

1 Opto-chemogenetic inhibition of L-type Cav1 channels in neurons  
2 through a membrane-assisted molecular linkage

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16 **Summary**

17 Acute, specific, and robust inhibition of L-type  $\text{Ca}^{2+}$  (Cav1) channels has been sought after for  
18 both research and therapeutic applications. Compared to other available Cav1 antagonists,  
19 genetically-encoded modulators, such as CMI (C-terminus mediated inhibition) peptides encoded  
20 by Cav1 DCT (distal C-terminus), hold great potentials due to its affirmative mechanisms of action  
21 on both gating and signaling. Here, we find that membrane-anchoring with a Ras tag could  
22 essentially help form a type of intramolecular-equivalent linkage, by which the tag anchored-  
23 peptide appears to dimerize with another protein or peptide on the membrane, supported by the  
24 evidence from patch-clamp electrophysiology and FRET imaging. We then design and implement  
25 the constitutive and inducible CMI modules, with appropriate dynamic ranges targeting the short  
26 and long variants of Cav1.3, both naturally occurring in neurons. Upon optical (infrared-  
27 responsive nanoparticles) and/or chemical (rapamycin) induction of FRB/FKBP binding, DCT  
28 peptides with no CMI in the cytosol acutely translocate onto the membrane via FRB-Ras, where  
29 the physical linkage requirement could be fulfilled. The peptides robustly produce acute and  
30 potent inhibitions on both recombinant Cav1.3 channels and neuronal Cav1 activities, and thus  
31 the  $\text{Ca}^{2+}$  influx-neuritogenesis coupling. Validated through opto-chemogenetic induction, this  
32 prototype demonstrates channel modulation via membrane-assisted molecular linkage, promising  
33 broad applicability to diverse membrane proteins.

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35 **Keywords:** voltage-gated calcium channels, C-terminus mediated inhibition, membrane-  
36 anchoring Ras tag, rapamycin-mediated heterodimerization, opto-chemogenetics

37

38 **Introduction**

39 L-type voltage-gated (Cav1.1-1.4) calcium channels are membrane proteins that mediate  $\text{Ca}^{2+}$   
40 influx into excitable cells in response to transmembrane potentials <sup>1,2</sup>. Cav1 channels play critical  
41 roles in a variety of pathophysiological processes related to muscle contraction, vesicle secretion,  
42 and gene transcription in cardiomyocytes or neurons <sup>3</sup>. In particular, Cav1.3 and its close relative  
43 Cav1.2 are involved in the diseases (channelopathy) such as sinoatrial node dysfunction and  
44 deafness (SANDD) syndrome <sup>4,5</sup>, adrenal hypertension <sup>6</sup>, and Timothy syndrome <sup>7,8</sup>, all of which  
45 are due to the mutations on these channel genes. Cav1.3 and Cav1.2 are also implicated in  
46 neurodegenerative diseases including Parkinson's disease and Alzheimer's disease <sup>9,10</sup>.  
47 Therefore, Cav1 agonists and antagonists have drawn significant interest and attention in both  
48 fundamental research and therapeutic development <sup>11-13</sup>.

49 C-terminus mediated inhibition (CMI) is one emerging modality of Cav1 antagonism <sup>14-17</sup>,  
50 which is closely related to calmodulin (CaM) modulation of the channels <sup>15</sup>. Calmodulin, a  $\text{Ca}^{2+}$ -  
51 binding protein containing EF-hands, is the molecular moderator of  $\text{Ca}^{2+}$ -dependent inactivation  
52 (CDI); and its  $\text{Ca}^{2+}$ -free form (apoCaM) is able to upregulate channel activation. Upon  
53 depolarization, the apoCaM-bound channel opens to induce  $\text{Ca}^{2+}$  influx and subsequently  
54 inactivates by conformational rearrangements associated with  $\text{Ca}^{2+}$ -bound CaM ( $\text{Ca}^{2+}/\text{CaM}$ ). It  
55 has been proposed that the Cav1 channel is switched between the two states of high- versus low-  
56 opening controlled by apoCaM and  $\text{Ca}^{2+}/\text{CaM}$  respectively <sup>14,18,19</sup>. In this context, CMI sets the  
57 channel to its low-opening state, which is functionally and quantitatively equivalent to CDI or the  
58 low-opening state <sup>14</sup>. In detail, two key motifs of distal C-terminus (DCT) in the pore-forming  
59 subunit (e.g.,  $\alpha_{1D}$  of Cav1.3), the proximal and distal C-terminal regulatory domains (PCRD and  
60 DCRD, respectively), compete against CaM by cooperatively binding the IQ domain (also known  
61 as CaM-binding domain, CaMBD) of the channel, where apoCaM is otherwise pre-associated  
62 <sup>14,19</sup>. Such competitive binding underlying CMI serves as a unified principle applicable to all the  
63 DCT variants across the Cav1 family, only varying in their binding affinities <sup>17</sup>. As one central  
64 principle of CMI, a physical linkage of any two modules among PCRD, DCRD and CaMBD  
65 (representing the channel with no DCT) is required and sufficient to induce CMI when the third  
66 module is present in the cell. The requirement of physical inter-module connection could be  
67 fulfilled either by constitutive linkage such as the fusion of PCRD with CaMBD or with DCRD, or  
68 by acute connection such as rapamycin-induced FRB/FKBP binding <sup>14</sup>.

69 In this study, we aim to employ the above knowledge and tools to develop applicable CMI-  
70 based antagonists, for which high inhibition potency and ample dynamic range with acute  
71 induction are desired. However, such task is challenging in several aspects. Firstly, both short  
72 (without DCT) and long (with DCT) Cav1.3 variants are expressed in brain and heart cells <sup>20-24</sup>.  
73 For the short variant of Cav1.3 (42A or  $\alpha_{1DS}$ ), to achieve high CMI potency, it is necessary to

74 utilize an engineered form of the channel, rather than its native form <sup>14</sup>, to fulfill the requirement of  
75 “three-module principle” as mentioned above. Meanwhile, for the long form Cav1.3 ( $\alpha_{1\text{DL}}$ ), the  
76 dynamic range is rather limited as DCT peptides directly result in either potent inhibition or  
77 no/minor CMI <sup>14,17</sup>. The breakthrough began with our discovery of an unexpected, effective  
78 membrane-assisted connection between CMI modules. With the aid of the membrane-targeting  
79 CAAX tag from the Ras protein <sup>25</sup>, aforementioned bottleneck problems could all be resolved by  
80 bringing the CMI modules onto the membrane. Lastly, for acute CMI induction, our previous  
81 rapamycin-inducible system or chemo-genetics in general provides a strong foundation for the  
82 development of the prototype <sup>14</sup>, but with intrinsic limitations in spatiotemporal resolution, for  
83 which we proposed an approach by integrating with near infrared (NIR)-responsive nanoparticles,  
84 to release rapamycin and thus induce CMI.

85 In this work, we have developed a prototype of opto-chemogenetics, which consists of NIR-  
86 responsive rapamycin-encapsulated nanoparticles, and FRB/FKBP- and Ras-tagged peptides.  
87 Induction of membrane translocation helps form equivalent linkages to the targeted Cav1  
88 channels, which potently inhibits Cav1 activities and neuronal development.

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## 91 **Results**

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### 93 **Unexpected CMI on $\alpha_{1\text{DS}}$ by membrane-anchored P+D peptides**

94 For the representative channel of short Cav1.3 (splice variant 42A, i.e., $\alpha_{1\text{DS}}$ ) (Figure 1A, top), due  
95 to the lack of DCT, each channel (around IQ) is bound with apoCaM, thus supposedly having the  
96 maximum opening and ensuing inactivation <sup>14,18</sup>, the latter of which was verified by examining the  
97 CDI strength of the whole-cell  $\text{Ca}^{2+}$  current (Figure 1A, middle). Briefly, the  $\text{Ca}^{2+}$  current ( $I_{\text{Ca}}$ , in  
98 red) of  $\alpha_{1\text{DS}}$  upon depolarization reached its instantaneous peak, and rapidly (within tens of  
99 milliseconds) inactivated until reaching its steady-state plateau. In contrast, nearly no or rather  
100 weak inactivation/decay was observed from the  $\text{Ba}^{2+}$  current ( $I_{\text{Ba}}$ , in gray) during the 300 ms  
101 depolarization step. The differences between  $\text{Ca}^{2+}$  currents and  $\text{Ba}^{2+}$  currents reflect the  
102 dependency of inactivation on  $\text{Ca}^{2+}$ , quantified by the index of CDI or  $S_{\text{Ca}}$  (Figure 1A, bottom).  
103 According to the prerequisite of CMI, both PCRD and DCRD are required to be present for  
104 eventual association with the channel at the IQ domain as the trio complex; moreover, if there is  
105 no physical linkage among the three modules, no CMI would be produced <sup>14,17</sup>. As expected,  
106 when PCRD and DCRD (encoding corresponding motifs of Cav1.3/1.4 DCT, denoted as P+D)  
107 were co-expressed with  $\alpha_{1\text{DS}}$ , the  $\text{Ca}^{2+}$  currents were indistinguishable from the control group  
108 (Figure 1B). Next, the Ras tag, as the membrane-targeting signal <sup>25</sup>, was fused onto PCRD,  
109 DCRD or both, which were then co-expressed with the other untagged modules for further

110 examination. Unexpectedly, when PCRD was anchored to the membrane (by CAAX motif of the  
111 Ras tag), CDI was significantly reduced (Scheme I, Figure 1C), compared to the control level of  
112 CDI obtained from  $\alpha_{1DS}$  alone (Figure 1A). Similar results of strong CMI effects on CDI were  
113 obtained with Ras-tagged DCRD (Scheme II, Figure 1D), and with co-expression of both Ras-  
114 tagged PCRD and Ras-tagged DCRD (Scheme III, Figure 1E). To quantify the inhibitory effects  
115 on  $\alpha_{1DS}$ , *CMI* (in percentage) is defined as the normalized fraction of channels that switch from  
116 apoCaM-bound to DCT-bound according to our previous study <sup>17</sup>. *CMI* is inversely proportional to  
117  $S_{Ca}$ , therefore substantial reduction of  $S_{Ca}$  corresponds to high *CMI*. All three schemes exhibited  
118 remarkable *CMI* (Figure 1F), apparently breaking the rule of CMI in that no bipartite linkage  
119 seemed to exist among the modules expressed in the cell. Meanwhile, except for the leakage  
120 requirement, the 'trio' working model of CMI is still valid. If only the PCRD or DCRD peptides  
121 were expressed alone, even if tagged with Ras—thereby lacking the third party—the channels did  
122 not exhibit any significant change in CDI (Figure S1). Taken together, these results regarding  
123 P+D peptides led us to hypothesize that the bipartite linkage requirement could be met by way of  
124 the Ras tag and the membrane, presumably as an unconventional type of 'physical' linkage  
125 allowing the CMI modules to form effective inter-module connections.

## 126 Additional evidence from FRET supports the effective membrane-assisted linkage

127 Although electrophysiological recordings for P+D peptides have already strongly suggested that  
128 the membrane-targeting CAAX motif is critical to effectively link PCRD to DCRD or the channel,  
129 more direct evidence was sought after, for which Förster resonance energy transfer analysis  
130 (FRET) would serve as one suitable tool to address the molecular interactions in the cytosol or  
131 membrane <sup>26,27</sup> (Figure 2A-2C). Cytosolic peptides of P+D were co-expressed as a FRET pair,  
132 i.e., YFP-PCRD and CFP-DCRD, which resulted in low FRET efficiency (indexed by FRET ratio,  
133 *FR*), consistent with the weak *CMI* (Figure 1). By employing the membrane-targeting Ras tag,  
134 PCRD-YFP-Ras and DCRD-CFP-Ras peptides were constitutively expressed on the membrane  
135 (Figure 2A and 2B). Notably, Ras-tagged P+D peptides exhibited much higher *FR* than the  
136 cytosolic peptides (Figure 2C), indicating that a substantial number of donor and acceptor  
137 molecules are within the distance of 50Å according to the  $r_0$  (Förster radius of FRET pair)  
138 between CFP and YFP <sup>28</sup>. For the pair of membrane-anchored P+D that exhibited high *FR*, the  
139 PCRD and DCRD peptides are in such close proximity that they seem to be physically connected,  
140 apparently by a linkage equivalent to the one in the fusion protein of P-D. As expected,  
141 membrane-anchored CFP-YFP-Ras dimer resulted in high *FR*. Notably, after inserting an ER/K  
142 linker <sup>29</sup> into such dimer, i.e., CFP-ER/K-YFP-Ras, only produced low FRET thus serving as an  
143 important negative control (Figure 2D-2F). Assured by these control groups, intriguing results  
144 were obtained from CFP-Ras and YFP-Ras. This Ras-tagged FRET pair exhibited high *FR* on the

145 membrane, mirroring the high *FR* observed from the PCRD-YFP-Ras and DCRD-CFP-Ras pair  
146 (Figure 2C). The similar results between Figure 2C and Figure 2F (indicated by the pink areas)  
147 argue no or ultraweak interaction present between PCRD and DCRD<sup>19</sup> consistent with our earlier  
148 reports (but see<sup>30</sup>); otherwise, overall higher *FR* in Figure 2C should be expected because of  
149 additional PCRD/DCRD interactions. Combining electrophysiology and FRET results, we  
150 conclude that the P+D peptides with no cytosolic CMI, when anchored onto the membrane,  
151 effectively connect  $\alpha_{1DS}$  channels, thus fulfilling the physical linkage requirement for strong CMI  
152 on  $\alpha_{1DS}$  channels.

