1 2 3	LUXendins reveal endogenous glucagon-like peptide-1 receptor distribution and dynamics
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43 ABSTRACT (150 words)

44 The glucagon-like peptide-1 receptor (GLP1R) is a class B G protein-coupled receptor (GPCR) involved in metabolism. Presently, its visualization is limited to genetic manipulation, 45 antibody detection or the use of probes that stimulate receptor activation. Herein, we present 46 47 LUXendin645, a far-red fluorescent GLP1R antagonistic peptide label. LUXendin645 48 produces intense and specific membrane labeling throughout live and fixed tissue. GLP1R signaling can additionally be evoked when the receptor is allosterically modulated in the 49 50 presence of LUXendin645. Using LUXendin645 and STED-compatible LUXendin651 we describe islet GLP1R expression patterns, reveal higher-order GLP1R organization including 51 52 the existence of membrane nanodomains, and track single receptor subpopulations. We furthermore show that different fluorophores can confer agonistic behavior on the LUXendin 53 backbone, with implications for the design of stabilized incretin-mimetics. Thus, our labeling 54 probes possess divergent activation modes, allow visualization of endogenous GLP1R, and 55 56 provide new insight into class B GPCR distribution and dynamics.

58 INTRODUCTION

The glucagon-like peptide-1 receptor (GLP1R) is a secretin family class B G protein-coupled 59 receptor (GPCR) characterized by hormone regulation.¹ Due to its involvement in glucose 60 homeostasis, the GLP1R has become a blockbuster target for the treatment of type 2 61 diabetes mellitus.² The endogenous ligand, glucagon-like peptide-1 (GLP-1) is released from 62 enteroendocrine L-cells in the gut in response to food intake,³ from where it travels to the 63 pancreas before binding to its cognate receptor expressed in β-cells. Following activation, 64 the GLP1R engages a cascade of signaling pathways including Ca²⁺, cAMP, ERK and β -65 arrestin, which ultimately converge on β-cell survival and the glucose-dependent 66 amplification of insulin release.^{4,5} GLP1R is also expressed in the brain⁶ and muscle⁷ where 67 it further contributes to metabolism via effects on food intake, energy expenditure, 68 locomotion and insulin sensitivity. Despite this, GLP1R localization remains a challenge and 69 70 is impeding functional characterization of GLP-1 and drug action.

Chemical biology and recombinant genetics have made available a diverse range of 71 methods for the visualization of biological entities. Thus, classical fluorescent protein-72 fusions,⁸ self-labeling suicide enzymes (SNAP-, CLIP-, and Halo-tag),⁹⁻¹¹ "click 73 chemistry"^{12,13} and fluorogenic probes¹⁴⁻¹⁶ have provided unprecedented insight into the 74 75 localization and distribution of their respective targets in living cells. In particular, current 76 approaches for visualizing the GLP1R have so far relied on monoclonal antibodies (mAbs) directed against GLP1R epitopes,^{17,18} or fluorescent analogues of Exendin4(1-39),¹⁹⁻²¹ a 77 stabilized form of GLP-1 and the basis for the incretin-mimetic class of drugs. Moreover, 78 79 floxed mouse models exist in which Cre recombinase is driven by the Glp1r promoter, allowing labeling of GLP1R-expressing cells when crossed with reporter mice.^{6,7} 80

81 Such methods have a number of shortcomings. Antibodies possess variable specificity¹⁸ and tissue penetration, and GLP1R epitopes might be hidden or preferentially affected by fixation 82 83 in different cell types. Even more, fluorescent analogues of Exendin4(1-39) activate and internalize the receptor, which could confound results in live cells, particularly when used as 84 a tool to sort purified populations (*i.e.* β-cells) for transcriptomic analysis.^{22,23} On the other 85 hand, reporter mouse strategies possess high fidelity, but cannot account for post-86 translational processing, protein stability and trafficking of native receptor.²⁴ Lastly, none of 87 the aforementioned approaches are amenable to super-resolution imaging of GLP1R. 88

Given the wider reported roles of GLP-1 signaling in the heart,²⁵ liver,²⁶ immune system² and 89 brain,²⁷ it is clear that new tools are urgently required to help identify GLP-1 target sites, with 90 repercussions for drug treatment and its side effects. In the present study, we therefore set 91 out to generate a specific probe for endogenous GLP1R detection in its native, surface-92 exposed state in live and fixed tissue, without receptor activation. Herein, we report 93 LUXendin645 and LUXendin651, Cy5- and SiR- conjugated far-red fluorescent antagonists 94 with unprecedented specificity, live tissue penetration and super-resolution capability. Using 95 96 our tools, we provide an updated view of GLP1R expression patterns in the islet of Langerhans, show that endogenous GLP1Rs form nanodomains at the membrane and 97 reveal receptor subpopulations with distinct diffusion modes. Lastly, we find that installation 98 of a TMR fluorophore unexpectedly confers potent agonist properties. As such, the 99 LUXendins provide the first nanoscopic characterization of a class B GPCR, with wider 100 flexibility for detection and interrogation of GLP1R in the tissue setting. 101

102 **RESULTS**

103 **Design and synthesis of LUXendin555, LUXendin651 and LUXendin645**

Ideally, a fluorescent probe to specifically visualize a biomolecule should have the following 104 characteristics: straightforward synthesis and easy accessibility, high solubility, relative small 105 size, high specificity and affinity, and a fluorescent moiety that exhibits photostability, 106 brightness, (far-)red fluorescence with an additional two-photon cross-section. Moreover, the 107 probe should be devoid of biological effects when applied to live cells and show good or no 108 cell permeability, depending on its target localization. While some of these points were 109 addressed in the past (vide infra), we set out to achieve this high bar by designing a highly 110 specific fluorescent GLP1R antagonist using TMR, Cy5 and SiR fluorophores. As no small 111 molecule antagonists for the GLP1R are known, we turned to Exendin4(9-39), a potent 112 antagonistic scaffold amenable to modification (Fig. 1).²⁸ We used solid-phase peptide 113 synthesis (SPPS) to generate an S39C mutant,²⁹ which provides a C-terminal thiol handle 114 for late-stage installation of different fluorophores. As such, TMR-, Cy5- and SiR-conjugated 115 versions were obtained by means of cysteine-maleimide chemistry, termed LUXendin555, 116 LUXendin645, and LUXendin651, respectively (spectral properties are shown in Table 1, 117 HPLC traces and HRMS characterization can be found in the SI) (Fig. 1). 118

Table 1: Spectral properties of GLP1R labeling probes. Maximal excitation and emission
 wavelengths, and quantum yields were acquired using probes dissolved at 10 μM in PBS, pH
 7.4 at 21 °C.

	dye	λ_{Ex} / nm	λ _{Em} / nm	ε ^[a] / M ⁻¹ cm ⁻¹	Φ
LUXendin555	TMR	555	579	84,000	0.31
LUXendin645	Cy5	645	664	250,000	0.22
LUXendin651	SiR	651	669	100,000	0.43

^[a] For maleimide-conjugated fluorophores

123

124 LUXendin645 intensely labels GLP1R in cells and tissue

GLP-1-induced cAMP production (EC_{50} (cAMP) = 2.8 nM, 95% CI [1.5-5.2]) was similarly 125 blocked by Exendin4(9-39) (EC₅₀(cAMP) = 38.4 nM, 95% CI [19.0-77.8]) and its S39C 126 mutant (EC_{50} (cAMP) = 34.8 nM, 95% CI [18.8-64.4]) (Fig. 2a). Installation of Cy5 to produce 127 **LUXendin645** did not affect these antagonist properties (EC_{50} (cAMP) = 73.1 nM, 95% CI 128 [54.9-97.5]) (Fig. 2a). As expected, addition of the GLP1R positive allosteric modulator 129 (PAM) BETP³⁰ conferred agonist activity on **LUXendin645** (EC_{50} (cAMP) = 9.3 nM, 95% CI 130 [2.2-40.0]), with a potency similar to Exendin4(1-39) (*EC*₅₀(cAMP) = 18.3 nM, 95% CI [8.0-131 42.1]) (Fig. 2b). 132

As a first assessment of GLP1R labeling efficiency, we probed YFP-AD293-SNAP_GLP1R cells with increasing concentrations of **LUXendin645**. Maximum labeling occurred at 100 nM (Fig. 2c), in good agreement with the previously published $K_d = 15.8$ nM of native Exendin4(9-39)³¹. **LUXendin645** was unable to label YFP-AD293 cells in which the GLP1R was absent (Fig. 2d).

