# Distinct bandwidths of orexin neuron activity independently encode body movement and metabolic state

**Author List:** Alexander L. Tesmer[1], Paulius Viskaitis[1], Dane Donegan[1], Eva F. Bracey[1], Nikola Grujic[1], Tommaso Patriarchi[2,3], Daria Peleg-Raibstein[1,3], Denis Burdakov[1,3]

**Affiliations:**

1: *Swiss Federal Institute of Technology (ETH Zürich), Department of Health Sciences and Technology, Zürich, Switzerland*

2: *Institute of Pharmacology and Toxicology, University of Zürich, Zürich, Switzerland*

3: *Neuroscience Center Zürich (ZNZ), Zürich, Switzerland*

## Abstract

Hypothalamic orexin/hypocretin neurons (HONs) are key orchestrators of metabolism and adaptive behaviors. HON activity varies rapidly across behavioral and metabolic states: active during periods of high arousal, and silent during quiescence. However, it is unknown whether HON activity tracks specific behaviors, or a general aspect of all behaviors, and whether this depends on metabolic state. After recording HON population dynamics in awake behaving mice, we performed a spectral analysis of HON encoding of spontaneous body movements and behaviors recorded via video-tracking. Multivariate analyses of distinct HON activity bandwidths revealed that movements were encoded at a higher frequency bandwidth than blood glucose, and imposing distinct metabolic states did not interfere with HON movement encoding. HON population activity tracked the total amount of body movement across multiple classified behaviors with a high degree of precision. At key projection targets, orexin/hypocretin peptide outputs correlated with self-initiated movement in a projection-specific manner, indicating functional heterogeneity in HON outputs. Finally, we found that body movement was not encoded to the same extent in other key neural clusters related to arousal or energy. Collectively, these data reveal a general principle behind HON activation in behaving animals, that is orthogonal to their reactions to metabolic shifts. This not only enhances our understanding of the fundamental roles of HONs in brain-body coordination, but also suggests novel non-invasive methods for monitoring HON population activity using video-tracked biometrics, which are pivotal for future investigations into how movement and energy demands are encoded by the brain.

## Introduction

Neural activity related to body movement has recently received renewed attention [1-4]. Although the cortex is classically subdivided into sensory and motor regions[5], movement-related signals make up a large proportion of single-neuron activity across both regions [1-4, 6-18]. Modern technologies for recording large numbers of neurochemically-undefined neurons also detected movement-related activity across subcortical brain areas[1], but suggested some differences between brain areas[3]. This raises the question of whether population activities of neurochemically-distinct subcortical neurons are shaped by the magnitude and frequency of body movements.

We explored this question by examining the population activity of hypothalamic neurons producing the peptide transmitters hypocretins/orexins [19, 20]. Hypocretin/orexin neurons (HONs) track the body's glycemic dynamics and hunger states [20-23], and orchestrate consciousness and arousal [24-27]. Metrics and interpretations of HON activity are of substantial interest in both basic and clinical sciences, due to their brain-wide influence and link to diagnosis and treatment of multiple brain disorders[28-36]. Yet, fundamental questions remain unresolved in relation to HONs and movement:

- Does HON population activity track specific behaviors, or the general magnitude of body movement?
- Given that hunger attenuates some neural operations [37], does it disable HON movement tracking?
- Is movement vs glycemic information tracked by quantitatively distinct bandwidths of HON activity?
- How does HON tracking of body movement compare to other genetically-defined neural subcortical clusters linked to arousal and metabolism?

Here, we address these questions by simultaneously measuring population HON activity and body movement. We report that HONs strongly encode the instantaneous magnitude of body movement; a feature that was observed across and within unique behaviors. HON movement encoding occurs in an activity bandwidth quantitatively distinct from their glucose-tracking bandwidth and is independent of metabolic or glycemic states. We further find that orexin/hypocretin peptide release dynamics related to body movement differ between various projection targets of orexin neurons. These results define a low-cost video biometric of HONs in a widely-used experimental setting, and add to our understanding of movement-related activation of genetically-distinct subcortical neural clusters.

## Results

**A general movement metric statistically explains rapid HON population dynamics across and within behaviors**

To correlate HON dynamics with general body movement, we used a video camera to monitor a head-fixed mouse on a running wheel. Head fixation allowed us to repeatedly record movement from a fixed angle while focusing on factors other than head acceleration, as done in other recent studies[1, 2]. Simultaneously, we recorded HON activity via intrahypothalamic fiber photometry of HON-selective GCaMP6s activity sensor (Figure 1A). Movement artifacts were controlled for via isosbestic excitation. To measure body movement, we derived a 1-dimensional movement metric by calculating the total per-pixel difference between consecutive frames, and then convolving with a decay kernel matched to the known dynamics of the GCaMP6s sensor (Figure 1B; [38]). We then quantified the correlation between recorded HON dynamics, movement, and running speed on the wheel. HON dynamics exhibited a positive correlation to both running-speed ($r = 0.51 \pm 0.03$) and the movement metric ($r = 0.68 \pm 0.04$, Figure 1C-D). The movement metric's correlation was significantly stronger than running ($p < 0.0001$). Notably, we also observed a strong positive correlation with the movement metric within epochs containing no locomotion on the wheel ($r = 0.54 \pm 0.03$), demonstrating that movement encoding by HON dynamics is not limited to running (Figure 1C,D).

Does HON activity represent discrete behavioral states, or rather, encode movement magnitude generalized across behaviors? Both hypotheses could potentially explain the strong correlation in Figure 1. To compare our movement metric (Figure 1B) across different behaviors, we trained a deep-learning network to classify video recordings into the five most commonly observed behaviors: resting, running, grooming, chewing, and sniffing (Figure 2A). Recorded HON activity was the highest during running, and lowest during resting showing significantly different activity levels across behaviors ($p < 0.0001$, Figure 2B,C). The average HON activity during specific behaviors followed a nearly 1:1 relationship against its average movement metric (Figure 2D). Movement was also correlated with HON population dynamics within classified non-locomotor behaviors of grooming, chewing, and sniffing (Figure 2E). Overall, these results reveal HON population activity precisely tracks a general degree of body movement across recorded behaviors.

**Movement tracking within different frequencies and phases of HON population signal**

Recorded HON dynamics varied over multiple timescales, exhibiting sub-second to several-minute oscillations. Due to this observation, we asked if HON encoding of movement was similar across frequency domains of HON activity. Empirical mode decomposition (EMD) adaptively decomposes a signal into a set of intrinsic mode functions (IMFs) which provide a time-frequency representation of the data, and is robust to the non-stationary and non-linear nature of biological signals[39]. Each IMF can be assigned a characteristic frequency which approximates the average oscillation in that signal component. Thus, we were able to "break down" hORX-GCaMP6s photometry into a set of simple IMFs, each capturing a different characteristic frequency of HON dynamics (Figure 3A). When plotting the average power of each HON IMF versus its characteristic frequency, we noted that maximum power generally occurred around 0.1 to 0.01 Hz (Figure 3B). A parallel EMD performed on the body movement metric revealed a maximum power in a similar frequency band (Figure 3C), suggesting that body movement and HONs have similar spectral profiles.

Do movements occur at specific phases within the HON activity rhythms? To examine this, we performed a phase preference analysis which tells us when, on average, a movement event occurs in the cycle of a HON oscillation. By convention, within each HON IMF, we defined the crest ("upstate") to be at $\pi/2$ radians and the trough ("downstate") at $3\pi/2$ radians. In turn, we split the movement metric (z-score) above and below zero to define "active" and "quiescent" movement epochs, respectively. We found that active epochs preferred the $\pi/2$ HON phase while quiescent epochs preferred the $3\pi/2$ HON phase, especially in the 0.1 to 0.01 Hz frequency domain (Figure 3D). Strongest phase coupling between HONs and movement was also observed in this frequency domain (Figure 3E).