153 **Design of P-D peptides for  $\alpha_{1DL}$  inspired by membrane-assisted CMI on  $\alpha_{1DS}$**

154 So now we have partially achieved our goal by providing P+D peptides which, with the assistance  
155 of the membrane, target  $\alpha_{1DS}$  with high potency. With respect to  $\alpha_{1DL}$ , which is the full-length  
156 variant of Cav1.3, the potency of CMI is expected to correlate quantitatively with the affinity  
157 between DCT peptides and  $\alpha_{1DL}$  channels. Accordingly, in contrast to the DCT peptides encoded  
158 by Cav1.3 or Cav1.4, the DCT peptides encoded by Cav1.1- or Cav1.2 such as CCAT<sub>C</sub> containing  
159 the linked PCRD<sub>C</sub> and DCRD<sub>C</sub> of Cav1.2 are barely able to produce any inhibition on  $\alpha_{1DL}$ <sup>17</sup>. This  
160 type of peptide is denoted as P-D (to compare with P+D), since PCRD and DCRD are physically  
161 linked together. Consistent results were achieved that CDI of the CCAT<sub>C</sub> group is  
162 indistinguishable from the  $\alpha_{1DL}$  control (Figure 3A and 3B). Inspired by the discovery that  
163 membrane-assisted molecular linkage significantly enhances CMI, we then proposed the design  
164 of Ras-mRuby-CCAT<sub>C</sub>, where the Ras is fused, as a novel type of applicable P-D peptides. In  
165 contrast to cytosolic CCAT<sub>C</sub> (or Cav1.2-encoded P-D), membrane-anchored CCAT<sub>C</sub> significantly  
166 attenuated CDI of  $\alpha_{1DL}$  (Figure 3C), resulting in potent CMI of 57 ± 9% (Figure 3D). A major  
167 feature of CMI effects is the concurrent inhibition of both inactivation and activation processes. In  
168 support of this notion, membrane-anchored P-D exhibited smaller  $\text{Ca}^{2+}$  currents (pA/pF) in  
169 comparison with cytosolic P-D producing nearly no effect on  $\alpha_{1DL}$  (Figure S2). Thus, we have  
170 designed and implemented the Cav1.2-encoded P-D peptides that are highly applicable to  $\alpha_{1DL}$ .  
171 They produce nearly no inhibition in the cytosol, yet exhibit potent CMI effects when translocated  
172 onto the membrane.

173 **Chemical and optical induction of rapid cytosol-membrane peptide translocation**

174 In the context of membrane-assisted physical linkage for CMI, the induction method is crucial for  
175 CMI peptides to acutely translocate onto the membrane. Following the previous design of acute  
176 CMI<sup>14</sup>, a series of chemical/rapamycin-inducible versions targeting  $\alpha_{1DS}$  were developed by  
177 introducing rapamycin binding peptides of FRB/FKBP alongside the membrane-anchoring Ras  
178 tag. The primary rationale behind such a design is to swiftly fulfill the requirement of physical

179 linkage to the peptides (Figure 4A). By design, various DCT-encoded motifs in the cytosol are  
180 able to acutely translocate onto the membrane through the tight binding of rapamycin to FKBP-  
181 tagged peptides which would eventually form the complex with FRB-Ras on the membrane<sup>14,31</sup>.  
182 YFP-FKBP-DCRD, YFP-FKBP-PCRD, and FRB-CFP-Ras were expressed in HEK293 cells.  
183 Time-lapse imaging by confocal microscopy was conducted to monitor the process of membrane  
184 translocation at the interval of 30 s (Figure 4B). To quantify the membrane translocation, a red  
185 line was drawn to cross the whole cell from which the ratio of fluorescence intensity between  
186 membrane (Fm) versus cytosol (Fc) was calculated as a quantitative index. Direct application of 1  
187  $\mu$ M rapamycin to the bath induces the binding of FRB fused in the membrane by Ras tag and  
188 FKBP, leading to translocation of YFP-FKBP-PCRD and YFP-FKBP-DCRD on the membrane,  
189 while treatment with 0.1% DMSO, serving as a vehicle control, did not cause any membrane  
190 association with FKBP (Figure 4B and 4C).

191 Our strategy for achieving optical induction fully leverages the previously established  
192 method. NIR-responsive nanoparticles encapsulating rapamycin (rapamycin@PDPP) may  
193 provide additional benefits in spatial control, tissue penetration, biocompatibility and drug release.

194 As shown in Figure S3, rapamycin@PDPP nanoparticles were prepared via the  
195 nanoprecipitation of PDPP, DPPC, DSPE-PEG2000-NH<sub>2</sub> and rapamycin. PDPP cores convert  
196 NIR light into heat, triggering a phase-transition of DPPC lipid coating at a temperature of 41°C.  
197 An additional lipid coating, DSPE-PEG2000-NH<sub>2</sub>, enhances the biocompatibility of the  
198 nanoparticles. Encapsulated rapamycin is released from the nanoparticles under 808nm NIR  
199 irradiation. The NIR-responsive nanoparticles have been proven to be biocompatible in HEK293  
200 cells and tissues<sup>32,33</sup>. To approach the design goals, rapamycin@PDPP nanoparticles were then  
201 deployed to gain opto-chemical control of membrane translocation of CMI modules. The first key  
202 step was to develop NIR-responsive binding between FRB-Ras and FKBP. Fluorescent tag YFP  
203 was fused onto FKBP to visualize its subcellular distribution. As illustrated in the design scheme  
204 (Figure 4A), NIR light triggers the release of rapamycin from rapamycin@PDPP nanoparticles,  
205 and subsequently induces the binding (heterodimerization) of Ras-tagged FRB and cytosolic  
206 FKBP in the cell, leading to translocation of YFP-FKBP-PCRD and/or YFP-FKBP-DCRD onto the  
207 membrane. The concentration of rapamycin@PDPP nanoparticles was calibrated according to  
208 the UV standard curve of conjugated polymer PDPP. Considering the efficacies of drug loading  
209 and release of nanoparticles, cells were incubated with 25  $\mu$ g/ml rapamycin@PDPP and  
210 irradiated by NIR for 5 min to release the rapamycin resulting in a final concentration of 1  $\mu$ M  
211 rapamycin in the bath solution. No basal leakage of rapamycin from rapamycin@PDPP was  
212 detected without NIR stimulation during the 15-minute imaging period. After 5 minutes of *in situ*  
213 NIR exposure to trigger rapamycin release, we observed rapid mobilization of the YFP-tagged  
214 proteins (Figure 4D). As demonstrated by histogram analyses of positions along the red line,

215 distinct intensity profiles were observed at 0 or 15 minutes (prior to NIR exposure) compared to  
216 37 minutes (following NIR exposure) (Figure 4E). This temporal analysis of the Fm/Fc ratio further  
217 underscored the stability of rapamycin encapsulated within PDPP in the absence of NIR  
218 stimulation, and its rapid membrane translocation triggered by opto-chemical activation of  
219 FRB/FKBP dimerization (Figure 4F).

220 **Chemically and optically inducible membrane-assisted CMI peptides of P+D.** Leveraging  
221 the membrane-assisted peptide linkage (Figure 1) and rapid induction of cytosol-membrane  
222 translocation (Figure 4), we designed a prototype of membrane-assisted Cav1.3-encoded P+D  
223 peptides, enabling CMI on  $\alpha_{1DS}$  (Figure 5A). Following our design, we used rapamycin or  
224 rapamycin@PDPP to acutely induce the translocation of YFP-FKBP-PCRD or YFP-FKBP-DCRD  
225 onto the membrane via Ras-tagged FRB. As anticipated,  $\text{Ca}^{2+}$  currents of  $\alpha_{1DS}$  were potently  
226 inhibited upon 1  $\mu\text{M}$  rapamycin, demonstrated by the time-dependent inactivation ( $S_{Ca}$ ) and  
227 activation (indexed by the current amplitude,  $I_{peak}$ ) (Figure 5B and 5C). In control  $\alpha_{1DS}$  channels  
228 lacking P+D expression, 1  $\mu\text{M}$  rapamycin had no effect, as shown by unchanged  $S_{Ca}$  and  $I_{peak}$   
229 values (Figure S4A-S4C). Vehicle control (0.1% DMSO) did not impact  $\text{Ca}^{2+}$  currents when  $\alpha_{1DS}$   
230 was co-expressed with inducible P+D peptides (Figure S4D-S4F).

231 In principle, three possible schemes can be deployed according to the particular peptides  
232 translocated onto the membrane: PCRD (Scheme I), DCRD (Scheme II) or both (Scheme III).  
233 According to the first scheme (Figure S5A-S5C), the two DCT modules of FKBP-PCRD and  
234 DCRD were co-expressed with the third module, IQ-containing membrane channels. Upon  
235 administration of rapamycin, both inactivation and activation as indexed by  $S_{Ca}$  and  $I_{peak}$ , were  
236 gradually attenuated, causing clear CMI effects (potency  $14 \pm 1\%$ ). Presumably, an effective  
237 connection formed between the channel and FKBP-PCRD, the latter of which was rapidly  
238 mobilized onto the membrane through rapamycin-triggered FKBP binding to membranous FRB-  
239 Ras. In the presence of cytosolic DCRD, the effectively-connected IQ (channel) and PCRD would  
240 further form a ternary complex according to the established principle of CMI. Consistently, despite  
241 the apparent contradiction of concurrent attenuation on both activation and inactivation, the net  
242 reduction of  $\text{Ca}^{2+}$  influx was ensured by the stereotypical  $I_{300}$  (current amplitude at 300 ms), which  
243 remained unaltered (Figure S5A).

244 In the second scheme, similar rapamycin-induced CMI effects were observed from  $\text{Ca}^{2+}$   
245 current recordings (Figure S5D-S5F), with FKBP-DCRD and cytosolic PCRD co-expressed  
246 alongside  $\alpha_{1DS}$ . Consistent with the data and interpretation from the first scheme, effective  
247 connections between FKBP-tagged DCRD and  $\alpha_{1DS}$  presumably formed in response to  
248 rapamycin, leading to cooperative binding and channel inhibition.

249 Notably, in the third scheme (Figure 5B and 5C), both PCRD and DCRD were recruited to  
250 the membrane, directly corresponding to its constitutive version (Figure 1E). The CMI potency of

251 this scheme appeared relatively more pronounced than the other schemes. This was evident from  
252 the exemplar  $\text{Ca}^{2+}$  current traces before and after rapamycin stimuli, and from the temporal  
253 profiles of inactivation ( $S_{\text{Ca}}$ ) and activation ( $I_{\text{peak}}$ ).

254 We then explored the optical induction of CMI, following our strategy of NIR-responsive  
255 rapamycin release and subsequent peptide translocation onto the membrane.  
256 Rapamycin@PDPP nanoparticles without NIR light did not cause any significant effect, indicated  
257 by unaltered CDI ( $S_{\text{Ca}}$ ) and peak current ( $I_{\text{peak}}$ ) during the whole time-course (Figure S6A and  
258 S6B). Five minutes of NIR irradiation successfully induced inhibitory effects on  $\text{Ca}^{2+}$  currents  
259 (Figure 5D), presumably by triggering the release of rapamycin, leading to typical attenuation on  
260 both inactivation ( $S_{\text{Ca}}$ ) and activation ( $I_{\text{peak}}$ ) (Figure 5E). Moreover, the CMI potency associated  
261 with optical induction here was close to the potency of CMI by direct rapamycin induction (cyan  
262 lines based on Figure 5B and 5C), further confirming the effectiveness of the combined  
263 optical/chemical induction as proposed in our design. As a negative control, rapamycin@PDPP  
264 nanoparticles with NIR light had no significant effect on HEK293 cells only expressing  $\alpha_{1\text{DS}}$   
265 (Figure S6C and S6D).

266 Lastly, detailed profiles of  $S_{\text{Ca}}$  and  $I_{\text{peak}}$  across the full range of membrane potentials were  
267 measured for  $\text{Ca}^{2+}$  currents toward the protocol's end (Figure S7), yielding consistent conclusions  
268 in all cases, including the three basic schemes and the optical induction design (P+D) (Figure 5;  
269 Figure S5). The potencies for the Scheme I, II and III are  $19 \pm 2\%$ ,  $36 \pm 15\%$  and  $67 \pm 9\%$ ,  
270 respectively, in addition to opto-chemogenetic CMI of  $56 \pm 9\%$ .

271 **P-D peptides inducibly suppressed the Cav1 activity-neuritogenesis coupling**

272 According to our newly designed P-D peptides (Figure 3), the Cav1.2-encoded P-D peptides of  
273 PCRD<sub>C</sub>-DCRD<sub>C</sub> (P<sub>C</sub>D<sub>C</sub>) on the membrane are able to produce CMI effects. An inducible version of  
274 P-D was developed using the rapamycin/FRB/FKBP module similar to what is depicted in Figure  
275 5A. First, FKBP-YFP-P<sub>C</sub>D<sub>C</sub> and FRB-CFP-Ras were tested for the inducible CMI effects on  $\alpha_{1\text{DL}}$ .  
276 P<sub>C</sub>D<sub>C</sub> was recruited by acute induction to the membrane resembling its constitutive version  
277 (Figure 6A-6C). Upon rapamycin, both inactivation and activation as indexed by  $S_{\text{Ca}}$  (Figure 6B)  
278 and  $I_{\text{peak}}$  (Figure 6C; Figure S8A) were gradually attenuated, causing unambiguous CMI effects  
279 (CMI  $44 \pm 7\%$ ), further confirmed by the full voltage-dependent profiles (Figure S8B).  
280 Interestingly, FKBP-YFP-P<sub>C</sub>D<sub>C</sub> also significantly induced strong CMI inhibition ( $41 \pm 6\%$ ) on  $\alpha_{1\text{DS}}$ ,  
281 evidenced by gradual attenuations in inactivation ( $S_{\text{Ca}}$ ) and activation ( $I_{\text{peak}}$ ) (Figure 6D-6F).  
282 Toward the ending point of the time course, attenuated CDI of  $\alpha_{1\text{DS}}$  was close to that of  $\alpha_{1\text{DL}}$   
283 (Figure 6A-6C). The affinity of P<sub>C</sub>D<sub>C</sub> for the channel should be enhanced by about two orders of  
284 magnitude before and after membrane-translocation <sup>17</sup>, which could be well accounted for by a  
285 membrane-assisted dimerization-like linkage as proposed earlier.

