Title: A Brain Reward Circuit Inhibited By Next-Generation Weight Loss Drugs

Authors

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Abstract

Glucagon-like peptide-1 receptor agonists (GLP1RAs) effectively reduce body weight and improve metabolic outcomes, yet established peptide-based therapies require injections and complex manufacturing. Small-molecule GLP1RAs promise oral bioavailability and scalable manufacturing, but their selective binding to human versus rodent receptors has limited mechanistic studies. The neural circuits through which these emerging therapeutics modulate feeding behavior remain undefined, particularly in comparison to established peptide-based GLP1RAs. Here, we developed humanized GLP1R mouse models to investigate how small-molecule GLP1RAs influence feeding behavior. Integrating genetic manipulations, calcium imaging, and behavior profiling, we discovered that these compounds regulate both homeostatic and hedonic feeding through parallel neural circuits. Beyond engaging canonical hypothalamic and hindbrain networks that control metabolic homeostasis, GLP1RAs recruit a discrete population of Glp1r-expressing neurons in the central amygdala, which selectively suppress the consumption of palatable foods by reducing dopamine release in the nucleus accumbens. Stimulating these central amygdalar neurons curtail hedonic feeding, whereas targeted deletion of the receptor in this cell population specifically diminishes the anorectic efficacy of GLP1RAs for reward-driven intake. These findings reveal a dedicated neural circuit through which small molecule GLP1RAs modulate reward processing, suggesting broad therapeutic potential in conditions of dysregulated dopamine signaling including substance use disorder and binge eating.

Main

The global obesity epidemic has catalyzed an urgent search for effective pharmacological interventions, with glucagon-like peptide-1 receptor agonists (GLP1RAs) emerging as leading candidates. These compounds, notably liraglutide (Saxenda, Victoza) and semaglutide (Wegovy, Ozempic), promote weight loss by enhancing insulin secretion, suppressing glucagon release, and inducing satiety (**Fig. 1a,b**) [1–5,1,6,7–17]. Recent studies have highlighted crucial roles for hypothalamic and hindbrain regions in GLP1RA-mediated feeding suppression [18–25]. However, peptide-based GLP1RAs require injection, cold storage, and complex manufacturing processes, with widespread global supply chain issues restricting patient access [26–29]. Next-generation small-molecule GLP1RAs like danuglipron (PF06882961) and orforglipron (LY3502970) offer transformative advantages through oral bioavailability and scalable manufacturing (**Fig. 1a**) [30,31–36]. Yet a critical challenge in developing these compounds has been their species-specific binding properties—many small-molecule GLP1RAs that effectively activate human GLP1R show minimal activity at rodent receptors, severely limiting preclinical investigation of their mechanisms of action [35,37,38,39]. Notably, orforglipron has advanced into over ten registered Phase 3 clinical trials [31–33,40]. The imminent clinical deployment of these small-molecules demands urgent investigation of their neural mechanisms, particularly given emerging evidence of GLP1RAs' effects on mood, motivation, and reward processing [41–45]. To overcome the species specificity of small-molecule GLP1RAs and enable preclinical investigation of their neural mechanisms, we engineered humanized GLP1R mouse models, providing an essential platform for *in vivo* studies that would otherwise be unattainable. Through integrated behavioral, neuroanatomical, and functional analyses, we uncovered a previously unknown multi-synaptic hindbrain-amygdala-midbrain circuit that specifically modulates rewarding food consumption through striatal dopaminergic signaling. This discovery advances our understanding of how Glp1R signaling influences not only feeding behavior but also fundamental reward processes, including addiction, mood disorders, and motivation, [7–17,46] highlighting both the therapeutic potential and the need for caution as these treatments see broader use.

Generation and Validation of Humanized Glp1r^{S33W} Mice for Investigating Small-Molecule GLP1RAs

While peptide GLP1RAs, like liraglutide, reduce food consumption in C57BL6J mice, many small-molecule GLP1RAs do not effectively activate rodent Glp1r (**Fig. 1b**) due to a single amino acid difference from tryptophan to serine at position 33 (**Fig. 1c**) [37,38,39]. Using CRISPR-Cas9-mediated genome editing, we inserted the S33W mutation into the mouse *Glp1r* locus, effectively humanizing it (**Fig. 1d,e**). Homozygous humanized Glp1r S33W mice (Glp1r^{S33W}) and wild type (WT) littermates did not exhibit differences in respiratory exchange ratio (RER) (**Extended Data Fig. 1a-d**), energy expenditure (EE) (**Extended Data Fig. 1e-h**) or body weight (**Extended Data Fig. 1i-j**), demonstrating that Glp1r^{S33W} mice maintain normal metabolic functions and energy homeostasis comparable to WT littermates. To evaluate the *in vivo* functionality of the S33W mutation, we performed glucose tolerance tests (GTT) and found that liraglutide improved glucose tolerance in both Glp1r^{S33W} mice and WT mice (**Fig. 1f**), whereas danuglipron and orforglipron were effective only in Glp1r^{S33W} mice (**Fig. 1g,h**). These results demonstrate that Glp1r^{S33W} mice retain responsiveness to peptide-based GLP1RAs while gaining sensitivity to human-specific small molecule GLP1RAs, establishing a valuable *in vivo* model system for investigating this next-generation class of drugs.

Small-Molecule GLP1RAs Mirror Liraglutide Effects in Suppressing Feeding in Glp1r[S33W] Mice

GLP1RAs induce significant weight loss through multiple mechanisms beyond their effects on insulin secretion and glucose control[1,5,32,47]. To systematically characterize their impact on distinct feeding modalities, we employed parallel behavioral paradigms examining both homeostatic and hedonic feeding patterns. Homeostatic feeding was quantified through standard diet (SD) consumption during the active-phase (zeitgeber time (ZT)12-16), while hedonic feeding was assessed via high-fat diet (HFD) intake during the inactive-phase (ZT2-6) when baseline SD consumption is minimal[48,49,50]. In Glp1r[S33W] mice, administration of liraglutide, danuglipron, and orforglipron significantly attenuated both active-phase SD (**Fig. 1j,l,n**) and inactive-phase HFD (**Fig. 1p,r,t**) consumption compared to vehicle controls. As predicted by the species specific receptor activation profile, WT mice exhibited reduced SD (**Fig. 1i,k,m**) and HFD (**Fig. 1o,q,s**) intake exclusively following liraglutide administration. Notably, both liraglutide and orforglipron demonstrated sustained 24-hour inhibition of food intake (**Extended Data Fig. 2a-c**), consistent with their extended pharmacokinetic profiles relative to danuglipron (**Fig. 1a**). To validate the clinical relevance of these orally bioavailable small-molecule GLP1RAs, we confirmed that oral danuglipron significantly reduced blood glucose levels (**Fig. 1u**) and acute HFD intake comparable to intraperitoneal injection effects (**Fig. 1v, w**). Similarly, oral orforglipron inhibited acute HFD intake (**Fig. 1x,y**) and its chronic daily administration in overweight Glp1r[S33W] mice significantly reduced body weight compared to saline controls (**Fig. 1z**), establishing its efficacy in weight management [32] .

GLP1RAs Exhibit Distinct Neural Activation Patterns in Feeding Circuits

Because small-molecule GLP1RAs may have greater brain penetration than large peptide-based GLP1RAs—potentially leading to distinct neural activation patterns—we aimed to identify the brain regions involved in their inhibition of food consumption. First, we focused on nuclei previously reported to be activated by peptide-based GLP1RAs and expressed Glp1r (**Fig. 2a-d**), specifically the dorsomedial hypothalamus (DMH), nucleus tractus solitarius (NTS), area postrema (AP), and central amygdala (CeA)[19,22–24,51–54]. We used cFos expression as a surrogate for GLP1RA-dependent neuronal activation in WT and Glp1r[S33W] mice treated with danuglipron, orforglipron, and liraglutide (**Fig. 2a-d**). Danuglipron and orforglipron induced significant cFos expression in the NTS (**Fig. 2f**), AP (**Fig. 2g**), and CeA (**Fig. 2h**), but not in the DMH (**Fig. 2e**) of Glp1r[S33W] mice compared to WT controls, mirroring previous studies using peptide-based GLP1RAs[19,51,55,56]. As expected, liraglutide induced comparable cFos expression in both groups, matching the small-molecule responses in Glp1r[S33W] mice across all regions, confirming its effective binding to and activation of the Glp1r[S33W] variant (**Fig. 2e-h**).

Given that activation of the AP is known to induce nausea and malaise, while Glp1R activation in the NTS signals satiation[23,57], we aimed to determine whether the relative cFos activation between these two regions could reveal potential mechanisms underlying the differential effects of GLP1RAs observed in clinical trials[5,32,58,59]. By comparing the ratio of cFos activation in the NTS to that in the AP, we observed significant differences among the drugs tested (**Fig. 2i**). Specifically, orforglipron exhibited greater activation in the NTS and less activation in the AP compared to both danuglipron and liraglutide. To determine whether oral administration of danuglipron replicates the NTS-favored activation pattern observed with orforglipron, we compared intraperitoneal (IP) and oral administration of danuglipron in Glp1r[S33W] and WT mice (**Fig. 2j,k and Extended Data Fig. 3a-c**). Glp1r[S33W] NTS cFos activation was comparable

between both routes, but oral delivery significantly reduced AP cFos activation (**Fig. 2l**). These
findings indicate that oral danuglipron, its designed route of administration, replicates the NTS-
favored activation pattern while minimizing AP activation. This preferential activation is
advantageous because it may reduce negative side effects associated with AP activation, such
as nausea and malaise, while preserving therapeutic effects mediated by the NTS. Therefore,
orally delivered small-molecule GLP1RAs represent a promising advancement in weight loss
therapies by enhancing both efficacy and tolerability (**Fig. 1u-y**).