We next examined whether LUXendin645 would allow labeling of endogenous GLP1R.
 Following 60 min application of 50 nM LUXendin645, isolated islets demonstrated intense
 and clean labeling, which was restricted to the membrane (Fig. 2e). Using conventional

141 confocal microscopy, we were able to detect bright staining even 60 μ m into the islet (Fig. 142 2e). Given these results, we next attempted to penetrate deeper into the islet by taking 143 advantage of the superior axial resolution of two-photon excitation (Fig. 2f). Remarkably, this 144 imaging modality revealed **LUXendin645** labeling at high resolution throughout the entire 145 volume of the islet (170 μ m in this case) (Fig. 2f). Consistent with the cAMP assays, 146 profound GLP1R internalization was detected following co-application of **LUXendin645** and 147 BETP to MIN6 β-cells, which endogenously express the receptor (Fig. 2g, h).

148 LUXendin645 allows multiplexed GLP1R detection

Demonstrating flexibility, LUXendin645 labeling was still present following formaldehyde 149 fixation (Fig. 2i, j). Immunostaining using a specific primary monoclonal antibody against the 150 GLP1R revealed strong co-localization with LUXendin645 in both islets (Fig. 2i) and MIN6 151 cells (Fig. 2i). Notably, LUXendin645 displayed superior signal-to-noise-ratio and membrane 152 resolution compared to the antibody (Fig. 2k), expected to be even better in live tissue where 153 auto-fluorescence is less. Likewise, LUXendin645 co-localized with SNAP-Surface 488 in 154 SNAP GLP1R-INS1 rat β-cells generated on an endogenous null background (Fig. 2I). 155 Suggesting that LUXendin645 requires the presence of surface GLP1R, labeling was 156 markedly reduced following prior internalization with Exendin4(1-39) (Fig. 2I, m). 157

158 LUXendin645 specifically binds the GLP1R

To further validate the specificity of **LUXendin645** labeling in primary tissue, we generated *Glp1r* knock-out mice. This was achieved using CRISPR-Cas9 genome editing to introduce a deletion into exon 1 of the *Glp1r*. The consequent frameshift was associated with absence of translation and therefore a global GLP1R knockout, termed *Glp1r*^{(GE)-/-}, in which all intronic regions, and thus regulatory elements, are preserved (Fig. 3a, b). Wild-type (*Glp1r*^{+/+}), heterozygous and homozygous littermates were phenotypically normal and possessed similar body weights (Fig. 3c).

Confirming successful GLP1R knock-out, insulin secretion assays in islets isolated from 166 Glp1r^{(GE)-/-} mice showed intact responses to glucose, but absence of Exendin4(1-39)-167 stimulated insulin secretion (Fig. 3d). Reflecting this finding, the incretin-mimetic Liraglutide 168 was only able to stimulate cAMP rises in islets from wild-type ($Glp1r^{+/+}$) littermates, 169 measured using the FRET probe Epac2-camps (Fig. 3e, f). As expected, immunostaining 170 with monoclonal antibody showed complete absence of GLP1R protein (Fig. 3g). Suggesting 171 that LUXendin645 specifically targets GLP1R, with little to no cross-talk from glucagon-172 receptors,³² signal could not be detected in $Glp1r^{(GE)-/-}$ islets (Fig. 3g). 173

Together, these data provide strong evidence for a specific mode of **LUXendin645** action *via* the GLP1R.

176 LUXendin645 highlights weak GLP1R expression

Previous approaches have shown low abundance of *Glp1r* transcripts in the other major islet endocrine cell type, *i.e.* glucagon-secreting α-cells.^{7,33} This is associated with detection of GLP1R protein in ~1-10% of cells,^{7,34} providing an excellent testbed for **LUXendin645** sensitivity. Studies in intact islets showed that **LUXendin645** labeling was widespread in the islet and well co-localized with insulin immunostaining (Fig. 4a). However, **LUXendin645** could also be seen on membranes very closely associated with α-cells and somatostatin183 secreting δ -cells (Fig. 4b, c), similarly to results obtained with GLP1R mAb. Due to the close apposition of β -, α - and δ -cell membranes, we were unable to accurately assign cell-type 184 specificity to LUXendin645. Instead, using cell clusters plated onto coverslips, we could 185 better discern LUXendin645 labeling, revealing GLP1R expression in 18 \pm 6% of α -cells 186 (Fig. 4d–f), higher than that shown before using antibodies^{19,34} and reporter genes⁷. Notably, 187 GLP1R-expressing α -cells tended to adjoin, whereas those without the receptor were next to 188 β -cells. Confirming previous findings, a majority (86 ± 3%) of β -cells were positive for 189 **LUXendin645** (Fig 4d-f).^{7,19} 190

We wondered whether fixation required for immunostaining might increase background 191 fluorescence and decrease LUXendin645 signal such that GLP1R detection sensitivity was 192 reduced. To circumvent this, studies were repeated in live islets where LUXendin645 signal 193 was found to be much brighter and background almost non-existent. GLP1R was detected in 194 26.2 ± 1.1 % of non- β -cells (Fig 4g, h) using Ins1Cre^{Thor}; R26^{mTmG} reporter mice in which β -195 196 cells are labeled green and all other cell types are labeled red following Cre-mediated recombination. Once adjusted for the previously reported GLP1R expression in δ-cells 197 (assuming 100%), which constitute ~5-10% of the islet population,³⁵ this leaves ~16-21% of 198 GLP1R+ α-cells, reflecting results obtained with immunostaining of dissociated islets. This 199 was not an artefact of optical section, since two-photon islet reconstructions showed similar 200 absence of LUXendin645 staining in discrete regions near the surface (where α -cells 201 predominate) (Movie S1). 202

203 LUXendin645 and Luxendin651 reveal higher-order GLP1R organization

By combining LUXendin645 with Super-Resolution Radial Fluctuations (SRRF) analysis,³⁶ 204 GLP1R could be imaged at super-resolution using streamed images (~ 1000) from a 205 conventional widefield microscope (Fig. 5a). To image endogenous GLP1R at < 100 nm 206 207 lateral resolution, we combined STED nanoscopy with LUXendin651, which bears silicon rhodamine (SiR) instead of Cy5. LUXendin651 produced bright labeling of wild-type but not 208 Glp1r^{(GE)-/-} islets, with an identical distribution to LUXendin645 (Supplementary Fig. S1). 209 Incubation of MIN6 cells with LUXendin651 and subsequent fixation allowed STED imaging 210 of the endogenous GLP1R with a FWHM = 70 ± 10 nm (Fig. 5b, c). STED snapshots of MIN6 211 β-cells revealed GLP1R distribution with unprecedented detail: receptors were not randomly 212 arranged but rather tended to organize into nanodomains with neighbors (Fig. 5b, c). This 213 was confirmed using the F- and G-functions, which showed a non-random and more 214 215 clustered GLP1R distribution (Fig. 5d, e). Differences in GLP1R expression level and pattern 216 could clearly be seen between neighboring cells with a subpopulation possessing highly 217 concentrated GLP1R clusters (Fig. 5f).