286 Our next step was to investigate inducible membrane-assisted P-D peptides in live neurons  
287 under physiological conditions, following the validation of CMI impacts on recombinant Cav1.3  
288 channels. Furthermore, peptides encoded by DCT, including CCAT<sub>C</sub>, are endogenously present  
289 in native cells, playing pivotal roles in the regulation of channels and neurons. Subsequently,  
290 FKBP-CFP-P<sub>C</sub>D<sub>C</sub> and FRB-mRuby-Ras were virally introduced into cultured cortical neurons. An  
291 improved version of GCaMP, jGCaMP7b-X<sub>C</sub><sup>34</sup>, was utilized to monitor neuronal Ca<sup>2+</sup> dynamics.  
292 Following rapamycin induction, P<sub>C</sub>D<sub>C</sub> translocated onto the cortical neuron membrane (Figure 6G-  
293 6I). In cortical neurons expressing FKBP-CFP-P<sub>C</sub>D<sub>C</sub> and FRB-mRuby-Ras, we observed  
294 spontaneous Ca<sup>2+</sup> oscillations, quantified using the indices of frequency (mHz), amplitude ( $\Delta F/F_0$ )  
295 and influx (AUC, or Area Under the Curve). Oscillatory Ca<sup>2+</sup> activities post 10 and 20 minutes of  
296 rapamycin treatment were compared to pre-treatment levels (Figure 6J-6M). In control neurons  
297 not expressing FKBP-CFP-P<sub>C</sub>D<sub>C</sub>, no perceptible difference was observed (Figure 6J and 6I).  
298 Conversely, the membrane-anchored P-D type peptides of P<sub>C</sub>D<sub>C</sub> significantly reduced Ca<sup>2+</sup>  
299 oscillations, as indicated by all three major indices (Figure 6K and 6M). Following rapamycin  
300 induction, hippocampal neurons also exhibited a similar reduction in spontaneous Ca<sup>2+</sup> activities  
301 (Figure S9).

302 Neurite outgrowth and neuronal development are closely related to Ca<sup>2+</sup>, particularly due to  
303 Cav1 channels<sup>17,35</sup>. To explore the Cav1 activity-neuritogenesis coupling in the context of  
304 inducible CMI, we examined cultured cortical neurons at different timepoints (days *in vitro*, DIV)  
305 after rapamycin treatment (Figure 7A and 7B). As expected, both neuritogenesis (total length)  
306 and Ca<sup>2+</sup> influx (AUC) of cortical neurons expressing FKBP-CFP-P<sub>C</sub>D<sub>C</sub> and FRB-mRuby-Ras  
307 were significantly attenuated compared to the control group not expressing the CMI modules.  
308 Consistent with previous results<sup>34</sup>, the neurite length of each neuron in accordance to its DIV  
309 followed a sigmoidal-like curve, as evidenced from the control (Figure 7C). We qualitatively  
310 assumed that Cav1 influx to be the key factor responsible for neuritogenesis, despite the  
311 complexity of frequency, amplitude and other parameters of Ca<sup>2+</sup> dynamics<sup>34</sup>. In this study, Ca<sup>2+</sup>  
312 influx was explicitly quantified as AUC, represented as a bell-shaped curve (Figure 7D), aligning  
313 well with the two-phase trend of neurite growth rate (NGR,  $\mu\text{m}/\text{day}$ ) (Figure 7E), thereby directly  
314 supporting a clear yet simple correlation between Ca<sup>2+</sup> influx and neurite outgrowth (Figure 7F).

315 Our earlier data demonstrate that cultured cortical neurons go through an initial phase (~14  
316 days) of rapid outgrowth before entering into the plateau phase, forming a monotonic increasing  
317 curve (Figure 7C, sigmoidal-like curve in solid black), of which the first derivative indicates NGR  
318 of cultured cortical neurons (Figure 7E, bell-shaped curve in solid black). Inducing CMI by  
319 membrane association of P<sub>C</sub>D<sub>C</sub> led to reduction of Ca<sup>2+</sup> oscillations, causing significant changes  
320 in neurite length, AUC and NGR, reflected as abrupt and large deviations from the curves of  
321 control neurons (Figure 7C-7E). Notably, the correlation between NGR of neuronal development

322 and AUC of  $\text{Ca}^{2+}$  activities appeared to be a phase-plane plot that the trajectory for the control  
323 neurons was suddenly dragged down by CMI induction to the negative range of growth rate  
324 (Figure 7F).

325 Hippocampal neurons, well known for oscillatory activities, play vital roles in brain functions  
326 <sup>36</sup>. We speculated that the CMI effects on the Cav1 activities-neuritogenesis coupling in cortical  
327 neurons should be generalizable, e.g., onto hippocampus. Membrane-anchored P-D peptides of  
328 Ras-YFP-PcDc significantly reduced oscillatory  $\text{Ca}^{2+}$  activity in hippocampal neurons, as  
329 quantified by AUC (Figure S9A and S9B). Meanwhile, the neurite length of hippocampal neurons  
330 expressing Ras-YFP-PcDc was significantly shorter than the control group of cytosolic peptides  
331 (Figure S9C and S9D).

332

### 333 **Discussion**

334

335 In this study, we have developed a prototype of membrane-assisted CMI with opto-chemogenetic  
336 induction. It comprises NIR-responsive nanoparticles encapsulating rapamycin and peptides  
337 tagged with FRB/FKBP and Ras, encoding the DCT of Cav1.2 (P-D) or Cav1.3/1.4 (P+D) (Figure  
338 8). Upon induction of membrane translocation, the peptides can form molecular-scale linkages to  
339 the targeted Cav1 channels, whether in long or short variants. Robust and potent inhibitory effects  
340 on Cav1 activities and neuronal development were acutely induced with ample dynamic range.

341

### 342 **Insights into protein-protein interaction facilitated by membrane-anchoring**

343 Besides ion channels, certain membrane proteins are known to interact with each other to form  
344 dimers or even oligomers, as the prerequisite of their subsequent signaling and activities <sup>25,37,38</sup>. A  
345 prominent example is the Ras protein, whose dimerization on plasma membrane promotes RAF  
346 and MAPK cell signaling <sup>25</sup>. In fact, the C-terminal domain containing CAAX as the membrane-  
347 anchoring tag in this study was adopted from H-Ras, one isoform of the Ras family <sup>14,31</sup>. The G  
348 domain is critical to Ras dimerization, for which membrane-anchoring is also required in the first  
349 place <sup>39</sup>. Our data, from both electrophysiology and FRET on the peptides tagged with Ras CAAX  
350 box, suggest that similar membrane-facilitated physical linkages and protein interactions may  
351 underlie Ras dimerization. This implies that CAAX-assisted translocation onto the membrane  
352 could increase the proximity of the molecules to a scale of 50 Å or less (Förster Radius),  
353 equivalent to a physical linkage (as required by our CMI principle) which enhances effective  
354 affinity or relative concentration (between intramolecular binding partners) and thus promotes the  
355 interaction/dimerization of the binding domains (e.g., G domain) <sup>40,41</sup>. Another potential factor is  
356 via the lateral interactions between the transmembrane domains of membrane proteins <sup>42</sup>, which,  
357 however, is unlikely the case of Ras/CAAX. Here, we quantitatively examined the equivalent

358 peptide-channel dimerization using reliable biophysical methods (patch-clamp and 3-cube FRET)  
359 and mechanisms (DCT/CMI), which are readily expandable onto other membrane proteins  
360 including Ras. Interventions of Ras overactivation have been actively pursued as potential cancer  
361 therapeutics by targeting its membrane anchoring and dimerization, for which membrane-assisted  
362 CMI here may help develop (compound) screening assays, by taking advantage of the  
363 quantitative assays for CDI (electrophysiology) and  $\text{Ca}^{2+}$  dynamics (fluorescence imaging). The  
364 membrane-association tag of the tyrosine kinase Lyn and other c-Src family members is also  
365 important to dimerization and functions<sup>43-45</sup>. We expect that Ras and Lyn (and potentially other  
366 membrane proteins) would share similar membrane (anchoring tag)-assisted linkage to enhance  
367 protein-protein interaction or dimerization, all awaiting future investigations to explore.

368 When we revised and finalized this manuscript, another study reported a similar strategy of  
369 utilizing the CAAX tag to demonstrate that Rad (small RGK G-protein) regulation of Cav1.2  
370 channels is critically dependent on membrane-association<sup>46</sup>. Ras tag was also proved by their  
371 FRET data to have the capability to bring the donor and acceptor close enough to yield high  
372 FRET efficiency. However, a few points are worth mentioning here. First of all, we reached our  
373 conclusion of the equivalent physical linkage based on the 3-component principle of CMI we  
374 established in earlier independent studies mainly with electrophysiology<sup>14,17</sup>. Therefore, the core  
375 mechanism should be the membrane/Ras-assisted linkage in our view, leading to elevated  
376 effective concentration or enhanced apparent affinity as the consequences secondary to the  
377 formation of 'physical' linkage. In support, even Ras-tagged fluorophores could produce high FRET  
378 in both our study (cellular FRET with membrane-anchored CFP/YFP) and their report  
379 (flowcytometric FRET with Cer/Ven). In addition, our experiments and analyses on membrane-  
380 assisted linkage, interaction and dimerization were restricted within the proteins or peptides on  
381 the membrane, different from their study heavily based on cytosolic/dispersed  $\beta_2$ .

382

### 383 **Hints on mechanistic details of DCT, CaM and CMI**

384 Before this work, only DCRD showed an appreciable (channel) affinity whereas the binding of  
385 PCRD/channel has not been detected yet, and thus the nature of their cooperativity still remains  
386 elusive. In the context of membrane-assisted linkage and CMI, membrane-anchored PCRD  
387 should also bind the channel when its effective concentration gets high enough, due to the fact  
388 that PCRD behaves similarly as DCRD (Figure 1C; Figure S5A; Figure S7A). Our data provide  
389 the missing piece of evidence critical to a unified mechanism of cooperative binding.

390 To date, the consensus holds that both the proximal and distal regions (PCRD and DCRD)  
391 are crucial for modulating Cav1 channels. For Cav1.2, PCRD and DCRD may have some  
392 electrostatic interactions according to *in silico* modeling<sup>30</sup>, whereas for Cav1.3 no direct  
393 interaction could be detected between PCRD and DCRD<sup>14,19</sup>. Later reports systematically

394 comparing DCT across Cav1.1-1.4 demonstrate that a set of common principles are likely shared  
395 to induce inhibitory effects (CMI) on channel gating and  $\text{Ca}^{2+}$  influx <sup>14,17</sup>. For instance, DCRD  
396 modules/motifs contribute more significantly than PCRD in CMI and related interactions. In  
397 support, FRET binding data suggest that DCRD itself could bind the CaM-binding IQ domain in  
398 contrast to PCRD that has no detectable binding; and PCRD and DCRD cooperate with each  
399 other to form the ternary complex of PCRD/DCRD/IQ <sup>14</sup>. Meanwhile, the DCT peptide, as  
400 suggested, might behave as an apoCaM, the latter of which is known to bear intrinsic  
401 cooperativity between its two lobes <sup>47</sup>. In light of this view and our data, one would postulate that  
402 PCRD by itself (just resembling DCRD) is also able to bind the channel/IQ, but with even lower  
403 affinity than DCRD. When present in the cytosol, the concentrations of PCRD or DCRD are way  
404 below the levels for any discernable binding with the channel to actually happen, thus no  
405 cooperative binding or CMI. However, once PCRD and/or DCRD translocate onto the membrane,  
406 the membrane-assisted linkage and the consequent (local) concentrations relative to each other  
407 (PCRD, DCRD and IQ/channel) are increased by orders of magnitudes to the levels of realistic  
408 binding. In this context, the observed cooperativity between PCRD and DCRD would resemble  
409 the two lobes of CaM: once one lobe/module is bound, the consequent allosteric changes  
410 facilitate the target binding of the other lobe/module, as the underlying principles for all the  
411 scenarios of P+D or P-D (e.g, Figure 1 and Figure 3). Not only to elucidate the molecular details  
412 of CMI/DCT but also to gain insights into the binding mechanisms related to CaM, the results and  
413 hints from this study merit further investigation.

