two centroids, and normalized it to the centroid distance between two baseline controls in the same mouse to obtain the relative distance (Figs. 3A, B and S3C, D). In D1neurons, the relative distance of lever-press exhibited a peak at ~-5 s, followed by larger increases of ~0 s (Fig. 3C). In D2-neurons, the relative distance of lever-press exhibited an increase at ~-2.5 s, followed by larger increases at ~0 s (Fig. 3D). When assessed by the bootstrapped confidence interval (BCI; see Methods) analysis, although most intervals (n = 100 samples × fivefold points = 500/interval) of active leverpress trials exhibited higher relative distance values compared to control trials, the magnitudes of confidence around -5s (t value interval, 22. 5–27.2) were not overlapping with and were significantly higher than -2.5 s (7.6-11.9) in D1-neurons, as were D2-neurons at -2.5 s (32.7-38.1) compared to -5 s (5.6-9.7). When repeating this in a higher dimensional space with ten PCs, we observed similar results (Fig. S3E, F). These results confirm that D1- and D2-neurons display distinct temporal dynamics during the pre-press phase.

The linear assumption of PCA may omit some nonlinear aspects of neuronal dynamics, so we used  $MIND^{24}$  to conduct nonlinear dimensionality reduction. Using the seven-dimensional embedding of the manifold (Fig. S3G), we took the first two dimensions and built a series of support vector machine-based classifiers<sup>25,26</sup> to test whether neuronal activities during the pre-press phase predict the action of lever-pressing. Our results show that the ability of Support Vector Machine classifiers to predict the upcoming lever-press increased at ~-5 s for D1-neurons [*t* value BCI interval (*n* = 100 samples/intervals), 7.3–12.2] and at ~-2.5 s for D2-neurons [*t* value BCI interval (*n* = 100 samples/intervals), 16.0–21.2], respectively (Fig. 3E, F).

To further characterize the conserved neural dynamics of D1- and D2-neurons that may predict future lever-presses, we examined the flow of neural trajectories. In two-latent dimensions from MIND outputs, we plotted the coordinates of D1- or D2-neurons at individual timepoints over the 20-s trials, and used arrows that connected the two timepoints (1.5 s apart) to describe the neural trajectories through which neurons traveled (Figs. 3G–L and S3H–J). Our results show that the trajectories of D1-neurons to ~-5 s, and the trajectories of D2-neurons to either ~5 or ~2.5 s, converged better than the trajectories to randomly selected control timepoints (Figs. 3M and S3J). These results confirm—with some caveats (see Discussion) –the organized temporal dynamics of D1- and D2-neurons during the pre-press phase.

#### **Behavioral correlates**

To explore whether the two pre-press clusters are correlated with mice's movements, we used DeepLabCut (DLC)<sup>27</sup> to trace and analyze the motion of different body parts of the mouse during the 20-s leverpress trials, using trials without lever-press as baseline controls (Fig. 4A, B). Among the three major body parts (head, main body, and tail), the movement velocity of heads (averaged from 7 D1-Cre and 7 D2-Cre mice) exhibited relatively clear changes during pre-press phases, with an initial increase at ~-5 s and peak at ~2.5 s (Fig. S3K-M). Furthermore, over the 20-s lever-press trials, the activity intensities (zscores) of D1-neurons and D2-neurons were correlated positively with the velocities of head movement, and these correlations were more prominent for D1-neurons at -5 s and D2-neurons at -2.5 s, compared to other timepoints (Fig. S3N-Q). These correlations suggest a potential role of NAc clusters in either locomotion or cognitive states that are behaviorally manifested by head movements. Nonetheless, within the operant chamber, locations (assessed by head locations) of either D1-Cre or D2-Cre mice were rather random at -7.5 and -5 s, but moved close to the final responding zone (i.e., the mouse's location at -0.5 s) at -2.5 s (Fig. S3R-X). Moreover, the synchronized movement trajectories toward the final responding zone were not detected at -5 s, but at -2.5 s (Fig. S3Y, CC). These results suggest that the increase in head movement at -5 s may not signal locomotion, but reflect certain cognitive states.

To directly examine the roles of specifically-timed NAc clusters in launching the final act of lever-pressing for sucrose, we optimized a DLC-based algorithm to predict individual lever-presses during SA sessions. Our plan was to use in vivo optogenetics to interfere with the activity of NAc neurons in vivo at -5, -2.5, or -0.5 s, and examine whether these cluster-targeted interferences influence the likelihood of subsequent lever-presses. The first two timepoints (-5 and -2.5 s) correspond to the two pre-press neuronal clusters. The -0.5-s time-point corresponds to the rising phase of the 0-s cluster (Figs. 1L, 2I, J). We did not target 0 s per se, at which point the action of lever-pressing was already under way.

We trained the DeepLabCut algorithm using the combined information of the mouse's postures, positions, and movements during the pre-press phase (Figs. 4A, B and S4A). For each intended timepoint, the prediction was made 1s earlier, using the 5-s video immediately before the prediction-making timepoint, such that there was sufficient lead time for the computer to process positive



Fig. 3 | Populational activities of D1- and D2-neurons before lever-pressing for sucrose. A, B Two-dimensional PCA projections of NAc neuronal activities at -10 (A) and 0 s (B) from an example mouse. Each dot represents neuronal activities of a single trial (purple, baseline; green, lever-press). Center dots and lines represent means and standard deviations, respectively. C, D The distance of PCA centroids of D1-neurons (C) or D2-neurons (D) between lever-press and baseline trials. Solid lines, the mean distance of all tested mice; shade, standard errors. Dashed lines/ arrows indicate timepoints of 0, -2.5 or -5 s. E, F Support vector machine accuracy of lever-press prediction based on two latents extracted from D1-neuron (E) and D2-neuron (F) activities using MIND. Solid lines, mean accuracy of all tested mice, shade, standard errors. G, H Example mouse (D1-Cre) showing two-latent projections of D1-neuron activity of all lever-press trials. Each dot indicates the two-latent position of neurons at a single timepoint in a trial. Solid lines connecting two sets of latent coordinates of neurons at the times of (t-1.5 s) and (t) in each trial. "t" was either randomly selected (G) or set to --5 s (H), with arrows indicating the direction

from (t-1.5 s) to (t), to represent the trajectories through which neurons traveled over the 1.5-s period. Arrows at angles within  $\pm 75^{\circ}$  with the mean direction of all arrows were coded in blue, and others were coded in red. **I**, **J** Arrow plots of neural trajectories of D1-neurons over the 1.5-s periods with randomly selected t (**I**) or t = -- 5 s (**J**) from an example D1-Cre mouse. **K**, **L** Arrow plots of neural trajectories of D2-neurons over the 1.5-s periods with randomly selected t (**K**) or t = --2.5 s (**L**) from an example D2-Cre mouse. Insets in **I**–**L**: blue arrow, mean direction calculated as the mean angle of all arrows; red arrow, the opposite direction of the blue arrow; black arrows, describing the range of included angle of  $\pm 75^{\circ}$  with the mean direction. **M** Summaries showing synchronized trajectories of D1-neurons to --2.5 s (*p* = 0.03 rdm versus -5, two-sided paired *t*-test). Each dot represents data from a single mouse (5 D1-cre and 6 D2-cre mice). Black dots and vertical lines represent means and standard errors, respectively. \**p* < 0.05. Source data are provided in the Source Data file associated with this manuscript.

predictions and trigger optogenetic inhibitions exactly at the intended timepoint. For all three timepoints for the following experiments in both D1- and D2-Cre mice, the prediction efficacy was reasonably high, with both the true positive rate and balanced accuracy (see Methods) >50%, substantially higher than randomized predictions (Figs. 4C, D and S4B, C). Thus, ~50% of the actual lever-presses could be captured by our DeepLabCut algorithm for the –5-s timepoint. The prediction efficacy increased further for the –2.5-s and –0.5-s timepoints. Taken together, our DeepLabCut algorithm predicts a portion of, but not all, lever-presses.