Finally, to test whether LUXendin645 and LUXendin651 would be capable of tracking 218 GLP1Rs in live cells, we performed single-molecule microscopy experiments in which 219 individual receptors labeled with either fluorescent probe were imaged by total internal 220 reflection fluorescence (TIRF) microscopy.^{37,38} Both probes allowed GLP1R to be tracked at 221 the single-molecule level in CHO-K1-SNAP_GLP1R cells, but brightness and bleaching 222 precluded longer recordings with LUXendin645 (Fig. 5g and Supplementary Movies S2, 223 224 S3). By combining single-particle tracking with LUXendin651, we were able to show that most GLP1Rs diffuse rapidly at the membrane (Fig. 5g and Supplementary Movie S4). 225 However, a mean square displacement (MSD) analysis³⁷ revealed a high heterogeneity in 226

the diffusion of GLP1Rs on the plasma membrane, ranging from virtually immobile receptorsto some displaying features of directed motion (superdiffusion) (Fig. 5h).

229 Altering fluorophore to produce LUXendin555 confers different ligand behavior

230 Lastly, we explored whether swapping the far-red Cy5/SiR for a TMR dye would be tolerated to obtain a spectrally orthogonal probe, termed LUXendin555. Labeling was detected in 231 YFP-AD293-SNAP GLP1R (Fig. 6a) but not YFP-AD293 cells (Fig. 6b). However, we 232 noticed a more punctate LUXendin555 staining pattern when viewed at high-resolutions 233 (Fig. 6c). Further experiments with MIN6 cells and islets showed similar internalization of the 234 GLP1R (Fig. 6d), suggesting that LUXendin555 acts as an agonist, presumably via 235 interactions mediated by the ectodomain. This was confirmed using cAMP assays where 236 **LUXendin555** was found to potently activate GLP1R signaling (EC_{50} (cAMP) = 129.8 nM; 237 95% CI = 56.9-296.2) (Fig. 6e). Intriguingly, LUXendin555 potency could be further 238 increased using a PAM (EC_{50} (cAMP) = 28.4 nM; 95% CI = 11.3-71.8) (Fig. 6f), suggesting a 239 unique binding conformation at the orthosteric site compared to agonists such as 240 Exendin4(1-39), which cannot be allosterically-modulated.³⁰ As for the other probes, 241 **LUXendin555** was unable to label *Glp1r^{(GE)-/-}* islets (Fig. S2). 242

243 LUXendins label islets in vivo

We thought that the high quantum yield of TMR, coupled with good two-photon cross-section 244 and agonistic behaviour might suit LUXendin555 well to in vivo imaging where maintenance 245 of normoglycemia under anaesthesia can be an advantage for some experiments. Two-246 photon imaging was applied to an anaesthetized mouse to allow visualization of the intact 247 248 pancreas, exposed through an abdominal incision (Fig. 6g). Vessels and nuclei were first 249 labeled using FITC-dextran and Hoechst before injecting LUXendin555 intravenously. Labeling occurred rapidly within 5 min post-injection, produced intense membrane staining 250 confined to the islet where GLP1R is expressed (Fig. 6h), and normoglycemia was 251 maintained (250 mg/dl). No obvious internalization could be seen, most likely reflecting the 252 253 time of exposure to LUXendin555, as well as the concentration achieved in vivo at the islet.

254 **DISCUSSION**

In the present study, we synthesize and validate far-red fluorescent labels, termed 255 LUXendins for the real-time detection of GLP1R in live cells. Nanomolar concentrations of 256 LUXendin645 and LUXendin651 led to intense membrane-labeling of the GLP1R, with best 257 258 in class tissue penetration and signal-to-noise ratio, as well as super-resolution capability. Notably, LUXendin645 and LUXendin651 did not activate the GLP1R unless agonist 259 activity is conferred with the widely-available PAM BETP. LUXendin645 and LUXendin651 260 are highly specific, as shown using a novel CRISPR-Cas9 mouse line lacking GLP1R 261 expression. Lastly, the analogous compound LUXendin555 bearing a different fluorophore 262 unusually displays agonistic activity, expanding the color palette and activity profile without 263 changing the peptidic pharmacophore. 264

Compared to present chemical biology approaches, LUXendins possess a number of 265 advantages for GLP1R labeling, which generally rely on Exendin4(1-39) labeled with for 266 instance Cy3, Cy5 or FITC.^{19-21,30} Firstly, the use of an antagonist encourages receptor 267 recycling back to the membrane and retains receptor at the cell surface, which likely 268 increases detection capability. Secondly, the GLP1R is not activated, meaning that results 269 can be interpreted in the absence of potentially confounding cell signaling, such as that 270 expected with agonists.¹⁹ Thirdly, Cy5 occupies the far-red range, leading to less 271 272 background fluorescence, increasing depth penetration due to reduced scatter, and avoiding the use of more phototoxic wavelengths.³⁹ Together, these desirable properties open up the 273 possibility to image expression and trafficking of native GLP1R over extended periods of 274 time, when LUXendins are used in conjunction with a PAM. 275

To test the specificity of LUXendins, we used CRISPR-Cas9 genome-editing to globally 276 277 knock out the GLP1R in mice. Protein deletion was confirmed by absence of detectable 278 GLP1R signal following labeling with monoclonal antibody, LUXendin555, LUXendin645 and LUXendin651. While Glp1r^{-/-} animals already exist and have made important 279 contributions to our understanding of incretin biology, they were produced using a targeted 280 mutation to replace exons encoding transmembrane regions 1 and 3 (encoded by exons 5 281 and 7), presumably leading to deletion of the introns in between (~6.25 kb).⁴⁰ By contrast, 282 *Glp1r*^{(GE)-/-} mice possess intact introns. Since introns contain regulatory elements, such as 283 distant-acting enhancers⁴¹, miRNAs⁴² and lncRNAs,⁴³ their loss in transgenic knockouts 284 could have wider influence on the transcriptome. GLP1R knock-out mice might therefore be 285 useful alongside conventional approaches for validating GLP1R reagents, including 286 antibodies, agonist and antagonist, and derivatives thereof. 287

Demonstrating the excellent sensitivity of the Cy5-linked LUXendin645 in particular, we 288 were able to detect GLP1R in ~20% of α -cells. Understanding α -cell GLP1R expression 289 patterns is important because incretin-mimetics reduce glucagon secretion,⁴⁴ which would 290 otherwise act to aggravate blood glucose levels. However, previous studies using 291 292 antibodies, reporter animals and agonist-fluorophores have shown only ~1-10% GLP1R expression in mouse and rat α -cells, in line with the low transcript abundance^{7,19,33,45}, despite 293 reports that GLP-1 can directly suppress glucagon release.^{34,46} Our data are in general 294 concordance with these findings, but provide a 2-fold increase in detection capability. This 295 296 improvement is likely related to the superior SNR of LUXendin645, which increases the ability to resolve relatively low levels of GLP1R. A recent report showed GLP1R expression 297 298 in ~80% of α -cells using a novel antibody raised against the *N*-terminal region, with both 299 membrane and cytosolic staining evident⁴⁷. While the reasons for this discrepancy are 300 unknown, it should be noted that **LUXendin645** binds the orthosteric site and so reports the 301 proportion of GLP1R that is "signaling competent".^{7, 19, 32}.

