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Vitamin B₁₂ modulates Parkinson's disease LRRK2 kinase activity through allosteric regulation and confers neuroprotection

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(Short title: Vitamin B₁₂ modulates LRRK2 activity and toxicity)

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39 Abstract

Missense mutations in Leucine-Rich Repeat Kinase 2 (LRRK2) cause the majority of familial 40 and some sporadic forms of Parkinson's disease (PD). The hyperactivity of LRRK2 kinase 41 42 induced by the pathogenic mutations underlies neurotoxicity, promoting the development of LRRK2 kinase inhibitors as therapeutics. Many potent and specific small molecule LRRK2 43 inhibitors have been reported with promise. However, nearly all inhibitors are ATP competitive 44 - some with unwanted side effects and unclear clinical outcome - alternative types of LRRK2 45 inhibitors are lacking. Herein we find 5'-deoxyadenosylcobalamin (AdoCbl), a physiological 46 form of the essential micronutrient vitamin B₁₂ as a mixed-type allosteric inhibitor of LRRK2 47 kinase activity. Multiple assays show that AdoCbl directly binds LRRK2, leading to the 48 alterations of protein conformation and ATP binding in LRRK2. STD-NMR analysis of a 49 LRRK2 homologous kinase reveals the contact sites in AdoCbl that interface with the kinase 50 domain. Furthermore, we provide evidence that AdoCbl modulates LRRK2 activity through 51 disruption of LRRK2 dimerization. Treatment with AdoCbl inhibits LRRK2 kinase activity in 52 cultured cells and brain tissue, and importantly prevents neurotoxicity in primary rodent cultures 53 as well as in transgenic C. elegans and D. melanogaster expressing LRRK2 disease variants. 54 Finally, AdoCbl alleviates deficits in dopamine release sustainability caused by LRRK2 disease 55 variants in mouse models. Our study uncovers vitamin B₁₂ as a novel class of LRRK2 kinase 56 modulator with a distinct mechanism, which can be harnessed to develop new LRRK2-based PD 57 58 therapeutics in the future.

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60 Key words: Vitamin B₁₂, LRRK2, Parkinson's disease, kinase

61 Introduction

Parkinson's disease (PD) is the most common chronic neurodegenerative movement 62 disorder affecting 1% of the world population over the age of sixty. The pathological hallmarks 63 of PD include the age-dependent loss of dopaminergic neurons in the substantia nigra and the 64 progressive spatiotemporal distribution of Lewy bodies and Lewy neurites¹. There is currently no 65 cure or disease-modifying therapy for PD, and available treatments target only the symptoms of 66 the disease but not its progression². In addition, the pathogenesis of PD remains poorly 67 understood. Discovered over a decade ago, Leucine-Rich Repeat Kinase 2 (LRRK2) has now 68 emerged as a major target not only for understanding the molecular basis of PD pathogenesis but 69 also for therapeutic intervention³. 70

Missense mutations in the PARK8/LRRK2 gene represent the prevalent cause for 71 autosomal-dominant PD^{4,5}. In addition, *LRRK2* mutations have been implicated in a significant 72 number of sporadic PD cases⁶⁻⁹. PD-linked LRRK2 variants associate with neuropathologies and 73 clinical symptoms indistinguishable from idiopathic PD cases^{10,11}, suggesting that both inherited 74 and sporadic forms of the disease share a similar pathogenic mechanism. LRRK2 encodes a 75 286kDa protein containing catalytic GTPase and kinase domains, as well as Armadillo, Ankyrin, 76 LRR and WD40 protein-protein interaction accessory domains (Fig. 1a). LRRK2 adopts a highly 77 compact dimer structure with extensive intramolecular interactions¹², and dimerization has been 78 proposed to correlate with LRRK2 kinase activity in vitro¹³. Of the six reported pathogenic 79 mutations, the G2019S variant has the highest prevalence¹⁴, accounting for 1% of sporadic and 80 5% of hereditary PD cases worldwide¹⁰, and up to 30-40% of all PD cases among North 81 Africans and Ashkenazi Jews¹⁵. Located in a conserved region of the kinase activation loop, the 82 83 G2019S variant has been consistently associated with increased LRRK2 kinase activity in

vitro^{13,16-18} and *in vivo*¹⁹⁻²². In addition, the G2019S variant also increases the phosphorylation of
a subset of Rab GTPases, recently identified as promising physiological LRRK2 substrates^{23,24}.

Multiple lines of evidence demonstrate that LRRK2 kinase hyperactivity caused by PD 86 pathogenic mutations, including G2019S, is causal to neurotoxicity or neuronal dysfunctions. 87 LRRK2 kinase inhibitors attenuate the cell toxicity caused by the G2019S mutation in primary 88 cortical neurons²⁵ and normalize G2019S-mediated postsynaptic abnormal activity in brain slice 89 cultures²⁶. In addition, LRRK2 kinase activity inhibitors prevent G2019S-potentiated α -90 synuclein accumulation in dopaminergic neurons^{27,28}, and their administration suppressed 91 neurodegeneration in C. elegans, D. melanogaster and mouse PD models^{25,29-31}. Consequently, 92 93 extensive effort has been devoted to the development of ATP-competitive small molecule 94 LRRK2 kinase inhibitors. Early generation kinase inhibitors displayed high potency against LRRK2, but lacked the specificity required to be considered for therapeutics^{25,32-34}. Among the 95 next generation, several inhibitors were highly potent and specific, but did not possess the 96 pharmacokinetic properties for effective brain penetration^{35,36}, while others elicited dose toxicity 97 and abnormal lung phenotypes in nonhuman primates³⁷. The current generation of ATP-98 competitive inhibitors show promise, but will require further modification³⁸ and preclinical 99 testing³⁹ before their therapeutic potential can be fully assessed. Remarkably, LRRK2 kinase 100 101 activity inhibitors displaying alternative mechanisms of inhibition to these ATP-competitive 102 inhibitors have yet to be reported.

discovered 5'-103 Here we that the FDA-approved natural compound deoxyadenosylcobalamin (AdoCbl), one of two physiological forms of the essential human 104 micronutrient vitamin B₁₂, is a unique mixed-type allosteric modulator of LRRK2 kinase 105 activity. AdoCbl is capable of disturbing LRRK2 protein conformation and dimerization. In 106

addition, we explore the ability of AdoCbl to prevent mutant *LRRK2* induced neurotoxicity and Parkinson-like phenotypes in PD animal models. We conclude that vitamin B_{12} is a novel type of LRRK2 kinase modulator, which is distinguished from other ATP competitive inhibitors. Future experiment should investigate the structural basis for LRRK2- vitamin B_{12} interaction that can be harnessed to develop new therapeutics for LRRK2-based PD.

112

113 **Results**

114 Identification of vitamin B₁₂ as a LRRK2 kinase activity inhibitor

AdoCbl (Supplimentary information, Fig. S1a) was identified as a kinase activity inhibitor of 115 FLAG-tagged wild type (WT) LRRK2 purified from BAC transgenic mouse brain¹⁹ 116 (Supplimentary information, Fig. S1b) from a high-throughput screen (HTS) of a small library of 117 2,080 FDA-approved compounds (Supplimentary information, Table S1). To assay LRRK2 118 kinase activity we measured the time-resolved fluorescence resonance energy transfer (TR-119 FRET) between phosphorylated Fluorescein-LRRKtide peptide and Terbidium-labeled anti-120 pLRRKtide antibody⁴⁰. In this screen AdoCbl displayed a half-maximal inhibitory concentration 121 (IC₅₀) of 1.2 μ M (Fig. 1b). Vitamin B₁₂ consists of a central cobalt ion that is equatorially 122 chelated by a tetradentate corrin macrocycle and up to two axially coordinating ligands 123 (Supplimentary information, Fig. S1a). The 'lower' (α)-coordinating ligand is usually a 124 dimethylbenzimidazole (DMZ) base that connects to the f-side chain of the chelator by an α -125 ribazole containing backbone⁴¹. 126

127 Vitamin B_{12} has additional forms in addition to AdoCbl, including cyanocobalamin 128 (CNCbl), hydroxycobalamin (HOCbl), and methylcobalamin (MeCbl), which are distinguished 129 by their (β)-coordinating ligand⁴² (Supplimentary information, **Fig. S1a**). Only MeCbl and AdoCbl are physiologically active in cells, as coenzymes of MeCbl-dependent methionine synthase and AdoCbl-dependent methylmalonyl coenzyme A mutase⁴². In humans, these enzymatic reactions play a key role in the metabolism of amino acids, nucleotides, and fatty acids, in addition to the normal functioning of the nervous system, and the formation of red blood cells⁴³.