414

#### 415 **The development of molecular tools for protein dimerization**

416 Controllable protein heterodimerization allows to modulate diverse biological processes such as  
417 protease activity, transcription and translocation <sup>48-51</sup>, thus applicable to a broad spectrum of  
418 scenarios as powerful molecular tools <sup>52,53</sup>. Rapamycin-inducible FKBP/FRB heterodimerization  
419 has been widely applied due to its ultra-high affinity of rapamycin towards its protein binding  
420 partners FKBP and FRB ( $K_d = 12 \text{ nM}$  for FKBP-rapamycin-FRB), with a clear baseline (no  
421 detectable binding) in the absence of rapamycin <sup>54,55</sup>. To improve the spatial control of rapamycin  
422 system, photocaged rapamycin analogues have been developed, such as cRb, which features a  
423 nitrobenzyl cage linked to a rapamycin analogue <sup>56</sup>, dRap, a photo-cleavable rapamycin dimer <sup>57</sup>,  
424 pRap, a caged rapamycin with nitro-piperonyloxycarbonyl N-hydroxysuccinimide carbonate  
425 (NPOC-NHS) <sup>58</sup>, DMNB caged rapamycin <sup>59</sup>, and arylazopyrazole rapamycin analogs <sup>60</sup>.  
426 However, all of these photocaged rapamycin variants are triggered by the ultraviolet light (UV),  
427 unfavored by biological applications. In fact, most approaches for optical control of protein-protein  
428 interaction by photocaged drugs are limited by the short wavelength stimulation <sup>61,62</sup>. In  
429 comparison, NIR light has less cell damage and deeper tissue penetration. Moreover, unlike

430 rapamycin analogues, our design of rapamycin@PDPP does not change the skeleton of  
431 rapamycin, thus relieving the concerns regarding potential reduction in membrane permeability  
432 and increase in cellular toxicity due to covalent modifications of rapamycin. And nanoparticles are  
433 recognized as a well-established platform for controlled drug delivery, which promises extra  
434 benefits for *in vivo* applications<sup>32</sup>.

435 Besides opto-chemogenetics based on rapamycin@PDPP and FKBP/FRB in this work, other  
436 optically-controlled dimerization methods (such as CRY2/CIB, UVR8/UVR8, and light-switchable  
437 nanobodies) are commonly triggered by blue light or UV light<sup>63-65</sup>. Some newly designed  
438 optogenetic systems could be triggered by NIR light but suffer from low efficacy when compared  
439 to the FKBP/rapamycin/FRB system in practice<sup>66,67</sup>. Here in this work, by taking advantage of two  
440 separate but established lines of work, we designed and implemented a prototype of NIR-  
441 triggered heterodimerization, as a feasible strategy of optogenetics.

442 Moreover, the membrane-assisted molecular linkage as proposed in this work opens up new  
443 avenue to design dimerization tools. The first step is to adopt or devise cytosolic modules with no  
444 or low weak affinities to dimerize; then, the cytosolic modules need to translocate onto the  
445 membrane, e.g., by attaching membrane-anchoring tags such as Ras CAAX to monomeric  
446 proteins or peptides. Combining with other molecular tools (such as rapamycin@PDPP in this  
447 work), a general platform with controllable binding/dimerization can be achieved. It is a  
448 challenging task to specifically design and implement optical control within each particular  
449 molecule, considering the diverse interactions and mechanisms often difficult to intervene/control.  
450 Instead, through a more universal strategy as demonstrated in this work, the desired dimer or  
451 even binding complex can be achieved on the membrane with high spatiotemporal resolutions  
452 without having to dig into the binding details.

#### 453 **Insights into the coupling of Cav1 activities with neuronal development**

454 Cellular Ca<sup>2+</sup> signals, especially transmembrane Ca<sup>2+</sup> influx, play a central role in neural  
455 development<sup>35,68</sup>. Spontaneous, regenerative and correlated or even synchronized Ca<sup>2+</sup> activities  
456 are particularly important to neurite outgrowth, presumably owing to enhanced efficiency in gene  
457 transcription in the nucleus and related downstream events<sup>69</sup>. In addition, L-type Ca<sup>2+</sup> channels  
458 are proposed as the core mediator to specifically and mechanistically link Ca<sup>2+</sup> oscillations, the  
459 CaMKII-CREB signaling pathway, and also neuritogenesis altogether, i.e., the Cav1 activity-  
460 neuritogenesis coupling<sup>17</sup>. However, due to multiple complications, this coupling needs additional  
461 evidence before it can be fully established. The first complication is that transmembrane Ca<sup>2+</sup> has  
462 an array of sources, e.g., N-Methyl-D-aspartate (NMDA) receptors, TRP channels, Orai/STIM,  
463 and Cav2<sup>70</sup>. Another complication comes from the molecular tools that most studies are relying  
464 on: pharmaceutical interventions based on DHP derivatives. Both Cav1 inhibitors and potentiators  
465 have generated the data supporting the proposed coupling, but also encountered with many

466 complicated scenarios, e.g., the unexpected neuroprotection by DHP inhibitors, the differential  
467 effects of Cd<sup>2+</sup> and nimodipine on transcription signaling, and the off-target effects and  
468 neurotoxicity of Bay-K-8644<sup>71-73</sup>. Moreover, knock-out mice of Cav1.3-/- and Cav1.2-/- could also  
469 provide useful information<sup>69,74</sup>; however, they may not be suitable to certain studies on neural  
470 development due to compensatory effects as reported<sup>75,76</sup>. CMI peptides stand out as a  
471 promising toolset to explore the molecular physiology of Cav1<sup>17</sup>. Now in this study, with optimized  
472 P-D peptides and membrane-assisted inducible CMI, unprecedented evidence has been provided  
473 to quantitatively characterize the coupling and its modulation. In this work, we not only validate  
474 our design in both recombinant and neuronal systems, but also provide the direct evidence  
475 strongly supporting that (apoCaM-bound) Cav1 is the molecular basis of the oscillatory Ca<sup>2+</sup>  
476 signals in tight coupling with neurite outgrowth in cultured cortical neurons (Figure 7). We expect  
477 that future studies deploying the findings and tools from this study will greatly help elucidate the  
478 signaling pathways, mechanistic details and relevant pathophysiology of Cav1 in neurons.

479 **Therapeutic potentials of opto-chemogenetics and rapamycin@PDPP nanoparticles**

480 The proof-of-concept of opto-chemogenetic CMI highlights the therapeutic potential of CMI-based  
481 antagonism in Cav1-related disorders, such as Parkinson's disease<sup>14</sup>. In fact, some subtypes of  
482 congenital long QT syndromes are genetically associated with Cav1 and CaM, both of which lead  
483 to alternations in channel activities and severe cardiac arrhythmias<sup>77,78</sup>. Thus, Cav1 antagonisms  
484 based on CMI may serve as the candidate treatments for LQT or like diseases. Moreover, NIR-  
485 controlled CMI may enable noninvasive, high spatiotemporal, and tissue compatible interventions  
486 of Cav1 in the heart and the brain. Notably, our design targets Cav1.3 as the representative  
487 subtype, presumably expandable on Cav1.2 due to their shared CMI effects and mechanisms<sup>17</sup>.  
488 Multiple variants and isoforms are expressed in the brain and heart<sup>20,22,23,79-82</sup>. As demonstrated,  
489 P+D and P-D peptides have differential capabilities to deal with Cav1.3 variants, which include  
490 both the long and short  $\alpha_{1D}$  in cortical and hippocampal neurons (Figure 8). For any particular  
491 type of primary cells, it is necessary to conduct tests and analyses on each channel variant with  
492 different peptides before proceeding further. Cav1.2-encoded P-D peptides derived from this work  
493 have displayed excellent performance and characteristics, which invite additional optimizations  
494 and further explorations with healthy and diseased neurons.

495 Enlightened and encouraged by optogenetics (e.g., channelrhodopsin), an increasing number of  
496 optical tools have been developed for precise spatiotemporal control of physiological processes in  
497 living cells, which are designated as 'optophysiology'<sup>83</sup>. Optically-controlled and genetically-  
498 encoded Ca<sup>2+</sup> channel actuators/modulators are promising research directions in 'optophysiology'  
499<sup>84</sup>. In parallel, chemogenetics provides potent and robust control of physiological processes<sup>85</sup>.  
500 Development of chemogenetic Ca<sup>2+</sup> channel modulators has also been actively pursued to  
501 facilitate both basic and therapeutic research<sup>31</sup>. Our NIR-triggered CMI has seamlessly

502 integrated rapamycin@PDPP with chemogenetics, offering at least three aspects of advantages:  
503 1. effective and robust control of FRB/FKBP binding (rapamycin); 2. high precision of  
504 spatiotemporal control at single-cell resolution (photosensitive nanoparticles); 3. deep tissue  
505 penetration with long-wavelength photostimulation (NIR) and high biocompatibility (nanomaterials  
506 and genetically-encoded modulators). With all these benefits including the unique feature of NIR  
507<sup>86,87</sup>, we expect that our opto-chemogenetics prototype would be applicable broadly and  
508 particularly beneficial to future *in vivo* applications.

509 **Author Contributions**

510 X.D.L. conceived, designed and supervised the project; Y.B.F. and C.F.X. helped organize and  
511 oversee the project. J.L.G., Y.X.Y., B.Y.L., Z.Y., S.Q., W.Z., S.X.G., Y.L. and B.W. performed  
512 the experiments and analyzed the data. N.L. provided preliminary patch-clamp data on peptide  
513 effects. X.D.L. wrote and finalized the manuscript. All authors contributed to writing and revising  
514 the manuscript

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520

521 **Declaration of interest**

522 The authors declare no competing interests.

523

524 **Main figure titles and legends**

525 **Figure 1.** CMI effects on  $\alpha_{1DS}$  by P+D peptides.

526 (A) Top: cartoon illustration of the Cav1.3 (splice variant 42A, denoted as  $\alpha_{1DS}$ ) channel. Middle:  
527 representative current traces of  $\alpha_{1DS}$  at the membrane potential ( $V$ ) of -10 mV.  $\text{Ca}^{2+}$  current ( $I_{Ca}$ ,  
528 with the scale bar on the left) and  $\text{Ba}^{2+}$  current ( $I_{Ba}$ , rescaled to  $I_{Ca}$ ) are colored in red and gray,  
529 respectively. The peak current ( $I_{peak}$  representing the peak amplitude in pA or alternatively the  
530 current density in pA/pF) and the current at 50 ms ( $I_{50}$ ) are to calculate  $r_{50}$  (ratio between  $I_{50}$  and  
531  $I_{peak}$  for both  $I_{Ca}$  and  $I_{Ba}$ , i.e.,  $r_{Ca}$  and  $r_{Ba}$ ). Bottom: inactivation ( $r_{50}$ ) profiles across the full range of  
532  $V$ . The differences between  $r_{Ca}$  and  $r_{Ba}$  reflect CDI ( $\text{Ca}^{2+}$ -dependent inactivation), for which  $S_{Ca}$   
533 (defined as  $1-r_{Ca}$  at -10 mV) serves as the major index of CDI strength.

534 (B) The negative control: two separate DCRD and PCRD (i.e., P+D) peptides in the cytoplasm.  
535 Both CFP-DCRD and YFP-PCRD were expressed together with  $\alpha_{1DS}$  channels. The schematic  
536 illustration, current traces and  $r_{50}$  profiles are shown. The inactivation  $r_{Ca}$  profiles of the  $\alpha_{1DS}$  group  
537 (in pale red) versus the group of cytosolic P+D peptides (in red) are compared.  
538 (C) The design scheme (Scheme I) of PCRD on the membrane anchored by the Ras/CAAX tag  
539 while DCRD in the cytosol. The inactivation  $r_{Ca}$  profiles of the control group (in pale red) versus  
540 the peptide group (in red) are compared, for which their differences are highlighted by green  
541 shade.  
542 (D) The design scheme (Scheme II) of DCRD on the membrane while PCRD in the cytosol.  
543 (E) The design scheme (Scheme III) of anchoring both DCRD and PCRD on the membrane.  
544 (F) Statistical summary of CDI strength ( $S_{Ca}$ ) and CMI potency (CMI in percentage). CMI potency  
545 is defined as the change in CDI:  $(S_{Ca,Control} - S_{Ca,Peptide})/S_{Ca,Control}$ , where the control is  $\alpha_{1DS}$ . All  
546 statistical data are given as mean  $\pm$  SEM (Standard Error of the Mean), with One-way ANOVA  
547 followed by Dunnett for post hoc tests: \*\*,  $p<0.01$ ; n.s., or not significant,  $p>0.05$ .  
548 See also Figure S1.

549 **Figure 2.** High FRET efficiency promoted by membrane-anchoring Ras/CAAX tag.  
550 (A) Schematic diagram of cytosolic and membrane-anchored FRET pairs of CFP-DCRD and  
551 YFP-PCRD. Once DCRD-CFP and PCRD-YFP are anchored onto the membrane by the  
552 Ras/CAAX tag, a putative molecular linkage (pink area) appears to be formed.  
553 (B) FRET imaging to examine the relationship between DCRD-CFP-Ras and PCRD-YFP-Ras.  
554 (C) Quantitative 2-hybrid 3-cube FRET describing the relationship between the FRET ratio ( $FR$ )  
555 and the donor fluorescence intensity (or concentration, *Donor*). Each dot indicates one HEK293  
556 cell. The two FRET pairs of co-expressed P+D, i.e., Ras-tagged (pink) versus cytosolic (green)  
557 CFP-DCRD and YFP-PCRD, were compared. The CFP-YFP dimer and CFP/YFP co-expression  
558 serve as the positive (blue) and negative (gray) control, respectively.  
559 (D) Schematic diagram of cytosolic and membrane-anchored FRET pairs of CFP and YFP. The  
560 pink area indicates potential linkage between CFP and YFP.  
561 (E) FRET imaging to examine the relationship between CFP-Ras and YFP-Ras.  
562 (F) The FRET pairs were examined including CFP-Ras and YFP-Ras (co-expression, red), CFP-  
563 YFP-Ras (dimer, cyan), CFP-ER/K-Ras (dimer, dark green). The two control lines (gray and blue)  
564 are directly adopted from (C).  
565

566 **Figure 3.** CMI effects of Cav1.2-encoded peptides (P-D) on  $\alpha_{1DL}$ .