Finally, we sought to confirm whether HON simply tracked, or also shaped, the body movements characterized in Figure 3C. We reasoned that if HONs only tracked the movements, then HON ablation would not substantially alter the power spectrum of the movements; conversely, if HONs shaped the movements, then HON ablation would alter the movements. We selectively ablated HONs using an extensively validated HON-DTR mouse model[23, 40, 41] (Figure 3F). Maximum-power IMFs were found in a similar frequency range peaking around 0.1-0.01 Hz in HON-ablated and control mice (Figure 3G), suggesting HONs are not necessary to maintain movement frequency profiles. Overall, these results define frequencies and phases of HON activity that track body movement information.

**Orexinergic representation of movement at different HON projection targets**

Monoaminergic nuclei producing dopamine and noradrenaline, substantia nigra pars compacta (SNc) and locus coeruleus (LC) respectively, have long been studied for their involvement in arousal and movement [42, 43]. Both are densely innervated by HON axons and express orexin receptors [29, 44]. Do HONs transmit movement information equally to these projection targets? To investigate this, we expressed the genetically-encoded orexin peptide biosensor OxLight1[45] into the SNc and LC for simultaneous dual-site recording in the same mouse (Figure 4A). We found that the "active" epochs of the movement metric differed in phase preference to OxLight1 signal between the brain regions: SNc orexin recordings showed a phase preference to the "downstate" ($3\pi/2$) phase, while LC orexin recordings preferred the "upstate" ($\pi/2$) phase, particularly in the 0.1 to 0.01 Hz frequency band (Figure 4B), with the highest phase coupling in the lower frequency bands (Figure 4C). This suggests that orexin release may heterogeneously represent body movement at different HON projection targets. To further explore this using an alternative analysis, we used a K-Means clustering algorithm to sort self-initiated movements into two broad categorical clusters constituting "small" and "large" movements (Figure 4D). When orexin dynamics were aligned to these clusters, we observed rising signals in the LC, but falling signals in the SNc, which was especially apparent in association with "large" clustered movements (Figure 4E). Together, these analyses indicate that orexin peptide release related to movement is non-homogenous across two major HON projection targets.

**HON movement tracking across metabolic states**

Given the robust correlation of HON activity and movement across the behavioral and frequency spectra, we sought to contrast our findings against another major physiological factor thought to influence HON activity, the metabolic state [20-22]. First, we tested whether movement encoding by HONs depended on fasting state, which is known to strongly modulate HONs[20, 46]. We found that correlations of HON activity and movement were not significantly different in *ad-libitum* fed, 18h-fasted then re-fed, and 18h-fasted mice (Figure 5A). Second, we sought to quantify how the HON movement encoding compares to the recently-described HON encoding of lower-frequency blood glucose information, namely the negative relations between HONs and first temporal derivative of blood glucose[23]. Using a small number of mice from this pre-existing dataset [23] in which video recordings were also available (Figure 5B), we again performed an EMD to align individual HON IMFs to both movement and the first derivative of blood glucose after intragastric infusion of glucose (0.24 g/mL, 900 µL over 10 minutes; Figure 5C). Within the 1$^{st}$ and 4$^{th}$ quartile of blood glucose, movement-HON correlations were not significantly different (Q1: $r = 0.43 \pm 0.11$. Q4: $r = 0.45 \pm 0.07$. Mean ± SEM of $n = 6$ mice. Paired *t*-test: $t_5 = 0.2225$, $p=0.8327$). To explore and formally define the HON signal frequency bands that carry information about movement and blood glucose, we fit each HON IMF using a multivariate model with glucose derivative and movement as weighted predictors of each IMF. We plotted the two fitted weights against corresponding IMF frequency (Figure 5D). Large negative weights for the blood glucose derivative were assigned to lower frequency IMFs, while large positive weights for movement were assigned to higher frequency IMFs (Figure 5D). When binning across frequencies, statistical comparison of these weights indicated that movement had significantly different weights than glucose derivative both in the 0.1 to 0.01 Hz and <0.001 Hz frequency bands (Figure 5E). Notably, glucose derivative did not have significant weights in the higher frequency band, whereas movement did; conversely, movement did not have significant weights in the lower frequency band, whereas

glucose derivative did (Figure 5E). Overall, these data indicate that movement representation in the HON population signal is spectrally orthogonal to fasting state or blood glucose dynamics, and is carried selectively in the high-frequency (0.1-0.01 Hz) band of the signal, while glucose information is contained in lower frequency (<0.001 Hz) band.

**Movement tracking in HON versus other genetically-defined subcortical neural populations**

Finally, we sought to contrast the movement encoding in the HON population against other genetically defined subcortical neural clusters. We selected dopaminergic neurons of the SNc, glutamatergic neurons of the medial vestibular nucleus (MVe), and noradrenergic neurons of the LC, due to their links to HON and previously proposed roles in movement and/or arousal [47-52]. Additionally, we examined SF-1 expressing neurons in the ventral medial hypothalamus (VMH), which are thought to be sensitive to metabolic state [53-57]. We used different BL/6J-derived mouse cre-lines to express cre-dependent GCaMP6s activity indicators in each of these neural clusters, obtaining simultaneous fiber photometry neural activity and body movement recording in each mouse group, in the same way as for HONs (Figure 1A). We found that, like HONs ($LHA^{ORX}$, r = 0.68 ± 0.04), the MVe glutamatergic neurons ($MVe^{GLUT}$, r = 0.70 ± 0.06), strongly correlated with movement across the entire recording (Figure 6C). The strength of the correlation was not significantly different across these two populations (p= 0.8366). In contrast, $LC^{NA}$ had only weak positive correlation (r = 0.23 ± 0.07), while $SNc^{DA}$ had a weak negative correlation (r = -0.28 ± 0.08). $VMH^{SF-1}$ neurons had only a slight positive trend (r = 0.20 ± 0.11). Cross correlation between GCaMP6s and the movement metric showed that HON activity on average preceded movement by a few samples (-0.34 ± 0.12 seconds), as did the $LC^{NA}$ and $SNc^{DA}$ (-0.72 ± 0.15 and -1.08 ± 0.52 seconds, respectively). $MVe^{GLUT}$ activity was closely aligned to movement (-0.15 ± 0.09), and $VMH^{SF-1}$ activity followed movement by several seconds (4.23 ± 0.15) using the 1.5× inter quartile range to filter for outliers (Figure 6D). We then repeated the clustering analysis described in Figure 4, aligning the photometry signals to initiation of movements assigned to “small” or “large” movements (Figure 6E). For large movements, HON activity encoded movement similarly to $MVe^{GLUT}$ neurons (p = 0.3915, Figure 6G). However, for small movements, HON activity encoded the movement metric significantly better than $MVe^{GLUT}$ neurons (p = 0.0099, Figure 6G). Together, these data suggest HONs are uniquely positioned to track body movement to a degree not observed in the other subcortical populations we examined.