To interfere with neuronal clusters in vivo, we expressed Jaws, a chloride pump for optogenetic inhibition upon 635-nm laser stimulation<sup>28</sup>, selectively in NAc D1- or D2-neurons by bilateral injection of AAV8-Flex-Jaws in D1-Cre or D2-Cre mice (Figs. 4E, F and S4D). To target a particular cluster with minimal impact on other clusters, we verified a short inhibition duration, 250 ms, which was expected to interfere with, but not abolish, activities of the intended cluster. To verify the inhibition efficacy of this Jaws approach, we made whole-cell

current-clamp slice recordings from NAc neurons with or without Jaws expression. A 500-ms depolarizing current step evoked persistent firing of action potentials in both Jaws-expressing (visualized by co-expressed GFP) and control (without expressing Jaws) neurons, while a laser stimulation (250 ms) selectively suppressed the evoked action potential firing in Jaws-expressing neurons (Fig. 4G, H).

Through pre-installed optical fibers (Fig. S4M, N), we applied this short-duration optogenetic inhibition to Jaws-expressing NAc neurons at the –5-s, –2.5-s, or –0.5-s timepoint during a 1-h sucrose SA session after >10 d of sucrose SA training (Fig. 41). Compared to sessions without in vivo optogenetic stimulation (the "off" session), the same D1-Cre mice during the sessions with laser inhibition (the "on" session; 5–10 mW × 250 ms, bilateral) of NAc D1-neurons at –5 s, but not at –2.5 or –0.5 s, exhibited reduced levels of subsequent lever-presses for sucrose, as well as operant responses to the inactive lever without changes in responding accuracy [active/(active + inactive)] (Figs. 4J and S4E–G). Analogous results were obtained upon laser inhibition of NAc D2-neurons but with peak effects at –2.5 s and not at



Fig. 4 | Interfering with the pre-press temporal dynamics of NAc neurons reduces sucrose-motivated operant responses. A Illustration showing positions where tracing dots were assigned on the mouse's body in DeepLabCut (DLC) analysis. B Example DLC tracing of a mouse before and upon lever-pressing for sucrose. C Example DLC prediction of lever-presses for sucrose. The upper, yellow bars show the times when actual lever-presses occurred. Middle, blue bars show the times that were 0.5 s before yellow bars, the timepoints where the prediction should be made. Lower, black bars show DLC-predicted timepoints that were 0.5 s before the potential lever-presses. D Summaries showing the true positive rate and balanced accuracy of the 5-, -2.5-, and -0.5-s DLC models, with the control of random prediction (D1 true positive:  $-5 \text{ s} 0.50 \pm 0.04$ ,  $-2.5 \text{ s} 0.57 \pm 0.07$ , -0.5 s $0.71 \pm 0.04$ , random  $0.25 \pm 0.04$ , n = 12; D1 balanced accuracy:  $-5 \le 0.64 \pm 0.02$ ,  $-2.5 \pm 0.03$ ,  $-0.5 \pm 0.03$ ,  $-0.5 \pm 0.02$ , random,  $0.50 \pm 0.01$ , n = 12; D2 true positive:  $-5 \pm 0.44 \pm 0.02$ ,  $-2.5 \pm 0.63 \pm 0.02$ ,  $-0.5 \pm 0.80 \pm 0.03$ , random  $0.28 \pm 0.04$ , n = 17; D2 balanced accuracy: -5 s 0.57 ± 0.01, - 2.5 s 0.70 ± 0.01, -0.5 s 0.82 ± 0.02, random,  $0.50 \pm 0.01$ , n = 17). Each dot (n) indicates a session of a mouse. Middle and outer lines present means and standard errors, respectively. E Example slice showing intra-NAc viral-mediated expression of Jaws. F Images from an example D1-Cre mouse showing that Cre-positive neurons co-expressed Jaws. Note that Jaws was preferentially expressed on the plasma membrane. G Example neurons with or without Jaws expression in the NAc slice (left) and example recordings (right) showing that laser activation of Jaws silenced action potential firing in a Jawsexpressing neuron, but not control neuron. H Summaries showing that laser activation of Jaws decreased the frequency of evoked action potential firing in NAc

-5 or -0.5 s (Figs. 4K and S4I-K). In an additional analysis, we examined the lever-presses that were not predicted by DLC, thus without timecontingent optogenetic stimulation during the "on" session. In both D1-Cre and D2-Cre mice, the numbers of unpredicted lever-presses were similar between the "off" and "on" sessions (Fig. S4H, L). As such, the basic sucrose-motivated operant responding was similar across sessions, but reduced by specifically-timed inhibition of D1- or D2neurons.

The accuracy of DeepLabCut predictions can be quantified by the positive predictive value [PPV; =true positives/(true positives + false positives)]. In these mice, the predictions were made before laser inhibition. As such, laser inhibition did not affect the number of predicted lever-presses but should decrease the PPV if the inhibition reduced the number of actual lever-presses. Indeed, the relative PPV (normalized to sessions without laser inhibition) was decreased upon

neurons that expressed Jaws without affecting control neurons (in Hz; control: off1  $34.4 \pm 5.3$ , on  $39.6 \pm 4.9$ , off<sub>2</sub>  $36.8 \pm 4.1$ , n = 5 neurons from three mice,  $F_{2.12} = 0.43$ , p = 0.55; Jaws: off<sub>1</sub> 42.0 ± 5.2, on, 0.0 ± 0.0, off<sub>2</sub>, 37.7 ± 9.7, n = 6 neurons from three mice,  $F_{2,15} = 19.06$ , p = 0.00; p = 0.00 of  $f_1$  vs on, p = 0.04 of  $f_2$  vs on; one-way ANOVA repeated measures followed by Bonferroni's posttest). I Schematic showing optogenetic inhibition of NAc neurons at -5, -2.5, or -0.5 s before the predicted leverpress after 10 d of sucrose SA. J, K Summaries showing that optogenetic inhibition of NAc D1-neurons at -5 s (-5 s: off 138.0 ± 9.6, on 119.3 ± 13.7,  $t_6$  = 2.7, p = 0.03; -2.5 s: off 144.8 ± 17.1, on 142.4 ± 19.3,  $t_6$  = 0.2, p = 0.88; -0.5 s: off 146.2 ± 26.5, on  $163.0 \pm 25.1$ ,  $t_6 = 1.09$ ; p = 0.32, n = 7 mice; paired *t*-test; **J** or D2-neurons at -2.5 s  $(-5 \text{ s: off } 137.8 \pm 18.6, \text{ on } 124.4 \pm 26.8, t_6 = 0.67, p = 0.53; -2.5 \text{ s: off } 136.8 \pm 11.7, \text{ on}$ 96.1 ± 15.1,  $t_6$  = 2.86, p = 0.03; -0.5 s: off 155.4 ± 31.9, on 145.0 ± 21.1,  $t_6$  = 0.45, p = 0.67; n = 7 mice; two-sided paired t-test; **K**), but not other timepoints, decreased the number of lever-presses for sucrose. L, M Summaries showing decreased relative positive predictive value (PPV) of DLC-based prediction upon optogenetic inhibition of NAc D1-neurons at -5 s (-5 s, off 1.00 ± 0.09, on 0.76 ± 0.06,  $t_7 = 2.8$ , n = 8, p = 0.03; -2.5 s, off 1.00  $\pm$  0.12, on 1.09  $\pm$  0.16,  $t_7 = 0.4$ , n = 8 mice, p = 0.67; -0.5 s, off 1.00 ± 0.17, on 0.90 ± 0.20,  $t_6 = 0.5$ , n = 7 mice, p = 0.65; paired t-test; L) or D2-neurons at -2.5 s (5 s, off  $1.00 \pm 0.10$ , on  $1.03 \pm 0.23$ ,  $t_6 = 0.2$ , n = 7, p = 0.82; -2.5 s, off 1.00 ± 0.15, on 0.63 ± 0.09,  $t_6 = 2.7$ , n = 7, p = 0.04; -0.5 s: off 1.01 ± 0.17, on  $1.01 \pm 0.17$ ,  $t_6 = 0.13$ , n = 7, p = 0.93; two-sided paired *t*-test; **M**), but not other timepoints. \*p < 0.05; \*\*p < 0.01. Source data are provided in the Source Data file associated with this manuscript.

optogenetic inhibition of NAc D1-neurons at -5 s (Fig. 4L) or D2-neurons at -2.5 s (Fig. 4M), but not any other timepoints for either of these neuronal types.