567 (A) Top: illustration of Cav1.3 long (denoted as  $\alpha_{1DL}$ ). Middle: representative  $I_{Ca}$  and  $I_{Ba}$  traces of  
568  $\alpha_{1DL}$  at the membrane potential ( $V$ ) of -10 mV. Bottom: voltage-dependent inactivation profiles of  
569  $r_{50}$ .

570 (B) The design scheme for the P-D type of peptide CCATc (P-D) encoded by Cav1.2 DCT. The  
571 inactivation  $r_{Ca}$  profiles of the  $\alpha_{1DL}$  group (in pale red) versus the group of cytosolic P-D peptides  
572 (in red) are compared.

573 (C) The design scheme of membrane-anchored P-D peptides.  $\alpha_{1DL}$  channels were co-expressed  
574 with Ras-mRuby-CCATc. The inactivation  $r_{Ca}$  profiles of the group of P-D peptides (in red) versus  
575 the  $\alpha_{1DL}$  control group (in pale red) are compared, for which their differences are highlighted by  
576 green shade.

577 (D) Statistical summary of the strength of CDI ( $S_{Ca}$ ) and CMI potency ( $CM_I$ ). Data points are  
578 presented as mean  $\pm$  SEM, with the corresponding significance: \*\*\*,  $p<0.001$ ; n.s.,  $p>0.05$ .

579 See also Figure S2.

580

581 **Figure 4.** Chemical and optical induction of rapid cytosol-membrane translocation.

582 (A) The general design scheme for chemical or optical induction of membrane translocation.  
583 Rapamycin or encapsulated rapamycin releasing from rapamycin@PDPP nanoparticles after 808  
584 nm NIR laser irradiation induces FRB/FKBP heterodimerization. In response to chemical or  
585 optical induction, YFP-FKBP-DCRD and YFP-FKBP-PCRD (P+D) rapidly translocate from cytosol  
586 to the plasma membrane, where FRB-CFP-Ras is constitutively anchored on the membrane.

587 (B) Representative confocal images to illustrate the rapid translocations of cytosolic DCRD and  
588 PCRD onto the plasma membrane within 5 min upon rapamycin induction. HEK293 cells were  
589 transfected with YFP-FKBP-DCRD, YFP-FKBP-PCRD, and FRB-CFP-Ras. 1  $\mu$ M rapamycin or  
590 vehicle (0.1% DMSO, negative control) was applied. The scale bar is 5  $\mu$ m.

591 (C) The representative fluorescence intensity profiles before or 300 s after induction, based on  
592 the cross sections (red lines) in the images. Fm and Fc represent membranal fluorescence and  
593 cytosolic fluorescence, respectively.

594 (D) Representative confocal images to illustrate NIR induction of translocations of cytosolic YFP-  
595 FKBP-DCRD and YFP-FKBP-PCRD (P+D) to the plasma membrane in real-time and *in situ*. 25  
596  $\mu$ g/ml rapamycin@PDPP nanoparticles were incubated with cells for 15 min and irradiated by NIR  
597 for 5 min to release the rapamycin reaching the final concentration of 1  $\mu$ M *in situ*, then imaged  
598 for 22 min to monitor peptide translocations. The concentration of rapamycin@PDPP  
599 nanoparticles was calibrated according to the UV standard curve of conjugated polymer PDPP.

600 The scale bar is 5  $\mu$ m.

601 (E) The representative fluorescence intensity profiles at 0 min, 15 min and 37 min.

602 (F) Temporal profiles of the ratio of membranal fluorescence to cytosolic fluorescence (Fm/Fc).

603 The red bar indicates 5 min of NIR exposure.

604 All statistical data are given as mean  $\pm$  SEM.

605 See also Figure S3.

606

607 **Figure 5.** Opto-chemogenetics of membrane-assisted CMI on  $\alpha_{1DS}$  by P+D peptides.

608 (A) The design scheme of chemogenetic or opto-chemogenetic CMI. Rapamycin or opto-  
609 chemical control of rapamycin releasing from rapamycin@PDPP nanoparticles is intended to  
610 induce rapid translocation of YFP-FKBP-DCRD and YFP-FKBP-PCRD from the cytosol to the  
611 plasma membrane.

612 (B, C) Rapamycin-induced CMI through translocation of P+D peptides onto the membrane. YFP-  
613 FKBP-DCRD and YFP-FKBP-PCRD were co-expressed with FRB-CFP-Ras. Exemplars of  $Ca^{2+}$   
614 current traces demonstrate effective inhibition by 1  $\mu$ M rapamycin, where both the peak ( $I_{peak}$ ) and  
615 steady-state amplitude (at 300 ms, i.e.,  $I_{300}$ ) are indicated by the dashed lines (B). Temporal  
616 profiles of  $S_{Ca}$  along with CMI (left) and normalized  $I_{peak}$  (right) demonstrate rapamycin-induced  
617 attenuation in comparison with  $\alpha_{1DS}$  control (C). Data points connected by lines (in green and  
618 blue) represent the values of  $S_{Ca}$  or  $I_{peak}$  before and after rapamycin application, respectively.

619 (D) Opto-chemogenetic CMI for  $\alpha_{1DS}$ . HEK293 cells expressing recombinant  $\alpha_{1DS}$ , FRB-CFP-Ras,  
620 YFP-FKBP-PCRD, and YFP-FKBP-DCRD were treated with rapamycin@PDPP nanoparticles.  
621 NIR irradiation for 5 min to trigger the release of rapamycin reaching the final concentration of 1  
622  $\mu$ M. Representative  $Ca^{2+}$  traces at different timepoints are featured with a declining trend of  $I_{peak}$   
623 and the characteristic stable  $I_{300}$ .

624 (E) Temporal profiles of inactivation  $S_{Ca}$  along with potency CMI (left) and normalized  $I_{peak}$  (right).

625 Before (green) and after 5-min NIR exposure (blue),  $I_{Ca}$  currents were recorded every 30 s.

626 Dotted lines in black and cyan represent the control groups of the vehicle (0.1% DMSO, details in  
627 Figure S4D-S4F) or rapamycin (direct application, adapted from Figure 5C).

628 All statistical data are given as mean  $\pm$  SEM.

629 See also Figure S4-S7.

630

631 **Figure 6.** P-D peptides inducibly suppress recombinant Cav1.3 channels and neuronal  $Ca^{2+}$   
632 oscillations.

633 (A-C) Rapamycin-induced membrane-targeting of Cav1.2 DCT-encoded PCRD<sub>C</sub>-DCRD<sub>C</sub> (P<sub>C</sub>D<sub>C</sub>)  
634 and effective CMI for Cav1.3 long ( $\alpha_{1DL}$ ). Membrane-anchored FRB-CFP-Ras recruited FKBP-  
635 YFP-P<sub>C</sub>D<sub>C</sub> onto the membrane by rapamycin-mediated FRB/FKBP binding (A). CMI was induced  
636 presumably by effective linkage between membrane-anchored P<sub>C</sub>D<sub>C</sub> and  $\alpha_{1DL}$ . Exemplars of  $Ca^{2+}$

637 current traces demonstrate the reduction in the peak amplitude ( $I_{peak}$ , dotted line) by 1  $\mu$ M  
638 rapamycin (A). Temporal files of  $S_{Ca}$  along with CMI potency (CMI) (B) and normalized  $I_{peak}$  (C)  
639 are to show rapamycin-induced attenuation. Data points in green and blue (connected by lines)  
640 represent the values of  $S_{Ca}$  or  $I_{peak}$  before and after rapamycin administration, respectively.  
641 (D-F) Rapamycin-induced membrane-targeting of P<sub>c</sub>D<sub>c</sub> and effective CMI for  $\alpha_{1DS}$ . Membrane-  
642 anchored FRB-CFP-Ras recruited FKBP-YFP-P<sub>c</sub>D<sub>c</sub> to the membrane by rapamycin-mediated  
643 FRB/FKBP binding (D). Effective CMI was induced presumably by effective connection between  
644 membranous P<sub>c</sub>D<sub>c</sub> and  $\alpha_{1DS}$ . Exemplars of  $Ca^{2+}$  current traces demonstrate the effective  
645 inhibition on  $I_{peak}$  by 1  $\mu$ M rapamycin (D). Temporal files of  $S_{Ca}$  and CMI (E) and normalized  $I_{peak}$   
646 (F) are shown, where data points in green and blue (connected by lines) represent the values of  
647  $S_{Ca}$  or  $I_{peak}$  before and after rapamycin application, respectively.  
648 (G) Experimental protocol for acute inhibition on cultured cortical neurons. 10  $\mu$ M rapamycin was  
649 added to neurons expressing membrane-anchored FRB-mRuby-Ras and cytosolic FKBP-CFP-  
650 P<sub>c</sub>D<sub>c</sub> by lentivirus transfection at DIV 11. Confocal imaging was performed before and after  
651 rapamycin treatment at the indicated timepoints.  
652 (H) The  $Ca^{2+}$  probes, P-D peptides and induction modules were co-expressed in neurons, subject  
653 to confocal fluorescence imaging: jGCaMP7b-X<sub>C</sub> (green), FRB-mRuby-Ras (red), and FKBP-CFP-  
654 P<sub>c</sub>D<sub>c</sub> (blue).  
655 (I) Time-lapse confocal images of  $Ca^{2+}$  dynamics in cortical neurons at DIV 11. Color-coded  
656 fluorescence intensities (as shown in the scale bar) of jGCaMP7b-X<sub>C</sub> reflect the concentrations of  
657 cellular  $Ca^{2+}$  signals.  
658 (J, K) Spontaneous  $Ca^{2+}$  activities in a control neuron (J) or a neuron with rapamycin-inducible  
659 CMI (K).  
660 (L, M) Key indices to quantify  $Ca^{2+}$  dynamics in the control group (L) and the neurons expressing  
661 CMI modules (M), including the average frequency (mHz) (left), the peak amplitude ( $\Delta F/F_0$ )  
662 (middle), and the  $Ca^{2+}$  influx AUC (calculated as  $\Delta F/F_0$  per min) (right).  
663 All statistical data are given as mean  $\pm$  SEM. One-way ANOVA followed by Dunnett for post hoc  
664 test is used for L, M: \*\*\*,  $p<0.001$ ; n.s.,  $p>0.05$ .  
665 See also Figure S8 and S9.  
666

667 **Figure 7.** Inducible inhibition of the Cav1 influx-neuritogenesis coupling in cortical neurons.  
668 (A, B) Neurite tracing and fluorescence  $Ca^{2+}$  imaging, before (DIV 11) and after (represented by  
669 DIV 12 and DIV 18) 10  $\mu$ M rapamycin induction, from the control neurons (A) versus the neurons  
670 expressing FRB-mRuby-Ras and FKBP-CFP-P<sub>c</sub>D<sub>c</sub> (B).

671 (C) Time-dependent profiles of neurite outgrowth, described by the correlation between the total  
672 length per single neuron ( $\mu\text{m}$ ) and the development stage (DIV), corresponding to the control  
673 neurons and the neurons subject to rapamycin-induced inhibition.  
674 (D) Time-dependent profiles of  $\text{Ca}^{2+}$  influx, described by the correlation between AUC ( $\Delta F/F_0$  per  
675 min) of  $\text{Ca}^{2+}$  oscillations and the development stage (DIV).  
676 (E) Temporal profiles of NGR (neurite growth rate,  $\mu\text{m}$  per day), which is derived from the total  
677 length-DIV curve (C). The dotted line represents the process of CMI induction.  
678 (F) Relationships between AUC (D) and NGR (E). The arrows indicate the temporal trends of  
679 neuronal development and its inhibition.  
680 All data points are calculated by mean  $\pm$  SEM.  
681 See also Figure S10.  
682

683 **Figure 8.** Summary of membrane-assisted molecular linkage and Cav1 inhibition with opto-  
684 chemogenetic induction.  
685 In neurons, Cav1 channels of two particular subgroups are targeted by CMI, represented by  $\alpha_{1\text{DS}}$   
686 channels (without DCT) or a fraction of  $\alpha_{1\text{DL}}$  channels (containing the DCT domain but not auto-  
687 inhibited). This study designs and implements two major types of CMI peptides: P+D, represented  
688 by PCRD and DCRD peptides derived from Cav1.3/1.4 DCT; and P-D, represented by Cav1.2-  
689 encoded PCRD-DCRD. These peptides are devised mainly based on our data suggesting that  
690 the Ras/CAAX tags are able to form a type of effective linkage between the Ras-anchored  
691 peptides and the proteins on the membrane (indicated by pink shade). For  $\alpha_{1\text{DS}}$ , the P+D peptide  
692 has proven effective in creating a linkage; and for apoCaM-bound  $\alpha_{1\text{DL}}$ , P-D serves as the  
693 suitable solution, achieving minimum CMI at the basal state and potent CMI upon induction. The  
694 induction method is a combination of rapamycin-mediated FRB/FKBP binding and NIR-  
695 responsive rapamycin@PDPP nanoparticles, as our practical solution for opto-chemogenetics  
696 targeting Cav1. As proof of principle, P-D peptides are able to induce acute, specific and potent  
697 inhibitions on channels and neurons. This provides new evidence from a unique perspective,  
698 supporting the notion that Cav1-dependent  $\text{Ca}^{2+}$  oscillations and neurite outgrowth are tightly  
699 coupled.  
700

701 **Methods**

702

703 **Molecular biology.** YFP-FKBP-DCRD (Addgene ID: 87453), YFP-FKBP-PCRD (Addgene ID: 704 87452), and FRB-CFP-Ras (Addgene ID: 87451) are available on Addgene. YFP-PCRD, YFP- 705 DCRD, CFP-DCRD, YFP-CCAT<sub>C</sub>, Cav1.3  $\alpha_{1DS}$  (AF370009.1) and Cav1.3  $\alpha_{1DL}$  (NM\_001389225.2) 706 are from previous study<sup>14,17</sup>. PCRD-CFP-Ras and DCRD-CFP-Ras were generated by replacing 707 the FRB in FRB-CFP-Ras with PCRD or DCRD, respectively. Constructs of PCRD-YFP-Ras, 708 CFP-Ras, YFP-Ras and CFP-YFP-Ras were made by appropriate design. For CFP-ER/K-YFP- 709 Ras, ER/K  $\alpha$ -helix (206 a.a.) were inserted between CFP and YFP sequence of CFP-YFP-Ras 710 with BspEI sites<sup>29</sup>. For Ras-mRuby-CCAT<sub>C</sub>, the Ras tag (KLNPPDESGPGCMSCKCVLS) was 711 PCR-amplified and fused to the N-terminus of mRuby, then inserted into YFP-CCAT<sub>C</sub> with KpnI 712 and NotI to replace YFP. For FKBP-YFP-PcDc, the FKBP was PCR-amplified with KpnI and 713 BamHI sites and fused to the N-terminus of YFP-PcDc and then cloned into pcDNA4 vector. Ras- 714 FKBP-YFP-PcDc, with PCR-amplified Ras tag was fused to the N-terminus of FKBP-YFP-PcDc, 715 inserting into a customized pcDNA3 vector via unique KpnI and XbaI sites.