Similar to AdoCbl, these other forms of vitamin B₁₂ inhibited the LRRK2 catalyzed 135 phosphorylation of the LRRKtide peptide with an IC₅₀ of ~1 μ M (Fig. 1b), suggesting that the 136 nature of the (β) -coordinating ligand was not essential for the inhibition. Next, we validated the 137 LRRK2 kinase inhibition by the various forms of vitamin B₁₂ using highly pure strep-tagged 138 LRRK2-WT expressed in HEK293 cells (Supplimentary information, Fig. S1c). To this end, we 139 assayed LRRK2 autophosphorylation (Fig. 1c) and phosphorylation of the generic substrate 140 myelin basic protein (MBP) (Fig. 1d) by measuring the incorporation of radioactive ³²P. In both 141 cases, we determined IC₅₀s in the ~10 μ M range for each form of vitamin B₁₂. We note that 142 AdoCbl inhibited LRRK2-G2019S catalyzed phosphorylation of the recently identified LRRK2 143 physiological substrate Rab $10^{23,24}$ also with a ~10 μ M IC₅₀ (Fig. 1e). 144

Next, we derived Mouse Embryonic Fibroblast (MEF) cells from our LRRK2-G2019S 145 BAC transgenic mice¹⁹, and incubated them with AdoCbl, CNCbl, HOCbl, or MeCbl to measure 146 their effect on LRRK2 autophosphorylation. As a readout we measured autophosphorylation 147 using anti-LRRK2 pS935⁴⁴ and pS1292²⁰ antibodies. In this system both antibodies reported 148 decreased LRRK2 autophosphorylation levels upon treatment with the established LRRK2 GNE-149 1023²⁰ inhibitor (Supplimentary information, Figs. S2a-b). These MEFs constitutively 150 151 overexpress the pathogenic LRRK2-G2019S variant, which in accordance with literature displayed kinase hyperactivity compared to LRRK2-WT¹⁹⁻²² (Supplimentary information, Fig. 152

S2c). Interestingly, we found that only AdoCbl, but not the other forms of vitamin B_{12} , exhibited 153 inhibition of LRRK2-G2019S autophosphorylation in MEF cells with an IC₅₀ of ~10 µM, similar 154 to that measured in vitro (Figs. 1f-g). We observed a similar inhibition profile for the different 155 forms of vitamin B₁₂ in macrophages derived from the LRRK2-G2019S transgenic mice 156 (Supplimentary information, Fig. S2d). The lack of inhibition displayed by CNCbl, HOCbl, or 157 MeCbl is not understood at present, but one possibility is that differences in cellular uptake, 158 localization and metabolism in the cells affect their efficacy compared to AdoCbl. Because 159 AdoCbl showed the greatest potential for LRRK2 inhibition in cultured cells we focused our 160 research efforts on this physiological form of vitamin B₁₂. 161

162

163 AdoCbl binds directly to LRRK2

164 We next tested if AdoCbl binds directly to human LRRK2. We first used agarose functionalized with AdoCbl to pull-down purified LRRK2, which could be eluted as a function of AdoCbl 165 concentration (Fig. 2a and Supplimentary information, Fig. S3). In thermal shift assays 166 (TSA)⁴⁵ the melting temperature of LRRK2 increased substantially from 50 to 54°C in the 167 presence of AdoCbl (Fig. 2b). This thermostabilization by AdoCbl was comparable to that 168 measured in the presence of the established LRRK2 kinase inhibitor PF-06447475³⁸. 169 Furthermore, we applied microscale thermophoresis (MST)⁴⁶ to measure the binding affinity of 170 AdoCbl for LRRK2 and determined an apparent dissociation equilibrium constant (K_D) of 12.0 171 and 4.1 µM for purified LRRK2-WT and LRRK2-G2019S, respectively (Fig. 2c), in agreement 172 with our IC₅₀ values. As a validation of the MST assay, under the same conditions LRRK2-173 G2019S binds PF-06447475 with a K_D of 70 nM (Fig. 2d), in line with the reported IC₅₀ of 11 174 nM for this inhibitor³⁸. 175

176 We next sought to identify the functional groups in AdoCbl responsible for interacting with LRRK2 by using an extension of the saturation transfer difference (STD) NMR method 177 termed ATP-STD NMR⁴⁷. This method was developed to screen protein kinase inhibitors by 178 recording STD signals in the presence of competing ATP⁴⁸. Due to an unstable and aggregation 179 prone human LRRK2 kinase domain, which makes it intractable for biophysical/structural 180 analysis, we decided to use the humanized kinase domain of the Roco4 protein from 181 Dictyostelium discoideum⁴⁹. The kinase domain of Roco4 (amino acids 1018–1292) has a 47% 182 similarity with the kinase domain of human LRRK2 (amino acids 1879-2138), and its 183 humanized variant, where amino acid residues F1107 and F1161 are substituted for Leucine to 184 mimic the residues L1949 and L2001 in LRRK2, is considered a valuable model for the 185 structural characterization of LRRK2 kinase inhibitors^{47,49}. We first verified that AdoCbl 186 inhibited autophosphorylation of the humanized Roco4 kinase (Fig. 2e) with an IC₅₀ of 73.6 µM 187 (Fig. 2f). In agreement with published data⁴⁷, we obtained a clear STD signal for ATP binding to 188 Roco4 kinase (Fig. 2g, orange spectrum). Addition of AdoCbl to the ATP/Roco4 sample in a 189 1:1 AdoCbl:ATP ratio resulted in the emergence of additional STD signals corresponding to 190 AdoCbl protons, confirming a direct binding of AdoCbl to Roco4. At a 10:1 AdoCbl:ATP ratio, 191 the STD peaks corresponding to AdoCbl became much stronger while ATP peaks weakened, 192 demonstrating that AdoCbl diminished ATP binding to Roco4 kinase. Stronger STD signals 193 likely correspond to AdoCbl protons in the vicinity or at the protein binding interface. These 194 protons are distributed around one side of the molecule and are contributed by the adenine, 195 corrin, and DMZ moieties (Fig. 2h). 196

197

198 AdoCbl is a mixed-type allosteric LRRK2 kinase inhibitor

199 The current collection of commercially available LRRK2 kinase inhibitors, including the latest generation PF-06447475³⁸ and MLi-2³⁹, are considered to be ATP-competitive, with the 200 exception of FX2149 that is GTP-competitive⁵⁰. To determine the mode of inhibition of vitamin 201 B_{12} we measured V_{max} and K_m as a function of ATP and in the presence of an increasing 202 concentration of AdoCbl. For our *in vitro* inhibition kinetics assays we used purified full-length 203 LRRK2-WT and LRRK2-G2019S to measure relative velocity based on the quantification of 204 LRRK2 autophosphorylation pS1292 signal (Supplimentary information, Fig. S4). Consistent 205 with literature^{13,16-18}, the relative velocity of LRRK2-G2019S was two-fold higher than LRRK2-206 WT (Supplimentary information, Table S2). Titration of AdoCbl caused a decrease in apparent 207 V_{max} and an increase in apparent K_m (Figs. 3a-c), suggesting mixed-type inhibition, as confirmed 208 by reciprocal Lineweaver-Burk plots of the data (Figs. 3b-d and Supplementary information, 209 210 Table S2). Mixed-type inhibitors generally bind to an allosteric site and can affect an enzyme's ability to catalyze a reaction and to bind its substrate⁵¹. To further characterize the mode of 211 AdoCbl inhibition of LRRK2 we measured the competition with AMP-PNP using MST (Fig. 212 3e). Under our assay conditions AMP-PNP displayed a K_D of 0.9 µM against LRRK2 (Fig. 3f). 213 In further support of the mixed-inhibition mode of action, increasing concentrations of AMP-214 PNP reduced but did not overcome the binding of AdoCbl to LRRK2 (Fig. 3e). 215

We further compared AdoCbl with the reported ATP-competitive LRRK2 inhibitor IN-1 (LRRK2-IN-1) for its ability to inhibit the human LRRK2 A2016T variant. The A2016T substitution in the ATP-site of LRRK2 results in a normally active enzyme, which is, however, significantly less sensitive to the ATP-competitive inhibitors H-1152 and sunitinib⁵², and up to 400-fold less sensitive against LRRK2-IN-1 compared to the WT protein³⁵. Using the G2019S mutation as a background we confirmed that the A2016T substitution confers resistance to LRRK2-IN-1 (Supplimentary information, Figs. S5a-b). In contrast, this variant displayed a similar level of inhibition by AdoCbl as the G2019S protein alone. Similarly WT Roco4 from *D. discoideum*^{47,49}, which has a 241-fold lower affinity for LRRK2-IN-1 than humanized Roco4⁴⁷, was inhibited by the same degree as the humanized version (Supplimentary information, Figs. S5c-d). The data suggests distinct mechanisms of LRRK2 binding between LRRK2-IN-1 and AdoCbl.

228

229 AdoCbl induces conformational changes and disrupts dimerization of LRRK2

Allosteric inhibitor binding normally induces a conformational change in the enzyme that results 230 in reduced affinity for the substrate⁵³. To test the possibility of an AdoCbl-induced 231 conformational change in LRRK2 we conducted limited proteolysis assays in the presence of 232 AdoCbl. The addition of AdoCbl markedly increased the susceptibility of LRRK2 to proteolysis 233 by both trypsin and chymotrypsin (Fig. 4a). At a 90-min. interval, we showed that the presence 234 of AdoCbl significantly increases the sensitivity of trypsin degradation of LRRK2 protein in a 235 dose dependent manner (Fig. 4b). This observation does not result from an enhancement of the 236 intrinsic activity of these proteases, as demonstrated by the fact that AdoCbl did not affect the 237 proteolysis rate of a control kinase TBK1 (Supplimentary information, Fig. S6a). Of note, the 238 well-known ATP-competitive LRRK2 kinase inhibitors GSK2578215A³⁶, GNE-1023²⁰ and PF-239 06447475³⁸, produced the opposite effect as AdoCbl, i.e. they protected LRRK2 from proteolytic 240 digestion (Fig. 4b), whereas AMP-PNP had no effect (Supplimentary information, Fig. S6b). 241 For more evidence in support of conformational changes in LRRK2 upon binding to AdoCbl we 242 measured the intrinsic fluorescence of LRRK2 as a function of AdoCbl. With 27 tryptophan 243 amino acid residues, the fluorescence emission spectra of LRRK2 at an excitation wavelength of 244 295 nm displayed an AdoCbl dose-dependent decrease in fluorescence intensity (Fig. 4c). Note 245

that AdoCbl absorbs light at 295 nm and 340-360 nm, thus it was necessary to correct for the
inner-filter effect (Supplimentary information, Figs. S6c-d). Such a decrease in fluorescence
intensity is consistent with conformational changes in LRRK2 where initially buried tryptophan
residues become exposed to the solvent as a function of AdoCbl.