Danuglipron Suppress Food-Motivated Behaviors During Homeostatic and Hedonic
Feeding

Building on our observation that peptide-based and small-molecule GLP1RAs produce distinct
neuronal activation patterns, we next examined how these differences manifest in the behavior of
$Glp1r^{S33W}$ mice. We focused on liraglutide and danuglipron, which share similar pharmacokinetic
properties, and monitored mice in a home-cage environment using infrared video over two hours
following GLP1RA or vehicle/saline administration in their active phase (ZT12-14) (**Fig. 3a and**
Extended Data Fig. 4). By integrating pose estimation (SLEAP[60]) with a probabilistic model for
behavior classification (Keypoint-MoSeq[61]), we identified 23 discrete behaviors corroborated by
sensor data (**Fig. 3b-d and Extended Data Fig. 5 & 6**). These behaviors were grouped into five
principal categories— food-motivated, drinking, resting, moving, and grooming. Principal
component analysis (PCA) revealed that both liraglutide and danuglipron induced significant,
overall behavioral shifts from control conditions (**Fig. 3e,f and Extended Data Fig. 7a-d**).
Specifically, both treatments similarly reduced feeding and drinking while increasing resting-
related activity, suggesting a conserved effect on satiety-related behaviors (**Fig. 3g-k**). Linear
discriminant analysis (LDA) further supported these findings, clustering the drug-treated groups
together and distinctly apart from controls (**Fig. 3l**).

To determine the influence of danuglipron on hedonic feeding, we examined behavioral patterns
in SD and HFD-fed mice during the inactive phase (ZT 3-5). Vehicle-treated HFD-fed mice
exhibited a behavioral profile distinct from SD-fed mice, with more food-motivated behaviors and
drinking, and less resting (**Fig. 3m and Extended Data Fig. 7g-k**), indicating a diet-induced
behavioral shift. In contrast, danuglipron-treated HFD-fed mice closely resembled their SD-fed
counterparts, showing similar levels of food-motivated activity, drinking, movement, and resting
(**Fig. 3m and Extended Data Fig. 7g-k**)). Danuglipron-treated mice on either diet displayed less
grooming compared to vehicle-treated counterparts, likely due to reduced food intake naturally
shortening the behavioral satiety sequence, which includes a grooming phase following feeding[62].
Together, these findings demonstrate that GLP1RA treatments can realign the behavior of HFD-
fed animals toward SD-fed norms (**Fig. 3n and Supplementary Video 1**), effectively neutralizing
the behavioral hallmarks of hedonic feeding and reinforcing the notion that distinct neuronal
activation patterns translate into meaningful, diet-dependent behavioral outcomes.

Danuglipron Activates Hypothalamic and Hindbrain GLP1R Circuits

To distinguish direct from indirect effects of small-molecule GLP1RAs in specific brain regions,
we developed a Cre-dependent adeno-associated virus (AAV) vector expressing full-length
human GLP1R (AAV-hSyn-DIO-hGLP1R) (**Fig. 4a**). When applied in Glp1r-Cre mice, this
approach enables selective expression of hGLP1R in Glp1r-positive cells, allowing us to isolate

direct activation effects from secondary circuit responses. In Glp1r-Cre mice conditionally
expressing hGLP1R in their basomedial hypothalamus (BMH-hGLP1R) (**Extended Data Fig.**
8a,b), danuglipron significantly decreased active-phase SD intake without affecting inactive-
phase HFD consumption (**Fig. 4c,h**) while control mice expressing mCherry in the same region
showed no changes in consumption (**Fig. 4b,g**). When targeting the DMH, a BMH subnucleus
recently implicated in encoding satiation[24,54,63], we found similar selective effects on SD intake
(**Fig. 4d,i and Extended Data Fig. 8c,d**). Targeting the hindbrain NTS/AP complex resulted in
decreased consumption of both SD and HFD (**Fig. 4e,j and Extended Data Fig. 8e,f**), aligning
with recent findings on hindbrain Glp1R circuits in aversion and satiety[23].

Danuglipron Directly Activates CeA^{Glp1r} Neurons to Regulate Hedonic Feeding

Recognizing the limited understanding of the CeA's role in GLP1RA responses[53], we focused our
investigation on Glp1r-positive neurons in this region (CeA^{Glp1r}). First, we confirmed CeA^{Glp1r}
neurons that conditionally express hGLP1R directly respond to small-molecule GLP1RAs by co-
injecting AAV-hSyn-DIO-hGLP1R and AAV-DIO-eYFP into the CeA of Glp1r-Cre mice and
performing whole-cell patch-clamp recordings (**Extended Data Fig. 9c-f**). We measured the
resting membrane potential of hGLP1R-expressing neurons before and after infusion of 10 µM
danuglipron (**Extended Data Fig. 9a**). Consistent with activation of the G_s/cAMP pathway via
hGLP1R [64,65], danuglipron elicited significant membrane depolarization, confirming functional
expression (**Extended Data Fig. 9b**). Next, to determine whether this responsiveness translates
into changes in feeding behavior, we assessed Glp1r-Cre mice conditionally expressing hGLP1R
in the CeA (CeA-hGLP1R) under both SD and HFD conditions. Remarkably, CeA-hGLP1R mice
showed a selective reduction in inactive-phase HFD consumption without any effect on active-
phase SD intake (**Fig. 4f,k and Extended Data Fig. 8g,h**). We corroborated these findings with
an alternative virus expressing the small molecule-sensitive mouse SNP, Glp1r^{S33W} and its
wildtype control (AAV-DIO-mGlp1r^{S33W} and AAV-DIO-mGlp1r) (**Extended Data Fig. 10a,d**).
These results demonstrate that CeA^{Glp1R} neurons selectively modulate hedonic feeding in
response to small-molecule GLP1RAs (**Extended Data Fig. 10b,c**), revealing a previously
uncharacterized neural substrate for GLP1RA-mediated regulation of feeding behavior.

The relatively small molecular mass of danuglipron (555.6 Da) and its robust effects in CeA-
hGLP1R mice suggest this compound can access brain structures beyond the circumventricular
organs (CVOs). Although the extent of brain penetration by different GLP1RAs remains an open
question[19,51,66,67], definitively establishing their direct engagement of deep nuclear structures is
critical for understanding their mechanisms of action. To test whether danuglipron can directly
induce neuronal activity in the CeA, we expressed GCaMP7s along with either hGLP1R or mGlp1r
in the CeA of Glp1r-Cre mice and recorded calcium transients via fiber photometry *in vivo* (**Fig.**
4l and Extended Data Fig. 11a-d). Since previous work showed peptide-based GLP1RAs induce
cFos expression in the CeA of wildtype mice[19,51,55,56]—though whether through direct or indirect
pathways remains unclear—we first used liraglutide as a positive control and confirmed it elicited
significant calcium transients in CeA-hGLP1R mice (**Extended Data Fig. 11e,f**). Importantly,
danuglipron treatment also elicited robust increases in calcium transients in CeA-hGLP1R mice,
a response that was absent in mGlp1r-expressing negative controls (**Fig. 4m–p**). These findings
provide direct evidence that danuglipron penetrates beyond the CVOs to functionally engage CeA
neurons expressing human GLP1R.
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Next, we sought to establish the physiological role of CeA^{Glp1R} neurons in hedonic feeding by
optogenetically stimulating them independently of any pharmacological agonists and observed

reduced HFD consumption (**Fig. 4q-r**), mirroring the inhibitory feeding effects observed in
response to danuglipron in CeA-hGLP1R mice (**Fig. 4k and Extended Data Fig. 10b,c**). To
determine whether the CeA is essential for the inhibitory effects of GLP1RAs on feeding, we
selectively knocked out Glp1r in the CeA by bilaterally injecting AAV-Cre or AAV-GFP into the
CeA of Glp1r$^{flox/flox}$ mice (**Fig. 4s**). Although the loss of CeA Glp1R signaling had no impact on SD
intake, it significantly increased HFD consumption following liraglutide injection (**Fig. 4t**). These
results pinpoint CeA^{Glp1R} neurons as a critical node in the GLP1RA-responsive circuitry specifically
regulating reward-driven feeding behaviors. To further clarify the physiological relevance of this
circuit, we asked whether CeA^{Glp1R} neurons receive endogenous GLP-1 input. By expressing
synaptophysin in NTS Gcg-Cre neurons, we detected Gcg-positive fibers and synaptic terminals
in the CeA (**Fig. 4u**). This demonstrates that CeA^{Glp1R} neurons not only respond to exogenous
agonists, but also can receive endogenous GLP-1 signals from the NTS. Together, these findings
underscore the CeA as a key integrative hub where GLP-1 signaling—both pharmacologically
induced and naturally occurring—converges to curb hedonic feeding[68].

Small-Molecule GLP1RAs Engage CeA to Modulate Mesolimbic Dopamine Release in Response to HFD

Given the selective role of CeA^{Glp1R} neurons in hedonic feeding regulation, we investigated their
connectivity to mesolimbic reward circuitry. Anatomical tracing in Glp1r-Cre mice, using AAV-DIO-
Synaptophysin or AAV-DIO-eYFP, revealed pronounced projections from CeA-GLP1R neurons
to the ventral tegmental area (VTA) (**Fig. 5a and Extended Data Fig. 12a-e**). These findings
support a model in which NTS^{Gcg} neurons drive CeA^{Glp1R} activity, which in turn influences VTA
neurons and ultimately the nucleus accumbens (NAc) (**Fig. 5b**). Based on our observations that
CeA^{Glp1R} activation suppresses hedonic feeding while receptor ablation negates this effect, we
hypothesized that these neurons modulate VTA dopaminergic output to reduce NAc dopamine
signaling during reward-driven feeding.