## Discussion

We found that, across behaviors, HONs tracked the amount of body movement with a high degree of precision. This tracking occurred in a higher frequency bandwidth than their tracking of blood glucose, contributing to effective multiplexing of these two fundamental physiological variables. The HON movement tracking was not significantly different across hunger and glycemic states, suggesting orthogonal multiplexing of the movement and energy states. At two key projection targets of HONs, orexin/hypocretin peptide output was also related to movements, but in a projection-specific way, implying a heterogeneity in the movement-related HON outputs. Among the multiple neurochemically-defined subcortical neural clusters examined here, HONs were dominant in the precision of their movement tracking.

What would be the evolutionary advantages of coupling body movement to proportional changes in HONs? A central hypothesis for the meaning of HON activation is increased arousal, with evidence including electroencephalography [26], pupil dilation [58, 59], and cardiorespiratory adaptations [60 61-63]. Though our projection-specific data imply that there may be subsets of HONs that are negatively related to movement (Figure 4), at the HON population level overall the coupling between neural activity and movement was strongly positive (Figure 1). A simple interpretation of these data is that, via the HON movement tracking, the brain creates a "wake up" signal in proportion to movement, which could be helpful since dealing with challenges and opportunities created by movement may benefit from increased arousal. Importantly, HONs are also implicated in the mobilization of body glucose stores and shuttling glucose from liver to muscle [64]. Multiplexing their activation to both movement and glucose-sensing may allow movement process to be optimally matched to movement energy demands.

It is tempting to speculate on the breadth at which HON population activity encode physiological derivatives (i.e. rate-of-change in physiological parameters) multiplexed across the frequency domain. This study highlights how HONs strongly represent instantaneous movement magnitude, which can be rephrased as a change in body position over time. Similarly, we previously reported population HON activity predominantly tracks the derivative of blood glucose, rather than proportionally encode glycemic state [23]. Knowing the rate at which a physiological variable is changing allows for anticipatory responses, such as in Proportional-Integral-Derivative (PID) sensorimotor control loops, where the derivative-control component enables adaptive prediction of erroneous deviations from a set-point [65, 66].

Do HONs "read" or "write" movements? From the perspective of sensorimotor control loops, the answer should be both. In theory, HONs could "read" movements either by sensing them, or by receiving efference copies and/or corollary discharges corresponding to motor commands[67]. Prior studies indicate that acute, targeted HON stimulation can evoke or modulate certain kinds of movement [68-71]. However, note that we found the power-frequency spectrum of the self-paced movements studied here was not strongly dependent on presence of HONs themselves (Figure 3G). This indicates that, while HONs may be sufficient to "write" movements, they are not necessary. Furthermore, it is tempting to speculate on the implications of HON loss-of-function viewed from the lens of a sensorimotor control loop. Without derivative-control, a system is still able to measure and perturb a variable, however its ability to dampen unwanted oscillations from a set-point is strongly impaired. From this perspective we can speculate that narcolepsy-cataplexy, caused by HON loss-of-function, is perhaps explained by oscillations into unwanted sleep-states and motor programs due to impaired control loops for wakefulness and movement.

In addition to these fundamental implications, there is an applied implication of our findings for basic neuroscience research. Ever since the importance of HONs for brain function and brain-body coordination was established [24, 25, 31, 72], a demand appeared for tracking their function across research and clinical settings, and many useful (but invasive) techniques for this were developed [40, 45, 73-75]. The high correlation between body movement and HON activity demonstrated here suggests that video-tracked pixel difference could serve as a simple non-invasive biometric for real-time estimation of HON population state, at least as validated here in

head-fixed behaving mice, a widely used model in neuroscience research [76, 77], where assessment of arousal-linked signals is in continuing demand [15, 78-80 81, 82].

Our results open multiple directions for further study. Upstream of HONs, it would be important to solve the challenging puzzle of how movement information is conveyed to these neurons. This challenge may likely require an extensive functional screen, because of the wide-spread monosynaptic inputs to HONs, with many of these coming from areas where some movement-associated activity has been reported [83]. Within the HON population activity studied here, individual cells and their possibly heterogeneous responses to movement also remain to be defined, since the present results likely represent only a dominant subpopulation of HONs. Downstream of HONs, the findings in Figure 4 could be extended to probe the role in movement communications of the multiple transmitters released by HONs[84-86] to the genetically-distinct, brain-wide targets of their terminal projections[29]. In future work, it will also be important to test whether movement tracking by HONs is used for optimal adjustments of the many cognitive and autonomic processes linked to HON outputs.

In summary, our findings define a key aspect of brain activity that is rapidly and precisely synchronized to even small alterations in body movement. The brain needs to sense movement for predicting future states and energy needs. Our results show that movement is encoded in parallel within glycemic state within different frequency domains of HON activity, presumably allowing these cells to communicate both energy supply and a key aspect of energy demand in the body. Deeper insights of how defined neurons and connection turn body movement into adaptive responses will enable insights into the impact of body movement on brain function in health and disease.

## Materials and Methods

### Experimental Subjects

All animal experiments followed the Swiss Federal Food Safety and Veterinary Office Welfare Ordinance (TSchV 455.1, approved by the Zürich Cantonal Veterinary Office). Adult C57BL/6J-derived lines were studied. For experiments performed in Figure 4, we used previously validated cre-dependent transgenic mice: Vglut2-ires-Cre (Slc17a6$^{tm2(cre)Lowl}$/J, JAX:016963), SF1-Cre (Tg(Nr5a1-cre)7Lowl/J, JAX:012462), DAT-Cre (*Slc6a3*$^{tm1(cre)Xz}$/J, JAX:020080), or DBH-iCre (Tg(Dbh-icre)1Gsc, MGI:4355551). For HON ablation experiments we used the previously validated orexin-DTR mice, wherein all HONs were ablated via injection with diphtheria toxin >2 weeks before experiments began [40, 41]. All mice were male except for a small number of Vglut2-ires-Cre and DBH-iCre mice, which were similar to males and therefore pooled. Thus, whether all conclusions apply to female mice remains to be determined. Animals were housed in a 12:12 hour light-dark cycle and had *ad libitum* access to water and food (3430 Maintenance Standard diet, Kliba-Nafag) unless stated otherwise. All experiments were performed in the dark phase. Studies were repeated in at least two independent cohorts and, when relevant, used a semi-randomized crossover design for fasting state.

### Surgeries and Viral Vectors

To record photometry across a range of brain regions, we stereotaxically injected viral vectors into adult mice as follows. In all cases, mice were anesthetized with 2-5% isoflurane following operative analgesia of buprenorphine and site-specific lidocaine. Viruses were stereotaxically injected at 1-2 nL/s (NanoInject III injector) either unilaterally, or bilaterally, at the following coordinates relative to bregma: anteroposterior (AP), mediolateral (ML), and dorsoventral (DV).

The previously validated promotor-driven AAV1-hORX-GCaMP6s.hGH (2.0x$10^{13}$ GC/mL, Vigene Biosciences) was used to record from HONs in the **LHA:** AP -1.35, ML ± 0.95, DV -5.70, -5.40, and -5.10 mm. 70 nL per site. For cre-dependent mouse lines, we injected AAV9.CAG.Flex.GCaMP6s.WPRE.SV40, a gift from Douglas Kim & GENIE Project (Addgene plasmid # 100842; 1.9x$10^{13}$ GC/mL, 1:5 dilution in sterile PBS) in the **MVe:** AP -6.05, ML ± 0.95, DV -4.40 mm. 200 nL per site. In the **VMH:** AP -1.35, ML ± 0.45, DV -5.75, -5.50, and -5.25 mm. 70 nL per site. In the **SNc:** AP -3.20, ML ± 1.40, DV -4.20. 200 nL per site. In the **LC:** AP -5.35, ML ± 0.90, DV -3.70 and -3.50 mm. 100 nL per site. The orexin-sensor, AAVDJ.hSynapsin1.OxLight1 (7x$10^{12}$ GC/mL, UZH Viral Vector Facility, 1:3 dilution in sterile PBS) was injected into both the SNc or LC at the above coordinates. 150 nL per site. Optic fiber cannula of 200 um diameter, 0.39 numerical aperture (NA) with a 1.25 mm ceramic ferrule (Thorlabs) were implanted 0.1 mm above the most dorsal injection site. A custom-made aluminum head-plate was secured to the skull using dental cement (C&B Metabond). Mice were given postoperative analgesia and allowed to recover for at least two weeks before the first experiment.