LUXendin645 showed excellent signal-to-noise ratio using conventional 302 Since 303 epifluorescence, it was highly amenable to SRRF analysis. As such, LUXendin645 and its congeners open up the possibility to image the GLP1R at super-resolution using simple 304 widefield microscopy available in most laboratories. For stimulated emission depletion 305 306 (STED) microscopy experiments, Cy5 was replaced with SiR to give LUXendin651. STED imaging showed that endogenous GLP1R possess a higher structural order, namely 307 organization into nanodomains at the cell membrane. The presence of nanodomains under 308 non-stimulated conditions might reflect differences in palmitoylation, which has recently been 309 shown to influence GLP1R membrane distribution in response to agonists.⁴⁸ Notably, a 310 subpopulation of β-cells appeared to possess highly-concentrated GLP1R clusters. It will be 311 312 important in the future to investigate whether this is a cell autonomous heterogenous trait, or instead reflects biased orientation of membranes toward specific β -cells. Lastly, both 313 LUXendin645 and LUXendin651 allowed GLP1Rs to be imaged in live cells by single-314 molecular microscopy, revealing variability in their diffusion at the plasma membrane. 315 Particle tracking analyses segregated GLP1R into four different populations based upon 316 diffusion mode, in keeping with data from beta adrenergic receptors.³⁷ Together, these 317 experiments provide the first super-resolution characterization of a class B GPCR and 318 suggest a degree of complexity not readily appreciated with previous approaches. 319

Intriguingly, we saw that swapping Cy5 for a TMR moiety to give **LUXendin555** completely 320 changed the pharmacological behavior. The reasons for this are unknown, but we speculate 321 that the rhodamine scaffold engages a secondary binding site in the GLP1R ectodomain, 322 leading to activation. This finding is remarkable because it suggests that the agonist \rightarrow 323 antagonist switch that occurs following removal of eight N-terminal amino acids (as 324 physiologically mediated by the protease DPP-4)⁴⁹ can be counteracted simply by installing 325 a C-terminal linked rhodamine fluorophore, with implications for the design of more stable 326 327 GLP1R activators. More generally, this shift in compound behaviour following a fluorophore modification serves as another instructive example for the thorough validation of all new 328 chemical labels.⁵⁰ Nonetheless, LUXendin555 possessed advantageous properties for in 329 vivo imaging including maintenance of relatively stable glycemia, good two-photon cross-330 section and high quantum yield. 331

In summary, we provide a comprehensively-tested and unique GLP1R detection toolbox consisting of far-red antagonist labels, **LUXendin645** and **LUXendin651**, an agonist **LUXendin555**, and knockout $Glp1r^{(GE)-/-}$ animals. Using these freely-available probes, we provide an updated view of GLP1R organization, with relevance for the treatment of complex metabolic diseases such as obesity and diabetes, as well as production of more stable GLP1R activators. Thus, the stage is set for visualizing GLP1R in various tissues using a range of imaging techniques, as well as the production of novel peptidic labels and agonists.

340 METHODS

341 Synthesis

Solid-phase peptide synthesis of S39C-Exendin4(9-39) was performed as previously 342 reported.²⁹ Maleimide-conjugated-6-TMR, -6-SiR and -Cy5 were obtained by TSTU 343 activation of the corresponding acids and reaction with 1-(2-amino-ethyl)-pyrrole-2,5-dione 344 (TFA salt, Aldrich). Fluorophore coupling via thiol-maleimide chemistry to peptides was 345 performed in PBS. All compounds were characterized by HRMS and purity was assessed to 346 be >95% by HPLC. Extinction coefficients were based upon known manufacturer bulk 347 material measures for TMR-Mal, Cy5-Mal (both Lumiprobe) and SiR-Mal (Spirochrome). 348 Details for synthesis including further characterization of all LUXendins are detailed in the 349 Supporting Information. LUXendin555, LUXendin651 and LUXendin645 are freely 350 available for academic use upon request. 351

352

353 Cell culture

AD293 cells (Agilent) were maintained in Dulbecco's Modified Eagles medium (DMEM) 354 355 supplemented with 10% fetal calf serum (FCS), 1% *L*-glutamine and 1% penicillin/streptomycin. CHO-K1 cells (a kind gift from Dr Ben Jones, Imperial College 356 London) stably expressing the human SNAP GLP1R (Cisbio) (CHO-K1-SNAP GLP1R) 357 were maintained in DMEM supplemented with 10% FCS, 1% penicillin/streptomycin, 500 358 µg/mL G418, 5 mM *D*-glucose, 10 mM HEPES and 1% nonessential amino acids. MIN6 β-359 cells (a kind gift from Prof. Jun-ichi Miyazaki, Osaka University) were maintained in DMEM 360 361 supplemented with 15% FCS, 25 mM D-glucose, 71 µM BME, 2 mM L-glutamine, 100 U/mL penicillin, and 100 µg/mL streptomycin. INS1 832/3 CRISPR-deleted for the endogenous 362 GLP1R locus (a kind gift from Dr. Jacqui Naylor, MedImmune)⁵¹ were transfected with 363 human SNAP_GLP1R, before FACS of the SNAP-Surface488-positive population and 364 selection using G418.48 The resulting SNAP_GLP1R_INS1^{GLP1R-/-} cells were maintained in 365 RPMI-1640 supplemented with 10% FBS, 10 mM HEPES, 2 mM L-glutamine, 1 mM 366 367 pyruvate, 72 μM β-mercaptoethanol, 1% penicillin/streptomycin and 500 μg/mL G418.

368 Animals

Glp1r^{(GE)-/-}: CRISPR-Cas9 genome-editing was used to introduce a single base pair deletion 369 into exon 1 of the *Glp1r* locus. Fertilized eggs of female Cas9-overexpressing mice (strain 370 Gt(ROSA)26Sor^{tm1.1(CAG-cas9*,-EGFP)Fezh}/J) were harvested following super-ovulation. Modified 371 single-guide RNA (Synthego) targeting exon 1 of Glp1r and a single-stranded repair-372 373 template were injected at 20 ng/µl into the pronucleus of embryos at the 1-cell stage. In 374 culture, 80% of embryos reached the 2-cell stage and were transplanted into surrogate mice. The targeted locus of offspring was analyzed by PCR and sequencing. Besides the insertion 375 of the repair template, deletions of up to 27 nucleotides could be detected in 2 out of 6 376 offspring. Design of the repair template will be described elsewhere. Off-target sites were 377 predicted using the CRISPR Guide Design Tool (crispr.mit.edu). Loci of the top ten off-target 378 hits were amplified by PCR and analyzed via Sanger sequencing. Founder animals carrying 379 380 alleles with small deletions were backcrossed to wild type animals (strain C57BL/6J) for 1-2 381 generations to outbreed affected off-targets and then bred to homozygosity. Animals with the 382 larger deletion of 27 nucleotides were not taken forward, as GLP1R protein was still present. Animals were born in Mendelian ratios and genotyping was performed using Sanger 383

sequencing. Animals were bred as heterozygous pairs to ensure $Glp1r^{+/+}$ littermates. *Glp1r*^{(GE)-/-} animals are freely available for academic use, subject to a Material Transfer Agreement.