To test this hypothesis, we first examined whether GLP1RAs broadly affect dopamine responses
in the NAc. By expressing AAV-dLight1.3b in Glp1r^{S33W} mice, we monitored dopamine responses
to HFD following peptide (liraglutide) or small-molecule (danuglipron, orforglipron) GLP1RA
administration (**Fig. 5c**). Strikingly, all three compounds significantly diminished both the peak
and consumption-associated dopamine response (**Fig. 5d–i and Extended Data Fig. 13a-c**),
indicating that despite their pharmacological differences, these agents converge on a common
central mechanism to reduce dopamine-mediated reward.

To establish a causal link between CeA^{Glp1R} neuron activity and mesolimbic dopamine output, we
selectively expressed hGLP1R in the CeA of Glp1r-Cre mice and monitored NAc dopamine
dynamics during HFD consumption following danuglipron or orforglipron administration (**Fig. 5j**
and Extended Data Fig. 12f-h). Remarkably, both treatments substantially blunted the peak and
consumption-associated dopamine responses (**Fig. 5k–p**). This finding demonstrates that
activation of GABAergic CeA^{Glp1R} neurons[53] inhibits reward-driven dopamine signaling. By
establishing that the CeA-VTA-NAc axis operates in parallel with previously characterized
hindbrain to midbrain Glp1R circuits[69–71], our findings reveal a distributed network of Glp1R-
expressing neurons orchestrating the suppression of food consumption[23,24,72,73,23,72,74–76].

Discussion

Our findings identify a previously unrecognized amygdalar circuit through which next-generation GLP1RAs modulate reward-driven feeding. In particular, our data indicate that CeA[Glp1R] neurons receive GLP-1 input from the NTS and influence VTA activity, thereby providing a framework for integrating metabolic signals into dopamine-dependent reward circuits[13,69,74–76]. This insight aligns with an expanding body of evidence that GLP1RAs influence motivational and reward-related processes, raising the possibility of their therapeutic potential for disorders characterized by dysregulated reward, such as substance use[15,16,17,46,77,78]. Looking ahead, our findings raise critical questions about the broader impact of chronic GLP1RA treatment on reward processing. With small-molecule GLP1RAs like orforglipron—described as 'a product for the masses'[31]— gaining traction as accessible, scalable therapies, understanding their long-term effects on brain function becomes essential.

Figures

319 **Figure 1: Generation and validation of a novel mouse model responsive to small molecule
320 **GLP1R agonists: a**, Structure, naming convention, molecular formula, molecular weight (MW),
321 half-life in humans, and species binding specificity of glucagon-like peptide-1 (GLP-1), liraglutide,
322 danuglipron, and orforglipron. Amino acid sequences of liraglutide shown with its substitution and
323 additions to GLP-1 highlighted in green and purple, respectively. **b**, Standard diet (SD)
324 consumption over 2 hours post-administration of saline (Sal), liraglutide (Lira), vehicle (Veh), or
325 danuglipron (Dan) (n = 11 per injection, one-way ANOVA with Bonferroni correction, ***P<0.001).
326 **c**, Schematic of the serine (TCA or S) to tryptophan (TGG or W) CRISPR-mediated substitution
327 in Glp1r^{S33W} (bottom) or in mouse Glp1r (top). **d,e**, Sanger sequencing chromatograms of (**d**) WT
328 mouse Glp1r and (**e**) Glp1r^{S33W} sequence, confirming the Glp1r S33W substitution in mice. **f-h**,
329 Glucose tolerance test (GTT) on GLP1RAs. Comparison of blood glucose levels on (**f**) liraglutide
330 (Lira), (**g**) danuglipron (Dan), (**h**) orforglipron (Orfo) followed by dextrose (Dex) in WT and
331 Glp1r^{S33W} mice (n = 5-9 per injection, two-way ANOVA with Bonferroni correction, **P<0.01;
332 ***P<0.001). **i-n**, SD intake 1, 2, and 4 hours post-treatment of (**i, j**) Lira (n = 9-11), (**k, l**) Dan (n

= 15-16), and (**m, n**) Orfo (n = 8-9) and vehicle controls in WT and Glp1r^{S33W} mice. **o-t**, High fat
diet (HFD) intake 1, 2, and 4 hours post-treatment of (**o, p**) Lira (n = 8-10), (**q, r**) Dan (n = 14-16),
and (**s, t**) Orfo (n = 8-9) and their vehicle controls in WT and Glp1r^{S33W} mice (two-way ANOVA
with Bonferroni correction, *P<0.05; **P<0.01; ***P<0.001). **u**, GTT measuring blood glucose
levels following oral administration of danuglipron (oDan) and dextrose in Glp1r^{S33W} and WT mice
(n = 6 per genotype, two-way ANOVA with Bonferroni correction, **P<0.01; ***P<0.001). **v-y**, HFD
intake 1, 2, and 4 hours after oral gavage of (**v**) danuglipron or vehicle and (**x**) orforglipron or
saline (n = 8-9, two-way ANOVA with Bonferroni correction, **P<0.01; ***P<0.001). Comparison
of the 4th hour between intraperitoneal (IP) and oral routes of administration with (**w**) danuglipron
or (**y**) orforglipron (two-way ANOVA with Bonferroni correction, **P<0.01; ***P<0.001). **z**, 7-day
weight changes of mice on chronic HFD treated with orforglipron or saline daily at ZT6 (n = 7 per
injection, paired t-test, ***P<0.001). Data are represented as means ± SEM. *P<0.05; **P<0.01;
***P<0.001. See Supplementary Table 1 for statistical details for all figures and Extended Data
figures.
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Figure 2: GLP1RA activation across targeted GLP1R-expressing brain regions. **a-d**, GLP1R protein expression validated by a Glp1r-Cre;tdTomato mouse line and neuronal cFos activation 2 hours after danuglipron or liraglutide or 6 hours after orforglipron injection in WT and Glp1r^{S33W}

mice in the (**a**) DMH, (**b**) NTS, (**c**) AP, or (**d**) CeA. Scale bars = 200 μm. **e-h**, Quantification of cFos in the (**e**) DMH, (**f**) NTS, (**g**) AP and (**h**) CeA (n = 3-4 per genotype, two-way ANOVA with Bonferroni correction, *P<0.05; **P<0.01; ***P<0.001). **i**, Ratio of NTS/AP cFos activation in Glp1r^{S33W} mice after danuglipron, orforglipron, and liraglutide (n = 3-4 per injection, Kruskal-Wallis test, *P<0.05). **j,k**, Neuronal cFos activation in the NTS and AP 2 hours after danuglipron was administered to Glp1r^{S33W} mice via (**j**) IP injection or (**k**) oral gavage. **l**, Quantification of cFos expression in the NTS (left) or AP (right) following danuglipron IP or oral delivery in Glp1r^{S33W} mice (n = 3 per delivery route, Welch's t-test, *P<0.05). Data are represented as means ± SEM. *P<0.05; **P<0.01; ***P<0.001.

Figure 3: Machine-learning assisted behavior profiling reveals distinct phenotypes associated with GLP1RA and diet. a, Representative heatmap of Glp1r^S33W mouse nose location and home cage setup. Color indicates time spent in minutes over 2 hours. **b,** Simplified pipeline for machine learning analysis of behavior[60,61]. Analysis parameters: SLEAP tracking with 9 keypoints at 25 fps, Keypoint-MoSeq fit an autoregressive hidden Markov model (AR-HMM) to PCA-reduced keypoints. A full model was then trained, producing 91 behavioral syllables with a minimum frequency threshold of ≥0.01%. Trained raters manually named behaviors, incorporating locational context via OpenCV. **c,d**, Correlation between sensor data and video analysis across all conditions tested for (**c**) food hopper nose pokes and food motivated behaviors and (**d**) water bottle spout licks and drinking (*n* = 78, Pearson regression, ***P<0.0001). **e,f**, Proportion of time spent performing each of the 23 behaviors identified using Keypoint-MoSeq and averaged across all mice per condition, binned into 5 behavior categories. A MANOVA was run on the PCA of the proportion of time spent performing each behavioral category. PCA was ran for (**e**) Veh and Dan and (**f**) Saline and Lira (*n* = 9 Veh/Dan, *n* = 10 Sal/ Lira, RM MANOVA with resampling MATS,