Expression was confirmed experimentally by observing dynamics at 465 nm excitation. A small number of mice without any observable dynamics at 465 nm, or with strong artifacts in the 405 nm isosbestic, were excluded from analysis. Expression was additionally confirmed terminally, via perfusion with 4% PFA in sterile PBS, histological slicing, and then imaging with a fluorescence microscope (Nikon Eclipse Ti2).

For intragastric infusion surgeries as in Figure 5, a small number of experiments from Viskaitis et al. 2024 were re-analyzed if video was also available, the detailed methods for these glucose experiments are given in this source publication [23].

### Fiber Photometry

For fiber photometry, we used a custom-build camera-based photometry system. GCaMP6s (or OxLight1) activity was recorded at 10-20 Hz via alternating excitation between 405 nm and 465 nm LEDs (Doric; average power 20 µW at fiber tip) in multiple animals simultaneously. The 405 nm excitation was used as an isosbestic control for movement artifacts. Most recordings were either 20 or 40 minutes long, except in Figure 5 when recording lasted for >1 hour. The first minute of each photometry trace was removed due to bleaching artifacts.

Further 465 mm fluorescence bleaching was accounted for by subtracting a triple exponential curve fit to the trace. Finally, each trace was z-score normalized to its standard deviation and mean. For visual clarity only, photometry traces in Figure 1D, Figure 4A, and Figure 6A were smoothed using a 1-second moving average filter; all statistical comparisons and derived metrics were calculated using raw data.

**Movement Metrics**

All experiments were performed in a closed container illuminated via infrared LEDs to achieve constant luminance during the recording. The movement metric was generated from videos captured using a commercial infrared camera (Blackfly S USB3, Teledyne FLIR) at the same sampling rate as photometry (10-20 Hz). To generate the metric, per-pixel differences were calculated across consecutive frames with 8-bit resolution. Then, the absolute value of the difference across every pixel was summed for each consecutive frame to generate one value for each sample, excluding the first frame. To compare this movement metric to concurrently measured photometry, the resulting trace was convolved with a "GCaMP6s kernel" which consisted of a 60 second exponential decay kernel with a decay rate equivalent to the reported GCaMP6s half-life (1.796 s [38]). Then, the first minute of convolution was removed to match the photometry trace and the resulting trace transformed to a z-score using its standard deviation and mean. When relevant, locomotion-specific motion was recorded using an optical encoder (Honeywell, 128 ppr 300 rpm Axial) and digital acquisition box (BNC-2110, National Instruments). Locomotion was filtered using a 5-sample (250 ms) moving average filter for visualization only.

For bout-related analyses, we detected movement-bouts by first smoothing the z-scored movement-metric with a 20-sample (1 second) moving average filter and then aligning to sample indices where movement was < 0 SD for at least 4 seconds before exceeding the threshold. For subsequent clustering, a K-Means algorithm (scikit-learn) in the default configuration was implemented to identify k = 2 clusters of movement from the identified bouts. Photometry signals were aligned to bout indices then baselined by calculating a z-score of 1-3 seconds before bout initiation.

**Concurrent monitoring of glucose and intragastric infusions**

The HD-XG telemetry system (DSI) as described in Viskaitis et al. 2024 was used to measure and preprocess blood glucose concentrations as per manufacturer instructions. For intragastric (IG) glucose infusions, 900 µL 0.24g/mL glucose dissolved in sterile saline was infused at a rate of 90 µL/minute for 10 minutes. Saline controls are shown in the source publication and did not perturb HONs[23]. Missing samples were linearly interpolated, and the resulting glucose trace was resampled (scipy.signal.resample) to align to the photometry recording Hz. To generate the derivative traces, the raw glucose trace was smoothed using a 10 minute moving average filter then resampled to align to the photometry recording Hz before the first derivative was calculated.

**Empirical mode decomposition**

The logic of empirical mode decomposition analysis was largely based on [87], and was performed using the default settings of the python EMD toolbox version 0.6.2 [88]. Briefly, traces were first normalized (z-score) before IMFs were calculated using the sift algorithm [39]. The instantaneous phase, amplitude, and frequency across each IMF were calculated using the Normalized Hilbert Transform Method. The characteristic frequency was determined by taking the mean of each IMF's frequency data weighted per-sample by the IMF's amplitude data. Extremely low-frequency (< $10^{-3}$ Hz) IMFs were excluded as they did not complete enough cycles to allow sufficient sampling for the following statistics. Power was taken as the means of the squared amplitude data and expressed as a percentage of the total power from each IMF. The preferred phase (direction) and coupling strength (length) for each IMF's phase data was then calculated from the 1$^{st}$ trigonometric circular moment with weights corresponding to positive ("active") or negative ("quiescent") signed samples of the movement metric. Note that in the "active" case, for example, all negative values of the movement metric would be assigned weights of zero.

**Behavioral classification**

To classify behaviors, we used the video captures used to generate the movement-metric and manually labeled five behavioral classes: chewing, grooming, resting, running, and sniffing, from greyscale frames using the previous, current, and subsequent frames to form an RBG input image. A convolutional neural network (ResNet18) was trained using PyTorch 2.2.0 to over 98.6% accuracy by stratified ten-percent holdout validation. The trained network was then used to classify photometry-synchronized videos.

**Data analysis and statistics**

Raw data were processed with custom scripts in Python 3.9, using Seaborn and Matplotlib libraries for plot-generation. Statistical analysis was similarly performed in Python using Pinguoin v0.5.4, SciPy v1.14.0, and scikit-learn 1.2.1 libraries. In Figure 2 and 3, local regressions were performed using statsmodels v0.14.1 with a 0.5 fraction of the data. Confidence intervals were generated using 1000 bootstrapped samples. Circular regressions were similarly performed using scikit-learn and a multi-output support vector regression whereby the phase (θ) in radians was evaluated over 7 evenly spaced samples on the log-scale frequency by converting the phase into a multidimensional vector y:

$$y = [\sin(\theta), \cos(\theta)]$$

Linear regression models for Figure 5 were calculated using the statsmodels library following the formula:

$$IMF_n = \beta_0 + \beta_1 X_1 + \beta_2 X_2 + \epsilon$$

Where $IMF_n$ is the $n^{th}$ IMF of the GCaMP6s signal, $\beta_0$ is the intercept term, $\beta_1$ and $\beta_2$ are the coefficients for $X_1$, blood-glucose derivative, and $X_2$: movement metric, respectively, and $\epsilon$ is the error term.

Statistical tests, sample sizes, and their results are indicated in the figures, legends, and/or descriptions in the text. Where significance is presented, p-values are as follows: *p<0.05, **p<0.01, ***p<0.001, and ****p<0.0001, n.s. p>=0.05. We made no assumptions regarding the directionality of our effects; all statistical tests were two-tailed. When relevant, multiple comparisons adjustments were made using the Bonferroni correction as indicated in figure legends / or text. Data are presented as means and standard error of the mean (SEM) unless stated otherwise. Boxplots always represent the maximum, minimum, interquartile range, and median of the data.