Taken together, these results establish that the -5-s D1-neuron and -2.5-s D2-neuron clustering activities represent two distinct steps in the sequence of neuronal events by which the NAc contributes to the initiation of sucrose-motivated operant responses.

#### Discussion

In well-learned reward-motivated behaviors, the act of reward-taking can be regarded as the final behavioral output of a sequence of cognitive-behavioral events. We propose that the clusters of neuronal dynamics in the NAc revealed by the present study contribute importantly to the circuit basis for some of these preluding events that launch reward-seeking and taking behavior.

## The three clusters

Constituting >90% of neuronal populations in the NAc. MSNs were expected to be predominantly represented in the NAc clusters in our current study. Without intrinsic pace-making mechanisms, activation of NAc MSNs is driven primarily by glutamatergic inputs<sup>29</sup>. A single NAc MSN receives convergent inputs from the hippocampus, amygdala, several subregions of the prefrontal cortex, and other limbic/paralimbic regions that encode different aspects of reward incentive<sup>30,31</sup>. These inputs often adjacently synapse on the same MSN dendrites, together with heterosynaptically aligned dopaminergic and other monoaminergic presynaptic terminals<sup>30,32,33</sup>. Furthermore, these glutamatergic and monoaminergic inputs influence NAc interneurons, such as fast-spiking and cholinergic interneurons, which, in turn, regulate the firing pattern of MSNs<sup>34-36</sup>. Thus, the timing and intensity of the neuronal dynamics in each NAc cluster are likely dictated by temporally distinct glutamatergic inputs and regulated by neuromodulators and local circuits.

We identified three temporally defined NAc neuronal clusters, among which the -5-s and -2.5-s clusters may correspond to key cognitive/behavioral events during the pre-press phase. One potential pre-press feature is appetitive behavior-animals are exploring and searching for reward–which relies on the proper functioning of NAc neurons<sup>5,37-40</sup>. However, appetitive behaviors are typically continuous, with temporal features that do not correlate with the clear peaks of the two identified clusters. Furthermore, having been well-trained, the mice can approach rewards without major searching efforts. Rather, the -5-s D1-neuron cluster correlated temporally with a rise in head movement without apparent locomotion initiation, suggesting changes in attention or some related cognitive events (Fig. S3K-CC). On the other hand, the -2.5-s D2-neuron cluster correlated temporally with peak movements of the head and locomotion toward reward, suggesting the onset of approach behavior toward sucrose (Fig. S3K-CC). Together, these results suggest that the -5-s D1-neuron cluster versus the -2.5-s D2-neuron cluster contributes to different components of the cognitive-behavioral sequence toward lever-pressing.

During the pre-press phase, a chain of interwoven cognitive and behavioral events must occur to launch a successful operant response for sucrose. For example, the motivation for sucrose must be prioritized and engaged. In our experimental procedure, sucrose-seeking and taking behaviors are self-initiated. As such, the motivation for sucrose may remain dormant (circulating in the "background") until it is engaged. Intrinsically related to this motivation is the anticipation of reward. Occurring during the pre-press phase, the anticipation of reward is correlated with increases in dopamine release in the NAc<sup>41-44</sup>, with such increases peaking at -5 s before the operant response in rats performing self-paced sucrose-seeking<sup>45</sup>. It is thus tempting to speculate that the -5-s cluster preferentially contributes to the cognitive or behavioral states of motivation-engaging or reward-anticipating.

The -5-s cluster is primarily composed of D1-neurons (Fig. 2). Extensive studies indicate a critical role for NAc D1-neurons in motivation-invigorating and reward-anticipating processes<sup>8-11</sup>. For example, mice establish much stronger optogenetic self-stimulation of NAc D1-neurons compared to D2-neurons, suggesting the dominant role of D1-neurons in motivation invigoration<sup>46</sup>. Echoing this, persistently elevating activities of NAc D1-neurons improves rewarded operant responses, while disrupting the function of NAc D1-neurons causes the opposite effects<sup>47-50</sup>. On the other hand, in both humans and rodents, anticipation of reward is correlated with increased NAc activity<sup>51-53</sup>. Extending these findings, our current study identified the temporal dynamics of D1-neurons during the pre-press phase, and demonstrated that interference with these neuronal dynamics reduced the likelihood of subsequent sucrose-seeking. These results reveal that, rather than the constitutive activity of these neurons, the temporal dynamics of NAc D1-neurons are the key for engaging reward motivation to reward-seeking and taking.

After motivation is engaged, mice switch from spontaneous behaviors to task performance, initiating the action sequence toward reward consumption<sup>54</sup>. Meanwhile, other extraneous signals must be ignored to ensure undistracted behavioral performance. These two processes are expected to occur during the late pre-press phase, for which the -2.5-s cluster fits with respect to timeframe. While MSNs in the dorsolateral striatum have long been implicated in the initiation of rewarded action sequences<sup>55-57</sup>, recent results show that NAc MSNs are also essential<sup>58,59</sup>. Compared to the -5-s timepoint, we observed abrupt motion changes in mice at -2.5 s, suggesting initiation of new behavior (Fig. S3K-CC). The -2.5-s cluster is mainly composed of D2-neurons, inhibition of which at -2.5 s, but not other timepoints, decreased leverpressing for sucrose (Fig. 4). Thus, the -2.5-s cluster may represent another essential set of NAc dynamics that constitutes the behavioral sequence for reward-seeking once the mouse is motivationally committed.

Neurons in the 0-s cluster started increasing activities ~1 s before lever-pressing, which peaked upon the initiation of lever-pressing, and declined over the next 2-3s (Figs. 1, 2). This lever-press-contingent pattern is consistent with previous findings that select populations of NAc neurons increase firing rates during the on- and post-lever-press phases<sup>19,60,61</sup>. The 0-s cluster overlaps with at least four major motor responses, including lever-pressing, sucrose taking, sucrose consumption, and receding from sucrose magazine/sipper. In rats, Nicola et al. detect increased activities of NAc neurons during their entry, stay-in, and exit from the sucrose receptable entry<sup>40</sup>, suggesting motor-related functions of the 0-s cluster. On the other hand, this cluster may also participate in the cognitive processing of unconditioned stimuli. In nonhuman primates, a population of ventral striatal neurons exhibits increased activities during rewarded operant responses, and this increase in activity is sensitive to the magnitude of the reward, but absent when only the reward-associated cues are present without reward delivery<sup>62-65</sup>. Furthermore, several cognitive events occur immediately after lever-pressing, such as experiencing reward and recalibrating anticipation with outcome, for which the 0-s cluster may be involved, given the prominent role of NAc in reward learning<sup>3,29,66</sup>.

It is worth mentioning that, for most populational data, a clearcut separation of subpopulations is not possible. This is also true for our cluster analyses. For example, it appears that a small population of D1-neurons exhibited increased activities at -2.5 s (Fig. S2K-G). However, optogenetic inhibition of D1-neurons at -2.5 s did not affect operant responding, leaving the behavioral significance of this cluster unknown. It is also worth mentioning that the three NAc clusters were identified using an operant procedure with a fixed ratio 1 schedule. Under more demanding reinforcement schedules, for which higher motivational states are required, we speculate that, if the -5-s cluster contributes to motivation-engaging as hypothesized above, this cluster will become more prominent, e.g., exhibiting higher collective z-scores.