We hypothesize that the effect of AdoCbl binding in LRRK2 conformation alters 250 oligomeric state of LRRK2. Ample evidence now supports dimeric LRRK2 as the main 251 oligomeric species of the enzyme in vitro¹², and available data indicates that LRRK2 252 dimerization correlates with kinase activity¹³. We quantified cellular LRRK2 dimers using a 253 novel adaptation of the proximity biotinylation approach. We expressed recombinant LRRK2 254 protein fusion to BirA (biotin ligase) or to AP (acceptor peptide) in HEK293T cells in the 255 presence of vehicle or AdoCbl. As a negative control BirA- and AP-LRRK2 expressing cells 256 257 were lysed without having been given the biotin pulse; and in such samples, the number of labeled LRRK2 dimers purified on streptavidin plates is negligible (Fig. 4d). Expression levels 258 of both forms of LRRK2 are comparable as determined by ELISA or Western immunoblot. Cells 259 co-expressing BirA-LRRK2/AP-LRRK2 contain robust levels of biotinylated LRRK2 dimers, 260 normalized to total expression of LRRK2. However, in cells treated with AdoCbl, we detected a 261 dose-dependent reduction in the levels of LRRK2 dimers, both in cells expressing WT LRRK2, 262 as well as in cells expressing the LRRK2-G2019S or LRRK2-I2020T variant proteins (Fig. 4e). 263 In contrast to other LRRK2 kinase inhibitors⁵⁴⁻⁵⁶, we did not observe a significant decrease in 264 LRRK2 expression following treatment with AdoCbl (Figs. 4d-f), indicating that this compound 265 disrupts LRRK2 dimers without affecting expression. 266

AdoCbl protects dopaminergic neurons from *LRRK2-G2019S* induced neurotoxicity in C. elegans

The degeneration of dopaminergic (DAergic) neurons is the pathological hallmark of PD^2 . 270 271 However, recapitulating this phenotype in mammalian models of LRRK2-linked PD has been a challenge, nearly all reported genetic models (either transgenic overexpression or knock-in) 272 failed to display clear neurodegeneration^{19,57-59}. In contrast, invertebrate PD models of LRRK2 273 show a robust degeneration of DAergic neurons⁶⁰⁻⁶³. The DAergic pathway in C. elegans is 274 important for the basal slowing response, a behavior by which worms slow their locomotive 275 movement when encountering food⁶⁴. Transgenic *LRRK2-G2019S* nematodes exhibit progressive 276 impairment of the basal slowing response, but this locomotive behavioral deficit can be restored 277 by treatment with the LRRK2 kinase inhibitors LRRK2-IN-1 and TTT-3002³⁰. In this C. elegans 278 model of LRRK2 PD, these two inhibitors targeted specifically LRRK2, as they were ineffective 279 against the neurodegenerative phenotype displayed in transgenic LRRK2-A2016T/G2019S worms 280 carrying the inhibitor-resistant LRRK2 A2016T mutation³⁰. Therefore, we selected the 281 established human LRRK2-G2019S C. elegans model to ask if AdoCbl protects against DAergic 282 neuron degeneration. LRRK2-G2019S transgenic worms that were fed up to 1.25 µM AdoCbl 283 during their larval stage resisted the locomotive behavioral deficit on adult day 3 in a dose-284 dependent manner with a half-maximal effective concentration (EC₅₀) value of 0.53 µM (Fig. 285 5a). Consistent with the lack of an effect of the LRRK2 A2016T mutation on the inhibition by 286 AdoCbl in vitro (Supplimentary information, Figs. S5a-b), treating transgenic LRRK2-287 A2016T/G2019S worms with AdoCbl resulted in a rescued neurodegenerative phenotype 288 289 (Supplimentary information, Fig. S7a). The data also supports the distinct mechanism of AdoCbl in blocking LRRK2 activity and LRRK2 associated neurodegeneration from IN-1. Additionally, 290

291 the AdoCbl-induced rescue was observed in transgenic LRRK2-R1441C worms as well, which also display an impaired basal slowing response (Supplimentary information, Fig. S7b). C. 292 elegans possess eight DAergic neurons that can be readily visualized by coupling GFP to a DA-293 294 neuron-specific promoter. Four GFP-tagged DAergic neurons of cephalic sensilla (CEP neurons) in the head were examined using fluorescence microscopy. Overexpression of LRRK2-G2019S 295 causes age-dependent degeneration of these DAergic neurons, where less than 60% remain on 296 adult day 9, compared to 75% in control worms expressing GFP alone. When fed 1.25 µM 297 AdoCbl during their larval stage, age-synchronized adult LRRK2-G2019S worms displayed a 298 robust increase in DAergic neuron survival, nearly back to the levels of the GFP-control worms 299 (Figs. 5b-c). As in the case of TTT-3002 and LRRK2-IN-1³⁰, treatment of WT worms 300 expressing GFP marker alone with AdoCbl did not result in any significant changes in basal 301 302 slowing response or DAergic neuron survival, suggesting that the effect of AdoCbl was specific to the transgenic LRRK2-G2019S worms. 303

304

305 AdoCbl prevents LRRK2-G2019S induced neurotoxicity in D. melanogaster model of PD

Signal regulation in the human retina depends largely on dopamine⁶⁵, and this process can be 306 affected by the loss of DA that is characteristic in PD patients⁶⁶. In D. melanogaster, vision is 307 also regulated by comparable DAergic circuits^{67,68}. Transgenic overexpression of the human 308 LRRK2-G2019S gene in D. melanogaster has been shown to elicit DA-dependent retinal 309 degeneration and loss of visual response due to an abnormal increase in contrast sensitivity, 310 which can be rescued using LRRK2 kinase activity inhibitors^{31,69}. After feeding Drosophila 311 larvae with AdoCbl at concentrations up to 2.5 µM, we recorded the visual response to flickering 312 blue light in 1-day-old flies. Our Fast Fourier Transform (FFT) algorithm separates this visual 313

314 response according to the first three stages of the fly visual system: photoreceptors, lamina neurons, and medulla neurons (Fig. 6a). Increasing the contrast of the flickering light resulted in 315 a greater retinal response of the fly, revealing characteristic Contrast Response Functions (CRFs) 316 that are dependent on the combination of genotype and AdoCbl treatment (Fig. 6b). In the 317 photoreceptors and lamina neurons, the physiological response increased and plateaued at 70% 318 applied contrast, while the medulla neurons generated a complex response, as indicated by the 319 peak response at 40% applied contrast. In each case, flies with dopaminergic expression of 320 LRRK2-G2019S have a much greater response compared to those expressing LRRK-WT. 321 Notably, feeding flies with 2.5 µM AdoCbl throughout larval life rescued the LRRK2-G2019S 322 phenotype completely, with the photoreceptor, lamina neurons and medulla neurons all showing 323 324 a CRF close to that of WT flies (Fig. 6b). Furthermore, titration of AdoCbl revealed an EC_{50} 325 between 250 and 500 nM in all three stages of the visual pathway (Fig. 6c, and Supplimentary information, Fig. S8). To determine the specificity of AdoCbl toward LRRK2 kinase activity, 326 we tested a 2.5 µM concentration against flies with a kinase-dead background (LRRK2-G2019S-327 328 K1906M) and found no significant change in any of the three measured regions (Fig. 6d). In contrast to the results from C. elegans, treating wild-type drosophila with a 2.5 µM 329 concentration of AdoCbl significantly rescues the visual response (Fig. 6e). Finally, we tested for 330 331 off-target effects by feeding 2.5 µM of AdoCbl to flies with little expression of the LRRK2 homolog (dLRRK) and found no statistically significant difference between any of the 332 photoreceptor, lamina and medulla neurons (Fig. 6f). 333

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AdoCbl prevents *LRRK2-G2019S* induced neurotoxicity and rescues deficits in dopamine
 transmission in LRRK2-PD mouse models

Previous studies have demonstrated that transient overexpression of *LRRK2-G2019S*, but not *LRRK2-WT*, leads to toxicity in primary cortical neuron cultures^{70,71}. We employed the same approach and found that transfection of *LRRK2-G2019S* indeed caused neurotoxicity in dissociated cortical neurons, as evidenced by apoptotic nuclear features. Treatment of the transfected neurons with AdoCbl, however, suppressed the frequency of apoptotic neurons in a dose-dependent manner (**Fig. 7a**). As a positive control in this assay, the most recent generation *LRRK2* inhibitor MLi-2³⁹ showed potent protection at a 10 nM concentration.

The lack of frank neurodegeneration in nearly all LRRK2 transgenic mouse models 344 345 prevents us from testing AdoCbl neuroprotection in vivo. However, a common pathological feature for reported LRRK2 models is the deficit in DA transmission^{19,72}. To investigate if 346 AdoCbl prevents such a defect, we first tested the inhibition of neuronal LRRK2 by AdoCbl 347 using striatal brain slices from LRRK2-G2019S BAC transgenic mice under ex vivo conditions. 348 Striatal slices were incubated in oxygenated artificial cerebrospinal fluid (ACSF) for two hours 349 in the presence of LRRK2 inhibitor or vehicle. Administration of AdoCbl in the ACSF caused 350 dose-dependent inhibition of LRRK2 autophosphorylation in slice lysates (Fig. 7b). Similarly, 351 GNE-1023 exhibited dose dependent inhibition of LRRK2 under the same conditions (SI 352 Supplimentary information, Figs. S9a-b). Compared to WT controls, LRRK2-G2019S BAC 353 transgenic mice were reported to have decreased sustainability of evoked DA release at the age 354 of 12 months old¹⁹. Therefore, we measured single-pulse evoked DA release sustainability in 355 striatal slices from LRRK2-G2019S BAC transgenic mice and WT littermates at the age of 12-15 356 months using Fast Scan Cyclic Voltammetry (FSCV)⁷³(Figs. 7c-d). A bipolar stimulating 357 electrode was placed in the dorsal striatum ~150 µm from the recording microelectrode and 358 359 depolarizing currents were applied at 2-minute intervals for 20 minutes. In control slices, the

amplitude of DA release at a given site evoked by single pulses decreased with the first few stimulations and declined by 20% by the end of the 20-minute period. Consistent with a previous report¹⁹, this decline was much more profound in the brain slices of the G2019S mice. Remarkably, AdoCbl alleviated this deficit and restored the sustainability to the level of WT control slices.