Ins1Cre^{Thor};R26^{mT/mG}: To allow identification of β- and non-β-cells, *Ins1Cre^{Thor} a*nimals with Cre knocked-in at the *Ins1* locus (strain B6(Cg)-*Ins1^{tm1.1(cre)Thor}/J*) were crossed with *R26^{mT/mG}* reporter mice (strain B6.129(Cg)-*Gt(ROSA)26Sor^{tm4(ACTB-tdTomato,-EGFP)Luo/J*). Cre-dependent excision of the floxed allele results in deletion of tdTomato, expression of membranelocalized GFP and thus identification of recombined and non-recombined cells.}

All studies were performed with 6-12 week old male and female animals, and regulated by the Animals (Scientific Procedures) Act 1986 of the U.K. Approval was granted by the University of Birmingham's Animal Welfare and Ethical Review Body.

395 Islet isolation

Islets were isolated from male and female $Glp1r^{(GE)-/-}$ and $Ins1Cre^{Thor};R26^{mT/mG}$ mice, as well as CD1 wild-type animals, maintained under specific-pathogen free conditions, with *ad lib* access to food and water. Briefly, animals were humanely euthanized before injection of collagenase 1 mg/mL (Serva NB8) into the bile duct. Following removal of the inflated pancreas and digestion for 12 min at 37 °C, islets were separated using a Histopaque (Sigma-Aldrich) gradient. Islets were cultured in RPMI medium containing 10% FCS, 100 units/mL penicillin, and 100 µg/mL streptomycin.

403 **Binding and potency assays**

Binding assays were performed in transiently-transfected YFP-AD293-SNAP_GLP1R cells 404 (using PolyJet reagent; SignaGen). Increasing concentrations of compound were applied for 405 60 min, before imaging using a Zeiss LSM880 meta-confocal microscope configured with 406 GaAsP detectors and 10x/0.45 W, 40x/1.00 W and 63x/1.20 W objectives. YFP, TMR 407 (LUXendin555) and Cy5 (LUXendin645) were excited using λ = 514 nm, λ = 561 nm and λ 408 = 633 nm lasers, respectively. Emitted signals were captured at λ = 519–574 nm, λ = 570– 409 641 nm and λ = 638-759 nm for YFP, TMR (LUXendin555) and Cy5 (LUXendin645), 410 respectively. Control experiments were performed in YFP-AD293-SNAP cells, as above. 411

Potency for cAMP generation and inhibition was tested in heterologous expression systems, comprising either stable CHO-K1-SNAP_GLP1R cells or transiently-transfected YFP-AD293-SNAP_GLP1R cells, as previously described.²⁹ Briefly, cells were incubated with increasing concentrations of compound +/- allosteric modulator for 30 min, before harvesting, lysis and measurement of cAMP using cAMP-GloTM Assay (Promega), according to the manufacturer's instructions. EC_{50} values were calculated using log concentrationresponse curves fitted with a three-parameter equation.

419 Live imaging

Islets were incubated for 1 h at 37 °C in culture medium supplemented with either 100-250 nM LUXendin555, 50-100 nM LUXendin645 or 100 nM LUXendin651, based upon binding assays. Islets were imaged using either a Zeiss LSM780 or LSM880 microscope, as above (LUXendin651 was imaged as for LUXendin645). *Ins1Cre^{Thor};R26^{mT/mG}* islets were excited at λ = 488 nm (emission, λ = 493-555 nm) and λ = 561 nm (emission, λ = 570-624 nm) for

425 mGFP and tdTomato, respectively. Two-photon imaging of **LUXendin645** was performed 426 using a Zeiss LSM 880 NLO equipped with a Spectra-Physics Insight X3 femtosecond-427 pulsed laser and 20x/1.00 W objective. Excitation was performed at λ = 800 nm and emitted 428 signals detected at λ = 638-759 nm.

429 cAMP imaging

Islets were transduced with adenovirus harboring the FRET sensor, Epac2-camps, before 430 imaging using a Crest X-Light spinning disk system coupled to a Nikon Ti-E base and 431 10x/0.4 NA objective. Excitation was delivered at λ = 430–450 nm using a Lumencor Spectra 432 X light engine. Emitted signals were detected at λ = 460–500 and λ = 520–550 nm for 433 Cerulean and Citrine, respectively, using a Photometrics Delta Evolve EM-CCD. Imaging 434 was performed in HEPES-bicarbonate buffer, containing (in mmol/L) 120 NaCl, 4.8 KCl, 24 435 NaHCO₃, 0.5 Na₂HPO₄, 5 HEPES, 2.5 CaCl₂, 1.2 MgCl₂, and 3-17 *D*-glucose. Vehicle 436 (H₂0), Exendin4(1-39) (10-20 nM) or Liraglutide (10 nM) were applied at the indicated time 437 points, with forskolin (10 μ M) acting as a positive control. 438

439 Immunostaining

LUXendin555- or LUXendin645-treated cells or tissue were fixed for 60 min in 4% 440 paraformaldehyde. Primary antibodies were applied overnight at 4 °C in PBS + 0.1% Triton 441 442 + 1% BSA. Secondary antibodies were applied in the same buffer for 1 h at room 443 temperature, before mounting on slides using Vectashield Hardset containing DAPI. Primary antibodies were mouse monoclonal anti-GLP1R 1:30 (Iowa DHSB; mAb #7F38), rabbit anti-444 insulin 1:500 (Cell Signaling Technology, #3014), mouse monoclonal anti-glucagon 1:2000 445 (Sigma-Aldrich, #G2654) and mouse anti-somatostatin 1:5000 (Invitrogen, #14-9751-80). 446 Secondary antibodies were goat anti-mouse Alexa Fluor 568 and donkey anti-rabbit DyLight 447 488 1:1000. Images were captured using an LSM880 meta-confocal microscope. Alexa 448 Fluor 488 and Alexa Fluor 568 were excited at λ = 488 nm and λ = 568 nm, respectively. 449 Emitted signals were detected at λ = 500–550 nm (Alexa Fluor 488) and λ = 519–574 nm 450 (Alexa Fluor 568). 451

452 Super-resolution microscopy

SRRF: MIN6 were treated with LUXendin645 before fixation and mounting on slides using 453 454 Vectashield Hardset containing DAPI. Imaging was performed using a Crest X-Light spinning disk system in bypass (widefield) mode. Excitation was delivered at λ = 640/30 nm 455 through a 63x/1.4 NA objective using a Lumencor Spectra X light engine. Emission was 456 457 collected at λ = 700/75 nm using a Photometrics Delta Evolve EM-CDD. A 1000 image 458 sequence was captured (~ 2 min) before offline super resolution radial fluctuation (SRRF) analysis to generate a single super-resolution snapshot using the NanoJ plugin for ImageJ 459 (NIH).³⁶ 460

461 Stimulated emission depletion (STED) microscopy: MIN6 cells were treated with 100, 200 462 and 400 nM **LUXendin651** before fixation (4% paraformaldehyde, 20 min). Cells were 463 mounted in Mowiol supplemented with DABCO and imaged on an Abberior STED 464 775/595/RESOLFT QUAD scanning microscope (Abberior Instruments GmbH, Germany) 465 equipped with STED lines at λ = 595 and λ = 775 nm, excitation lines at λ = 355 nm, 405 nm, 466 485 nm, 561 nm, and 640 nm, spectral detection, and a UPIanSApo 100x/1.4 oil immersion 467 objective lens. Following excitation at λ = 640 nm, fluorescence was acquired in the spectral 468 window λ = 650-800 nm. Deconvolution was performed with Richardson-Lucy algorithm on Imspector software. FWHM was measured on raw data and calculated using OriginPro 2017 469 software with Gaussian fitting (n=15 profiles). Spatial GLP1R expression patterns were 470 analyzed using the F- and G-functions, where F = distance between an object of interest and 471 its nearest neighbor, and G = distance from a given position to the nearest object of interest 472 (FIJI Spatial Statistic 2D/3D plugin).⁵² Both measures were compared to a random 473 distribution of the same measured objects, with a shift away from the mean +/- 95% 474 475 confidence intervals indicating a non-random or clustered organization (*i.e.* more space or 476 smaller distance between objects).