#### D1-neurons versus D2-neurons

In D1-Cre and D2-Cre mice, Cre-dependent viral-mediated gene expression can also occur in non-MSN cell types that express D1 or D2 receptors, although recent single-cell RNA-sequencing data confirm that -1% of Cre+ cells are non-MSN cell types<sup>67</sup>. Thus, the neuronal dynamics in D1-Cre or D2-Cre mice should be interpreted with this caveat in mind.

Increased activities of both D1- and D2-neurons are observed during reward-taking, cue-conditioned reward-seeking, or rewardassociated learning<sup>7,11,13,68,69</sup>. While functionally contrasting each other on many occasions, D1- and D2-NAc neurons have also been recognized for their complementary roles in motivated behaviors<sup>7–9,70-72</sup>. For example, when applied persistently in a temporally noncontingent manner, optogenetics-mediated activity downregulation of either D1or D2-neurons decreases the likelihood of operant responding to sucrose<sup>73</sup>. Our results show that D1- and then D2-neurons sequentially dominate in the NAc circuit activity during the pre-press phase (Fig. 2), suggesting their distinct but temporally linked functions. Hinted by their differential coupling with motor changes (Fig. S3), we propose a heuristic model that the –5-s D1-neuron versus –2.5-s D2-neuron clusters preferentially contribute to distinct cognitive/behavioral events, such as motivation-engaging or sucrose-anticipating versus behavior-initiating responses. Specifically-timed inhibition of D1- or D2-neurons reduced subsequent lever-presses for sucrose (Fig. 4), indicating that both the D1-neuron and D2-neuron-dominated NAc temporal dynamics, and the cognitive/behavioral events they mediate, are essential for launching self-paced operant response for reward.

Although our current study focuses on activity increases, a portion of neurons exhibited decreased activities clustering at the three key timepoints (Figs. 1, 2). These activity decreases were observed for both D1- and D2-neurons at 0 s, such that there were indeed four clusters at 0 s: increased D1-neurons, increased D2-neurons, decreased D1-neurons, and decreased D2-neurons (Fig. 2II). This observation is consistent with results from in vivo recordings that reveal distinct populations of NAc neurons exhibiting increased versus decreased activity in response to the same stimulus<sup>19,74,75</sup>. However, the decrease cluster at 0 s is not composed of an independent neuronal population but includes a portion of the increase clusters during the pre-press phase. For example, in the two-cluster analysis of D1-neurons, most of the same neurons that exhibited increased activity at -5 s subsequently exhibited decreased activity at ~0 s (Fig. 2I). Similar activity patterns were observed for D2-neurons in the -2.5-s cluster (Fig. 2]). Thus, the decrease cluster can be regarded as the second part of a biphasic pattern of both neuronal subtypes in the -5-s and -2.5-s clusters. In theory, decreases and increases in neuronal activity could contribute equally to the overall circuit dynamics at a given timepoint. In this case, the increase and decrease clusters at ~0 s can be captured and combined by PCA, resulting in a higher separation than at ~-5 or ~-2.5 s where the increased cluster alone dominated (Figs. 2II, 3C, D). In addition, the same sets of D1- and D2-neurons participate in different functional ensembles with different temporal-dynamic features-i.e., the NAc ensemble can be organized by the timing of populational activities, not necessarily a fixed population of neurons. Furthermore, the decrease could connote inhibition, with which the corresponding cognitive or behavioral events during the pre-press phase are prevented from entering the on-press phase.

## **Computational analyses**

The PCA-distance results suggest that D1- versus D2-neurons enter a different activity state at ~-5 versus ~-2.5 s compared to their basal activities (Fig. 3C, D). In the support vector machine accuracy test, the ~5-s activity state of D1-neurons and ~2.5-s activity state of D2-neurons exhibited increased correlation to subsequent lever-press actions (Fig. 3E, F). Thus, both the PCA-distance and support vector machine accuracy tests similarly revealed that D1- and D2-neurons exhibited temporally sequential activity states that may contribute to the prepress cognitive/behavioral sequence.

Given the overrepresentation of pre-press neuronal activity and the ability to decode upcoming lever-presses, we also examined whether the neural trajectories through which NAc neurons reached their pre-press clustering activity states were the same, i.e., how much variability was there when NAc neurons aligned their activity to the two key pre-press timepoints? We found similar trajectories for D1- or D2neurons (Fig. 3G–M). In fact, trajectories of D1- and D2-neurons in >75% lever-presses traveled in the same relative direction when reaching ~–5 or ~–2.5 s, respectively, suggesting that the NAc neuron-mediated processing of the pre-press cognitive-behavioral sequence is similar over trials. Extrapolated from these results are two additional conceptual considerations. First, an elevated synchronization was observed for the trajectories of D2-neurons to -5 s (Fig. S3J), the timepoint at which the activity of the -2.5-s cluster was in the early rising phase (Figs. 1L, 2J). Thus, the trajectory synchronization may also reflect key features of NAc neurons during the "preparatory" phase toward their peak activity increases. Second, at 0 s, the activity increase of one cluster overlaps with the activity decline of another cluster (Fig. 2I, J), presumably resulting in diverse activity states and unsynchronized trajectories among neurons when clusters were sampled together. As such, although synchronized trajectories of D1 or D2-neurons were not detected at 0 s (Fig. S3J), we speculate that such a trajectory synchronization exists in neurons from each individual cluster.

#### **Behavioral correlates**

We speculate that the -5-s D1-neuron cluster preferentially contributes to motivation-engaging, reward-anticipating, or other cognitive events. Our behavioral tests did not measure these cognitive events directly, but the results are in line with this speculation. For example, interfering with the -5-s cluster activity decreased the likelihood of subsequent operant responses for sucrose (Fig. 4), an effect that may result from compromised reward motivation or anticipation. Importantly, interfering with the -5-s cluster activity decreased the presses of both active and inactive levers, but not the ratio of active versus total (active + inactive) lever-presses (Fig. S4), suggesting that the -5-s cluster activities are correlated with reward motivation or anticipation but not the accuracy of operant performance. In parallel, although there are basal activities of D1-neurons at -2.5 s (Figs. 2 and S2), inhibiting D1-neurons at this timepoint did not affect subsequent operant responding (Figs. 4 and S4). Thus, rather than their general or constitutive activities, it is the temporally confined activities of D1-neurons that mediate key cognitive/behavioral events.

Correlated with movement changes, we speculate that the -2.5-s cluster contributes to the initiation of the behavioral sequence toward sucrose taking. While NAc D2-neurons are often associated with behavioral inhibition, their roles in motion initiation or performance are emerging. In trial-based food-taking tests, inhibition of D2-neurons immediately after predictive cues decreases the likelihood of operant responding, suggesting compromised initiation of reward-seeking upon insufficient activation of D2-neurons<sup>76</sup>. In addition to movement initiation, NAc D2-neurons are also implicated in reward motivation. For example, mice establish intracranial self-stimulation of NAc D2neurons, albeit with a much lower magnitude compared to D1-neuron stimulation<sup>46</sup>. Furthermore, mice with optogenetic up- versus downregulation of NAc D2-neuron activities exhibit increased versus decreased persistence in obtaining a reward, respectively<sup>73,77</sup>. Thus, like D1-neurons, the behavioral function of NAc D2-neurons is also likely to be multi-dimensional, depending upon their temporal dynamics and the phases of motivational responses. Particularly for the -2.5-s D2-neuron cluster, the sharp movement changes at -2.5 s (Fig. S3) implicate a strong locomotor component, potentially initiating the behavioral sequence of sucrose-seeking.