## Conflict of interest statement

The authors declare to competing financial interest.

## Acknowledgements

This work was funded by ETH Zürich. DB and ALT conceived the study and designed the protocol, with contributions from PV. ALT, PV, NG, DD, and EB performed the surgeries. ALT and PV performed most of the experiments. ALT designed and performed data analyses with contributions from PV and DD. TP provided and advised on the orexin sensor. DB and ALT wrote the text with inputs from DPR and NG. The authors have no competing interests to declare.

## Data availability

Data will be deposited in a publicly available database (osf.io) before time of publication.

## Figures and Legends

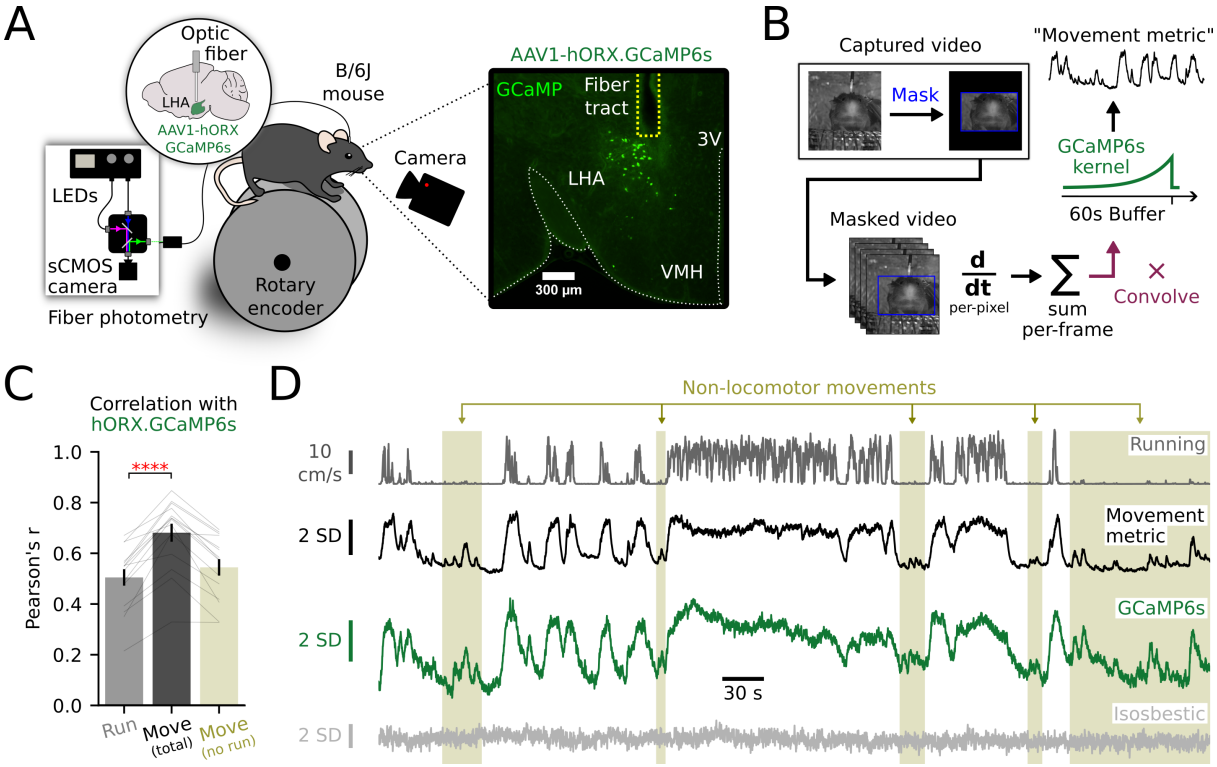


**Figure 1.** Movement magnitude is represented by rapid HON dynamics.

***A,*** Schematic depicting the photometry system and voluntary wheel-running apparatus with video capture (left) and representative expression (right) of AAV1-hORX-GCaMP6s in HONs (see Gonzalez et al. 2016). LHA; lateral hypothalamic area; 3V; third ventricle; VMH; ventral medial hypothalamus. ***B,*** Processing pipeline to generate a "movement metric" from video recording of voluntary movement. ***C,*** Whole-trace correlation of HON photometry with simultaneously recorded behavior metrics from n = 15 mice: running (r = 0.50 ± 0.03), the movement metric (r = 0.68 ± 0.02), the movement metric in epochs where locomotion was < 1 cm·s$^{-1}$ (r = 0.54 ± 0.03). Metrics given as mean ± SEM, connected lines represent individual mice. Asterisks indicate comparison between running and movement metric (paired *t*-test: $t_{14}$ = 6.676, **** p < 0.0001). ***D,*** Traces from an example experiment. From top to bottom: running on the wheel, the video-derived movement-metric, HON GCaMP6s photometry, and isosbestic control. Shaded beige regions indicate non-locomotor epochs where the movement metric still reported strong positive correlations with HON activity.