Single-molecule microscopy: For single-molecule experiments, CHO-K1-SNAP_GLP1R cells 477 were seeded onto 25 mm clean glass coverslips at a density of 3x 10⁵ per well. On the 478 following day, cells were labeled in culture medium with 100 pM LUXendin645 or 479 LUXendin651 for 20 min. At the end of the incubation, cells were washed 3x 5 min in culture 480 481 medium. Cells were then imaged at 37 °C in phenol-red free Hank's balanced salt solution, using a custom built total internal reflection fluorescence microscope (Cairn Research) 482 based on an Eclipse Ti2 (Nikon, Japan) equipped with an EMCCD camera (iXon Ultra, 483 484 Andor), 637 nm diode laser, and a 100x oil-immersion objective (NA 1.49, Nikon). Image sequences were acquired with an exposure time of 60 ms. Single-molecule image 485 sequences were analyzed with an automated particle detection software (utrack) in the 486 MATLAB environment, as previously described.^{53,54}. Data were further analyzed using 487 custom MATLAB algorithms, as previously described.^{37,55} 488

489 **Two-photon** *in vivo* imaging

A 7 week old female C57BL/6J mouse was anesthetized with isoflurane and a small, 1 cm 490 vertical incision was made at the level of the pancreas. The exposed organ was orientated 491 492 underneath the animal and pressed against a 50 mm glass-bottom dish for imaging on an 493 inverted microscope. Body temperature was maintained using heat pads and heating 494 elements on the objective. The mouse received Hoechst 33342 (1 mg/kg in PBS) to label nuclei, a 150 kDalton fluorescein-conjugated dextran (1 mg/kg in PBS) to label vasculature, 495 and 75 uL of 30 µM LUXendin555 via retro-orbital IV injection. Images were collected using 496 a Leica SP8 microscope, equipped with a 25x/0.95 NA objective and Spectra Physics 497 MaiTai DeepSee mulitphoton laser. Excitation was delivered at λ = 850 nm, with signals 498 collected with a HyD detector at λ = 460/50, λ = 525/50, λ = 624/40 nm for Hoechst, FITC 499 500 and LUXendin555, respectively. All in vivo imaging experiments were performed with approval and oversight from the Indiana University Institutional Animal Care and Use 501 502 Committee (IACUC).

503 Statistical analyses

504 Measurements were performed on discrete samples unless otherwise stated. All analyses 505 were conducted using GraphPad Prism software. Unpaired or paired Students t-test was 506 used for pairwise comparisons. Multiple interactions were determined using one-way 507 ANOVA followed by Dunn's or Sidak's posthoc tests (accounting for degrees of freedom).

508 Data availability

509 The datasets generated during and/or analysed during the current study are available from

510 the corresponding author on reasonable request.

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671 CONTRIBUTIONS

J.A., K.J., T.P., J.B. and D.J.H. devised the studies. J.A., A.A., D.N., N.H.F.F., F.B.A., S.T.,
Z.S., B.H., A.T., T.P., J.B. and D.J.H. performed experiments and analyzed data. J.A. and
A.B. generated novel mice. B.J.J. provided reagents. Z.K. and E.D'E. performed superresolution imaging. C.A.R. and A.K.L. performed *in vivo* imaging experiments. D.C.
supervised and analyzed single-molecule microscopy experiments. J.A., K.J., T.P., J.B. and
D.J.H. supervised the work. J.A., T.P., J.B. and D.J.H. wrote the manuscript with input from
all the authors.

679 COMPETING INTERESTS

680 The authors declare no conflict of interest.

682 FIGURE LEGENDS

Figure 1: Sequence and structure of LUXendin555, LUXendin651 and LUXendin645 683 bound to GLP1R. LUXendins are based on the antagonist Exendin4(9-39), shown in 684 complex with GLP1R. The label can be any dye, such as TMR (top), SiR (middle) or Cy5 685 686 (bottom) to give LUXendin555, LUXendin651 and LUXendin645, respectively. The model was obtained by using the cryo-EM structure of the activated form of GLP1R in complex with 687 a G protein (pdb: 5VAI)⁵⁶, with the G protein and the 8 *N*-terminal amino acids of the ligand 688 removed from the structure while mutating S39C and adding the respective linker. Models 689 were obtained as representative cartoons by the in-built building capability of PyMOL (Palo 690 691 Alto, CA, USA) without energy optimization. Succinimide stereochemistry is unknown and neglected for clarity. 692

693

Figure 2: LUXendin645 binding, signaling and labeling. a, Exendin4(9-39), its S39C 694 mutant and LUXendin645 display similar antagonistic properties (n = 3 replicates). b, 695 696 LUXendin645 does not activate the GLP1R in CHO-K1-SNAP_GLP1R cells unless the 697 positive allosteric modulator (PAM) BETP is present (Exendin4; +ve control) (n = 3 assays). c, LUXendin645 labels CHO-K1-SNAP_GLP1R cells with a maximal labeling achieved at 698 100 nM. d, LUXendin645 signal can be detected in YFP-AD293-SNAP_GLP1R but not 699 YFP-AD293 cells (scale bar = $212.5 \mu m$) (n = 3 assays). **e**, Representative confocal z-stack 700 (1 µm steps) showing penetration of LUXendin645 deep into a live pancreatic islet (x-y, x-z 701 702 and y-z projections are shown) (n = 4 islets) (scale bar = 37.5 μ m). f, As for (e), but twophoton z-stack (1 µm steps) showing the entire volume of an islet labeled with LUXendin645 703 704 (scale bar = 37.5 μ m) (n = 9 islets). **g** and **h**, GLP1R is internalized in MIN6 cells when 705 agonist activity is conferred on LUXendin645 using the positive allosteric modulator BETP 706 (scale bar = 21 μ m) (n = 5 images, 693-722 cells; Student's unpaired t-test) (Bar graph 707 shows mean ± SEM). i and j, LUXendin645 signal can be detected even following fixation and co-localizes with a specific monoclonal antibody against the GLP1R in both islets (n =708 13 islets) and MIN6 β -cells (n = 6 images, 543 cells) (scale bar = 26 μ m). **k**, The superior 709 signal-to-noise-ratio of LUXendin645 allows more membrane detail to be visualized 710 compared to antibody (scale bar = $12.5 \mu m$). Representative images are shown, with a blue 711 bar indicating the location of intensity-over-distance measures (the islet was co-stained with 712 LUXendin645 + antibody to allow direct comparison) (n = 13 islets). I and m, LUXendin645 713 co-localizes with the SNAP label, Surface 488, in SNAP hGLP1R-INS1^{GLP1-/-}, which are 714 deleted for the endogenous Glp1r (I). Pre-treatment with Exendin4(9-39) to internalize the 715 GLP1R reduces LUXendin645-labeling (m) (a wash-step was used prior to application of 716 the label) (scale bar = 10 μ m) (n = 4-5 images; 57-64 cells). Mean ± SE are shown. 717 **P<0.01. 718