In summary, in reward-motivated operant responses, if the final act of lever-pressing is analogous to the takeoff of an Olympic long jump, the preluding cognitive/behavioral events would serve as the approach run. We propose that the two sets of temporal dynamics of NAc neurons identified during the pre-press phase may mediate some of these key approach-run events that launch reward-seeking behaviors. These findings thereby provide unique insight into understanding the circuit mechanisms through which motivation is engaged for behavioral output.

## Methods

#### Animals, reagents, and genotyping

Wild-type C57BL/6J mice were purchased from Jackson Laboratories. Both D1-Cre<sup>78</sup> and D2-Cre mice<sup>78</sup> on a C57BL/6J background were originally purchased from Jackson Laboratories and were bred in the University of Pittsburgh animal facility. Mice were 7 weeks old at the beginning of experimentation and, after initial surgical procedures, were singly housed on a 12-h light/dark cycle (light on/off at 7:00/ 19:00), at a room temperature of 22–24 °C and humidity 40–60%. Mice accessed food and water ad libitum, except a few days prior to sucrose self-administration (SA) (see below). Mice were 12-14 weeks old at the initiation of behavioral experiments. Both male and female mice were used in pilot experiments, but male mice exhibited more tolerance for Miniscope wearing and stability of behavioral performance compared to female mice. Male mice were thus used for all experiments during data collection. All animal care and use were approved and performed in accordance with NIH guidelines and the University of Pittsburgh's Institutional Animal Care and Use Committee.

For optogenetic manipulations, we used Jaws-expressing adenoassociated virus (AAV) for in vivo expression, with the virus rAAV8/ hsyn-Flex-Jaws-KGC-GFP-ER2 (titer  $\geq$ 4.1 × 10<sup>12</sup> virus molecules/ml) purchased from the University of North Carolina GTC Vector Core. For GCaMP-based in vivo Ca<sup>2+</sup> imaging, we used pAAV.hsyn.G-CaMP6m.WPRE.SV40 (titer  $\geq$ 2.7 × 10<sup>13</sup> GC/ml) in wild-type mice and pAAV.hsyn.Flex.GCaMP6m.WPRE.SV40 (titer  $\geq$ 2.7 × 10<sup>13</sup> GC/ml) in D1-Cre or D2-Cre mice, both purchased from Addgene.

Genotyping was performed using a PCR reaction containing AccuStart II GelTrack PCR SuperMix. The primers for Cre detection  $(5' \rightarrow 3')$  were: forward AATGCTTCTGTCCGTTTGCC and reverse GATCCGCCGCATAACCAGT). Amplified DNA was analyzed on a 20% agarose gel with ethidium bromide staining, with the signature bands determining the genotypes<sup>78</sup>.

#### In vivo viral injections

Mice were anesthetized with i.p. injection of ketamine (100 mg/kg) –xylazine (10 mg/kg) mixture and were held in a stereotaxic frame (Stoelting Co., Wood Dale, IL). Through a 10-µL NanoFil syringe with a 32-gauge needle controlled by UMP3 and Micro4 system (WPI, Sarasota, FL), the AAV solution was infused at a rate of 200 nL/min into the NAc (AP + 1.50 mm, ML ± 0.73 mm, DV –4.25 mm). For Ca<sup>2+</sup> imaging experiments, 1µL of GCaMP6m-expressing AAV was infused unilaterally, followed by the implantation of a GRIN lens (0.5 mm in diameter, 8.4 mm in length, Inscopix) directly above the viral injection site. In this process, the GRIN lens was slowly lowered into the brain tissue using a cannula holder for implantation, and a small metal bar was affixed into place via superglue and dental cement. Mice were then kept in their home cages for >4 weeks for viral expression before imaging experiments.

After >4 weeks of viral expression, the mice were anesthetized and placed in the stereotaxic frame again for the installation of of Miniscope baseplate. The protective cover over the GRIN lens was removed, and a Miniscope, along with a relay lens (1.8 mm, 0.25 pitch, Edmund Optics) equipped with a baseplate, was stereotaxically lowered above the lens. The baseplate was positioned at a focal plane where fluorescent cells were visible. Once the optimal focal plane was attained, the baseplate was secured to the head with dental cement. After dental cement solidified, the Miniscope was removed, and a protective cap was secured over the GRIN lens.

## Ca<sup>2+</sup> imaging in sucrose SA mice

Sucrose SA was conducted in operant chambers enclosed within sound-attenuating cabinets (Med Associates). Each chamber ( $29.53 \times 24.84 \times 18.67 \text{ cm}^3$ ) contained an active and an inactive lever, a lickometer, a sucrose sipper, a conditioned stimulus light above each lever, a house light, a speaker for audio cues, and a wide-angled infrared camera (ELP Camera USB 1080P Wide Angle Fisheye LED Infrared Webcam).

Prior to the training procedure, mice were habituated daily for >1 week (1 h/d) to head restraint, Miniscope carrying, and fiber optic

cable installation. Two days prior to the overnight procedure, mice were water-restricted. Following overnight training (12 h of SA session), mice underwent 11 d of self-administration training, during which pressing the active lever resulted in extraction of the sucrose sipper delivering 10% sucrose solution (0.1 mL/lick) and presentation of the compound cues (sound and light). During the 10-s period. additional active lever-presses were recorded but not reinforced. Pressing the inactive lever did not have any consequence. The end of the 10-s session following reward delivery was signaled by termination of the house light and retraction of the sucrose sipper. Sucrose crystalline was purchased from Fisher Chemical. Prior to each sucrose selfadministration session with in vivo Ca<sup>2+</sup> imaging, mice were briefly head-restrained to install the Miniscope before being placed in the operant chamber. We used a wire-free version of the UCLA Miniscope (v3)<sup>22</sup>. To avoid potential over-bleaching of fluorescence and best fit the capacity limit of the single-cell lipo battery (Open Ephys Production), our recordings were focused on the first 20 min of each imaging session. About 40% of lever-presses occurred during the first 20 min of the 1-h SA session (raw data provided via Research Data Deposition). Thus, neuronal activities over the first 20 min may be correlated with a relatively high motivational state for sucrose.

## Ca<sup>2+</sup> signal analysis

Preprocess by z-score standardization and downsampling Miniscope videos of Ca<sup>2+</sup> activities were recorded at a resolution of  $\sim$  320  $\times$  320  $\mu$ m and a framerate of 20 Hz. Raw video data from each imaging session were processed using an open-source package, Ca2+ imaging analysis (CalmAn) in Python<sup>79</sup>. The CalmAn involves the motion correction, source extraction, and deconvolution steps to extract fluorescence traces of Ca<sup>2+</sup> activities. Specifically, the motion artifacts of Miniscope videos were corrected by the NoRMCORRE algorithm<sup>80</sup>. A constrained non-negative matrix factorization (CNMF) algorithm was used to perform source extraction of fluorescence traces and eliminate overlapping spatial sources<sup>81</sup>. Sparse non-negative deconvolution was used to estimate the underlying neural activities<sup>81,82</sup>. Following signal extraction, each trace was manually examined to exclude artifacts. To normalize signals among trials, the extracted Ca<sup>2+</sup> traces were binned to 100-ms segments and z-scored with mean = 0 and standard deviation = 1.  $\Delta F/F_0$  was used in manifold analysis, in which  $F_0$  was the mean z-score over 5-min sliding baseline, and  $\Delta F = F_t - F_0$  at the timepoint of t.

## Heatmap and sorting

For all heatmap results, z-score data over the 20-s time window with lever-press were extracted from individual neurons across all trials. Trial-averaged data of individual neurons were calculated by averaging the z-score data of all trials over the 20-s time window. Data from randomly selected, trial number-matched 20-s time windows without lever-press were used as controls. For consistent visualization, heatmaps were generated by setting the mean of trial-averaged data to 0 for individual neurons. The heatmaps were created using the levelplot function in the R lattice package (R Core Team 2022 R: A Language and Environment for Statistical Computing. R Foundation for Statistical Computing, Vienna; https://cran.r-project.org/web/packages/lattice/ index.html). For sequence-based sorting heatmaps, we used two methods. The first method sorted neurons by the times at which they exhibited peak z-scores (Fig. S1C, D). The second method sorted neurons by the times at which neurons exhibited initial increases in activities (Fig. 1H, I). To focus on the most prominent activity changes in each neuron, we operationally grouped neurons into three sets based on their z-scores: z-scores >0.5, <0.5 but > 0.25, and <0.25, with the detection thresholds set at the z-score of 0.5, 0.25, and normalized trial-averaged z-score, respectively.