*P<0.05, ***P<0.001).   **g-k**, Percentage of time spent (**g**) food seeking, (**h**) drinking, (**i**)
moving/exploring, (**j**) grooming, and (**k**) resting. (n = 9 Veh/Dan, n = 10 Sal/Lira, generalized
linear mixed-effects model with beta regression, *P<0.05, **P<0.01, ***P<0.001). **l,** Linear
discriminant analysis (LDA) plot of the similarity between mean behavioral summaries of mice per
condition. Opaque centroid circles represent the mean behavioral summaries per condition, small
circles indicate the specific embedding locations of individual mice within each condition, and
ellipses denote two standard deviations from the mean for each group. **m,** Proportion of time
spent performing each of the 23 behaviors, and 5 larger behavioral categories in SD- and HFD-
fed mice during the light cycle after vehicle or danuglipron. MANOVA was run on PCA of the 23
behavior durations (n = 10, RM MANOVA with resampling MATS and holm correction, *P<0.05,
P<0.01). **n, LDA plot of the similarity between mean behavioral summaries of mice per condition.
Data are represented as medians ± Q1-Q3. *P<0.05; **P<0.01; ***P<0.001.
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Figure 4: Central amygdala GLP1R activation inhibits hedonic food intake via direct
activation by danuglipron. a, Representative schematic of AAV-DIO-hGLP1R viral construct
and injection into the basomedial hypothalamus (BMH). **b-k**, 1, 2, and 4-hour SD or HFD
consumption after vehicle (Veh) or danuglipron (Dan) in Glp1r-Cre mice expressing (**b,g**) AAV-
DIO-mCherry (BMH-mCherry, n = 6) or (**c,h**) AAV-DIO-hGLP1R (BMH-hGLP1R, n = 10) in the
BMH, (**d,i**) DMH (n = 7), (**e,j**) NTS/AP (n = 6), or (**f,k**) CeA (n = 9) (two-way ANOVA with Bonferroni
correction, *P<0.05; **P<0.01; ***P<0.001). **l**, Schematic of AAV-DIO-GCaMP7s + AAV-DIO-
hGLP1R or mGLP1R injection with a fiber optic implant to the CeA of Glp1r-Cre mice. **m-p**,
Representative heatmaps of %ΔF/F neuronal calcium signal per mouse during 1-hour of fiber
photometry recording after vehicle or danuglipron injection in (**m**) hGLP1R or (**o**) mGLP1R
expressing mice. Number of significant calcium events averaged per mouse during 1-hour
recording session following vehicle or danuglipron in (**n**) hGLP1R or (**p**) mGLP1R expressing
mice (n = 3-6 per injection, paired t-test, **P<0.01 and Wilcoxon signed-rank test). **q**, Schematic
of AAV-DIO-eYFP or AAV-DIO-ChR2-eYFP injection with a fiber optic implant to the CeA of Glp1r-
Cre mice. **r**, 30-minute HFD consumption in ChR2 and eYFP expressing controls after 20 Hz blue
light stimulation (ON) or no stimulation (OFF) (n = 6 per group, two-way ANOVA with Tukey's
HSD correction, *P<0.05). **s**, Schematic of AAV-Cre to conditionally knockout Glp1r, or AAV-GFP
control injection to the CeA of Glp1r$^{flox/flox}$ mice. **t**, SD (left) and HFD (right) consumption 4 hours
after injection of liraglutide in AAV-Cre or AAV-GFP expressing mice. (n = 6, Welch's t-test,
*P<0.05). **u**, Representative images of the CeA from Gcg-Cre mice injected with AAV-DIO-mGFP-

2A-Synaptophysin-mRuby in the NTS; scale bar = 200 µm. NTS^{GCG} fibers (red; pseudo-colored
mGFP; top left), synaptic terminals (green; pseudo-colored mRuby; top right) are shown, with a
magnified view (bottom right; scale bar = 100 µm). Data are represented as means ± SEM.
*P<0.05; **P<0.01; ***P<0.001.
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Figure 5: CeA^{GLP1R} neurons project to the VTA to modulate dopamine output to the NAc in response to HFD. a, Representative image of the VTA from Glp1r-Cre mice injected with AAV-DIO- mGFP-2A-Synaptophysin-mRuby in the CeA; scale bar = 100 μm. CeA^{GLP1R} fibers (red; pseudo-colored mGFP), synaptic terminals (green; pseudo-colored mRuby), and tyrosine hydroxylase-positive neurons (Th; blue, marking dopaminergic neurons) are shown, with a magnified view (right; scale bar = 50 μm). **b**, Schematic of proposed neural circuit from NTS → CeA → VTA → NAc. Arrows indicate neuron activation, blunted ends indicate neuron inhibition. Gray arrow from NTS → VTA indicates a known connection from NTS^{GLP-1} to VTA^{vGAT} neurons [71]. **c**, Schematic of genetically-encoded dopamine sensor, AAV-dLight1.3b, injection and fiber optic implant in the NAc of Glp1r^{S33W} mice. **d,g**, Averaged Z-score traces showing dopamine release in the NAc in response to HFD following administration of (**d**) vehicle or danuglipron and (**g**) saline or orforglipron in Glp1r^{S33W} mice. Traces are aligned to food retrieval time (t = 0) and averaged across five food trials per mouse. **e-i**, Quantified (**e,h**) area under the curve (AUC) for Z-scores and (**f,i**) maximum fluorescence Z-scores within the food retrieval window (*n* = 9 for danuglipron, *n* = 7 for orforglipron, paired t-test, *P<0.05). **j**, Schematic of AAV-dLight1.3b injection and fiber optic implant into the NAc and AAV-DIO-hGLP1R injection into the CeA of Glp1r-Cre mice. **k,n**, Averaged Z-score traces showing dopamine release in the NAc in response to HFD following administration of (**k**) vehicle or danuglipron and (**n**) saline or orforglipron in CeA-hGLP1R mice. Traces are aligned to food retrieval time (t = 0) and averaged across five food trials per mouse. **l-p**, Quantification of (**l,o**) AUC for Z-scores and (**m,p**) maximum fluorescence Z-scores within the food retrieval window (*n* = 8 for danuglipron, *n* = 7 for orforglipron, paired t-test, *P<0.05). Data are represented as means ± SEM. *P<0.05; **P<0.01; ***P<0.001.

Methods

Mouse lines

All experiments were carried out in compliance with the Association for Assessment of Laboratory Animal Care policies and approved by the University of Virginia Animal Care and Use Committee. Mice were housed on a 12:12-hour light/dark (LD) cycle with food (PicoLab Rodent Diet 5053) and water *ad libitum* unless otherwise indicated. For experiments, we used 8-week or older male and female C57BL6/J mice, Glp1r-IRES-Cre mice (Glp1rtm1.1(cre)Lbrl/RcngJ, strain #029283, RRID:IMSR_JAX:029283), Glp1r-IRES-Cre mice crossed to Ai14 tdTomato reporter line (B6.Cg-Gt(ROSA)26Sortm14(CAG-tdTomato)Hze/J, strain #007914, RRID:IMSR_JAX:007914), Glp1r$^{flox/flox}$ mice (B6(SJL)-Glp1rtm1.1Stof/J, strain #035238, RRID:IMSR_JAX:035238), Gcg-Cre mice (C57BL/6J-Tg(Gcg-cre)-1Mmsc/Mmmh, stock #051056-MU, RRID:MMRRC_051056-MU) and Glp1r^{S33W} mice (described below). Gcg-Cre mice were rederived by *in vitro* fertilization from frozen sperm (MMRRC, stock no. 051056-MU).

Generation of Glp1r^{S33W} mouse

The Glp1r^{S33W} mouse line was created with CRISPR-Cas9 homologous repair at the University of Virginia Genetically Engineered Murine Model Core. Briefly, Cas-9 (Alt-R™ S.p. Cas9 Nuclease V3, 100 µg, catalog no. 1081058), Alt-R™ HDR Donor Oligo repair template (below), tracrRNA (Alt-R® CRISPR-Cas9 tracrRNA, 5 nmol, catalog no. 1072532), and CRISPR-Cas9 crRNA XT (ATTTCTGCACCGTCTCTGAG) were microinjected into a fertilized B6SJL zygote and were implanted into a pseudopregnant female. Founder pups were genotyped as described below and backcrossed to C57BL6/J mice for at least 4 generations before experimentation.

Repair Template

aagagggtgggagtccagtgggaccagaggggctgctggagccacggggcttctgcttttatttctgctttcccttgtagGGTACCA CGGTG**TCGCTCTGGGAAACCGTCCAAAAGTGG**AGAGAATACCGGCGGCAGTGCCAGCGT TTCCTCACGGAAGCGCCACTCCTGGCCACAGgtgcgtccagatgaggcctcacg

Validating Glp1r^{S33W} mice

Tail snips were obtained from pups at 3 weeks of age. DNA was extracted with an extraction buffer (Sigma, catalog no. E7526) and tissue prep solution (Sigma, catalog no. T3073), heated for 10 and 3 minutes at 55°C and 100°C, respectively, then neutralized with a neutralization solution (Sigma, catalog no. N3910). PrimeSTAR High Fidelity PCR (Takara, catalog no. R050A) was performed with 1uL of cDNA and 10uM of 5′-3′ F (GATCCCCAAAGTGGCAGTCA) and 5′-3′ R (AGCTATGGACTGGGGATCGT) primers. After amplification, the PCR product was run on a 1.2% agarose gel and bands were cut out at 330 bp. DNA was gel extracted and purified (Qiagen, catalog no. 28704), mixed with 5uM right primer, H$_2$O, and subsequently sent to be analyzed via Sanger sequencing (Azenta). Chromatogram results were analyzed to assign wild type, heterozygous, or homozygous genotypes for each mouse.