In addition, we examined the effects of AdoCbl using striatal slices from another preclinical *LRRK2-R1441G* BAC transgenic mouse model. The declined DA release evoked by 2-minute intervals during a 20-minute period was robust in slices from LRRK2-R1441G mice compared to WT controls, and again, AdoCbl alleviated this deficit, restoring the sustainability to the level of WT control slices (**Figs. 7e-f**). Taken together, our data demonstrates that AdoCbl is capable of rescuing the impairment of DAergic neurons in evoked DA release caused by multiple LRRK2 PD mutants.

372 Discussion

LRRK2 has emerged as a most promising drug target for the treatment of PD. Although 373 extensive research has yielded potent and selective LRRK2 kinase inhibitors, they are ATP 374 competitors, some of which are associated with unwanted side effect and unclear clinical 375 outcome³⁷. Thus, an alternative class of inhibitors should be considered. Herein, we present 376 evidence that AdoCbl, one of two physiologically active forms of vitamin B₁₂, inhibits LRRK2 377 kinase activity with a distinct mechanism. Despite the less potent nature in LRRK2 inhibition 378 379 compared to many industrially produced compounds, AdoCbl displays a unique feature of LRRK2 binding and kinase activity modulation mechanism by disturbing LRRK2 protein 380 conformation or dimerization, which may serve as a base for the development of novel allosteric 381 382 inhibitors of LRRK2. Moreover, AdoCbl prevents neurotoxicity and dopamine deficits in animal

models carrying LRRK2 disease variants. Therefore, our study identifies a novel class of LRRK2
kinase modulator that can be used to probe LRRK2 structure and function relationship and
develop new allosteric LRRK2 inhibitors in the future.

Our studies demonstrated the ability of AdoCbl to bind directly human LRRK2 through 386 multiple methods including kinetics, TSA, MST and intrinsic fluorescence (Figs. 1-3). Our data 387 indicates that AdoCbl acts as a mixed-type allosteric inhibitor capable of affecting ATP binding 388 to LRRK2. To date, the majority of reported LRRK2 kinase inhibitors has been known as ATP-389 competitors. Although the structure details of the binding between LRRK2 kinase domain and 390 391 the inhibitors are unavailable, insight based on Roco4 kinase studies suggests they are type I and II inhibitors^{47,49}. These types of inhibitors target the kinase active site; but while Type I bind to 392 the active conformation, type II bind to the inactive conformation⁷⁴. Vitamin B_{12} was shown to 393 suppress the activity of nitric oxide synthase⁷⁵ and HIV-1 integrase⁷⁶, while the ability of B_{12} to 394 inhibit kinase activity has never been documented. Indeed, the structure of Vitamin B₁₂ does not 395 resemble any known kinase inhibitor and no Vitamin $B_{12}\xspace$ mediated kinase inhibition has ever 396 been reported. In the absence of detailed structural information, our STD-NMR analysis revealed 397 extensive contacts between vitamin B₁₂ and the Roco4 kinase domain involving the adenosyl 398 moiety, the bulky corrin ring of cobalamin, and the DMZ base (Fig. 2h). Although ATP and 399 AdoCbl share an adenosyl moiety, the fact that HOCbl, MeCbl and CNCbl could inhibit LRRK2 400 401 kinase activity in vitro with comparable IC₅₀s (Fig. 1) suggests that the (β) -coordinating ligand in vitamin B₁₂ is not essential for binding to LRRK2. In addition, the ATP-site LRRK2 variant 402 A2016T, which displays resistance against several ATP-competitive inhibitors such as LRRK2-403 404 IN-1 did not have an effect on AdoCbl inhibition in vitro, or in the rescuing by AdoCbl of behavioral abnormality and DA neuron degeneration in C. elegans expressing LRRK2-405

406 A2016T/G2019S. Thus, our study suggests that vitamin B_{12} modulates LRRK2 activity by 407 binding at distinct sites in kinase domain than those for other known LRRK2 inhibitors.

Mechanistically AdoCbl distinguishes itself from other LRRK2 inhibitors by being 408 capable of altering LRRK2 protein conformation and disturbing LRRK2 dimer status. Several 409 groups including ours have previously demonstrated that LRRK2 can form dimers^{12,17,18}, which 410 is thought to represent the kinase active form of LRRK2 in detriment of LRRK2 monomers¹³. 411 Since AdoCbl did not affect total LRRK2 levels in cells, it is likely that AdoCbl inhibits LRRK2 412 kinase activity by shifting the equilibrium from LRRK2 dimers to the kinase inactive monomeric 413 414 form (Fig. 4). This hypothesis is consistent with our observation that in contrast to ATPcompetitive inhibitors, AdoCbl renders LRRK2 susceptible to proteolysis, as the monomeric 415 species might be structurally more accessible to proteases than the dimer. Our study also raises a 416 possibility that AdoCbl prefers dimeric to monomeric LRRK2¹² for binding. While this idea is 417 under investigation, our data suggests that the ability of AdoCbl to disrupt dimerization might 418 offer advantages over known ATP-competitive inhibitors as an allosteric inhibitor to modulate 419 LRRK2 kinase function. A better understanding of the mode of LRRK2 - vitamin B₁₂ interaction 420 underlying the mechanism of inhibition of LRRK2 activity will depend on future efforts to solve 421 422 the structures of LRRK2-vitamin B₁₂ complexes.

Compared to the nM inhibition efficacy displayed by the second generation ATPcompetitive LRRK2 kinase inhibitors PF-06447475³⁸ and MLi-2³⁹, vitamin B₁₂ showed a modest μ M inhibition *in vitro*. However, it is surprising that the efficacy of AdoCbl in animal models (**Figs. 5-6**) was comparable to those high-affinity inhibitors^{25,30,31}. While the unusual increase in efficacy of AdoCbl inside the cells relative to *in vitro* condition is surprising and not understood at present, we speculate that a couple of factors may contribute to the unexpected efficacy of

429 AdoCbl in the cells. First, vitamin B_{12} enters the cells through active transport mediated by specific proteins transcobalamin and its receptor (CD320), which ubiquitously located on the cell 430 surface, rather than diffusion (e.g. small compounds)^{77,78}. This mechanism may enhance 431 intracellular AdoCbl bioavailability, especially in the mitochondria where AdoCbl is normally 432 located. Second, a potential cell non-autonomous mechanism, where a variety of cells (including 433 glial cells) produce and secret transcobalamin that could facilitate the uptake of cobalamins in 434 neurons, may help explain the observation⁷⁹. Third, vitamin B_{12} may provide benefits through 435 acting on additional targets. Thus, the increased efficacy could result from a combination of 436 multiple target effects including LRRK2 inhibition. Vitamin B₁₂ is capable of crossing the blood 437 brain barrier (BBB), and it plays a key role in the regulation of excitotoxic homocysteine levels 438 in the brain⁸⁰, as well as in the synthesis of fatty acids incorporated into neuronal lipids and 439 myelin sheaths⁸¹. Indeed, vitamin B₁₂ deficiency in humans is known to contribute to a variety of 440 neurological conditions^{80,81}. Low vitamin B₁₂ levels have been described in patients with 441 idiopathic PD⁸²⁻⁸⁴, and there is also evidence that chronic L-3,4-Dihydroxyphenylalanine (L-442 dopa) intake decreases vitamin B₁₂ plasma levels⁸⁵. A recent study showed that low levels of 443 vitamin B_{12} predicts worse motor symptom in early PD^{86} , however, the mechanism is unknown. 444 It is likely that vitamin B_{12} supplement provides some benefit in PD ^{84,88}, but the lack of 445 knowledge of bioavailability of specific forms of vitamin B₁₂ (particularly in CNS) due to the 446 limitation of measurements hinders the understanding of the beneficial effect of vitamin B₁₂ in 447 human tissues. 448

Although it is challenging to understand the benefit or therapeutic potential of vitamin B₁₂ in PD due to above obstacles, our study implies inhibition of LRRK2 through vitamin B₁₂ as a potential mechanism. Our observation raises a possibility that tissue levels of AdoCbl

 453 LRRK2 variants in light of current reports showing the involvement of peripheral tissue/cells in 454 LRRK2 related pathogenesis⁸⁷⁻⁹⁰. Related epidemiologic studies should be performed in the near 455 future to address the possible association⁹¹. Indeed, future studies should investigate biochemical 456 and structural basis underlying the modulation of LRRK2 activity by vitamin B₁₂ as well as 457 vitamin B₁₂ efficacy and bioavailability in tissues in order to understand the therapeutic potential 458 of vitamin B₁₂ in PD. Nonetheless, AdoCbl represents a starting point for the development of a 459 new class of LRRK2 activity modulators (e.g. allosteric inhibitor) for the much-needed treatment 460 of LRRK2-linked pathological conditions such as PD and inflammatory bowel disease (IBD)⁹². 461 462 463 464 465 466 466 467 468 468 469 469 469 469 469 469 460 460 460 461 462 463 464 465 466 466 467 468 468 469 469 469 460 460 461 462 462 463 464 465 466 466 467 468 468 469 469 469 460 460 461 462 462 463 464 465 466 466 467 468 468 469 469 469 469 460 460 461 462 462 463 464 465 466 466 467 468 469 469 469 469 460 460 461 462 462 463 464 464 <	452	(including CNS and peripheral tissues) might modulate disease penetrance or progression of
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	474	reduce photolability. GNE-1023 was kindly gifted to us by Genentech (South San Francisco, CA,

475 USA). The inhibitors GSK2578215A, PF-06447475, and MLi-2 were purchased from Tocris

476 (Bristol, UK). Bovine purified myelin basic protein was obtained from EMD Millipore

477 (Darmstadt, Germany) and purified Rab10 was purchased from Origene (Rockville, MD, USA).