716 **Transfection of cDNA constructs in HEK293 cells.** HEK293 cell line (ATCC) was free of 717 mycoplasma contamination, checked by PCR with primers 5'- GGCAGATGGGTGAGTAACACG - 718 3' and 5'- CGGATAACGCTTGCACCTATG -3'. For electrophysiology recording, cells were 719 cultured in 60 mm dishes. Recombinant channels were transiently transfected according to an 720 established calcium phosphate protocol<sup>19</sup>. We applied 4  $\mu$ g-5  $\mu$ g of cDNA encoding the desired 721 channel  $\alpha_{1D}$  subunit, along with 4  $\mu$ g of rat brain  $\beta_{2a}$  (NM\_053851.2) and 4  $\mu$ g of rat brain  $\alpha_{2\delta}$  722 (NM\_012919.3) subunits. Additional 2  $\mu$ g of cDNA was added as required in co-transfections. 723 cDNA for simian virus 40 T antigen (1  $\mu$ g) was also co-transfected to enhance the expression of 724 channels. Cells were washed with PBS 6 hours after transfection and maintained in culture 725 medium of supplemented DMEM, then incubated for at least 48 hours in a water-saturated 5% 726 CO<sub>2</sub> incubator at 37°C before whole-cell recordings. For confocal fluorescence imaging, HEK293 727 cells were cultured in 35 mm confocal dishes. 2  $\mu$ g of desired cDNA was transfected by 728 lipofectamine 2000 (Invitrogen) for 6 hours. Cells were used after 2 days.

729 **Whole-cell electrophysiological recording.** Whole-cell recordings of transfected HEK293 cells 730 were obtained at room temperature (25°C) using an Axopatch 700B amplifier (Axon Instruments). 731 Electrodes were pulled with borosilicate glass capillaries by a programmable puller (P-1000, 732 Sutter Instruments, Novato, CA) and heat-polished by a microforge (MF-830, Narishige, Japan), 733 resulting in 3-5 M $\Omega$  resistances, before series resistance compensation of about 70%. The 734 internal solutions contained (in mM): CsMeSO<sub>3</sub>, 135; CsCl, 5; MgCl<sub>2</sub>, 1; MgATP, 4; HEPES, 5; 735 and EGTA, 5, adjusted to 290~300 mOsm with glucose and pH 7.3 with CsOH. The extracellular

736 solutions contained (in mM): TEA-MeSO<sub>3</sub>, 135; HEPES, 10; CaCl<sub>2</sub> or BaCl<sub>2</sub>, 10, adjusted to  
737 300~310 mOsm with glucose and pH 7.3 with TEAOH. Whole-cell currents were generated from  
738 a family of step depolarization (-60 to +50 mV from a holding potential of -70 mV) or a series of  
739 repeated step depolarization (-10 mV from a holding potential of -70 mV). Currents were recorded  
740 at 2 kHz low-pass filtering. Traces were acquired at a minimum repetition interval of 30 s. P/8 leak  
741 subtraction was used throughout. Rapamycin (Solarbio, or Aladdin) was dissolved in DMSO as  
742 10 mM or 1 mM stock solution, stored at -20°C, and then diluted to 1 μM using extracellular Ca<sup>2+</sup>  
743 solution before electrophysiological recordings.

744 **2-hybrid 3-cube FRET.** All the FRET experiments were performed in Tyrode's buffer containing  
745 2 mM Ca<sup>2+</sup>. An inverted epi-fluorescence microscope (Ti-U, Nikon) was used with computer-  
746 controlled filter wheels (Sutter Instrument) to coordinate with dichroic mirrors for appropriate  
747 imaging at excitation, emission, and FRET channels. The following filters sets were utilized:  
748 excitation: 438/24 nm and 480/30 nm; emission: 483/32 nm and 535/40 nm; dichroic mirrors: 458  
749 nm and 505 nm. Fluorescence images were acquired with a Neo sCMOS camera (Andor  
750 Technology), which were analyzed with 3<sup>3</sup>-FRET algorithms coded in Matlab (Mathworks).

751 **Confocal fluorescence imaging.** Fluorescence images were obtained in HEK293 cells  
752 expressing membrane-localized CFP-tagged FRB and with YFP-tagged cytoplasmic FKBP-  
753 PCRD/DCRD on 30 mm confocal dishes. The images were captured at 30 s intervals. Cells were  
754 applied with 1 μM rapamycin, 0.1% DMSO (vehicle), and 25 μg/ml rapamycin@PDPP with or  
755 without the stimuli of 808 nm near-infrared laser using a Hi-Tech high power laser generator.  
756 Images were recorded with Olympus Fluoview FV300 or Zeiss LSM710 laser scanning confocal  
757 microscopes. Images were analyzed using Imaris 7.7.2 and ImageJ. Fluorescence imaging of  
758 cultured neurons was performed on Dragonfly High Speed Confocal Microscope (Dragonfly 200,  
759 Andor, England) and with Fusion software. Measurement of the total length for neurites was  
760 performed with Imaris 7.7.2 (Bitplane). Only non-overlapping neurons were selected for analysis  
761 and images of at least 21 neurons from two independent culture preparations were analyzed.

762 **Preparation of drugs@PDPP nanoparticles.** PDPP (0.5 μμ), DSPE-PEG2000-NH<sub>2</sub> (3 mg,  
763 Tansh-Tech Technology Company, Guangzhou, China) and rapamycin (0.5 mg) were dissolved  
764 in 1 ml of THF (tetrahydrofuran) and sonicated for 30 min, then DPPC (8 mg, Rowen) was  
765 dissolved in 200 μl of dichloromethane and sonicated. The two solutions were mixed and  
766 sonicated again for 30 min, and the mixture was quickly transferred to 9 ml of ultrapure water until  
767 the ultrasonic solution became clear, and then placed on a stirring table to stir for 8 hours. Argon  
768 was blown into the solution for 1.5 hours, and then the solution was placed on a stirring table to  
769 stir for 8 hours to obtain the rapamycin@PDPP solutions. The preparation of Cy5@PDPP  
770 solutions was similar to rapamycin@PDPP solutions. Briefly, rapamycin was not added to THF at

771 the first step. The mixture solution containing PDPP, DSPE-PEG2000-NH<sub>2</sub> and DPPC was  
772 heated to 65°C and then added with Cy5. After stirring for 10 min, the solution was ultrasonic for  
773 30 min to get Cy5@PDPP solution. In addition, the solution was transferred to a 3500k dialysis  
774 bag, and the excess organic solvent was removed by dialysis for two days to obtain the final  
775 rapamycin@PDPP or Cy5@PDPP nanoparticles. For Cy5&rapamycin@PDPP nanoparticles,  
776 rapamycin@PDPP solution was mixed with Cy5 (0.5 mg), heated to 65°C, stirred for 10 min, and  
777 sonicated for 30 min to obtain the Cy5&rapamycin@PDPP nanoparticles. All nanoparticle  
778 solutions were centrifuged at 6,500 rpm for 20 min to obtain concentrated solutions after  
779 ultrafiltration, and the concentration of nanoparticles was determined by ultraviolet absorption  
780 spectrum for subsequent experiments.

781 **Determination of UV absorption spectra of drug@PDPP nanoparticles.** Rapamycin@PDPP,  
782 Cy5@PDPP, and Cy5&rapamycin@PDPP nanoparticles were concentrated to a concentration  
783 greater than 500 µg/ml using a 100k ultrafiltration tube. The concentrated solution of 30 µl  
784 nanoparticles was diluted 20 times, then the sample was scanned by UV absorption spectrum.  
785 The UV absorbance of nanoparticles at 808 nm was recorded to calculate the concentration  
786 according to the standard curve equation of PDPP.

787 **Particle size measurement of drug@PDPP nanoparticles.** Ultrapure water was used to dilute  
788 the nanoparticles to an appropriate concentration for reserve. The dynamic light scattering  
789 particle size meter was turned on and preheated for 20 min in advance. 1 ml of the nanoparticle  
790 solution was added to the dedicated particle size colorimeter and put into the detection tank to  
791 measure the particle sizes.

792 **Analysis of temperature rise curve of rapamycin@PDPP nanoparticles.** 200 µl of ultra-pure  
793 water was added to a 96-well plate, and the temperature of the solution was recorded under near-  
794 infrared laser irradiation (808 nm, 5 min, Hi-Tech high power laser generator). Subsequently,  
795 rapamycin@PDPP nanoparticles with concentrations of 5 µg/ml, 10 µg/ml and 20 µg/ml were  
796 irradiated according to the requirements of sample addition and irradiation, and the change in  
797 solution temperature was recorded. The obtained data were imported into the drawing software  
798 for analysis, and the temperature rise statistics of nanoparticles were completed.

799 **Photothermal stability analysis of rapamycin@PDPP nanoparticles.** Rapamycin@PDPP  
800 (200 µl) nanoparticles were added to the 96-well plate and irradiated with a laser at 808 nm for 5  
801 min to achieve the highest temperature. Then the laser was turned off to allow cooling for 15 min  
802 to return to its original temperature. Real-time readings were taken every 30 seconds during  
803 heating and cooling cycles. This procedure was repeat 3 times to complete the whole cycle of  
804 heating and cooling.

805 **Near-infrared photothermal imaging analysis of rapamycin@PDPP nanoparticles.**

806 Rapamycin@PDPP (200  $\mu$ l) nanoparticles were placed in a 96-well plate, and the nanoparticles  
807 solution was irradiated by a laser at 808 nm. Photos were taken by a near-infrared imager (FLIR  
808 T420 infrared thermal imager camera) every 60 s, and the images were processed by data  
809 processing software to complete the near-infrared thermal imaging analysis of nanoparticles.

810 **Confocal fluorescence imaging of Cy5 released from Cy5&rapamycin@PDPP**

811 **nanoparticles.** 2 ml of prepared nanoparticles were dropped onto confocal dishes and  
812 irradiated with 808 nm laser for 0, 0.5, 1, 2, 3, 4 or 5 min, respectively. Then samples were dried  
813 and imaged with a Leica SP5 confocal laser scanning microscope to capture the fluorescence of  
814 Cy5.

815 **Dissection and culturing of cortical and hippocampus neurons.** Cortical neurons or  
816 hippocampus neurons were dissected from newborn ICR mice or SD rat, respectively. The  
817 tissues of cortex or hippocampus were isolated and then digested with 0.25% trypsin without  
818 EGTA for 15 min at 37°C. Then digestion was terminated by Dulbecco's modified Eagle medium  
819 (DMEM) supplemented with 10% fetal bovine serum (FBS) and 1% antibiotics. The cell  
820 suspension was sieved through a filter and centrifuged at 1,000 rpm for 5 min. The cell pellet was  
821 resuspended in DMEM supplemented with 10% FBS and were plated on poly-D-lysine-coated 35  
822 mm No. 0 confocal dishes (In Vitro Scientific). After 4 hours, neurons were maintained in  
823 Neurobasal medium supplemented with 2% B27 and 1% GlutaMAX-I (growth medium), and  
824 cultured in the incubator with temperature of 37°C and 5% CO<sub>2</sub>. All animals were obtained from  
825 Beijing Vital River Laboratory Animal Technology Co., Ltd. Procedures involving animals were  
826 approved by local institutional ethical committees (Beihang University).