Generation of GLP1R viruses

The full length human *Glp1r* gene was obtained by PCR, amplifying the human fragment from GLP1R-tango (plasmid from Addgene, #66295, RRID:Addgene_66295), including the leader sequence present in the GLP1R-tango. The primers used were: 5′-3′ F (AAAGCT-AGCGCCACCATGAAGACGATCATCGCCCTGAGC) and 5′-3′ R (TTTGGCGCGCCCTAA-GAGCAGGACGCCTGACAAGT), ligating the product into pAAV-hSyn-DIO-EGFP (plasmid from Addgene, #50457, RRID:Addgene_50457) in place of the EGFP in NheI and AscI sites to produce the human GLP1R virus construct (AAV-hSyn-DIO-hGLP1R). The full length mouse *Glp1r* wild type gene was synthesized by Twist Biosciences (USA), generating a NheI and AscI fragment. This construct included the same leader sequence present in the human construct, as well as an

HA-tag encoded at the C-terminus of the full length mouse protein coding region. The fragment
was inserted into pAAV-hSyn-DIO-EGFP (plasmid from Addgene, #50457,
RRID:Addgene_50457) in place of EGFP to produce the plasmid construct (AAV-hSyn-DIO-
mGLP1R-HA). The full length mouse *Glp1r* gene bearing a Ser to Trp mutation at position 33
(S33W) was made by inserting a synthetic NheI and StuI fragment prepared by Twist Biosciences,
containing the single mutation within this fragment. This was cloned into the sites present in the
wild type construct to produce the S33W mouse mutant, followed by an HA-tag encoded at the
C-terminus (AAV-hSyn-DIO-mGLP1R^{S33W}-HA). Viral plasmid constructs were confirmed by
Sanger sequencing. Virus plasmid constructs were prepared and sent to the University of North
Carolina Viral Core (Chapel Hill, NC) for preparation of the AAV (serotype 8).
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Stereotactic surgery
Mice were anesthetized with isoflurane (5% induction and 2 to 2.5% maintenance; Isothesia) and
placed in a stereotaxic apparatus (AWD). A heating pad was used for the duration of the surgery
to maintain body temperature, and ocular lubricant was applied to the eyes to prevent desiccation.
A total of 200-400 nL was microinjected per side of [rAAV8/AAV2-hSyn-DIO-hGLP1R, plasmid
from Addgene, virus packed at UNC GTC Vector Core, Lot #AV9862 (100 µL at titer ≥ 1.5 ×10^{13}
vg/mL); AAV8-hSyn-DIO-mGLP1R^{S33W}-HA, synthesized by Twist Biosciences, virus packed at
UNC GTC Vector Core, Lot #AV10104 (100 µL at titer ≥ 8.2×10^{12} vg/mL); AAV8-hSyn-DIO-
mGLP1R-HA, synthesized by Twist Biosciences, virus packed at UNC GTC Vector Core, Lot
#AV10103 (100 µL at titer ≥ 4.5×10^{12} vg/mL); pAAV9-syn-dLight1.3b, plasmid from Addgene,
#135762, RRID:Addgene_135762, virus packed at UNC GTC Vector Core (100 µL at titer ≥
1.5×10^{13} vg/mL); pAAV1-EF1a-DIO- hChR2(H134R)-EYFP-WPRE-HGHpA, plasmid from
Addgene, #20298, RRID:Addgene_20298, virus packed at UNC GTC Vector Core (100 µL at titer
≥ 7×10^{12} vg/mL); pGP-AAV1-syn-DIO-jGCaMP7s-WPRE, plasmid from Addgene, #104491,
RRID: Addgene_104491, virus packed at UNC GTC Vector Core (100 µL at titer ≥ 1×10^{13} vg/mL);
pAAV1-Ef1a-DIO-EYFP, plasmid from Addgene, #27056, RRID:Addgene_27056, virus packed at
UNC GTC Vector Core (100 µL at titer ≥ 1×10^{13} vg/mL); AAV8-hSyn-DIO-mCherry, plasmid from
Addgene #50459, RRID:Addgene_50459, and virus packed at UNC Vector Core (100 µL at titer
≥ 7×10^{12} vg/mL); pAAV-hSyn-FLEx-mGFP-2A-Synaptophysin-mRuby, plasmid from Addgene,
#71760, RRID:Addgene_71760, and virus packed at UNC Vector Core;
pENN.AAV.hSyn.HI.eGFP-Cre.WPRE.SV40, plasmid from Addgene, #105540-AAV8,
RRID:Addgene_105540-AAV8, and virus packed at UNC Vector Core (100 µL at titer ≥ 1×10^{13}
vg/mL); pAAV-hSyn-EGFP, plasmid from Addgene, #50465-AAV8, RRID:Addgene_50465-
AAV8, and virus packed at UNC Vector Core (100 µL at titer ≥ 7×10^{12} vg/mL)], plasmid was
delivered using a glass pipette at a flow rate of 50 nl/min driven by a microsyringe pump controller
(World Precision Instruments, model Micro 4). The syringe needle was left in place for 10 min and
was completely withdrawn 17 min after viral delivery. For *in vivo* calcium and dopamine imaging
and optogenetics, a unilateral fiber optic cannula (RWD, Ceramic Ferrule, Ø400-µm, 0.5
numerical aperture) was implanted 0.2-mm dorsal to the viral injection coordinates following viral
delivery and stabilized on the skull with dental cement (C&B METABOND, Parkell). Two weeks
minimum were allowed for recovery and transgene expression after surgery. Stereotaxic
coordinates relative to Bregma (George Paxinos and Keith B. J. Franklin): basomedial
hypothalamus, mediolateral (ML): ±0.3 mm, anterior posterior (AP): −1.4 mm, dorsoventral (DV):
−5.9 mm; DMH, ML: ±0.3 mm, AP: −1.8 mm, DV: −5.4 mm; CeA, ML: ±2.7 mm, AP: −1.3 mm,
DV: −4.6 mm; VTA, ML: ±0.5 mm, AP: −3.6 mm, DV: −4.5 mm; NAc, ML: ±1.25 mm, AP: +1.0
mm, DV: −4.7 mm from Bregma; and NTS/AP, ML: ± 0.15 mm, AP: −0.3 mm, DV: −0.1, −0.4 mm
from the Zero point of the calamus scriptorius. All surgical procedures were performed under
sterile conditions and in accordance with University of Virginia Institutional Animal Care and Use
Committee guidelines. Histological analysis was performed to validate the success of intracranial
surgeries. Mice with unsuccessful viral/implant targeting were excluded.

GLP1R agonists

Liraglutide powder (Selleck, catalog no. S8256) was dissolved in 0.9% NaCl sterile saline, lightly
sonicated, and further diluted in 0.9% NaCl sterile saline to 0.03mg/mL. Danuglipron powder
(Selleck, catalog no. S9851) was dissolved to 30 mg/mL in 100% ethanol with gentle sonication,
then diluted to 3mg/mL (food intake) or 0.3mg/mL (GTT) in vehicle [1N NaOH, 2% Tween 80, 5%
polyethylene glycol (PEG) 400, 5% dextrose][35]. Orforglipron powder (MedChemExpress, catalog
no. HY-112185) was dissolved to 10mg/mL in Dimethyl sulfoxide (DMSO) and further diluted in
0.9% NaCl sterile saline to 0.1mg/mL.

Histological analysis and imaging

For fixed tissue collection, mice were deeply anesthetized (ketamine:xylazine, 280:80 mg/kg,
intraperitoneally) and perfused intracardially with ice-cold 0.01M phosphate buffer solution (PBS),
followed by fixative solution [4% paraformaldehyde (PFA) in PBS at a pH of 7.4]. For testing brain
region cFos activation (Fig. 3), danuglipron (30 mg/kg), orforglipron (1 mg/kg), or liraglutide (0.3
mg/kg) was delivered via intraperitoneal injection or oral gavage 2 hours (or 6 hours for
orforglipron) before perfusion and brain harvesting. After perfusion, brains were harvested and
postfixed overnight at 4°C in PFA. Fixed brains were then transferred into 30% sucrose in PBS
for 24 hours and then frozen on dry ice. Frozen brains were sectioned immediately or stored in
−80°C for future processing. Coronal sections (30 μm) were collected with a cryostat (Microm HM
505 E). Sections were permeabilized with 0.3% Triton X-100 in PBS (PBS-T) and blocked with
3% normal donkey serum (Jackson ImmunoResearch, RRID:AB_2337258) in PBS-T (PBS-T DS)
for 30 min at room temperature. Sections were then incubated overnight at room temperature in
primary antibodies diluted in PBS-T DS. For visualization, sections were washed with PBS-T and
incubated with appropriate secondary antibodies diluted in the PBS-T DS for 2 hours at room
temperature. Sections were washed three times with PBS and mounted using DAPI Fluoromount-
G (Southern Biotech, catalog no. 0100-20). Images were captured on a Zeiss Axioplan 2 Imaging
microscope equipped with an AxioCam MRm camera using AxioVision 4.6 software (Zeiss) or
confocal microscope imaging was performed on a Zeiss LSM 800 microscope (Carl Zeiss). The
following primary antibodies were used for fluorescent labeling: anti-c-Fos (rabbit, 1:1000;
Synaptic Systems, #226003, RRID:AB_2231974), anti-DsRed (rabbit, 1:1000; Takara Bio,
catalog no. 632496, RRID:AB_10013483), anti-TdTomato (goat, 1:1000; Arigobio, catalog no.
ARG55724), anti-hGLP1R (rabbit, 1:200; Invitrogen, catalog no. PA5-97789, RRID:
AB_2812404), anti-HA (rabbit, 1:1000, Cell Signaling, catalog no. 3724), anti-Th (rabbit, 1:500;
Chemicon, catalog no. AB152), and anti-GFP (goat, 1:500; Rockland, catalog no. 600-101-215).
The secondary antibodies (Jackson ImmunoResearch) used were Cy2-conjugated donkey anti-
rabbit (1:250; catalog no. 711-225-152, RRID:AB_2340612), Cy3-conjugated donkey anti-rabbit
(1:250; catalog no. 711-165-152, RRID:AB_2307443), Cy5-conjugated donkey anti-rabbit (1:250;
catalog no. 711-175-152, RRID:AB_2340607), Cy3-conjugated donkey anti-goat (1:250; catalog
no. 705-165-147, RRID:AB_2307351), and Alexa-Fluor® 488 donkey anti-goat (1:250; catalog
no. 705-545-003, RRID:AB_2340428).