478 Purified full-length flag-tagged LRRK2 was purchased from Invitrogen (Carlsbad, CA, USA).

479

480 Antibodies

Anti-LRRK2 N241A/34 NeuroMab clone was obtained from the Michael J. Fox Foundation,
 anti-pS935⁴⁴ LRRK2 (ab133450) was from Abcam, and anti-pS1292²⁰ was kindly gifted by
 Genentech. Anti-Rab10 (8127) was purchased from Cell Signaling and anti-pRab10 pT73 was
 obtained from the University of Dundee, UK.

485

486 **Protein Purification**

BAC-transgenic mouse brain overexpressing flag-tagged LRRK2 was homogenized in 487 homogenization buffer (20 mM HEPES at pH 7.4, 0.32 M Sucrose, 1 mM NaHCO3, 0.25 mM 488 CaCl2, 1 mM MgCl2, 1 mM PMSF, and complete protease inhibitor cocktail), then Triton X-100 489 was added to a final concentration of 1% and incubated at 4°C on a rotator for 30 min. 490 Homogenized brain was clarified at 12,000 x g for 10 min at 4°C and the FLAG-LRRK2 protein 491 were purified using Anti-FLAG Affinity Gel (Sigma, A220) with extensive wash before elution. 492 The protein was eluted using 150 ng/µL FLAG-peptide (Sigma, F4799) and stored at 80°C until 493 494 use.

495

The human *LRRK2* pDEST-NSF-tandem affinity plasmid was kindly gifted by Dr. Christian
Johannes Gloeckner (University of Tubingen, Germany). Strep-tagged LRRK2 was expressed in

HEK293T cells through transient transfection for 48 hours, as described previously¹². Cells were
harvested and incubated in lysis buffer (50 mM Tris pH 7.5, 100 mM NaCl, 2 mM DTT, 5 mM
MgCl₂, 0.5 mM EGTA, 1% Triton X-100, 10% Glycerol, Roche protease inhibitors
(11836170001)) for 30 minutes at 4°C. Lysate was centrifuged at 13,000 x g for 15 minutes.
Supernatant was mixed with Strep-Tactin Sepharose (2-1206-002) from Iba Life Sciences for 2
hours and washed extensively with buffer above, substituting 0.02% Triton X-100 for 1%. StrepFlag LRRK2 was eluted using 10mM desthiobiotin and stored at 80°C until use.

505

The 6xHis-GST-tagged Roco4 kinase domain plasmid, kindly gifted by Dr. Andy West 506 (University of Alabama Birmingham, AL, USA), was transformed into BL21 (DE3) cells 507 (Agilent Technologies, 230132) and grown at 37°C in 2xYT broth until reaching an OD600 of 508 509 0.6. Overexpression was induced for 16 hours at 18°C with 300 µM IPTG. Cells were pelleted and resuspended in 50 mM Tris pH 7.5, 150 mM NaCl, 1 mM TCEP, 0.02% Reduced TX100, 1 510 mM PMSF, 25 µg/mL lysozyme, 4 ug/mL DNase. Protein was bound to Ni-NTA resin and 511 washed and eluted with increasing concentrations of imidazole. Protein was concentrated and 512 treated with TEV protease to cleave the 6xHis-GST tag, while dialyzing in buffer overnight to 513 remove imidazole. 6xHis-GST tag was separated using Ni-NTA resin and pure Roco4 kinase 514 domain was collected in the flow through. 515

The pGEX-6p-1 construct was expressed as above using BL21 (DE3) cells. Crude lysate was bound to Glutathione Sepharose 4B (17-0618-01, GE Healthcare) for 1 hour before beads were washed 3x with PBS. GST protein was eluted with reduced glutathione.

519

520 Compound Screen and TR-FRET Kinase Assay

521 Compounds from the FDA-Approved library were tested against flag-tagged LRRK2 purified from BAC transgenic mouse brain. LRRK2 kinase activity was monitored by measuring time 522 resolved fluorescence resonance energy transfer (TR-FRET) emission ratio upon the 523 524 phosphorylation of Fluorescein-LRRKtide (PV4901, Invitrogen) and subsequent binding of Terbidium-pLRRKtide antibody (PV4898, Invitrogen). This TR-FRET-based assay was used in 525 a high-throughput screen (HTS) of small molecule chemical compounds for LRRK2 using the 526 TECAN (Mannedorf, Switzerland) Freedom EVO 200 liquid handling system, and relative 527 fluorescence was measured using the TECAN Safire 2 fluorescence spectrometer. To determine 528 the TR-FRET ratio between Fluorescein-LRRKtide and Terbidium-pLRRKtide antibody, 529 fluorescent intensity was measured at wavelengths 515 nm and 485 nm. 530

Prior to the HTS, each compound was prepared at 4x final concentration (1.6 or 4% 531 532 residual DMSO volume) in Kinase Buffer S, containing 50 mM Tris pH 8.5, 10 mM MgCl₂, 0.01% Brij-35, 1 mM EGTA in 96-well polypropylene non-treated plates (Thermo Scientific, 533 #12-565-436). The kinase reaction was performed in 10 μ l total volume in a low-volume white 534 384-well plate (Corning, #3673), with 20 nM LRRK2, 400 nM Fluorescein-ERM (LRRKtide), 535 and small molecules in Kinase Buffer S supplemented with 2 mM DTT on the day of the 536 experiment. Small molecules were screened at 3.3 or 4 µM with 0.4 or 1% residual DMSO in 537 duplicate. The assay plates were prepared by adding 2.5 µl of 4x compound solutions, 2.5 µl of 538 4x LRRK2, and 5 µl of 2x LRRKtide and ATP mixture. After incubation at room temperature 539 540 for 4 hours, the kinase reaction was terminated by the addition of 10 µl of 2x EDTA and 2x Tbanti-pERM antibody in the detection buffer, containing 20 mM Tris-HCl, 0.01% NP40. EDTA 541 was mixed with the antibody right before the addition of the mixture to wells, as the antibody 542 543 was stable in EDTA only for several hours. The final concentration of EDTA and Tb-anti-pERM

544 were 5 mM and 2.5 nM, respectively. After 1-hour incubation at room temperature, TR-FRET measurements were obtained according to the parameters described in instrument settings. 545 During the incubation, 384-well plates were covered by aluminum sealing tapes (Corning, 546 547 #6570) to reduce evaporation and exposure to light. All the liquid handling was carried out using fixed 8-tip LiHa arms on TECAN EVO200 workstation. HTS was performed with 0.4 or 1% 548 DMSO as negative control and no LRRK2 as positive control. Hit compounds were selected 549 based on the normalized percent inhibition by first computing emission ratio (emission intensity 550 of acceptor divided by donor) and then computing percent inhibition of kinase activity relative to 551 the DMSO treated control as 0% inhibition and the control in the absence of LRRK2 as 100% 552 inhibition. Compounds in wells showing greater than 30% inhibition in either of the duplicates 553 were selected as hits. 554

555

556 In Vitro Kinase Assays

Kinase reactions were performed in 30 uL kinase buffer (20 mM Tris pH 7.5, 1 mM DTT, 15 557 mM MnCl₂, 20 mM β -glycerophosphate) at 37°C for 30 minutes in the presence of [γ -³²P] ATP 558 (3000 Ci/mmol; BLU502H250UC, PerkinElmer Life Sciences) and 50 µM cold ATP. 559 Beforehand, LRRK2 or Roco4 Kinase was loaded with inhibitor and/or substrate, followed by 30 560 min incubation on ice. Reactions were stopped by addition of Laemmli buffer and boiling at 561 95°C for 10 minutes. Samples were resolved on 4-12% SDS-PAGE pre-cast gels (NP0323BOX, 562 Invitrogen). Radioactive signal was captured onto a phosphor-screen (S0230, GE Lifesciences) 563 and was digitally collected using a Typhoon scanner. ImageQuant densitometry was used to 564 quantify the phosphor-signal. 565

567 GTP Hydrolysis Assay

GTPase activity of strep-tagged LRRK2 was measured in 30 uL GTPase buffer (20 mM Tris pH 568 7.5, 150 mM NaCl, 1 mM DTT, 5 mM MgCl₂ 1 mM EDTA) at 30°C for 90 minutes. LRRK2 569 570 was incubated with inhibitor for 30 min on ice before reactions were initiated with the addition of 50 µM cold GTP and [a-32P] GTP (3000Ci/mmol; BLU006H250UC, PerkinElmer Life 571 Sciences). Reactions were terminated with the addition of 0.5 M EDTA. 2 uL of the reaction 572 mixture were dotted onto TLC plates (M1055790001, EMD Millipore). GDP and GTP were 573 separated by TLC using 0.5 M KH₂PO₄ pH 3.5 for 60 minutes. The TLC plate was dried for 15 574 minutes and radioactive signal was captured and using a phosphor-screen and a Typhoon 575 scanner. ImageQuant densitometry was used to quantify the phosphor-signal. 576

577

578 **B12-Agarose Binding Assay**

579 500 μL of 40 nM strep-tagged LRRK2 or 500 uL of 100 nM GST, pre-loaded with AdoCbl or
580 buffer for 30 min on ice, were incubated with 50 uL B12-Agarose (V3254, Sigma Aldrich). B12581 Agarose was washed 3x with buffer (50 mM Tris-HCl pH 7.5, 150 mM NaCl, 1 mM TCEP,
582 0.02% Triton X-100, 1% Ficoll 400) and bound protein was eluted with Laemmli buffer and
583 boiling at 95°C. Bound LRRK2 or GST was analyzed by western blot.