For timing-based sorting heatmaps, neurons were sorted based on normalized trial-averaged z-scores at the targeted timepoint. K-means clustering (KMC) was performed using the *kmeans* function in the R *stats* package with a pre-set number of clusters to analyze the first 15 s of the time window. For cluster presentation, we performed timing-based sorting of neurons to the cluster center, defined as the timepoints at which neurons exhibited z-scores >95% (cutoff values) of their normalized trial-averaged z-scores during the first 15 s of the 20-s time window. A linear weight (= cutoff value × 4) was given to each neuron to partially filter out nonactive neurons. The cluster-wise assessment of cluster stability was performed using the *clusterboot* function in the R *fpc* package<sup>83</sup>.

## Collective z-scores

For a collective z-score-based description of the temporal dynamics, neurons were grouped based on their KMC-allocated clusters. Activated versus nonactive neurons were defined as neurons with mean z-scores > or <0, respectively, over the  $\pm$ 0.5-s range around the cluster center. Collective z-scores were calculated by summing the normalized trial-averaged z-scores of the selected neurons divided by the total number of neurons. In another grouping approach, we ranked neurons by their activity intensity around the cluster center ( $\pm$ 0.5 s), and included the top 50% of these neurons for subsequent plotting. The temporal changes of collective z-scores of activated neurons or the top 50% of neurons ranked by activity were plotted by R package *ggplot* (https://ggplot2.tidyverse.org). Pie charts were made using the R function *pie*.

## Histogram and statistics

Over the 20-s lever-press or randomly selected trials, trial-averaged zscores of each neuron were sliced into 0.1-s bins. For each slice, we calculated the populational mean of z-scores by trial-averaging zscores of all neurons. The high-activity neuron was defined as the neuron with the z-score >95% of the populational mean for each bin. The counts of high-activity neurons per bin were used to plot the distribution of highly active neurons over the 20-s trials. We also examined other cutoff options (e.g., 0.3-s bins or >90% of the populational mean) and obtained similar results.

A Chi-square test was conducted using the R function chisq.test to compare the distribution of high activity neurons between a timepoint of interest versus a randomly selected timepoint. To condense the dataset, we summed the number of high-activity neurons over a 10-bin, 1-s period across the timepoint of interest (e.g., -5.5 to -4.5 s for the timepoint of -5 s). We built a  $2 \times 2$  contingency table with 2 dimensions. Dimension one was the timepoints of interest versus randomly selected timepoints with 100 repeats. Dimension two was the total counts of high-activity neurons over 1 s across the timepoints of interest versus the averaged counts of high-activity neurons over each 1-s period over the entire 20-s trials.

Dimensionality reduction. Principal component analysis (PCA) was performed to depict a mathematical representation of neuronal activities. In this analysis, trial-averaged concatenated PCA was used to create a mathematical representation of neuronal activities. Activities of individual neurons over time were compared among two different trial types: 30-s trials with lever-presses (15 s before and 15 s after the lever-press), and 30-s random trials (baseline trials). The sample size of baseline trials was set 2x of lever-press trials to support comparison between baseline 1 and baseline 2. The mean activity of each neuron (N) over time (T) and across two trial types (each  $T \times N$ ) were concatenated into a matrix 3T × N, normalized to having a mean of 0 and standard deviation of 1, and fed into the sklearn PCA model (https:// scikit-learn.org/stable/about.html#citing-scikit-learn). The resulting PCs were ordered by the degrees of their explained variance. Scree plots were generated to illustrate the cumulative explained variance relative to the total variance for each PC. The first two PCs were selected for visualization and distance calculation (x- and y-axis in a two-dimensional Cartesian coordinate system). Thus, for a singular trial instance input  $T \times N$ , we obtained the trial output instance  $T \times 2$ . We also used PCA to reduce the MIND-transformed seven-dimensional manifold into three dimensions prior to inputting the data into the SVM. The same process of trial-averaged input to create the principal axis was used, such that we could transform a  $T \times 7$  input into a  $T \times 3$ .

For PCA-related lever-press data, once we obtained their leverpress timings, we removed "overlapping" lever-presses (repeats within 10 s from each other; e.g., for times 1, 8, 9, 15 s, we removed times 8 and 9 s). This matched the 10-s cooldown period in the operant procedure. We then took the filtered set of times T, and defined "lever-press" data F, so F contained all the times in the interval [t - 10, t + 10] for t in T. For PCA-related baseline data, we sampled same numbers of [t - 10, t + 10]for t in randomly available timepoints and defined them as baseline samples. Note that between sampling iterations, this set of baseline samples would change, so the data would vary slightly between runs. For MIND-related lever-press data, the definition for lever-press was identical to the handling of PCA-related data. For MIND-related baseline data, we defined the baseline as time-shuffled lever-presses. Thus, for an SVM testing/training on a time slice [-0.5, 0], while the leverpress data would respect its temporal relation relative to the original lever-press, baseline data could be any of the timepoints from the lever-press data F. The limitation mentioned earlier lies with how MIND generates its nonlinear transformation. Data points that lie outside of the set of lever-press data F are ill-defined (e.g., possibly null) and not suitable for a baseline definition due to the method only transforming F.

**Centroid distance.** To determine whether lever-press could be predicted by preceding neuronal activities, the spatial separation between different trial types was examined using PCA-transformed data across 20-s time windows with or without lever-presses. The centroid of a data group was computed by calculating the mathematical mean of all data points within the group. The distance between two centroids  $[(x_1, y_1) \text{ and } (x_2, y_2)]$  was calculated as Euclidean distance:  $d = \sqrt{(x_2 - x_1)^2 + (y_2 - y_1)^2}$ . Such distances were calculated for each animal between baseline trials 1 and 2, as well as between lever-press trials and baseline trial 1, with 100 repeats (50 for pair distance) to minimize potential randomization-related biases. The group mean was computed from all animals in the group. The distance was normalized by setting the maximum distance between lever-press and baseline to "1" for each repeat.

**Manifold inference from neural dynamics (MIND).** To generate data used for nonlinear dimensionality reduction, we smoothed  $\Delta$ F/F traces from each animal with a 5-bin Gaussian filter and thresholded at 2 $\sigma$ , for which we measured the robust  $\sigma$  across the time series and individually for each neuron. We then ran the dataset through MIND<sup>24,84</sup> and embedded into 2-22 dimensions. Figure S3G shows the  $r^2$  values using the 7-22 dimensional embeddings of the manifold to reconstruct the raw neural activity, where r is the correlation coefficient between the raw neural activity data and the reconstructed neural activity data.

**Support vector machine (SVM)**. Using the MIND outputs, a series of SVM were built on 0.5-s slices to determine the accuracy of neuronal activities in classifying lever-press versus baseline. An SVM was used to determine an optimal hyperplane that maximally separated different trial types. Data were split into 0.5-s collections and then divided into a training set and a test set at the ratio of 60/40. The training set from each collection was used to train an SVM, while the test set was left out to evaluate the model's performance. We used the sklearn LinearSVM api with the following parameters; L2 normalization penalty with squared hinge loss, regularization parameter of 0.9, no class weighting, primal optimization problem, and max iterations of 1e5. To create

consistent results from randomized baseline selections, we averaged the accuracies across 100 baseline selections.