Antigen retrieval for hGLP1R staining

606 Antigen retrieval was performed before immunohistochemistry staining of human GLP1R, by
607 incubating the sections in the following solutions sequentially in room temperature: 1% NaOH +
608 0.3% H_2O_2 in PBS for 20 min, 0.3% glycine in PBS for 10 min, and 0.03% sodium dodecyl sulfate
609 (SDS) in PBS for 10 min. Then, antigen retrieval–treated sections were stained following the
610 immunohistochemistry staining procedures described.

Fos analysis pipeline
Fos images were uploaded to ImageJ (FIJI) and cropped based on brain regions outlined in the Allen Brain Atlas. The area of the cropped regions were measured and recorded. Image thresholds were set per image and particles were analyzed within the size restriction of 50-500 pixels. cFos particles were analyzed per image, and total particles of each image were divided by total area of the image. At least three cFos images per region for each mouse was quantified and averaged per mouse and per genotype (WT or Glp1r^{S33W}). Ratios of NTS/AP Fos activation in Glp1r^{S33W} mice were calculated by dividing Fos/area of NTS over AP for each mouse and averaged per injection.

Behavioral Assays

Metabolic analysis in comprehensive lab animal monitoring system
Indirect calorimetry in the comprehensive lab animal monitoring system (CLAMS, Columbus Instruments) was used to evaluate metabolic parameters of WT and Glp1r^{S33W} mice. All WT and Glp1r^{S33W} mice were single housed and maintained on a 12:12-hour LD cycle with *ad libitum* access to food (PicoLab Rodent Diet 5053) and water. Metabolic measures of respiratory exchange ratio and energy expenditure were averaged over 3 days per mouse and per genotype. (n = 10/11 mice per genotype). Averaged LD cycle and total 24 hour respiratory exchange ratio and energy expenditure was analyzed per genotype and per sex.

Glucose tolerance tests
WT or Glp1r^{S33W} mice were overnight fasted for 16 hours prior to experiment start (zeitgeber time [ZT] 10 - ZT2). Mice received a tail snip and blood glucose measure using a Glucometer (OneTouch Ultra Test Strips for Diabetes), along with injection or oral gavage of danuglipron (3mg/kg) or liraglutide (0.3mg/kg) 15 minutes prior to dextrose (D-glucose) injection, or orforglipron (1mg/kg) 240 minutes prior to dextrose. At time point 0, mice received a blood glucose measure and injection of dextrose (1g/kg). At 15, 30, 60, 90, and 120 minutes after injection, blood glucose levels were measured.

Homeostatic food intake
Home cages were changed and food was removed from the home cage 1 hour prior to experiment start. Mice were injected with vehicle/saline or drug (danuglipron 30mg/kg, liraglutide 0.3mg/kg, orforglipron 1mg/kg) at ZT11.5 (ZT8 for orforglipron) and two pellets of standard diet (PicoLab Rodent Diet 5053) were placed on the home cage floor at ZT12. Food intake measurements were taken at 1, 2, and 4 hours after ZT12 using infrared night vision goggles (Nightfox Swift Night Vision Goggles).

Hedonic food intake
Mice were habituated to high fat diet (HFD; Open Source, D12451; 4.73 kcal/gram; 45% fat, 20% protein, 35% carbohydrates; 17% sucrose) for 1 hour over two days before testing days. Standard diet was removed from the home cage 1 hour prior to experiment start. Mice were injected with vehicle/saline or drug (danuglipron 30mg/kg, liraglutide 0.3mg/kg, orforglipron 1mg/kg) at ZT1.5 and one pellet of HFD was placed on the home cage floor at ZT2 (ZT5.5 for orforglipron). Food intake measurements were taken at 1, 2, and 4 hours after HFD delivery. The same parameters were used in oral gavage experiments with danuglipron and orforglipron

Optogenetic Food Intake Analysis
Mice were single-housed for at least five days and habituated to a fiber optic cable and high fat diet for one hour over two days. On the test day, home cages were changed and food was

removed 1 hour prior to the start of the experiment. During the test day, a pre-measured pellet of
high-fat diet (HFD) was provided to each mouse. The test paradigm was 30 minutes of laser
stimulation followed by 30 minutes without laser stimulation. Food intake during each 30-minute
interval was measured. The laser stimulation protocol was 20 Hz, 473 nm blue light with a 2-
second on and 3-second off pattern. The light power exiting the fiber optic cable, measured using
an optical power meter (Thorlabs), was maintained at 7-8 mW across all experiments. Experiment
performed during the light phase, between ZT3-ZT4. Mice with missed virus injection or off-target
fiber placement were excluded from analysis.
673
Weight loss experiment
Male Glp1r^{S33W} mice >8 weeks old were placed on a high fat diet (Open Source, D12451; 4.73
kcal/gram; 45% fat, 20% protein, 35% carbohydrates; 17% sucrose) for at least 8 weeks prior to
experiment start. Mice that did not gain at least 20% of their baseline body weight were excluded
from testing. Mice were randomly assigned to saline or orforglipron (1mg/kg) injection groups and
retested with the opposite treatment after a week of rest. Glp1r^{S33W} mice were injected daily at
ZT6 and food and body weight were measured.
681
Home cage monitoring of Glp1r^{S33W} mice
Mice were singly housed and acclimated to home cage PhenoTyper boxes (Noldus, Netherlands)
for 5 days prior to testing. The cages were maintained on a 12:12-hour light-dark (LD) cycle.
During the acclimation period, mice had *ad libitum* access to standard diet (SD) provided in a food
hopper, along with water bottles, running wheels, shelters, and bedding. Mice that failed to meet
a baseline threshold of food hopper activity (<50 nose pokes from ZT 12-14) after habituation
were excluded from the study to ensure sufficient engagement with the feeding setup. Of the 38
mice tested, 9 did not meet this criterion and were excluded. For the light cycle experiment, mice
were additionally habituated to high-fat diet (HFD) for 2 days prior to testing. For testing,
danuglipron (30 mg/kg) or vehicle was administered at ZT 11.5, with the injection order
counterbalanced. Liraglutide (0.3 mg/kg) or saline was administered at ZT 10. Behavior was
monitored for 4 hours starting at ZT 12. In the light cycle experiment, Danuglipron (30 mg/kg) or
vehicle was administered at ZT 2.5, and behavior was recorded for 4 hours starting at ZT 3. During
the 4-hour testing window, mice had *ad libitum* access to either SD or HFD, depending on the test
condition. On HFD test days, HFD was replaced with SD immediately after the recording period.
Danuglipron was not administered on consecutive days. Sensors in the PhenoTyper cages
recorded the following metrics: food hopper head entries, water bottle spout licks, and full running
wheel rotations. Behavioral sessions were recorded with top-down infrared cameras (Noldus) at
a resolution of 960 x 540 pixels at 25 frames per second, in grayscale. Videos were cropped to
2-hour segments using Adobe Premiere Pro and re-encoded with H.264 compression via FFmpeg
to ensure smooth playback and frame-seeking.
703
Machine-learning assisted pipeline
Animal pose estimation was performed on home cage monitoring videos of singly housed, free
roaming mice with Social LEAP Estimates Animal Poses (SLEAP, v1.3.3)[60,61]. The following 9
keypoints were tracked: nose, left ear, right ear, center 1-5, and tail base. We labeled 10,770
frames from 18 videos under conditions similar to the experimental ones, splitting them into 9,693
training and 1,077 validation frames (90% split). We used a U-Net based neural network with a
max stride of 32, 16 filters, and a rotation angle of ± 180. All other hyperparameters were default
using the single animal pipeline. The trained model's average distance (ground truth vs prediction)
was: 1.59 pixels, mean object keypoint similarity (OKS): 0.85, mean average precision (mAP):
0.81, and mean average recall (mAR): 0.84. Inferences were made on the first two hours of videos
(ZT 12-14), as this period was significant in the sensor data. Flow tracking and default
hyperparameters were used for inference. Representative heatmaps of the mouse nose keypoint

were generated in Python by cropping to remove the walls of the cage and creating 62 by 27 pixel
bins.
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Keypoint Motion Sequencing (Keypoint-MoSeq)[60,61] was then used to identify behavioral syllables
using a probabilistic model from the input keypoint coordinates of 80 hours of home cage videos.
Four latent dimensions accounted for 90% of the variance in aligned and centered keypoint
coordinates. A kappa of 10^5 was chosen to maintain the desired syllable time-scale. Using this
parameter, an autoregressive hidden Markov model (AR-HMM) was first fit to the data, followed
by the full model fit. Keypoint-MoSeq identified 91 behavioral syllables; 46 accounted for ≥ 0.5%
of instances, while those with frequencies < 0.5% but ≥ 0.01% were included, and < 0.01% were
excluded.
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To provide biologically meaningful interpretations, the syllables were grouped into broader
behavioral categories (Fig. S6) by two trained raters. Some syllables represented a combination
of behaviors or closely related actions that could not be distinguished due to the camera angle
(e.g., "groom/sniff"). Poor-quality syllables (~1% of the dataset), likely from keypoint tracking
issues under the wheel, were excluded from analysis.

To incorporate location context, the pixel coordinates of the food hopper, shelter, and water bottle
spout were defined in videos using the Python OpenCV package (OpenCV, 2024). Regions of
interest (ROIs) were established around these coordinates. SLEAP coordinates identified when
the mouse entered a specific ROI, with the nose keypoint for the food hopper and water bottle
spout, and center 3 for the shelter. Behaviors were categorized based on location, such as
distinguishing "sniff by food" from "sniff" outside the food hopper ROI.

This categorization resulted in 23 unique behaviors, which were further grouped into five general
categories: "move/explore," "rest," "groom," "food-motivated behaviors," and "drink." On average,
these behaviors accounted for 98.3% of the total time in the two-hour video recordings for each
video (mouse × condition). For each video, we calculated the total time spent performing each of
the 23 behaviors. Additionally, the proportion of time each mouse spent on the five general
behavior categories was calculated relative to their total behavioral time.