584

585 Thermal Shift Assay

300 nM strep-tagged LRRK2 was incubated with Sypro Orange and inhibitor or buffer to a final
volume of 30 uL. Using a Stratagene Mx3000 Real-time PCR machine, samples were heated to
95°C and fluorescence intensity of Sypro Orange was measured at every 0.5°C increment. For

each experiment, data was normalized to the maximum fluorescent intensity.

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591 Microscale Thermophoresis

Microscale Thermophoresis (MST) measurements were obtained using a Monolith NT.115 592 (NanoTemper Technologies). Purified strep-tagged LRRK2 was labeled with NT-647 dye 593 (NanoTemper Technologies) and experiments were performed using a 2 nM final concentration. 594 A 12-point dilution series of AdoCbl, ranging from 200 nM to 100 µM, was added to labeled 595 LRRK2. After 30 min incubation on ice, the binding reaction was loaded onto Standard 596 capillaries (NanoTemper Technologies) and measurements were taken using 30% LED power 597 598 and 50% MST power. Laser on-time was set to 30 seconds and laser off-time was set to 5 seconds. Data was processed using GraphPad Prism 6.0 and a $K_{\rm D}$ was derived from three 599 independent thermophoresis experiments by fitting a curve based on the law of mass action. 600 601 Quality of each MST run was assessed by performing a capillary scan before and after each data collection to check that the fluorescence between samples stays within \pm 10%. Furthermore, each 602 time-trace showed a smooth decrease in normalized fluorescence, suggesting that no 603 precipitation occurred during the experiments. 604

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606 *STD-NMR*

Saturation Transfer Difference (STD) NMR was carried out with 1024 scans on a Bruker 800MHz NMR spectrometer equipped with a cryogenic probe at 277 K according to Mayer et al⁹³. Saturation on and off frequencies were set to -1 and -20 ppm, respectively, with saturation achieved using a 2 s train of 50 ms Gaussian pulses at 86 Hz. 1024 scans were used. STD-NMR samples contained 50 mM Tris, 150 mM NaCl, 1 mM TCEP and 2 mM MgCl2 at a pH of 7.5, 612 20-30 μ M Roco4 protein, with vitamin B₁₂ at 100-fold excess over Roco4 in concentration.

613 Vitamin B_{12} resonances were assigned in D2O according to Summers et al⁹⁴.

614

615 Intrinsic Fluorescence

616 Strep-tagged LRRK2 at a concentration of 150 nM was incubated with AdoCbl or buffer in a total volume of 80uL. Samples were loaded onto a 96-well black-walled plate and fluorescence 617 618 was measured using a Tecan Safire microplate reader. For these experiments, a correction 619 equation must be applied to the fluorescent measurements to compensate for the inner filter 620 effect. AdoCbl absorbs light at 295 nm, which affects the excitation strength of the incident light, and from 340-360 nm, which affects the amount of light reaching the detector after tryptophan 621 622 emission. Therefore, we calculated a corrected fluorescence value (Supplementary information, Figs. S5c-d) for each sample by measuring the absorbance at the excitation and 623 emission wavelengths and multiplying by the original fluorescence value ⁹⁵. 624

625

626 Limited Proteolysis Assays

Strep-tagged LRRK2 or TBK1 was subjected to limited proteolysis by trypsin or chymotrypsin
with a 10:1 molar ratio of LRRK2 to protease at 37°C. LRRK2 was loaded with inhibitor for 30
min on ice before protease was added. Reactions were stopped with the addition of Laemmli
buffer and boiling at 95°C.

631

632 In situ labeling and detection of LRRK2 dimers.

For the biochemical detection and purification of biotinylated LRRK2 dimers, we used an 633 adaptation of the proximity biotinvlation approach⁹⁶. A manuscript describing the full 634 characterization of this assay is currently under review (Leandrou et al.; submitted to Biochem 635 636 J). HEK293T cells, maintained throughout the duration of the experiment in biotin-depleted media, were co-transfected with plasmids encoding WT LRRK2, fused to biotin ligase (BirA) or 637 an acceptor peptide (AP). The following day, the growth media was replaced and the indicated 638 concentrations of AdoCbl, diluted in media, were added, and the cultures maintained for an 639 additional 48h. Prior to cell lysis, the cells were washed in pre-warmed PBS and given a brief (5 640 min) pulse with 50 µM biotin, followed extensive washing with PBS. Cytoplasmic extracts were 641 prepared in lysis buffer (20mM HEPES, pH 7.4; 150 mM NaCl; 0.5% NP-40; 2mM EGTA; 2 642 mM MgCl₂; 10% glycerol; pH 7.2). Following lysis, 5 µg of total clarified cell extract was bound 643 644 to streptavidin-coated ELISA plates for 1h at 37°C under constant agitation. The supernatant was removed and retained, and the wells were washed, and the amount of biotinylated LRRK2 645 present in each sample was quantified using HRP-conjugated (in house) anti-LRRK2 (75-253, 646 647 NeuroMab/Antibodies Incorporated; clone N241A/B34). Duplicate samples were incubated in the parallel ELISA plates pre-coated with anti-LRRK2 (ab195024, Abcam) in order to quantify 648 the total amount of LRRK2 present in each sample. In each experiment, control samples were 649 650 prepared from cells co-expressing AP-LRRK2 together with Flag-LRRK2 (without the BirA biotin ligase). To visualize expression of both LRRK2 constructs, parallel extracts were 651 separated by SDS-PAGE (6%), and membranes probed with anti-LRRK2 (clone N241A/B34). 652

653

654 Generation of Mouse Embryonic Fibroblasts (MEFs)

655 LRRK2-G2019S and wild type control MEFs were isolated from mouse embryos at day E13.5 resulting from crosses between heterozygous LRRK2-G2019S and wild type C57/BL/6J mice. 656 All the MEFs were cultured for at least 30 passages to immortalize the cells. All cells were 657 658 cultured in DMEM containing 10% FBS, 2mM L-glutamine and 100 units/ml Penicillin-Streptomycin, and were maintained at 37°C with 5% CO₂. All cells lines were confirmed by 659 PCR genotyping and western blot, but were not tested for mycoplasma contamination. To test 660 inhibition, cells were treated with inhibitor or DMSO for 24 hours in DMEM with 3% FBS 661 before being lysed and subject to western blot for analysis. 662

663

664 Treatment of C. elegans with AdoCbl

C. elegans strains were cultured on standard nematode growth medium (NGM) agar plates 665 seeded with E. coli OP50 as a food source. Mixed stage animals were maintained as bulk culture 666 667 on NGM agar at room temperature (22°C). Prior to each experiment, animals were agesynchronized by standard bleaching and washing protocol to obtain embryos, from which 668 developmental stages were followed. The following transgenic C. elegans lines expressing green 669 670 fluorescent protein (GFP) either alone (SGC730: Pdat-1::GFP) or together with human LRRK2-G2019S (SGC856: Pdat-1::LRRK2-G2019S; Pdat-1::GFP) or human LRRK2-R1441C (SGC851: 671 Pdat-1::LRRK2-R1441C Pdat-1::GFP) in dopaminergic neurons were used⁶³. 672

673

Treatment with AdoCbl was done in liquid culture to ensure adequate drug exposure using the published protocol as described³⁰. Briefly, worms were age-synchronized to generate L1 larva in M9 buffer [For 1 liter: KH2PO4, 3 g; Na2HPO4, 6 g; NaCl, 5 g; MgSO4 (1 M), 1 ml], which were distributed into a 12-well microtiter plate seeded with *E. coli* OP50 with roughly 50 L1 worms in a total volume of 900 ml. AdoCbl stock made in water was added to achieve the desired concentrations. The 12-well plate was covered in aluminum foil to protect from light, maintained in a humidified chamber at room temperature and shaken at 100 rpm. Worms were monitored every day and placed onto agar plates with OP50 when most of them reached L4 larval stage (about 3 days). L4 worms were grown on NGM agar plates seeded with *E. coli* OP50 for 3 days for behavioral assay or 9 days for neuronal assessment as described below.

684

685 C. elegans Basal Slowing Assay

Well-fed worms with intact dopaminergic neural circuitry move slower in the presence of 686 bacterial food than in its absence⁶⁴. This basal slowing response was assaved as described 687 previously^{63,64}. Briefly, a set of NGM assay plates were seeded with bacterial food, *E. coli* OP50, 688 in a ring shape, and another set of NGM assay plates were uncoated. Age-synchronized worms 689 690 (about 10 worms of each strain) were washed twice in S basal buffer (100 mM NaCl, 10 mg/ml cholesterol, 50 mM potassium phosphate, pH 6.0). Worms were then transferred to the center of 691 the NGM plates coated with or without E. coli OP50 as described above, settled for 5 min, and 692 693 their locomotion were recorded with a digital camera in 20 s intervals. Body bends were examined using an unbiased machine-vision analysis system (WormLab, MBF Bioscience, 694 Williston, VT). Basal slowing was calculated as the percent slowing in body bends per 20 s in 695 the presence vs. the absence of bacterial lawn. 696

697

698 Assessment of Dopaminergic Neuron Survival in C. elegans

Dopaminergic neurons in live C. elegans were examined essentially as described⁶³. Briefly, 699 700 worms were immobilized in the presence of 3 mM levamisole and were mounted on glass slides. The dopaminergic neurons in the head regions [four cephalic neurons (CEPs)] were visualized 701 702 for GFP fluorescence under a Zeiss Axiovert 200M microscope. The total numbers of CEPs with the intact cell body (survived) as well as those missing most of the cell body and neurites 703 (degenerated) were counted. For each strain, about 30 worms were analyzed in at least three 704 independent experiments. The percent of dopaminergic neuron survival was calculated as the 705 number of intact CEPs observed in all animals divided by total number of CEPs expected if no 706 degeneration occurred (four in each animal times the number of animals tested), times 100. 707 Fluorescent images of DA neurons in the head region of worms were taken with a Zeiss Axiovert 708 200M microscope using 1 s exposure time at $20 \times$ magnification. 709

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Sample size was determined according to the Statistical Solutions LLC calculator 711 (http://www.statisticalsolutions.net/pssTtest calc.php). Assuming alpha value of 0.05, to detect 712 difference of 10% between 100% mean for the control group and 90% mean for an experimental 713 group, 5% expected standard deviation (two-sided t-test), and a power of 0.8, a sample site of 4 714 animals is obtained. In Fig. 4, more than 20 worms were used for each group. All live and age-715 synchronized worms were included in the experiments. Only dead worms, if any, were excluded. 716 The number of worms available for experiments was in general five times more than the number 717 of worms being assayed (e.g., 20 worms were randomly picked for from a culture of 100 718 worms). For these experiments, the investigator was not blinded to group allocations. Data is 719 normally distributed, and the variance was similar between the groups that are being statistically 720 721 compared.