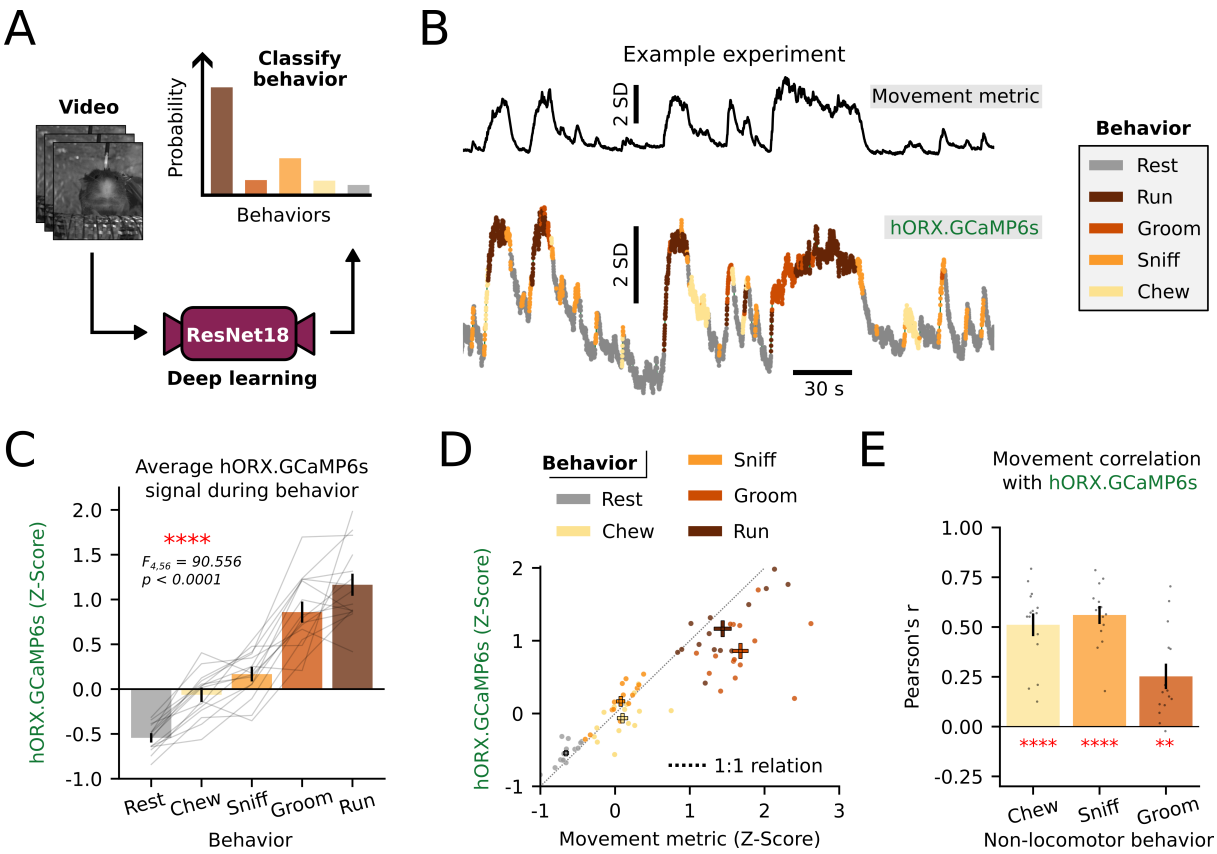


**Figure 2.** HON dynamics represent movement magnitude across classified behaviors.

***A,*** Diagram for classifying behaviors from video recordings via deep learning. ***B,*** Example experiments showing movement (upper, black) and color-coded photometry (lower) after behavioral classification. ***C,*** Average normalized hORX.GCaMP6s signal across classified behaviors in n = 15 mice (rmANOVA: $F_{4,56}$ = 90.556, p < 0.0001). ***D,*** Average value of the normalized hORX-GCaMP6s signal from n = 15 mice plotted against the average value of the movement metric in each classified behavior. Thick bars represent SEM across both metrics. The dotted line represents an idealized 1:1 linear relationship between movement and photometry with an intercept at zero. ***E,*** Correlation of hORX.GCaMP6s signal with the movement metric within classified behaviors. Asterisks represent two-tailed *t*-tests against mean of zero, after Bonferroni correction (Chew: $t_{14}$ = 10.007, p < 0.0001. Sniff: $t_{14}$ = 14.272, p < 0.0001. Groom: $t_{14}$ = 4.355, p = 0.0020).

*p < 0.05, **p < 0.01, ***p < 0.001, ****p < 0.0001 and ns, not significant by two-tailed tests.

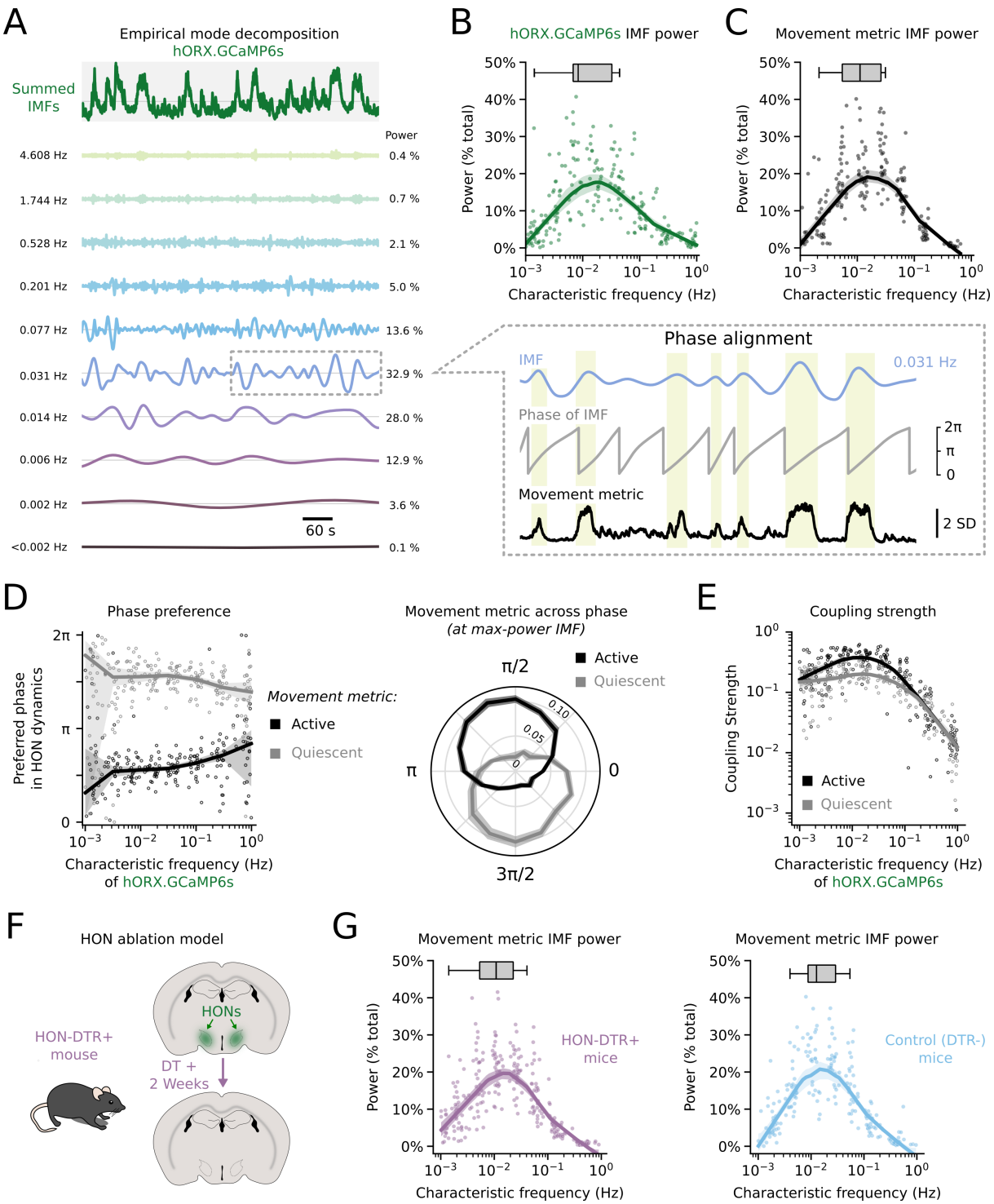


**Figure 3.** Movement magnitude is phase-aligned to HON activity across the frequency domain.

***A,*** Representative empirical mode decomposition (see methods) of HON GCaMP6s activity from one experiment. The top green trace displays a summation of all IMFs. Below are the first 10 IMFs sorted by characteristic frequency in Hz. Relative power is reported as a percentage of the total. Dashed grey box (middle right) represents a cutout of the 0.031 Hz IMF in which movement epochs (shaded beige regions) are clearly phase-aligned in the 0-π period. ***B,*** Average power plotted against characteristic frequency of n = 229 GCaMP6s-derived IMFs derived from 27 experiments using 15 mice. Thick line and shaded region represent a local regression and 95% CI. Boxplots represent the maximum power IMF from each experiment. ***C,*** Same as B, using n = 214 movement metric-derived IMFs. ***D,*** Left: Preferred phase of both active (black) and quiescent (grey) epochs of the movement metric plotted against characteristic frequency. Dots represent n = 229 GCaMP6s-derived IMFs derived from 27 experiments using 15 mice. Thick line and shaded region represent a circular regression and 95% CI. Right: average absolute value of the z-scored movement metric plotted on the radial axis

against the phase of the maximum-power IMF. Lines represent mean ± SEM from n = 15 mice. ***E,*** Coupling strength of the movement metric to GCaMP6s IMFs in both active (black) and quiescent (grey) epochs plotted against the IMF's characteristic frequency. Dots represent n = 229 GCaMP6s-derived IMFs derived from 27 experiments using 15 mice. Thick line and shaded region represent a local regression and 95% CI. ***F*** HON ablation in HON-DTR+ mice. ***G,*** Left: same as C, using n = 267 movement metric-derived IMFs from 34 experiments using 12 HON-DTR+ mice. Right: same, for n = 217 IMFs from 30 experiments using 11 control mice.