Proportional differences were assessed using a beta-distributed generalized linear mixed-effects
model with mouse as a random effect. For the inactive phase, the model included main effects of
drug and diet and their interaction. Behavioral collinearity was addressed with PCA, and the top
three principal components (PC 1–3) were analyzed via repeated measures MANOVA.

To reveal global differences in behavior by condition, linear discriminant analysis (LDA) with three
components was applied to the behavior duration dataset. LDA identified the linear combinations
of behavioral features that best separated conditions. Separate plots were generated for dark and
light cycle conditions, using the same LDA model fit across all tested conditions. Groups were
also visualized in PC space (PC 1 and PC 2) as used in the MANOVA analysis. LDA was
performed using the scikit-learn package [80,81]. All Python code for these analyses is available on
GitHub.

Electrophysiology recordings
Brain slice preparation
Preparation of acute brain slices for patch-clamp electrophysiology experiments was modified
from standard protocols previously described[82,83,84]. Mice were anesthetized with isoflurane and
decapitated. The brains were rapidly removed and kept in chilled artificial cerebrospinal fluid
(ACSF) (0°C) containing (in mM): 125 NaCl, 2.5 KCl, 1.25 NaH_2PO_4, 2 $CaCl_2$, 1 $MgCl_2$, 0.5 L-

ascorbic acid, 10 glucose, 25 $NaHCO_3$, and 2 Na-pyruvate (osmolarity 310 mOsm). Slices were
continuously oxygenated with 95% O2 and 5% CO2 throughout the preparation. Coronal brain
sections, 300 µm, were prepared using a Leica Microsystems VT1200 vibratome. Slices were
collected and placed in ACSF warmed to 37°C for 30 minutes and then kept at room temperature
for up to 5 hours.
767
Recordings
Brain slices were placed in a chamber superfused (~2 mL/min) with continuously oxygenated
ACSF solution warmed to 32 ± 1°C. hGLP1R-expressing Central amygdala neurons were
identified by video microscopy based on the expression of eYFP marker. Whole-cell
electrophysiology recordings were performed using a Multiclamp 700B amplifier with signals
digitized by a Digidata 1550B digitizer. Currents were amplified, lowpass-filtered at 2 kHz, and
sampled at 35 kHz. Borosilicate electrodes were fabricated using a Brown-Flaming puller (model
P1000, Sutter Instruments) to have pipette resistances between 2.5 and 4.5 mΩ. Current-clamp
recordings of membrane potentials were collected in ACSF solution identical to that used for
preparation of brain slices. The internal solution contained the following (in mM): 120 K-gluconate,
10 NaCl, 2 $MgCl_2$, 0.5 K_2EGTA, 10 HEPES, 4 Na_2ATP, and 0.3 NaGTP, pH 7.2 (osmolarity 290
mOsm). Resting membrane potential was recorded as previously described (1,2). After 5 mins of
baseline membrane potential recordings 10 µm of danuglipron was perfused for 5 mins followed
by washout.
782
Statistics
Electrophysiology recordings were analyzed using ClampFit 11.2. All statistical comparisons were
made using the appropriate test in GraphPad Prism 9.5.0. For membrane, AP properties, and
amplitude underwent descriptive statistics followed by normality and lognormality test using
gaussian distribution. Data were assessed for normality using the D'Agostino-Pearson omnibus
normality test, Anderson-Darling test, Shapiro-Wilk test, and Kolmogorov-Smirnov test with Dallal-
Wilkinson-Lillie for P-values. Data were tested for outliers using the ROUT method, and statistical
outliers were not included in data analysis. Followed by Tukey's test with no gaussian distribution
creating a nonparametric t-test using Wilcoxon matched-pairs signed rank test to compare
responses caused by the drug. Data are presented as individual data points and/or mean ± SEM.
793
Fiber Photometry Recordings
***In vivo* calcium recording (GCaMP)**
Mice underwent 20-minute daily habituation sessions over two consecutive days to acclimate to
the fiber-optic cable (Doric Lenses, Ø400-µm core, 0.57 numerical aperture). On the test day,
mice were injected with either vehicle, saline, danuglipron (30 mg/kg) or liraglutide (0.3 mg/kg)
two hours prior to recording. The order of injections was randomized to avoid order effects.
Following the two-hour post-injection period, mice were connected to patch cables which were
interfaced with rotary joints to enable free movement. Recordings were conducted for one hour.
Fiber photometry data were recorded using fluorescent signals from both calcium-dependent (465
nm) and calcium-independent isosbestic (405 nm) excitation wavelengths (Doric). The isosbestic
(405 nm) signal served to control for artifacts. The light power of the fiber optic cable was
measured before each experiment and maintained at approximately 20-30 µW for both the
calcium-independent isosbestic (405 nm) and calcium-dependent (465 nm) signals.
807
***In vivo* calcium analysis (GCaMP)**
The isosbestic signal (405 nm) was fitted to the calcium-dependent (465 nm) signal using a linear
least squares method implemented in a custom MATLAB script. Then ΔF/F was calculated as
(465 nm – fitted 405 nm) / fitted 405 nm. For significant calcium event detection analysis, we used
a combination of methodologies previously described [85]. Events were detected using a threshold

defined as the median plus two standard deviations of the entire recording, with events required
to be 1.5 seconds or longer. The number of events detected per trial was then extracted and
reported alongside heatmaps as %ΔF/F of entire recordings. Heatmaps were generated in Python
using Min-Max normalization, scaled to a range of 0–1. For each mouse, the normalization range
was determined based on the Vehicle condition: the average of the lowest 360 data points was
set as the minimum, and the average of the highest 360 data points was set as the maximum.
This normalization range, derived from the Vehicle condition, was then applied to the
corresponding paired Danuglipron data for the same mouse. A moving average with a window
and bin size of 10 smoothed the data, which was then plotted as a heatmap. Mice with missed
virus injection or off-target fiber placement were excluded from analysis.
823

***In vivo* dopamine recording (dLight1.3b)**
Mice were single-housed and habituated to the fiber optic cable and high-fat diet (HFD) for one
hour over two consecutive days. On the test day, mice received an injection of either a drug
(liraglutide [0.3 mg/kg], danuglipron [30 mg/kg], or orforglipron [1mg/kg]) or vehicle/saline, with
the order of drug versus vehicle/saline injections randomized. Liraglutide and danuglipron were
administered two hours before recording, while orforglipron was given four hours prior. Fiber
photometry data were recorded as described above. Fluorescent signals were collected from both
dopamine-dependent (465 nm) and dopamine-independent isosbestic (405 nm) excitation
wavelengths. During the testing sessions, small pellets of HFD (~10 mg) were dropped into a cup
at two-minute intervals after the mice retrieved the pellet. 5 to 6 trials were conducted per mouse.
The recording session was video recorded to timestamp food retrieval time. Dopamine recordings
were conducted during the light phase, between ZT3 and ZT6.
836

***In vivo* dopamine analysis (dLight1.3b)**
The isosbestic signal (405 nm) was fitted to the dopamine-dependent (465 nm) signal using a
linear least squares method implemented in a custom MATLAB script. Then ΔF/F was calculated
as (465 nm – fitted 405 nm) / fitted 405 nm. To account for inter-animal differences in signal
intensities, Z-scores were calculated for the ΔF/F signals. The baseline period for each food trial
was defined as the 30-second interval prior to food retrieval. The mean and standard deviation of
the baseline period were used to compute the Z-scores, with the formula: Z score = (F-
Fμ(baseline))/std(baseline), where F is the 405 nm corrected 465 nm signal (ΔF/F), μ(baseline)
is the mean, and std is the standard deviation of the baseline period. Video frames were analyzed
to determine the exact timestamp when the mouse retrieved the pellet, which was defined as time
0 for each retrieval. The 30-second window centered around the food retrieval time was extracted.
The area under the curve (AUC) and maximum fluorescence Z-scored within the food retrieval
window was further extracted and analyzed for quantification of dopaminergic activity. 5 food trials
were averaged per mouse. Mice with missed virus injections or off-target fiber placements were
excluded from the analysis.
852

Statistical analyses
All data are presented as mean ±SEM unless otherwise noted. Statistical tests including paired
or unpaired two-tailed t-tests, Kruskal-Wallis tests, Wilcoxon signed-rank tests, Pearson
regression, one-way ANOVA, two-way/repeated-measures ANOVA (with Bonferroni correction or
Tukey's HSD post hoc tests), MANOVA (with MATS resampling), linear mixed effect models with
beta regression (with Tukey's post hoc test) were performed using RStudio (v4.3.0), Python
(v3.11.5), JupyterLab (v3.6.3), MATLAB (R2023a), or GraphPad Prism (v10.4.0). Brief
descriptions of all experiments in each figure panel, sample sizes, mean ±SEM, statistical test,
test statistics, and *P*-values are presented in Supplementary Table 1. *P <0.05; **P <0.01;
***P <0.001.
863

864 **Data availability**
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866 All data will be available on Dryad upon publication and select code will also be available on
867 Github at https://github.com/UVACircMetNeuLab.
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 Extended Data

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Extended Data Fig. 1. Metabolic profiling of WT and Glp1r^{S33W} mice. a,e, Diurnal rhythms
averaged over 3 days of (**a**) respiratory exchange ratio (RER) and (**e**) energy expenditure (EE) in
WT and Glp1r^{S33W} mice. **b-g**, Average dark/light phase and total 24 hour (**b,c**) RER and (**f,g**) EE
between WT and Glp1r^{S33W} mice (n = 11-12 per genotype, two-way ANOVA with Bonferroni
correction or Welch's t-test). **d,h**, Total 24 hour (**d**) RER and (**h**) EE averaged by sex (n = 4-5
females, n = 7 males per genotype, two-way ANOVA with Bonferroni correction). **i**, Average
baseline body weight of WT and Glp1r^{S33W} mice 10 to 20 weeks old (n = 18-19 per genotype,
Welch's t-test). **j**, Average baseline body weight of WT and Glp1r^{S33W} male and female mice (n =
8-9 females, n = 10 males per group, two-way ANOVA with Bonferroni correction). Data are
represented as medians ± Q1-Q3. *P<0.05; **P<0.01; ***P<0.001.