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Figure 3: LUXendin645 is highly specific for the GLP1R. **a**, Schematic showing sgRNA targeting strategy for the production of $Glp1r^{(GE)-/-}$ mice. The sgRNA used targeted Glp1r and the double-strand break mediated by Cas9 lies within exon1 (capital letters); intron shown in gray. **b**, $Glp1r^{(GE)-/-}$ animals harbor a single-nucleotide deletion, as shown by sequencing traces. **c**, Body weights were similar in male 8 weeks old $Glp1r^{+/+}$, $Glp1r^{(GE)+/-}$ and $Glp1r^{(GE)-/-}$ littermates (n = 4–8 animals; one-way ANOVA with Bonferroni's post hoc test; F = 0.7982, DF = 2) (Bar graph shows mean ± SEM) **d**, The incretin-mimetic Exendin4(1-39) (10 nM) is

unable to significantly potentiate glucose-stimulated insulin secretion in $Glp1r^{(GE)-/-}$ islets (n = 727 6 replicates; two-way ANOVA with Sidak's post hoc test; F = 14.96, DF = 2 for $Glp1r^{+/+}$, F = 728 2.968, DF = 2 for $Glp1r^{(GE)-/-}$) (Bar graph shows mean ± SEM) **e**, Liraglutide (Lira) does not 729 stimulate cAMP beyond vehicle (Veh) control in *Glp1r^{(GE)-/-}* islets, measured using the FRET 730 probe Epac2-camps (traces represent mean ± SEM) (n = 14-17 islets). f, cAMP area-under-731 the-curve (AUC) quantification showing absence of significant Liraglutide-stimulation in 732 $Glp1r^{(GE)-/-}$ islets (n = 14–17 islets; Kruskal-Wallis test with Dunn's post hoc test; Kruskal-733 Wallis statistic = 7.6, DF = 2) (Box and Whiskers plot shows min-max and median) 734 (representative images displayed above each bar). g, LUXendin645 and GLP1R antibody 735 labeling is not detectable in $Glp1r^{(GE)-/-}$ islets (scale bar = 40 µm) (n = 12-14 islets for each 736 genotype). *P<0.05, **P<0.01 and NS, non-significant. 737

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Figure 4: LUXendin645 reveals GLP1R expression in a subpopulation of α -cells. a-c, 739 LUXendin645 labeling is widespread throughout the intact islet, co-localizing predominantly 740 with β -cells (a) and α -cells (b), but less so with δ -cells (c) stained for insulin, glucagon and 741 somatostatin, respectively (n = 7–9 islets) (scale bar = 26 μ m). **d**, Following dissociation of 742 743 islets into cell clusters, LUXendin645 labeling can be more accurately quantified (arrows highlight cells selected for zoom-in) (scale bar = 26 µm). e, Zoom-in of (d) showing a 744 LUXendin645- (left) and LUXendin645+ (right) α -cell (arrows highlight non-labeled cell 745 746 membrane, which is not bounded by a β -cell) (scale bar = 26 µm). f, Box-and-whiskers plot 747 showing proportion of β -cells (INS) and α -cells (GLU) co-localized with LUXendin645 (n = 5-6 images, 12 cell clusters) (Max-min shown together with the median). g, 748 Ins1Cre^{Thor};R26^{mT/mG} dual fluorophore reporter islets express tdTomato until Cre-mediated 749 replacement with mGFP, allowing identification of β -cells (~80% of the islet population) and 750 non- β -cells for live imaging (scale bar = 26 μ m). **LUXendin645** highlights GLP1R expression 751 752 in nearly all β -cells but relatively few non- β -cells (n = 24 islets, 809 cells). h, As for (g), but a zoom-in showing GLP1R expression in some non-β-cells (left) together with quantification 753 754 (right) (arrows show LUXendin645-labeled non- β cells) (scale bar = 5 μ m) (Box and 755 Whiskers plot shows min-max and median).

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757 Figure 5: LUXendin651 and LUXendin645 allow nanoscopic detection of GLP1R distribution and dynamics. a, LUXendin645 allows super-resolution snapshots of MIN6 β-758 cells using widefield microscopy combined with Super-Resolution Radial Fluctuations 759 (SRRF) (n = 3 images) (scale bar = 10 μ m). **b** and **c**, Confocal and STED snapshots of 760 endogenous GLP1R in LUXendin651-treated MIN6 cells at ~ 50 nm axial resolution. Note 761 the presence of punctate GLP1R expression as well as aggregation/clustering in images 762 captured above (b) and close to the coverslip (c) using STED microscopy (n = 3 images, 15 763 764 cells) (scale bar = $2 \mu m$). **d** and **e**, Spatial analysis of GLP1R expression patterns using the 765 F-function (d) and G-function (e) show a non-random distribution (red line) versus a random 766 model (black line; 95% confidence interval shown). f, Approximately 1 in 4 MIN6 β-cells possess highly concentrated GLP1R clusters (Bar graph shows mean ± SEM) (n = 3 images, 767 15 cells). g, Single molecule microscopy and tracking of LUXendin645- and LUXendin651-768 labeled GLP1R (n = 2 movies) (scale bar = 3 μ m). h, Mean square displacement (MSD) 769 analysis showing different GLP1R diffusion modes (representative trajectories are displayed) 770 (scale bar = 1 μ m). 771

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Figure 6: LUXendin555 displays agonist properties and allows in vivo labeling of 773 islets. a and b, LUXendin555 labels YFP-AD293_SNAP-GLP1R (a) but not YFP-AD293 (b) 774 controls (n = 3–4 assays) (10x scale bar = 213 μ m; 100x scale bar = 21 μ m). **c**, High 775 776 resolution snapshot of LUXendin555-labeling in MIN6 β -cells showing a punctate staining 777 pattern in the cytosol (n = 8 images, 142 cells) (scale bar = 9 μ m). d, Surface GLP1R expression is reduced in LUXendin555- compared to LUXendin645-treated islets 778 779 (representative images shown above each bar) (n = 5 islets; Student's unpaired t-test) (Bar graph shows mean ± SEM) (scale bar = 17 µm). e, LUXendin555 potently increases cAMP 780 levels in YFP-AD293 SNAP-GLP1R but not YFP-AD293 cells (n = 3 assays). f, Allosteric 781 modulation with BETP increases agonist activity of LUXendin555 (n = 3 assays). g, 782 Schematic depicting the two-photon imaging set up for visualization of the intact pancreas in 783 mice. h, Representative image showing that LUXendin555 labels cell membranes in an 784 islet surrounded by the vasculature *in vivo* (n = 2 islets from 1 mouse) (scale bar = 50 µm). 785 786 Mean \pm SE are shown. **P<0.01.

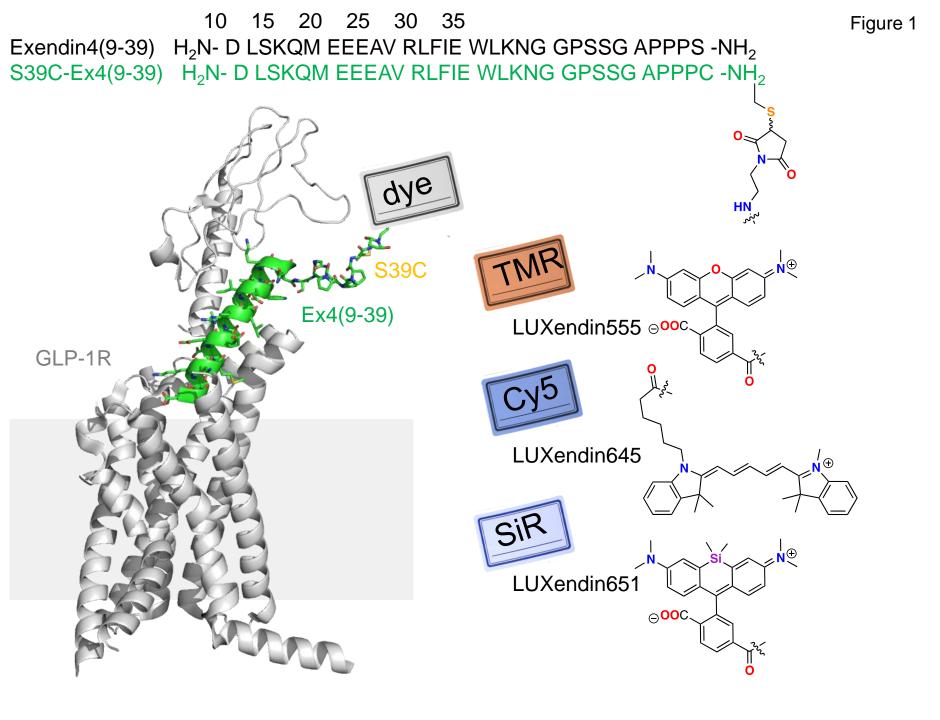
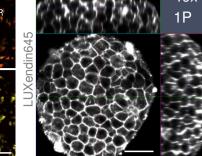
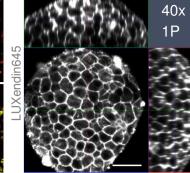
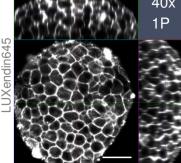