827 **Virus infection on cultured neurons.** AAV2/DJ-*hSyn*-jGCaMP7b-X<sub>C</sub> virus was used for  
828 infection of cultured neurons (Hanbio Biotechnology, China). Other viruses include pSLenti-*hSyn*-  
829 FKBP-CFP-P<sub>c</sub>D<sub>c</sub>-WPRE, pSLenti-*hSyn*-FRB-mRuby-Ras-WPRE and pAAV2/9 -*hSyn*-NES-  
830 jRGECO1a-WPRE viruses (OBiO Technology, China). 1  $\mu$ l of 1  $\times$  10<sup>12</sup> v.g./ml of the desired  
831 adeno-associated virus or 1-2  $\mu$ l of 1  $\times$  10<sup>8</sup> TU/ml of the desired lentivirus were added to growth  
832 medium at DIV 0 unless otherwise indicated. Neuronal experiments were repeated independently  
833 at least twice.

834 **Transfection of cDNA constructs in neurons.** 1  $\mu$ g of cDNA mixed with 1  $\mu$ l PLUS<sup>TM</sup> reagent  
835 were transiently transfected into DIV 3-7 cultured neurons by Lipofectamine<sup>TM</sup> LTX (Invitrogen)  
836 with a typical protocol according to the manual. The Opti-MEM containing plasmids and  
837 Lipofectamine<sup>TM</sup> LTX was added to the Neurobasal medium for transfection. After 2 hours,

838 neurons were maintained in Neurobasal medium supplemented with 2% B27 and 1% GlutaMAX-I  
839 for at least 2 days before imaging.

840 **Data analysis and statistics.** Data were analyzed in Matlab, OriginPro and GraphPad Prism  
841 software. The values of standard error of mean (S.E.M) or standard derivation (S.D.) were  
842 calculated. Two-tailed Student's *t*-test, paired *t*-test, or One-way ANOVA followed by Dunnett for  
843 post hoc test were applied when applicable. \*,  $p<0.05$ ; \*\*,  $p<0.01$ ; \*\*\*,  $p<0.001$ ; n.s. or not  
844 significant,  $p>0.05$ .

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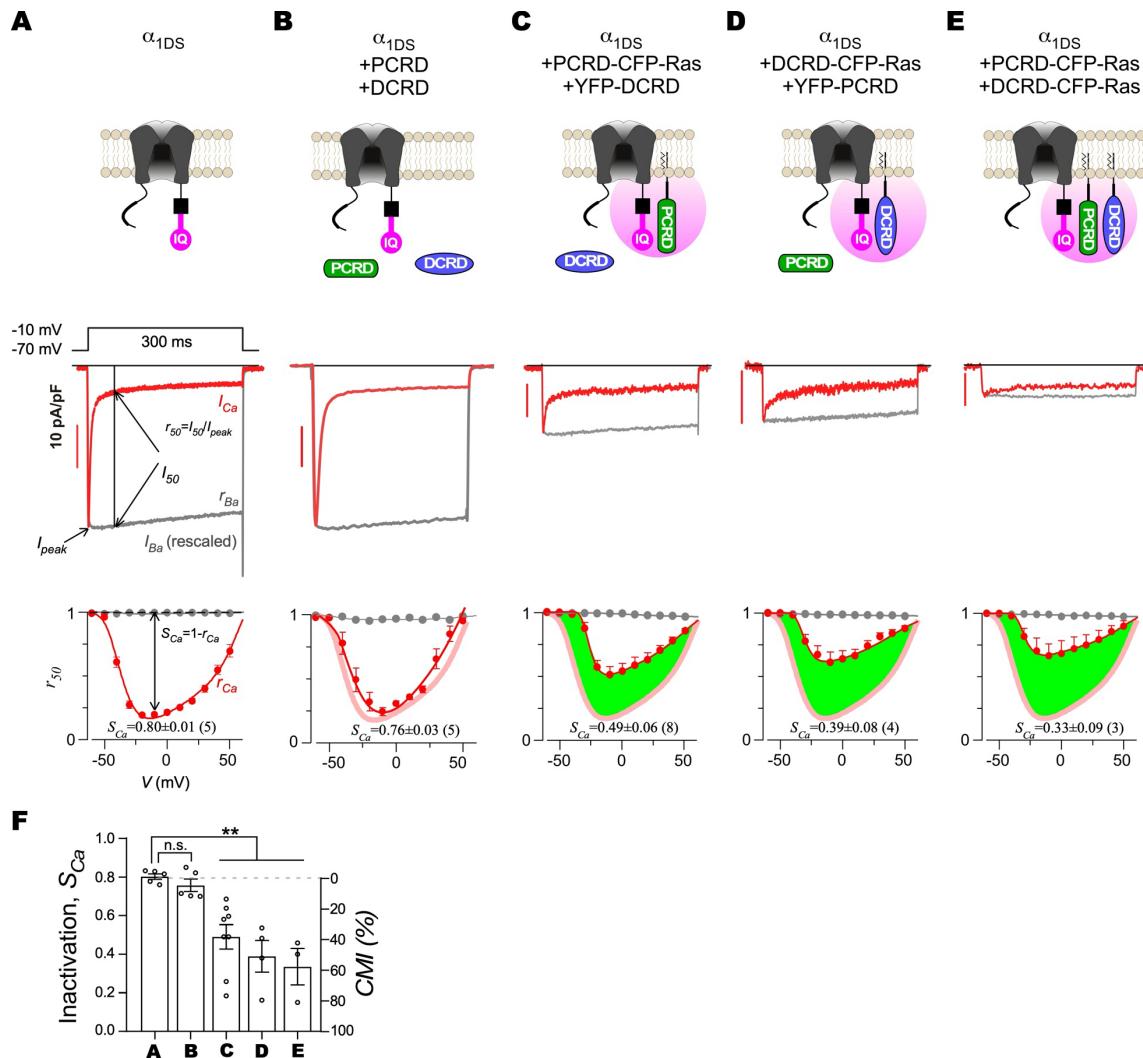
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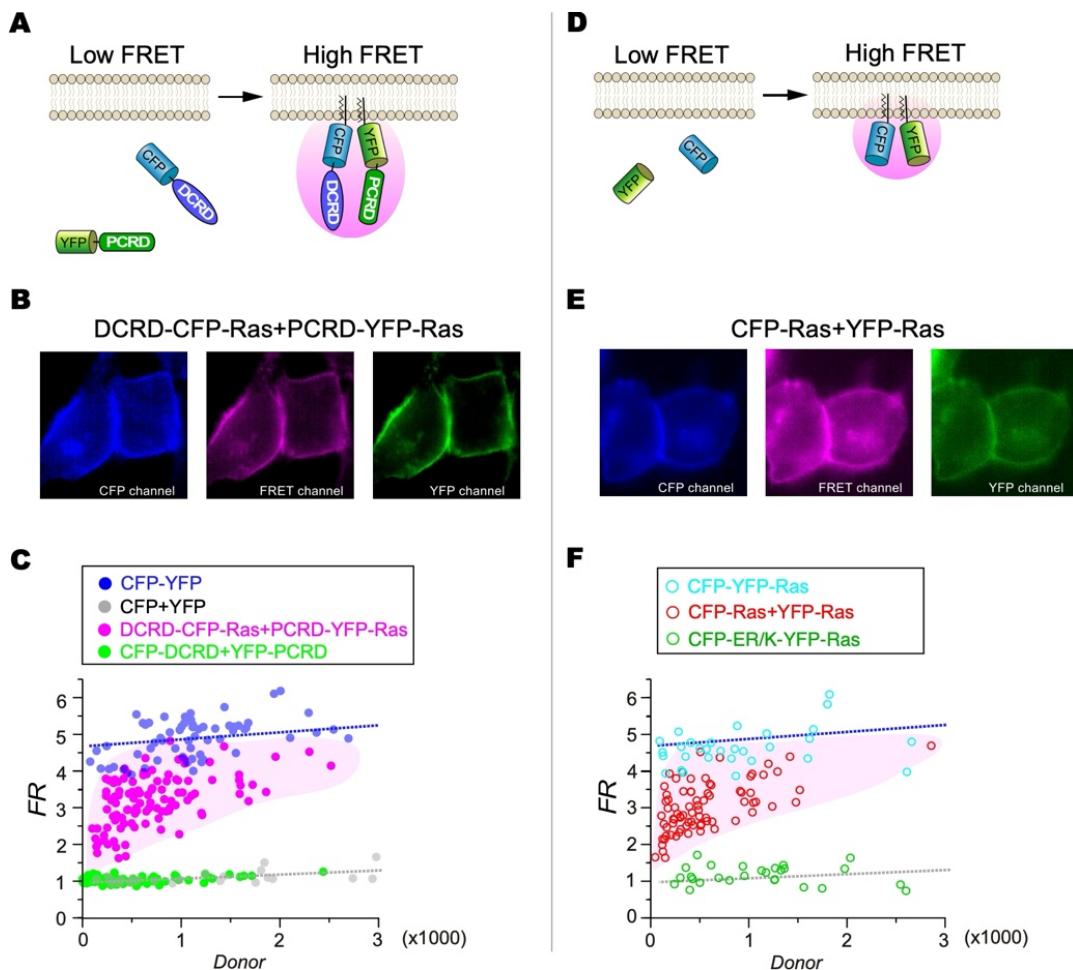
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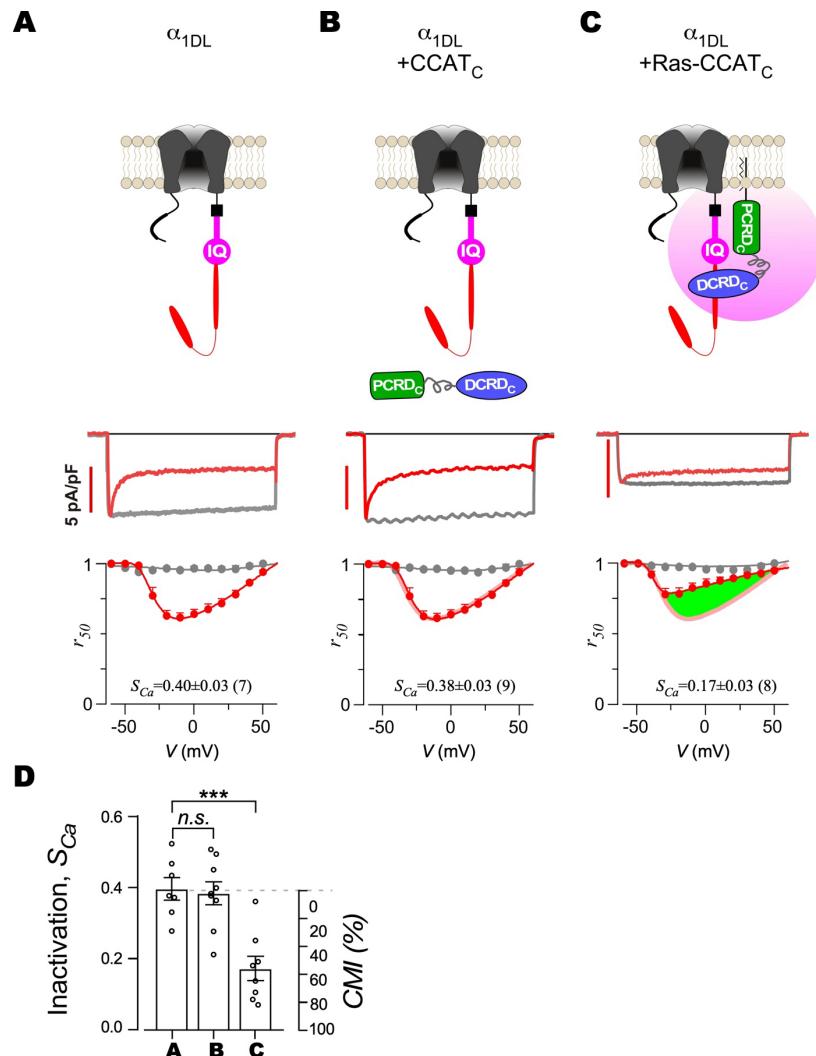
**Figure 1**