722

723 Treatment of Drosophila with AdoCbl

Flies were used and raised as described recently³¹. Briefly, the *TH* (*tyrosine hydroxylase*) GAL4 724 was crossed with either UAS-hLRRK2-wildtype, UAS-hLRRK2-G2019S or the kinase-dead 725 UAS-hLRRK2-G2019S-K1906M line to produce progeny dopaminergic expression of the 726 transgene ($DA \rightarrow hLRRK2$, $DA \rightarrow G2019S$, $DA \rightarrow KD$). The crosses were allowed to lay eggs 727 onto instant fly food (Carolina) or onto instant food supplemented with AdoCbl. The final 728 729 concentration of AdoCbl in the fly food ranged from 100 to 2500 nM. Females were collected on the day of emergence and transferred to new vials (no AdoCbl) for 24 hours. In control 730 experiments, low expression dLRRK flies (dLRRK^{e03680}) were fed instant fly food or food 731 732 supplemented with AdoCbl.

733

734 **Physiological recordings**: 18-24 hour old females were aspirated in a pipette tip, restrained with nail polish, and allowed to recover for >20 minutes. A recording electrode was placed in the 735 736 center of the eye, and a reference electrode in the mouthparts. After 2 minutes in the dark, the fly was illuminated with light from a blue flickering LED and the resulting electroretinogram signal 737 amplified and stored for off-line analysis. The response was analyzed by the Fast Fourier 738 739 Transform (FFT), generating components corresponding to the photoreceptors, second order lamina neurons, and third/fourth order medulla neurons. Stimulus generation, recording and 740 analysis were accomplished in Matlab, as described recently³¹; Matlab code available at 741 https://github.com/wadelab/flyCode). The number of flies used was sufficient according to 742 previously published data³¹. All data from tested flies were included. Male and female flies of 743 744 the required genotype were placed in randomly chosen vials (+/- drug) and allowed to mate and

lay eggs. Offspring were harvested daily and flies were sampled at random. The investigators
were blinded to the genotype while the experiments were in progress. For statistical analysis,
estimates of variation were made and are similar between groups being compared.

748

749 Determination of Survival of Primary Cortical Neurons

Primary rat embryonic cortical neurons were prepared and cultured as described^{70,97}. Briefly, 750 embryonic day 17 rat cortices were dissociated and plated on poly-d-lysine coated 12mm 751 diameter glass coverslips in Neurobasal medium (12348017, Invitrogen-ThermoScientific) with 752 753 B-27 serum free supplements (17504044, Invitrogen-ThermoScientific) at a density of 125,000 neurons per cm². On day four following plating, neurons were transiently co-transfected with 754 LRRK2-WT or LRRK2-G2019S and pcms-EGFP at a ratio of 4:1 using Lipofectamine 2000 755 according to the manufacturer's instructions. The indicated concentrations of AdoCbl or MLi-2 756 757 in Neurobasal/B-27 medium was added to the neurons on the morning following transfection and 758 supplemented one additional time at the mid-point (36 h) of the total duration of the experiment. Following a period of 72 h of expression, the coverslips were fixed in 4% formaldehyde and 759 760 stained with anti-GFP antibodies (ab13970, Abcam) and DAPI. We had determined in parallel neurons double stained with GFP and anti-LRRK2 antibodies (ab133474, Abcam) that the 761 percentage of GFP-positive neurons over-expressing LRRK2 was approximately 90% (not 762 shown). To simplify quantification of apoptotic degenerating neurons, GFP-positive neurons 763 were visualized and determine to be apoptotic or viable. For quantification, apoptotic neurons 764 were defined as those having condensed fragmented chromatin comprised of two or more 765 apoptotic bodies. More than 100 neurons per coverslip were assessed in triplicate coverslips in a 766

blinded fashion, from two to three independent cultures. The data are presented as the percentageof GFP-positive neurons containing apoptotic nuclear features.

769

770 Animals and Brain Slice Preparation

The use of the animals followed the National Institutes of Health guidelines and was approved
by the Institutional Animal Care and Use Committee at Thomas Jefferson University. All efforts
were made to minimize the number of animals used. BAC LRRK2(hR1441G) transgenic (TG)
mice were obtained from Chenjian Li's laboratory at Weill Medical College of Cornell
University and maintained on Taconic FVB/N background and BAC LRRK2(G2019S) TG mice
previously described¹⁹ maintained on C57/NJ background.

Three- to 5-month-old male transgenic LRRK2-G2019S mice and their non-transgenic 777 littermates were used for LRRK2 kinase inhibition in striatal brain slices. For preparing striatal 778 779 slices, mice were decapitated without anesthesia after cervical dislocation and brains were immediately dissected out. Coronal striatal brain slices at 250 µm were prepared on a vibratome 780 (VT1200, Leica, Solms, Germany). The striatal slices were allowed to recover for 0.5 to 1 hour 781 782 at 36°C in a holding chamber containing oxygenated artificial CSF (ASCF: 125 mM NaCl, 2.5 mM KCl, 26 mM NaHCO₃, 2.4 mM CaCl₂, 1.3 mM MgSO₄, 0.3 mM KH₂PO₄, and 10 mM 783 glucose, pH 7.3-7.4). To examine the effects of the LRRK2 inhibitors, slices were incubated for 784 2 h in oxygenated ACSF containing LRRK2 inhibitors. For the incubation treatment, striatal 785 slices were bisected, and one striatum was exposed to LRRK2 inhibitor (2 h) while the other was 786 exposed to vehicle (DMSO or water). After treatment, the slices were collected and rapidly 787 frozen in dry ice and stored in -80°C until assayed. 788

790 Slice Preparation for Evoked DA Transmission

Twelve- to 15-month-old male LRRK2-G2019S as well as 6- to 14-month-old male 791 LRRK2-R1441G BAC transgenic mice and their age-matched non-transgenic littermates were 792 used. For preparing striatal slices, mice were decapitated without anesthesia after cervical 793 dislocation and brains were immediately dissected out. Coronal striatal brain slices at 250 µm 794 were prepared on a vibratome (VT1200, Leica, Solms, Germany) for electrophysiological 795 recording. The striatal slices were allowed to recover for at least 1 hour at 36°C in a holding 796 chamber containing oxygenated artificial CSF (ASCF) and then placed in a recording chamber 797 superfused (1.5 ml/min) with ACSF at 36°C. The pH of all ACSF solutions were adjusted to 7.3-798 7.4 with concentrated hydrochloric acid and ACSF solutions were saturated with carbogen (95% 799 $O_2/5\%$ CO₂) prior to use to ensure stable pH buffering and adequate oxygenation. 800

801 Striatal slices were bisected, and one striatum was incubated for 2 hours in ACSF at 36° C 802 containing 300 μ M AdoCbl while the other was exposed to vehicle (water) as the control. Slices 803 were washed with ACSF for 20 min after treatment before fast scan cyclic voltammetry (FSCV) 804 recording.

805

806 *Fast scan cyclic voltammetry recording (FSCV)*

FSCV was used to measure evoked DA release in the dorsal striatum (dSTR). Electrochemical recordings and electrical stimulation were performed as previously described⁷³. Briefly, freshly cut carbon fiber electrodes ~5 μ m in diameter were inserted ~50 μ m into the dSTR slice. For FSCV, a triangular voltage wave (-400 to 900 mV at 280 V/sec versus Ag/AgCl) was applied to the electrode every 100 msec. Current was recorded with an Axopatch 200B amplifier (Axon Instruments, Foster City, CA), with a low-pass Bessel filter set at 10 kHz, digitized at 25 kHz (ITC-18 board; InstruTech, Great Neck, NY). Triangular wave generation and data acquisition were controlled by a personal computer running a locally written (Dr. E. Mosharov, Columbia University, New York, NY) IGOR program (WaveMetrics, Lake Oswego, OR). Striatal slices were electrically stimulated (400 μ A x 1 ms pulse duration) by an Iso-Flex stimulus isolator triggered by a Master-8 pulse generator (AMPI, Jerusalem, Israel) using a bipolar stimulating electrode placed at a distance of ~150 µm from the recording electrode. The slices were stimulated every 2 min. Background-subtracted cyclic voltammograms served for electrode calibration and to identify the released substance. DA oxidation current was converted to concentration based upon a calibration of 5 µM DA in ACSF after the experiment. For each experimental condition, at least three slices from at least three different mice were examined unless specified otherwise. The number of the recording sites was determined according to previously published experiments¹⁹ and SSD sample size power analysis. No randomization and no blinding were used for experimental groupings. All recorded data was included. Statistical tests were justified as appropriate, as data meets test assumptions, with a similar estimated variance between groups that are statistically compared.