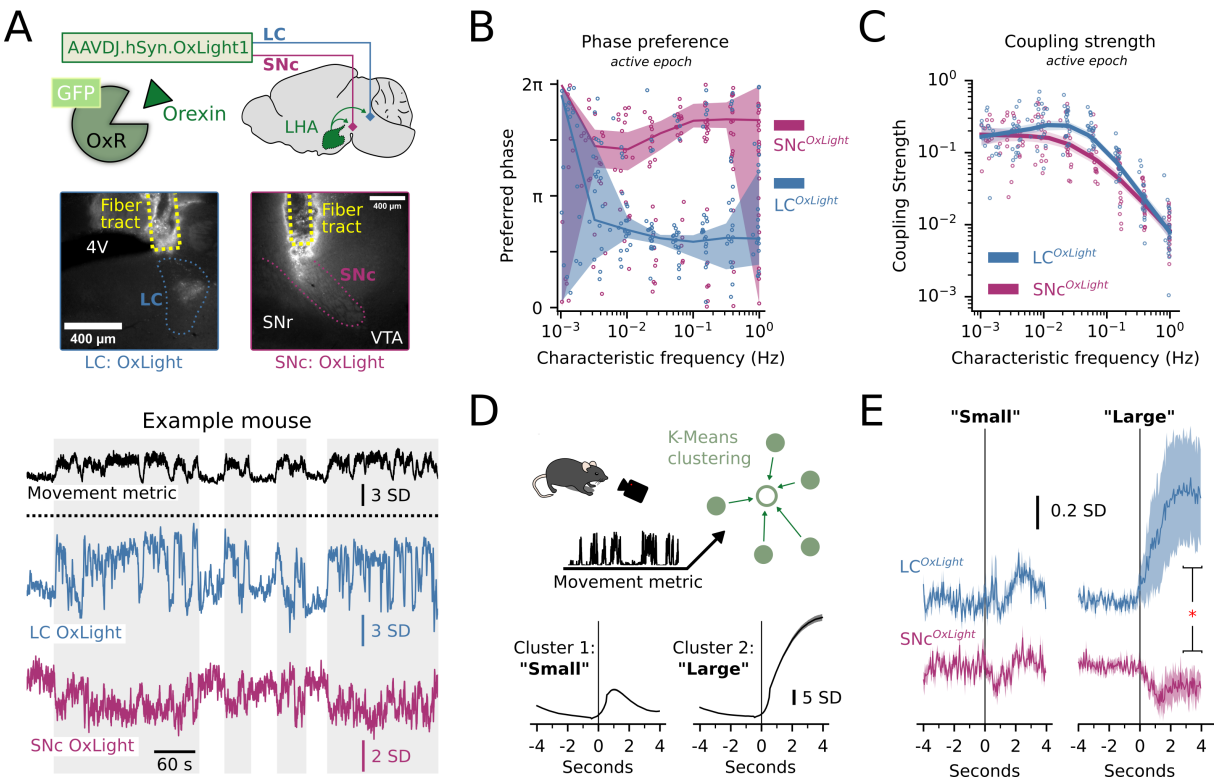


**Figure 4.** Movement-related orexin peptide release is non-homogenous across projection targets.

***A,*** Upper, schematic representing targeting of the orexin sensor OxLight1 to the LC and SNc, representative histology from n = 6 mice. Lower, example experiment displaying the movement metric and OxLight1 signal in the LC (blue) and SNc (purple) in the same mouse. Shaded regions represent movement epochs. ***B,*** Preferred phase of individual EMD-derived OxLight1 IMFs to active epochs of the movement metric plotted as a function of the IMF's characteristic frequency. n = 317 IMFs from 21 experiments using 7 mice. Thick line and shaded region represent a circular regression and 95% CI. ***C,*** Coupling strength of individual EMD-derived OxLight1 IMFs to active epochs of the movement metric plotted as a function of the IMF's characteristic frequency. n = 317 IMFs from 21 experiments using 7 mice. Thick line and shaded region represent a local regression and 95% CI. ***D,*** Diagram of K-Means clustering to generate two clusters of movement representing voluntary initiation motion following > 4s of no motion, see methods. ***E,*** Photometry baselined -3 to -1 seconds before movement initiation in two clusters: small movements (left) and large movements (right). Lines and shaded regions represent mean ± SEM of n = 6 mice. Asterisk represents a paired statistical comparison of mean signal 3 to 4 seconds after movement initiation (Wilcoxon test, $D_6$ = 1.0, * p = 0.03125).