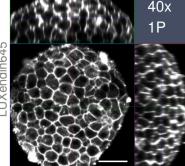
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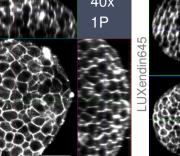


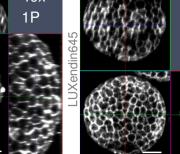


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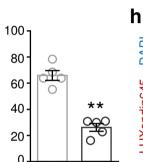








2P



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Log compound (M)

-GLP1 -GLP1 + Exendin4(9-39) -GLP1 + LUX645 -GLP1 + S39C

-7 -6

-8

а

150

cAMP (% min-max) 0 05 00 05

g

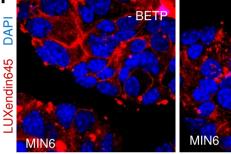
-11 -10 b

150

cAMP (% FSK max) 00 001 00 001

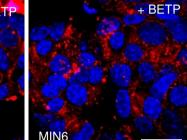
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← Exendin4 ← LUX645 - BETP ← LUX645 + BETP

2 -10 -8 Log compound (M)



C י125 י

% Labeling 75

-6

100

50 25-

0

d

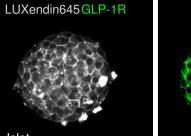
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YFP-AD293-SNAP

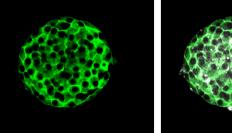
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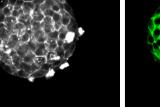
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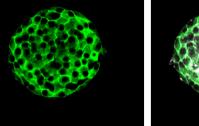
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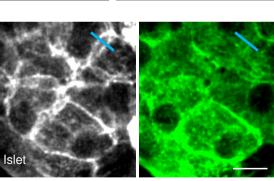
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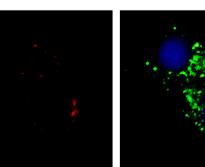


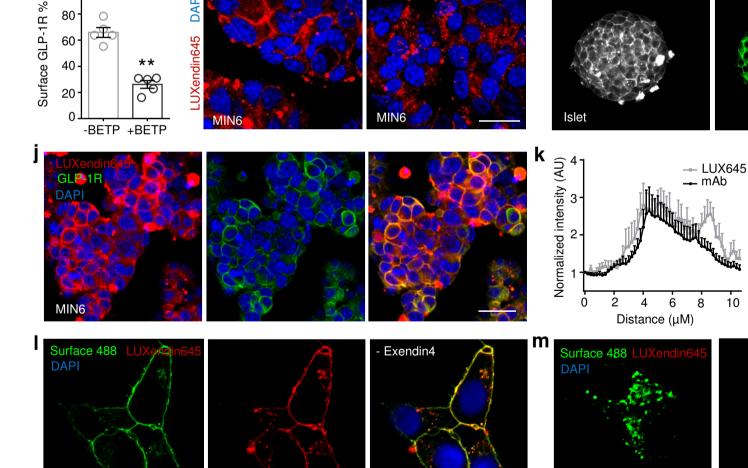


LUXendin645



GLP-1R





SNAP_GLP1R-INS1GLP1R-/-

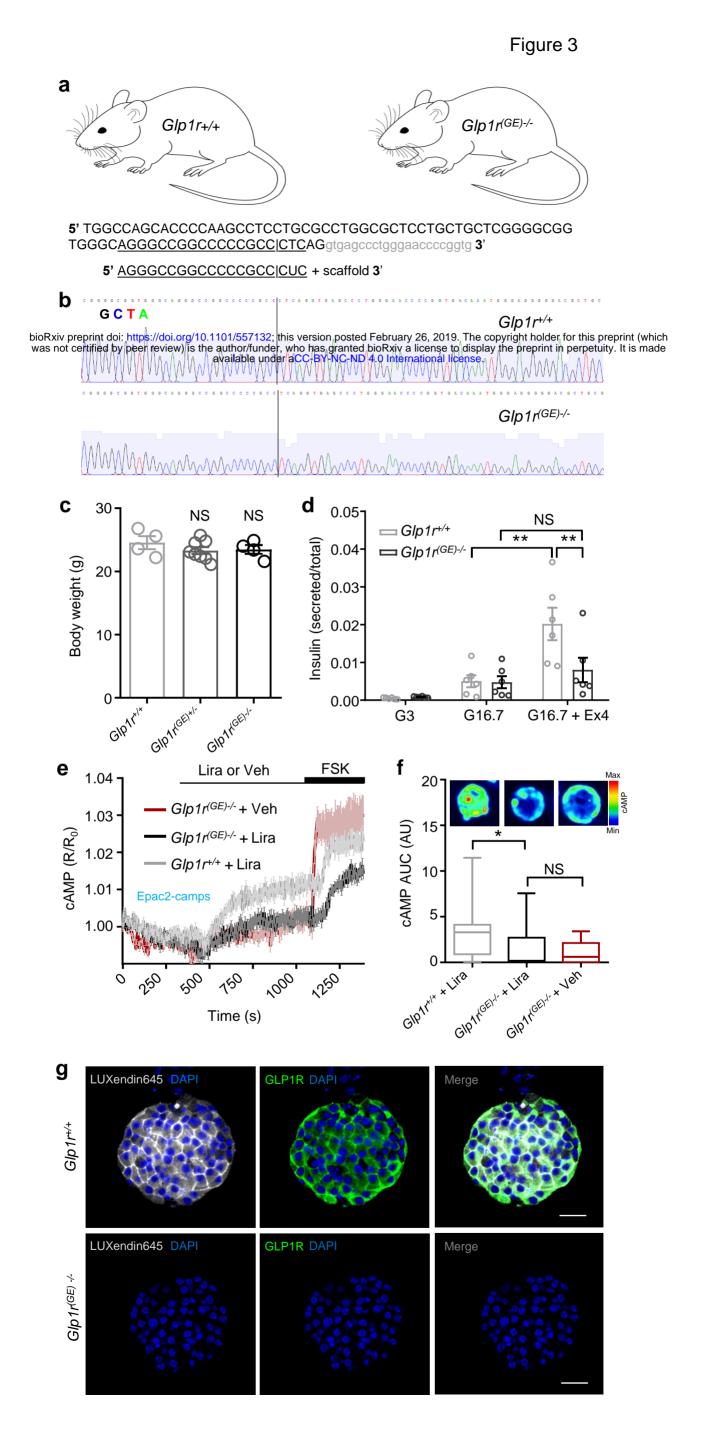


Figure 4