Bootstrapped confidence interval (BCI). We bootstrapped samples and calculated the t value of a 500-ms interval centered around the -5and -2.5 s to construct a 95% two-sided bootstrapped confidence interval using the scipy bootstrap and ttest ind apis in Python. The bootstrap settings used were method='basic' and confidence level = 0.95. The datasets used were the rodent-type arithmetic-mean averaged set of PCA centroid distances (n = 100 samples × fivefold prediction points = 500/interval)and MIND SVM data (n = 100 samples/interval). The PCA centroid distance confidence interval was constructed using data centered around -5 and -2.5  $(-5 \pm -0.2 \text{ s and } -2.5 \pm 0.2 \text{ s})$ , while the MIND data used the data from the [-5, -4.5] and [-2.5, -2.0] intervals.

## Arrow plot

Arrow plots were used to examine the directionality of the populational neural dynamics of D1- and D2-neurons in each individual mouse. Figure 3G-L shows the first two dimensions of manifolds embedded into seven dimensions. Each red dot represented the time (t s) before each lever-press, and the blue dot represented the time (t-1.5 s). Arrows were drawn from each blue to red dot. (t) for a timepoint of interest was determined as the time within a 1-s range of this timepoint, at which a maximal number of arrows exhibited synchronized direction. Arrows with length <mean length were considered nonactive and excluded. In Fig. 3G, I, K, random 1.5-s intervals with the number matching lever-press trials were similarly selected, aligned, and plotted. Arrows within 150° (±75°) of the mean direction (averaged from all arrows) were regarded as having synchronized direction; they were colored in blue and represent "synced angles". All other arrows were colored in red. The proportion of arrows classified as "synced angles" is shown in Fig. 3M and Fig. S3I.

## Slice preparation

To prepare acute brain slices<sup>85</sup>, mice were decapitated under isoflurane anesthesia. Coronal slices (250-µm thick) containing the NAc were prepared on a VT1200S vibratome (Leica) in a 4 °C cutting solution containing (in mM): 135 *N*-methyl-d-glucamine, 1 KCl, 1.2 KH<sub>2</sub>PO<sub>4</sub>, 0.5 CaCl<sub>2</sub>, 1.5 MgCl<sub>2</sub>, 20 choline-HCO<sub>3</sub>, and 11 glucose, saturated with 95%  $O_2/5\%$  CO<sub>2</sub>, and pH adjusted to 7.4 with HCl. The osmolality of the cutting solution was adjusted to 305–309 mOsm. Slices were incubated in the artificial cerebrospinal fluid (aCSF) containing (in mM): 119 NaCl, 2.5 KCl, 2.5 CaCl<sub>2</sub>, 1.3 MgCl<sub>2</sub>, 1 NaH<sub>2</sub>PO<sub>4</sub>, 26.2 NaHCO<sub>3</sub>, and 11 glucose, with the osmolality adjusted to 290–295 mOsm and saturated with 95%  $O_2/5\%$  CO<sub>2</sub>. The brain slices were incubated at 34 °C for 30 min and then allowed to recover for >30 min at 20–22 °C before electrophysiological recordings.

# Optogenetic electrophysiology

As detailed in previous studies<sup>86–89</sup>, current-clamp whole-cell recordings on NAc neurons were performed using an Axon MultiClamp 700B amplifier (Molecular Devices, San Jose, CA). Borosilicate glass pipettes pulled on a P-97 Puller (Sutter Instruments, Novato, CA), with a resistance of 2–5 MΩ when filled with a potassium-based internal solution containing (in mM): 130 K-methanesulfate, 10 KCl, 10 Hepes, 0.4 EGTA, 2 MgCl<sub>2</sub>, 3 Mg-ATP, 0.25 Na-GTP; pH 7.3 and osmolarity adjusted to 285–290 mOsm. Jaws-expressing versus noninfected control neurons were differentiated by the presence versus absence of GFP fluorescence. Action potentials were evoked by current steps multiple times with or without optogenetic stimulation (250 ms, 635-nm laser, 1–2 mW through a fluorescent port of the microscope; Sloc Lasers). The timing and duration of laser stimulation, as well as the recording, were controlled by preprogrammed Clampex 9.2 (Molecular Devices). Data were online filtered at 2.6-3 kHz, amplified five times, and digitized at 20 kHz.

## Time-specific interference of neuronal clusters

To perform in vivo laser stimulation of Jaws-expressing D1- or D2neurons, D1- or D2-Cre mice were injected bilaterally with rAAV8/hsyn-Flex-Jaws-KGC-GFP-ER2 (UNC GTC Vector Core) into the NAc (in mm: AP + 1.50; ML  $\pm$  0.73; DV -4.25). After stereotaxic insertion of injection needles, infusion of the virus was started at a rate of 200 nL/min. After infusion, the needle was held in place for 5 min before removal to minimize the backflow of the viral solution. After viral injection, the dual cannulae (0.37 NA, 1.5 mm Pitch, Ø200  $\mu$ m, Doric Lenses Inc. Quebec, QC, Canada) within a guiding socket receptacle were bilaterally inserted into the NAc (in mm: AP 1.50; ML  $\pm$  1.8; DV –4.2). Dental cement and screws were used to secure the cannulae on the skull.

For in vivo optogenetics, laser pulses were applied bilaterally to the NAc in freely moving mice (8 D1-Cre and 7 D2-Cre mice) via Ø200µm optical fibers connected to a Splitter Branching Patchcord (Core: 200 µm, NA: 0.37, Jacket: 900 µm; Doric Lenses). Prior to each sucrose SA session with in vivo optogenetics, mice were head-restrained, and the patchcord was connected to optical fibers. The patchcord was connected to a 635-nm laser diode controller (Sloc Lasers), and laser pulses (pulse duration, 250 ms) were generated through a waveform generator (Master 8). The light intensity through the patchcord was measured by a light sensor (S130A, Thor Labs) and adjusted to 5-10 mW prior to behavioral sessions. We trained the DLC algorithms for each mouse during the "off" session and then performed the test during an "on" session on the next day for a timepoint. We then trained the mice for two "off" sessions over another 2 days, to monitor behavioral stability and retrain the DLC. We then started another "on" session on the following day for another timepoint. Over this procedure, the mean performance of mice was similar over the "off" sessions, suggesting stable behavioral output under the control condition. The behavioral procedure for these optogenetics experiments was identical to the experiments for vivo imaging, except for laser stimulation.

## DeepLabCut (DLC)

We used DLC to label individual body parts, which were then converted to digital coordinates. The DLC algorithm used the sequences of movements in a long short-term memory (LSTM) model to predict lever-press in real time with low-latency<sup>27</sup>. Once a lever-press was predicted, the model sent an output with a custom code in Arduino (Uno R3) to the laser generator, which delivered a 250-ms laser stimulation via the patchcord at specified timepoints.

DLC-based prediction model. DLC model90,91 was trained using a complied 10-h sucrose SA video, in which we manually labeled 10 body and equipment parts. Key parameters for training were configured as: augmenter type was set to 'imgaug,' and the ImageNet pre-trained network used was ResNet-152. Other parameters were maintained at the DLC default settings. During training with optogenetic manipulations, the coordinates of 10 moving points were generated using DLClive through the chamber camera. The DLC-live recorded videos had a framerate ranging from 25 to 33 frames/s. Lever-presses during the timeout period and those that were partially overlapped were filtered out. The coordinates were grouped by 31 frames (-1s)/segment. Coordinate segments before lever-presses were used as positive samples. Coordinate segments of randomly selected timeframes excluding positive samples were used as negative samples. For the positive samples in the -5-, -2.5-, and -0.5-s models, we used the data from -6 to -5 s, -4 to -3 s, and -2.5 to -1.5 s, respectively. Data augmentation was implemented by shifting ~0.5 s of frames backward or forward, resulting in an x29-fold augmentation of the size of positive samples. The size of negative samples was determined in two ways: (1)

for mice with the number of verified active lever-presses >150 (-averaged number of lever-presses), the size of negative samples was adjusted to match the size of positive samples; (2) for mice with the number of active-presses <150 active lever-presses, the size of negative samples was set to match 150 lever-presses. These samples were then fitted to a PyTorch-constructed LSTM model (arXiv:1912.01703) with hidden dimensions set to 256, layer dimensions to 8, and a learning rate of 0.0001 using the torch.nn.LSTM function. Randomized predictions were made by a random model, which generated random positive versus negative outputs using the positive-negative frequencies determined by the input samples of each mouse. A filter was applied to the LSTM such that the positive outputs must repeat >1 over 1 s to generate a positive prediction.