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Extended Data Fig. 3. cFos activation in NTS and AP of WT mice administered oral or IP
danuglipron. a,b, Neuronal cFos activation in the NTS and AP 2-hours after danuglipron was
administered to WT mice via (**a**) IP injection or (**b**) oral gavage. **c**, Quantification of cFos
expression in the NTS (left) or AP (right) following danuglipron IP or oral delivery in WT mice (*n* =
3-4 per delivery route, Welch's t-test). Data are represented as means ± SEM. *$P<0.05$; **$P<0.01$;
***$P<0.001$.
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Extended Data Fig. 4. Home cage monitoring heatmaps of Glp1r^{S33W} mice. Representative
image of home cage set-up (dimensions: 30 x 30 x 43.5 cm) with calibrated positions of wheel,
IR translucent shelter (10.5 x 10.5 x 6 cm), food hopper (5.5 cm from floor), and water bottle spout
(5 cm from floor) identified in white outline (top). Coordinate-based heatmaps of nose keypoint
trajectories recorded at 25 fps over 2-hour sessions for each treatment group during active (ZT
12-14) or inactive (ZT 3-5) phase. Color scale represents dwelling time in seconds.
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Extended Data Fig. 5. Machine-learning assisted pipeline for home cage behavioral
analysis. Blue squares represent video pre-processing steps. Social LEAP Estimates Animal
Poses (SLEAP) was used to extract nine keypoint coordinates for each mouse in the videos (Fig.
3, A to B; fig. S4). Keypoint Motion Sequencing (Keypoint-MoSeq) identified behavioral syllables
from these coordinates (fig. S6). Red squares represent Python scripts used for the analysis of
Keypoint-MoSeq syllable results: locations (identify regions of interest), location_aware (**Fig. 3c-**
n), lda_cosine (**Fig. 3l,n**), and pie_timeline (**Fig. 3b,e,f,m**).

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Extended Data Fig. 6. Trajectory plots of main behavioral syllables identified by Keypoint-MoSeq. Syllables identified from keypoint coordinates by Keypoint-MoSeq were sorted into 11 categories by trained raters using grid movies generated for each syllable. The proportion of each syllable category is presented as a percentage. Rare syllables (minimum frequency < 0.5% but ≥ 0.01%) are not visually depicted but were included in the analysis.

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Extended Data Fig. 7. Principal component analysis and inactive phase behaviors. a–f,
Principal Component Analysis (PCA) of 23 behavioral durations recorded during 2-hour home
cage video sessions. PCA score plots for: (**a**) Vehicle and danuglipron-treated mice, (**c**) saline
and liraglutide-treated mice, and (**e**) inactive-phase SD- and HFD-fed mice treated with vehicle or
danuglipron. Corresponding PCA loading plots illustrating: (**b**) vehicle and danuglipron, (**d**) saline
and liraglutide, and (**f**) inactive-phase SD- and HFD-fed mice treated with vehicle or danuglipron.
g–k, Proportion of time allocated to five behavioral categories during the inactive phase for SD-
and HFD-fed mice on vehicle or danuglipron: (**g**) food-motivated behaviors, (**h**) drinking, (**i**)
movement/exploration, (**j**) grooming, and (**k**) resting behaviors (n = 10 per injection, (n = 10,
generalized linear mixed-effects model (beta distribution) with main effects of drug and diet, as
well as their interaction, followed by Tukey's post-hoc test, *$P<0.05$; **$P<0.01$; ***$P<0.001$). Data
are represented as medians ± Q1-Q3. *$P<0.05$; **$P<0.01$; ***$P<0.001$.

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1220 **Extended Data Fig. 8. Validation of AAV-hSyn-DIO-hGLP1R virus. a-h,** Fluorescent
1221 microscopy images of the brain regions stereotaxically injected with AAV-DIO-hGLP1R. Images
1222 from Allen Brain Atlas, with regions of interest in bold and hGLP1R antibody staining (green) in
1223 the (**a,b**) basomedial hypothalamus (BMH), (**c,d**) DMH, (**e,f**) NTS/AP, or (**g,h**) CeA. Scale bars =
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Extended Data Fig. 9. Danuglipron depolarizes the resting membrane potential in hGLP1R-
expressing CeA neurons. a, Representative trace showing the effect of 5 minutes of danuglipron
perfusion (10 µM) on the resting membrane potential of CeA neurons. **b,** Average depolarization
induced by danuglipron compared to baseline recording. Baseline: −62.72 ± 2.08 mV;
danuglipron: −54.87 ± 2.49 mV; average change: 7.8 mV (n = 7 cells, Wilcoxon signed-rank test,
*P<0.05). **c–f,** Localization of eYFP-labeled hGLP1R-expressing neurons in the central amygdala
(CeA). BrainJ software [79] analysis indicates prominent eYFP labeling in the capsular part of the
CeA, with additional labeling in the lateral part. Scale bars = 1000 µm.
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Extended Data Fig. 10. AAV-DIO-mGLP1R^S33W-HA targeted to the CeA of Glp1r-Cre mice
recapitulates effects of AAV-DIO-hGLP1R. a, Schematic of Glp1r-Cre mice injected with a Cre-
dependent AAV carrying full length mouse Glp1r (mGlp1r) or AAV carrying full length mouse
GLP1R with the S33W mutation at position 33 (mGLP1R^S33W) in the CeA. **b,c**, Normalized 4-hour
(**b**) SD and (**c**) HFD consumption post-injection of vehicle or danuglipron in mGlp1r, full length
human GLP1R (hGLP1R) or mGlp1r-S33W (S33W) expressing mice (n = 4-9 per group, two-way
ANOVA with Bonferroni correction, *$P<0.05$; **$P<0.01$). **d**, Representative image of AAV-DIO-
mGLP1R^S33W-HA expression in the CeA (green). Scale bars = 200 µm. Data are represented as
means ± SEM. *$P<0.05$; **$P<0.01$; ***$P<0.001$.

Extended Data Fig. 11. Fiber photometry recordings and validation of CeA^{GLP1R} neurons. a,
Representative traces of fiber photometry recordings showing calcium-dependent fluorescence
(465nm) and calcium-independent, isosbestic fluorescence (405nm) signals. **b**, Fitted 405nm
signal (pink) transformed for ΔF/F calculation. **c,** Representative trace of %ΔF/F used for
analysis. Blue dots indicate detected calcium events, identified using a threshold set at 2 standard
deviations plus the median of the entire 1-hour recording session, with an event required to be
longer than 1.5 seconds. **d**, Representative images of AAV-DIO-GCaMP7s + hGLP1R targeted
to the CeA. Validation with hGLP1R antibody (red; left), GCaMP7s (green; middle), and
verification of colocalization (right). Scale bars = 100 μm. **e**, Number of significant calcium events
averaged per mouse during 1-hour recording session following saline or liraglutide in CeA-
hGLP1R expressing mice (n = 6 per injection, paired t-test, *P<0.05). **f**, Representative heatmaps
of %ΔF/F neuronal calcium signal per mouse during 1-hour of fiber photometry recording after
saline (left) or liraglutide (right) injection in CeA-hGLP1R expressing mice. Data are represented
as means ± SEM. *P<0.05; **P<0.01; ***P<0.001.

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Extended Data Fig. 12. CeA^{GLP1R} neurons innervate the VTA and validation of AAVs
targeting CeA and NAc. a, Representative images of AAV-DIO-ChR2-eYFP expression targeted
to the CeA of Glp1r-Cre mice (green; *n* = 6). **b**, Tyrosine hydroxylase (Th) expression in the VTA
(magenta). **c**, Axon fiber projections from CeA^{GLP1R} neurons into the VTA, and **d**, colocalization of
Th with CeA^{GLP1R} fibers in the VTA. **e**, Traces of superimposed AAV-DIO-ChR2-eYFP injection
targeting per mouse, collapsed on the Allen Brain Atlas figure. **f**, Schematic showing AAV-
dLight1.3b injection into the NAc and AAV-DIO-hGLP1R injection into the CeA of Glp1r-Cre mice,
with fiber optic implants in the NAc. **g**, Validation of AAV-DIO-hGLP1R targeting the CeA using
hGLP1R antibody staining (red). **h**, Representative AAV-dLight expression in the NAc and fiber
optic implant placement (green). Scale bars = 200 μm.

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Extended Data Fig. 13. Liraglutide reduces NAc dopamine release in response to HFD. a,
Averaged Z-score traces showing dopamine release in the NAc in response to HFD following
administration of saline or liraglutide in Glp1r^{S33W} mice. Traces are aligned to food retrieval time
(t = 0) and averaged across five food trials per mouse. **b,c,** Quantified (**b**) area under the curve
(AUC) for Z-scores and (**c**) maximum fluorescence Z-scores within the food retrieval window (n =
7, paired t-test, *$P<0.05$). Data are represented as means ± SEM. *$P<0.05$; **$P<0.01$; ***$P<0.001$.
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