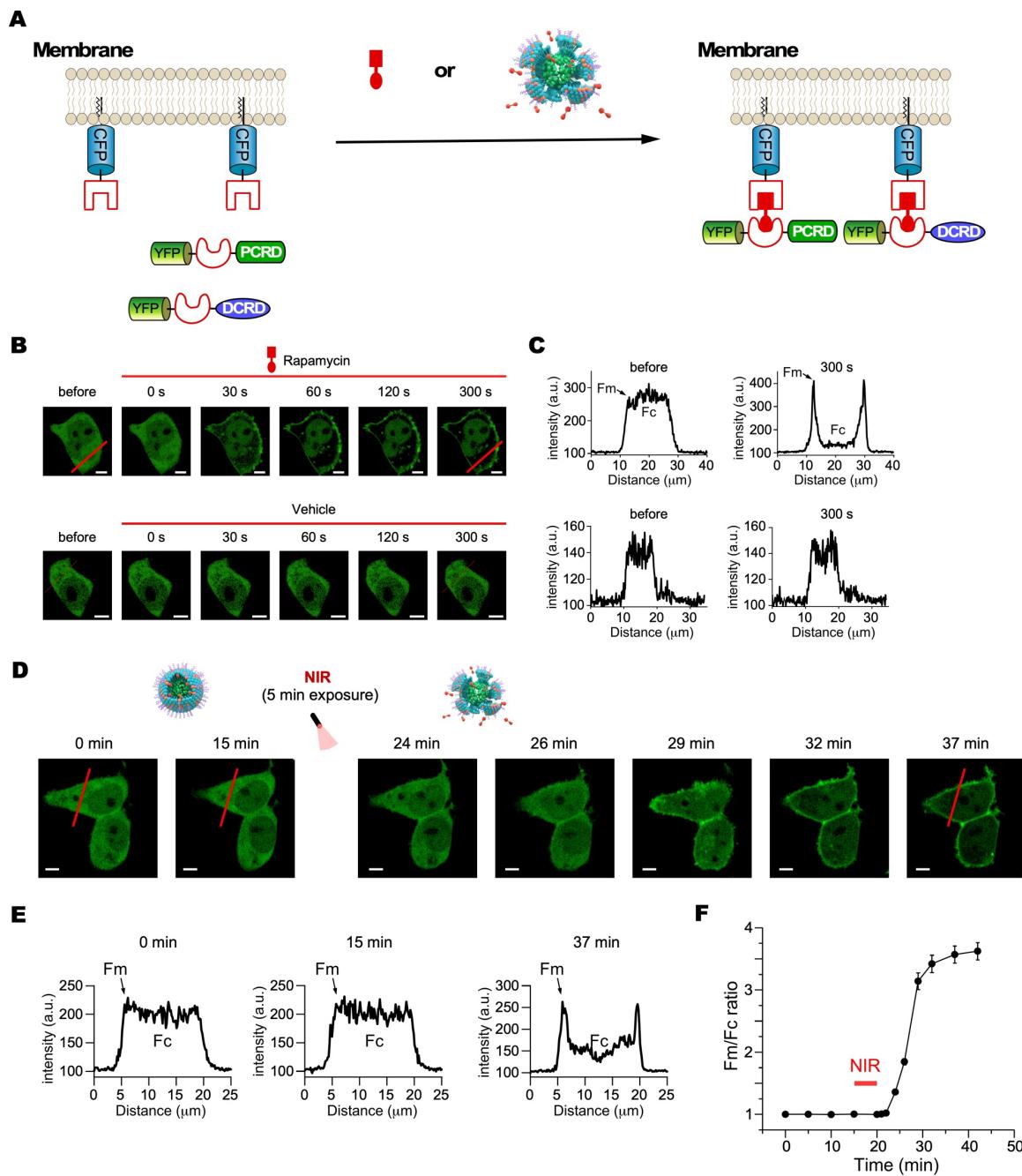
**Figure 2**



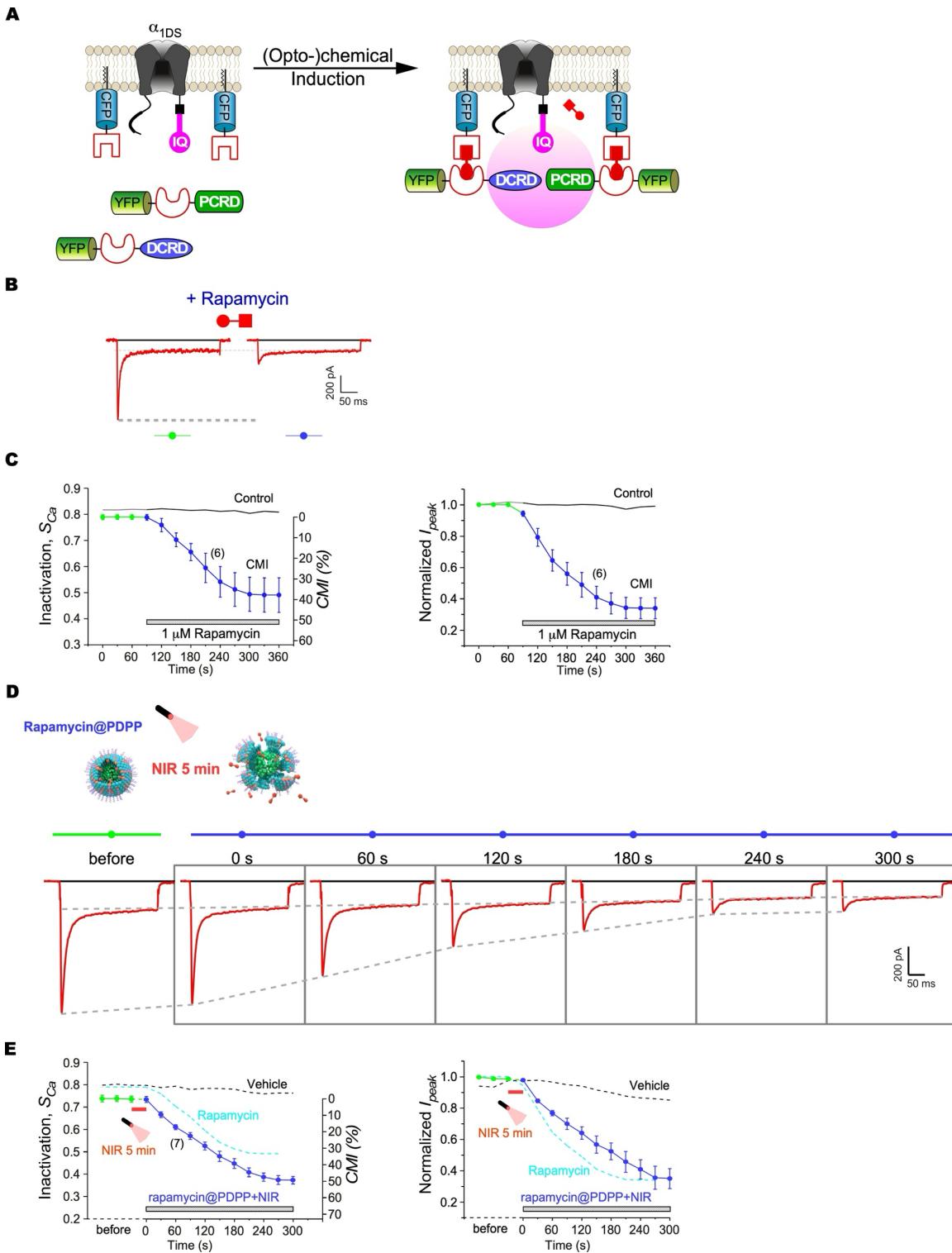
**Figure 3**



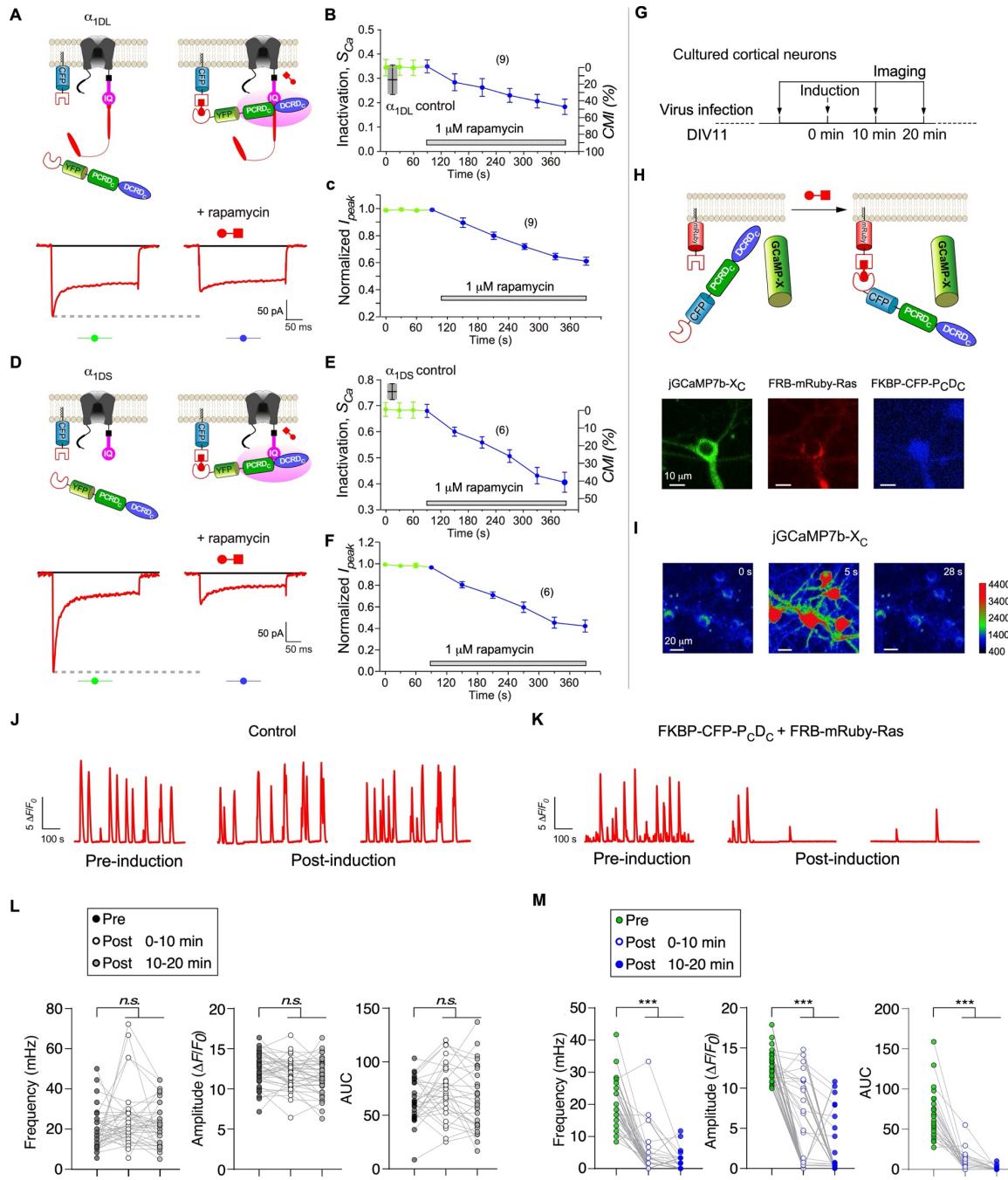
**Figure 4**



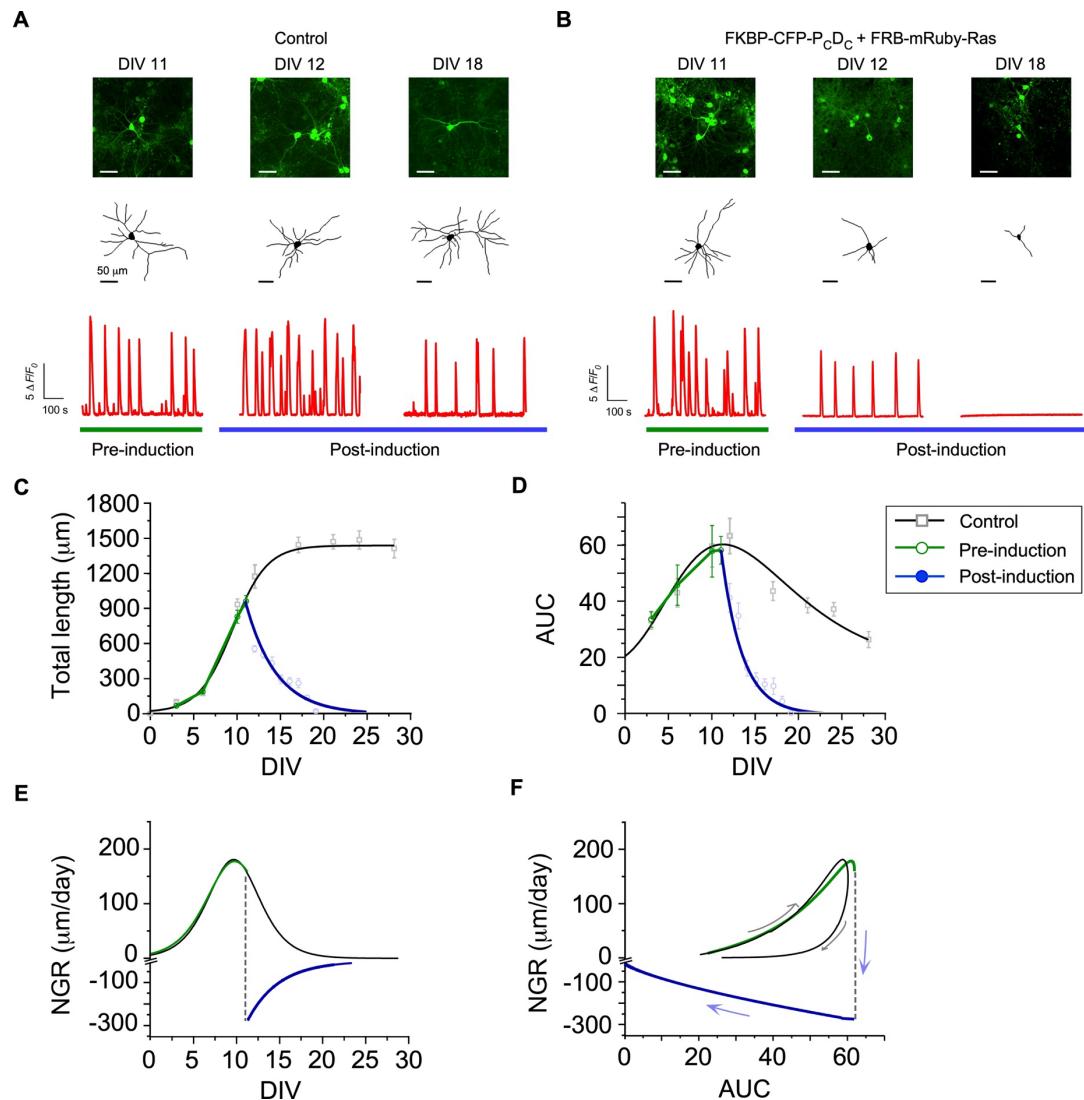
**Figure 5**



**Figure 6**



**Figure 7**



**Figure 8**