The balanced accuracy of DLC prediction was calculated using the formula: (true positives/positive samples + true negatives/negative samples)/2. The positive predictive value (PPV) was calculated as: true positives/predicted positives. Relative PPV in each mouse was calculated as PPV (on)/PPV (off). All lever-presses were treated as positive samples. Correction predictions of lever-presses were considered a true positive. Negative samples in the balanced accuracy and PPV calculation were collected at a rate of one sample/s.

DLC-based calculation of movement. The velocity of a mouse's movement was calculated based on ten DLC labels ("nose", "objectA", "left ear", "right ear", "neck", "middle back", "middle left", "middle right", "tail bottom", "tail mid") that traced the coordinates of different body parts. We categorized the labels into three parts: head ("nose", "objectA", "left ear", "right ear"), body ("neck", "middle back", "middle left", "middle right"), and tail ('tail bottom', "tail mid"). For both D1 and D2 mice, we performed the calculation on seven animals, using the day 9 and day 11 data, across a total of 14 experiments. We determined the trial-averaged speed for each body part in two types of trials. One type involved 20-s trials with lever-presses (from 10 s before to 10 s after lever-pressing), and the other consisted of 20-s random trials (baseline trials). To compute the speed at each timepoint, we filtered out coordinates with low confidence values (<0.95 for head and body, <0.5 for tail). We then measured the Euclidean distance between the coordinates of the current timepoint (x1, y1) and the next timepoint (x2, y2), which was 0.1 s after the current timepoint. After that, we divided the distance by the time elapsed between them (0.1 s) to calculate the movement averaged velocity of each body part. (speed =  $\sqrt{(x_2 - x_1)^2 + (y_2 - y_1)^2}/0.1$ ). The trial-averaged velocity was obtained from individual animals for statistical summarization. including the mean and the standard error. The plots were generated by the Python package Seaborn.

**Regression.** To explore the correlation between the movement and neuronal activity, we selected 20-s trials with lever-presses (from 10 s before to 10 s after lever-pressing) and calculated the trial-averaged velocity as well as trial-averaged neuronal activity. Then we put velocity as input and neuronal activity as output and used function stats.linregress in Python package scipy to fit a linear regression. We used Pearson's correlation coefficient to assess the relationship between velocity and neuronal activity. To analyze such correlations at -5, -2.5, and -0.5 s, we chose the data over the intervals of -5.5 to -4.5 s, -3 to -2 s, and -0.5 to 0.5 s, and calculated the orthogonal distance between the data points in each time interval and the regression line (d =  $\frac{|a^ttx1+b^ty1+c|}{\sqrt{a^2+b^2}}$ ), where the point is (x1, y1) and the line is  $a^*x + b^*y + c = 0$ . The regression plots were generated using the Python package Matplotlib. The statistical figures were generated using GraphPad Prism.

**Location**. The location of a mouse at a given timepoint was calculated using the mean coordinates of the head part of the labels ("nose",

"objectA", "left ear", "right ear"). We also calculated the mean and the standard deviation of all individual locations. Both individual location plots and mean location plots were generated using the Python package Matplotlib. The distance between the location of each animal at each timepoint (x1, y1) and the mean location at -0.5 s (x2, y2) was calculated using Euclidean distance (d =  $\sqrt{(x_2 - x_1)^2 + (y_2 - y_1)^2}$ ). The

calculated using Euclidean distance (d =  $\sqrt{(x_2 - x_1)^2 + (y_2 - y_1)^2}$ ). The statistical figures were generated using GraphPad Prism.

**Direction**. The direction of a mouse from one timepoint to another was calculated using atan2 function and degrees function in the Python package Math. The arrow plots were generated using the Python package Matplotlib. For the statistical figures, we first calculated the angle from the starting timepoint location towards the active lever, as well as the angle from the starting timepoint location towards the sipper. Then, we subtracted the two values by the angle from the starting timepoint location, and selected the minimum of the absolute values of these two as the angle difference. We performed these calculations for all pairs of locations. The statistical figures were generated using GraphPad Prism.

#### Staining and confocal imaging

After deep anesthesia with isoflurane, mice were perfused transcardially first with 20 mL of 0.01 M phosphate-buffered saline (PBS, pH 7.4) and then with 20 mL of 4% paraformaldehyde in 0.1 M phosphate buffer. The brains were removed and postfixed in 4% paraformaldehyde at 4 °C for 6-8 h, followed by incubation with sucrose solutions of graded concentrations (20% then 30%) in 0.01 M PBS at 4 °C for 24 h. The brain was sectioned into 35-µm-thick slices at -20 °C using a cryostat microtome (CryoStar NX50, Thermo Fisher). The brain slices containing the NAc (+1.8 to 0.8 mm from bregma) were washed with 0.01 M PBS, then blocked for 1 h in 4% normal goat serum and 0.4% Triton X-100 (TBS) in 0.01 M PBS. The sections were then incubated with the primary antibody (rabbit anti-Cre, 1:300 diluted in TBS, Cell Signaling Technology, #15036) for 48 h at 4 °C with gentle shaking. Next, the sections were rinsed in 0.01 M PBS three times (5 min each time) and then incubated with the secondary antibody (goat antirabbit Alexa Fluor 568.1:150 diluted in TBS Thermo Fisher. #A11011) for 2 h. The sections were then rinsed in 0.01 M PBS three times (5 min each time). After rinsing, the sections were mounted on glass slides with Mounting Medium with DAPI (Abcam, #AB104139). Fluorescence images were captured with a Leica TCS SP8 confocal laser-scanning microscope, using a 10X lens for low magnification and a 63X oil immersion objective for high magnification.

#### Data acquisition and statistics

For in vivo Ca<sup>2+</sup> imaging experiments, data were collected from seven wildtype, five D1-Cre, and six D2-Cre mice. For optogenetic electrophysiology, data were collected from five to six brain slices from three mice. For in vivo optogenetics experiments, data were collected from eight D1-Cre and 7 D2-Cre mice. Data of the optogenetic inhibition at -0.5 s were unable to be collected from one D1-Cre mouse, due to an unexpected incident (the mouse jumped out of the test chamber, resulting in termination of the experiment). Unaffected portions of data from this mouse were still used for DeepLabCut training. No statistical methods were used to predetermine sample sizes, but our sample sizes were consistent with those reported in previous publications with similar experimental designs<sup>73,92-94</sup>. All data collection was randomized. All data were analyzed offline, and investigators were not blinded to experimental conditions during the analyses. Statistical analyses were performed in GraphPad Prism (v10) or R (v4). All data collected from verified procedures were included in the final statistical analysis. Statistical significance was assessed using paired t-test or twotailed one-way ANOVA repeated measures, followed by Bonferroni's posttests. Differences were considered significant when the p value

<0.05. Statistical results were expressed as mean ± s.e.m. Standard deviations were used for some figure presentations.

## **Reporting summary**

Further information on research design is available in the Nature Portfolio Reporting Summary linked to this article.

# Data availability

Source data are reported in the Source Data sheet published together with this manuscript. Source data are provided with this paper.

# **Code availability**

All custom codes can be found at Code Ocean through the link: https:// codeocean.com/capsule/0290769/tree/v1.

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# **Competing interests**

The authors declare no competing interests.

# **Additional information**

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