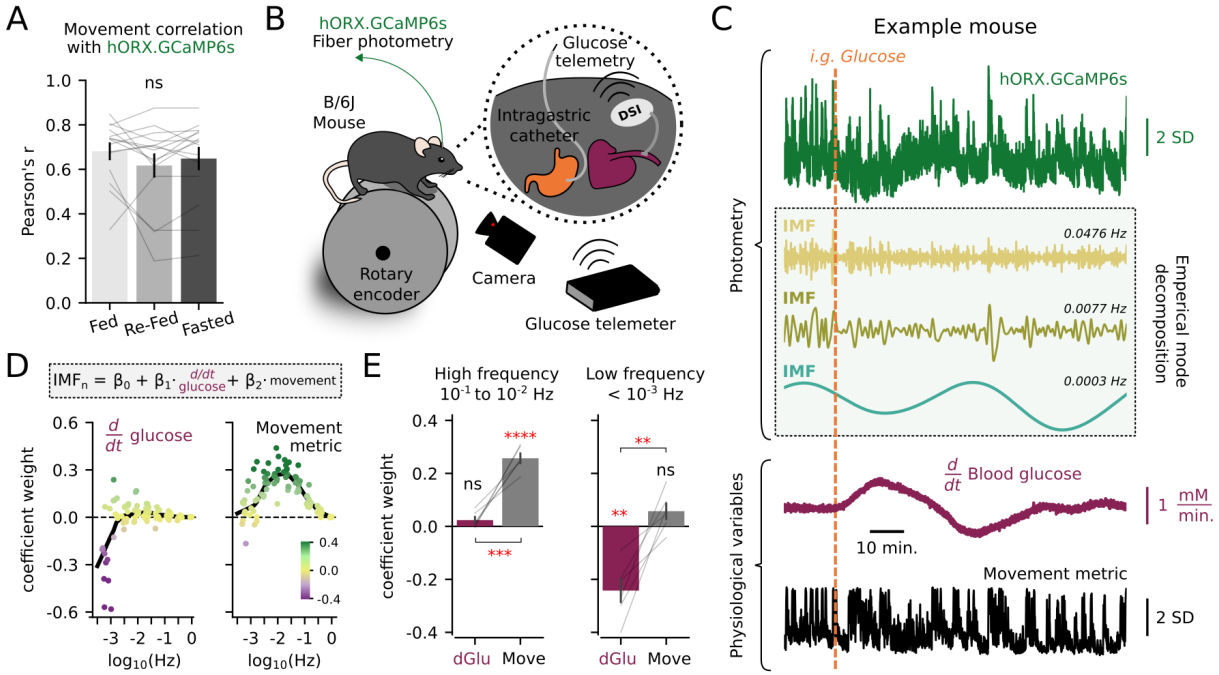


**Figure 5.** HONs multiplex movement and blood glucose across frequency domains.

***A,*** Correlation of movement with HON photometry across three states of fasting (n = 15 mice). Fed: ad-libitum access to chow. Re-fed: 18-hour fasted and then food returned 2 hours before experiment. Fasted: 18-hour fasted mice (rmANOVA: $F_{2,28}$ = 1.848, p = 0.176)**.** ***B,*** Scheme of experimental setup including photometry, glucose telemetry (DSI), video capture, and intragastric catheter infusions (Viskaitis et al., 2024). ***C***, Example HON GCaMP6s photometry trace (top), three derived IMFs (middle), and simultaneously recorded physiological variables of blood glucose (plotted as the first derivative) and movement magnitude (lower). A vertical dashed orange line represents an intragastric infusion of glucose. **D,** A linear model was fit to predict n = 94 IMFs using the glucose derivative and movement. Fitted coefficient weights are plotted as a function of the IMF's characteristic frequency. Note that glucose derivative (lower left) had large negative weights for low-frequency IMFs, while movement had large positive weights for higher-frequency IMFs. ***E,*** Per-mouse (n = 6) binned coefficient weights. For the higher frequency bin (left, $10^{-1}$ to $10^{-2}$ Hz), coefficient weights were tested against a population mean of zero (Bonferroni-corrected one-sample *t*-test: glucose derivative $t_5$ = 1.965, p = 0.2131; movement $t_5$ = 14.102 p < 0.0001). Coefficient weights of glucose derivative were compared to movement (paired *t*-test: $t_5$ = 8.331, p = 0.0004). For the lower frequency bin (right, < $10^{-3}$ Hz), coefficient weights were similarly tested against a population mean of zero (Bonferroni-corrected one-sample *t*-test: glucose derivative $t_5$ = -5.631, p = 0.0049; movement $t_5$ = 1.963, p = 0.2139). Coefficient weights of glucose derivative were compared to movement (paired t-test: $t_5$ = 5.385, p = 0.0030). Bar plots display mean ± SEM.

*p < 0.05, **p < 0.01, ***p < 0.001, ****p < 0.0001 and ns, not significant by two-tailed tests.

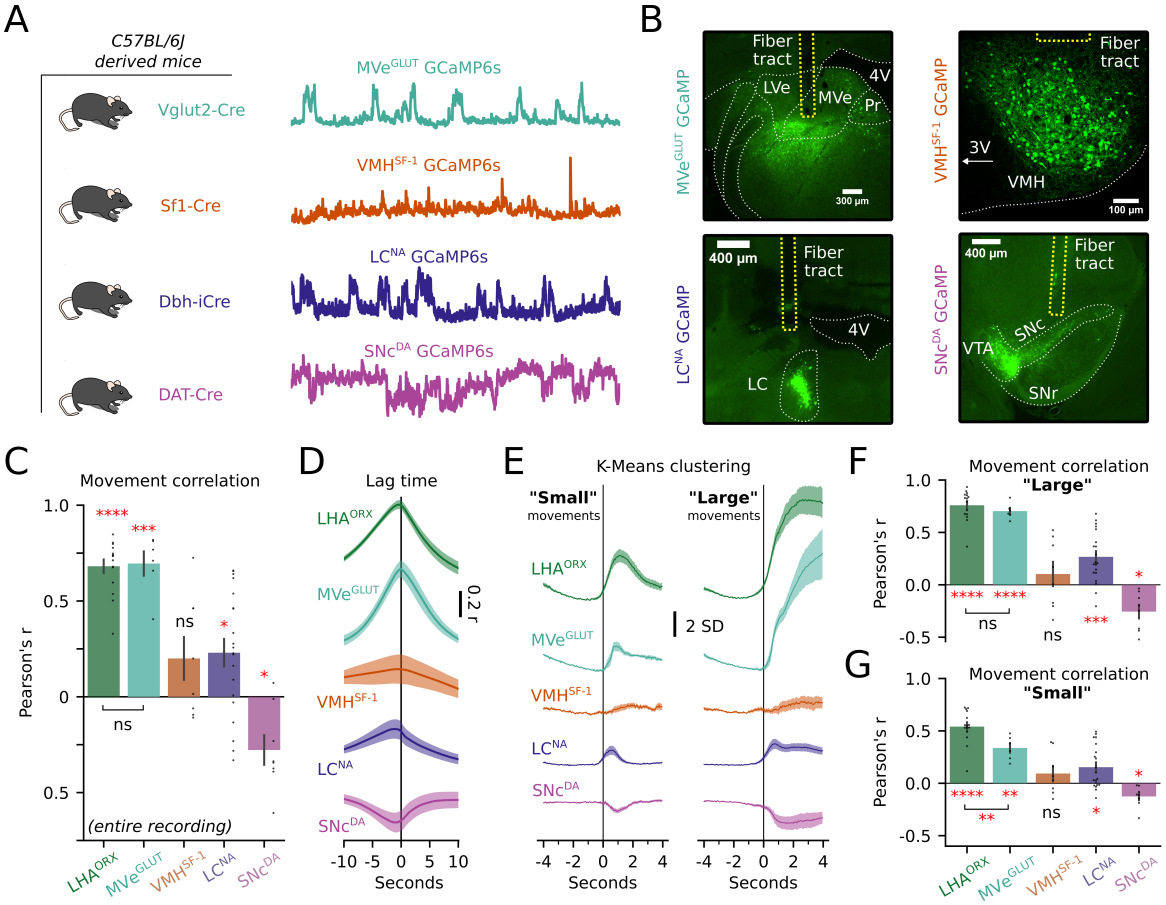


**Figure 6.** Representation of movement across genetically defined neurons**.**

***A,*** C57BL/6J-derived strains of mice permitted Cre-dependent photometry recordings from four separate neural populations ($MVe^{GLUT}$, n = 6; $VMH^{SF-1}$, n = 8; $LC^{NA}$, n = 20; and $SNc^{DA}$, n = 8 mice). ***B,*** Representative histology from each recording site. ***C,*** Movement correlation with photometry across neural subtypes. Asterisks represent one sample *t*-tests against mean of zero, after Bonferroni correction. Additional comparison is shown between $LHA^{ORX}$ (HONs) and $MVe^{GLUT}$ neurons (unpaired *t*-test: $t_{19}$ = 0.209, p = 0.8366). ***D,*** Cross correlation displaying lag time of each recorded population. Negative values imply photometry precedes movement. Lines and shaded regions represent mean ± SEM. ***E,*** Photometry baselined -3 to -1 seconds before movement initiation in two clusters: small movements (left) and large movements (right). Lines and shaded regions represent mean ± SEM. ***F.*** Correlation of movement and photometry during initiation of large movements. Asterisks represent one sample *t*-tests against mean of zero, after Bonferroni correction. Additional comparison is shown between HONs ($LHA^{ORX}$) and $MVe^{GLUT}$ (unpaired *t*-test: $t_{17}$ = 0.877, p = 0.3915). ***G.*** Correlation of movement and photometry during initiation of small movements. Asterisks represent one sample *t*-tests against mean of zero, after Bonferroni correction. Additional comparison is shown between $LHA^{ORX}$ (HONs) and $MVe^{GLUT}$ (unpaired *t*-test: $t_{17}$ = 2.864, p = 0.0099).

*p < 0.05, **p < 0.01, ***p < 0.001, ****p < 0.0001 and ns, not significant by two-tailed tests.

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