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866

867 Glossary of Terms

- 868 ACSF: artificial cerebrospinal fluid
- 869 AdoCbl: 5'-deoxyadenosylcobalamin, or adenosylcobalamin
- 870 AP: acceptor peptide
- 871 a.u.: arbitrary unit
- 872 BirA: biotin ligase
- 873 BAC: bacterial artificial chromosome
- 874 CEP: cephalic neurons
- 875 CNCbl: cyanocobalamin
- 876 CRF: contrast response function
- 877 DAergic: dopaminergic
- 878 DMZ: dimethylbenzimidazole
- 879 FFT: fast Fourier transform
- 880
- 881 FSCV: fast scan cyclic voltammetry

882	HOCbl: hydroxycobalamin
883	HTS: High-throughput Screen
884	LRRK2: Leucine-Riche Repeat Kinase 2
885	MBP: myelin basic protein
886	MeCbl: methylcobalamin
887	MEF: mouse embryonic fibroblast
888	MST: microscale thermophoresis
889	PD: Parkinson's Disease
890	STD-NMR: saturation transfer difference nuclear magnetic resonance
891	TR-FRET: time-resolved fluorescence resonance energy transfer
892	TSA: thermal stability assay
893	WT: wild-type
	w 1. white-type
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- 1182 Supplementary information is available at *Cell Research*'s website

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- 1187 Fig. 1. AdoCbl inhibits LRRK2 kinase activity. (a) Domain structure of LRRK2. (b) Dose-
- 1188 response curves of brain-purified flag-tagged LRRK2 kinase as a function of different forms of

1189	cobalamin. Phosphorylation is quantified by measuring TR-FRET emission ratios of fluorescein-
1190	LRRKtide and a Terbidium-labeled pLRRKtide antibody. (c) Dose-response curves of strep-
1191	tagged LRRK2 autophosphorylation or (d) phosphorylation of myelin basic protein as a function
1192	of different forms of cobalamin. (e) Dose-response curve of strep-tagged LRRK2-G2019S
1193	phosphorylation of purified Rab10 as a function of AdoCbl. (f) Dose-response curves of
1194	pS935/Total LRRK2 and (g) pS1292/Total LRRK2 after treatment with different forms of
1195	cobalamin in MEF cells derived from LRRK2-G2019S BAC transgenic mice. Data from each
1196	replicate was normalized to LRRK2 phosphorylation without cobalamin treatment. All data
1197	points represent the mean (\pm s.d.) of three biological replicates.
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1210	Fig. 2. Direct binding of AdoCbl to LRRK2 protein. (a) Binding of strep-tagged LRRK2 to
1211	AdoCbl-agarose in the presence of AdoCbl. Input represents the amount of protein that was

1212 added to beads, while pull-down denotes the amount of protein left on the beads after washes. Significance was calculated by one-way ANOVA using the mean $(\pm s.d.)$ of three biological 1213 replicates. * p < 0.05, ** p < 0.005 (b) Thermal shift assays showing melting temperatures of 1214 1215 strep-LRRK2 in the presence of AdoCbl or PF-06447475. (c) Microscale thermophoretic analysis of the interaction between AdoCbl or (d) PF-06447475 with strep-tagged LRRK2. (e) 1216 Coomassie stained SDS-PAGE of the Roco4 kinase domain purified from E. coli. (f) Dose-1217 response curve of Roco4 kinase activity as a function of AdoCbl. (g) ATP STD-NMR shows 1218 direct binding of AdoCbl to the Roco4 kinase domain and competition with ATP. From top to 1219 bottom, the spectra are as follows: 1D 1H NMR of ATP (blue), AdoCbl (red), STD negative 1220 control with ATP + AdoCbl only (green), STD positive control with ATP and Roco4 kinase 1221 domain (orange), STD of AdoCbl and Roco4 kinase domain with 1:1 ratio of AdoCbl to ATP 1222 1223 (purple), and STD of AdoCbl and Roco4 kinase domain with 10:1 ratio of AdoCbl to ATP (yellow). AdoCbl protons showing strong STD signals are labeled with assignment. All 1224 experiments were collected at 4°C on a Bruker 800MHz spectrometer equipped with a 1225 cryoprobe. (h) Protons with strong STD signals (highlighted in red) mapped onto the structure of 1226 AdoCbl. The NMR assignment and nomenclature of vitamin B12 is from Summers et al.⁹⁴ Data 1227 points in (a,c,d,f) represent the mean $(\pm s.d.)$ of three biological replicates. 1228

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Fig. 3. AdoCbl exhibits a mixed-mode of inhibition. (a) Michaelis-Menten kinetics curves of
full-length Invitrogen flag-tagged LRRK2-WT and (c) LRRK2-G2019S as a function of AdoCbl.

1235	Relative velocity represents the value of pS1292/Total LRRK2 after 20 minutes of reaction time
1236	at 30°C (during the linear reaction rate), as detected by western blot and quantified by
1237	densitometry. (b) Lineweaver-Burk plots of LRRK2-WT and (d) LRRK2-G2019S kinetics data.
1238	(e) Microscale thermophoretic analysis of the interaction between AdoCbl and strep-tagged
1239	LRRK2 in the presence of increasing concentrations of AMP-PNP. Fluorescently-labeled strep-
1240	tagged LRRK2 was pre-incubated with AMP-PNP before binding between LRRK2 and AdoCbl
1241	was measured by MST. (f) Microscale thermophoretic analysis of the interaction between AMP-
1242	PNP and LRRK2, showing a K_D of 0.9 μ M. Data points represent the mean (± s.d.) of three
1243	biological replicates.
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1256	Fig. 4. AdoCbl causes a LRRK2 conformational change and destabilizes LRRK2 dimers.
1257	(a) Coomassie stained SDS-PAGE showing limited proteolysis analysis using a 10:1 molar ratio

1258 of LRRK2: Trypsin (left panel) and LRRK2: Chymotrypsin (right panel). Proteolysis was performed at 30°C with or without 50 µM AdoCbl and reactions were quenched at the indicated 1259 times by the addition of sample loading buffer. The observed data was consistent across three 1260 1261 biological replicates. (b) Limited proteolysis of LRRK2-WT by trypsin in the presence of increasing concentrations of AdoCbl, or 1 µM LRRK2 kinase inhibitor. Proteolysis was 1262 performed for 90 minutes at 30°C. Shown is a representative SDS-PAGE of full-length LRRK2, 1263 in which bands were quantified and values were normalized to LRRK2 proteolysis without 1264 AdoCbl. (c) The peak intrinsic fluorescence of LRRK2 (339 nm) was measured as a function of 1265 AdoCbl. Strep-tagged LRRK2 was incubated with indicated concentrations of AdoCbl for 30 1266 1267 minutes prior to fluorescence measurements. Significance was measured by one-way ANOVA. * $p \le 0.05$, ** $p \le 0.005$. (d) HEK293T cells co-expressing BirA-WT (biotin ligase) and AP-WT 1268 1269 LRRK2 (acceptor peptide) were lysed following a biotin pulse to label dimeric LRRK2, and extracts bound to streptavidin-coated ELISA plates. LRRK2 was detected using anti-LRRK2 1270 conjugated to HRP (clone N241A/B34) and expressed as a ratio of total LRRK2 levels detected 1271 by ELISA in parallel plates coated with total LRRK2 antibodies (clone c41-2). In the plot, 1272 "WT/WT NP" refers to cells expressing WT LRRK2 dimers that were harvested without 1273 receiving a biotin pulse ("no pulse"). AdoCbl significantly reduced levels of dimeric WT-1274 LRRK2. Sub-panel shows representative immunoblot of parallel extracts detected with anti-1275 LRRK2 (clone N241A/B34). BirA-LRRK2 represents the top band, and AP-LRRK2 the bottom 1276 band. (e) HEK293T cells expressing BirA- G2019S or I2020T mutant LRRK2 together with AP-1277 G2019S or I2020T LRRK2, and dimeric LRRK2 quantified by ELISA. Treatment with AdoCbl 1278 significantly reduces dimeric mutant LRRK2. * p < 0.05 compared to WT/WT-LRRK2; *** p < 1279 1280 0.001 compared to G2019S-LRRK2 dimers or I2020T-LRRK2 dimers alone. (f) Representative

- immunoblot of parallel extracts detected with anti-LRRK2 (clone N241A/B34). BirA-LRRK2
- 1282 represents the top band, and AP-LRRK2 the bottom band.

- Fig. 5. AdoCbl rescues mutant human LRRK2-induced behavioral defects and
 dopaminergic neurodegeneration in *C. elegans*. (a) AdoCbl dose dependently rescues the loss

1304 of basal slowing response in transgenic hLRRK2-G2019S C. elegans. Age-synchronized nematodes expressing GFP marker only or additionally hLRRK2-G2019S in dopaminergic 1305 neurons were treated with either vehicle or AdoCbl in liquid culture during the larval stage L1 to 1306 1307 L4 (3 days), followed by growth on NGM plates for 3 days prior to behavior assay. Basal slowing response was assayed on NGM plates using an unbiased machine-vision analysis system 1308 (WormLab) as the percent slowing in body bends per 20 s in the presence vs. the absence of 1309 bacterial lawn. Data represent the mean (\pm s.d.) of three biological replicates, each with 20-25 1310 worms per treatment condition. (b) AdoCbl treatment attenuated the loss of dopaminergic 1311 neurons induced by hLRRK2-G2019S in C. elegans. Representative fluorescence images of 1312 dopaminergic neurons (CEP neurons within the outlined head region) in transgenic C. elegans 1313 expressing GFP marker only or additionally hLRRK2-G2019S following treatment with either 1314 1315 vehicle or 1.25 µM AdoCbl. Age-synchronized nematodes were treated with either vehicle or AdoCbl in liquid culture during the larval stage L1 to L4 (3 days), followed by growth on NGM 1316 plates for 9 days. GFP-tagged dopaminergic neurons in live animals were counted under a 1317 fluorescence microscope. (c) Quantification of percent dopaminergic neurons survived. Data are 1318 presented as the mean (\pm s.d.) of three biological replicates, each with approximately 30-50 1319 worms per treatment condition. P < 0.01, Student's t-test. n.s., not statistically significant. 1320

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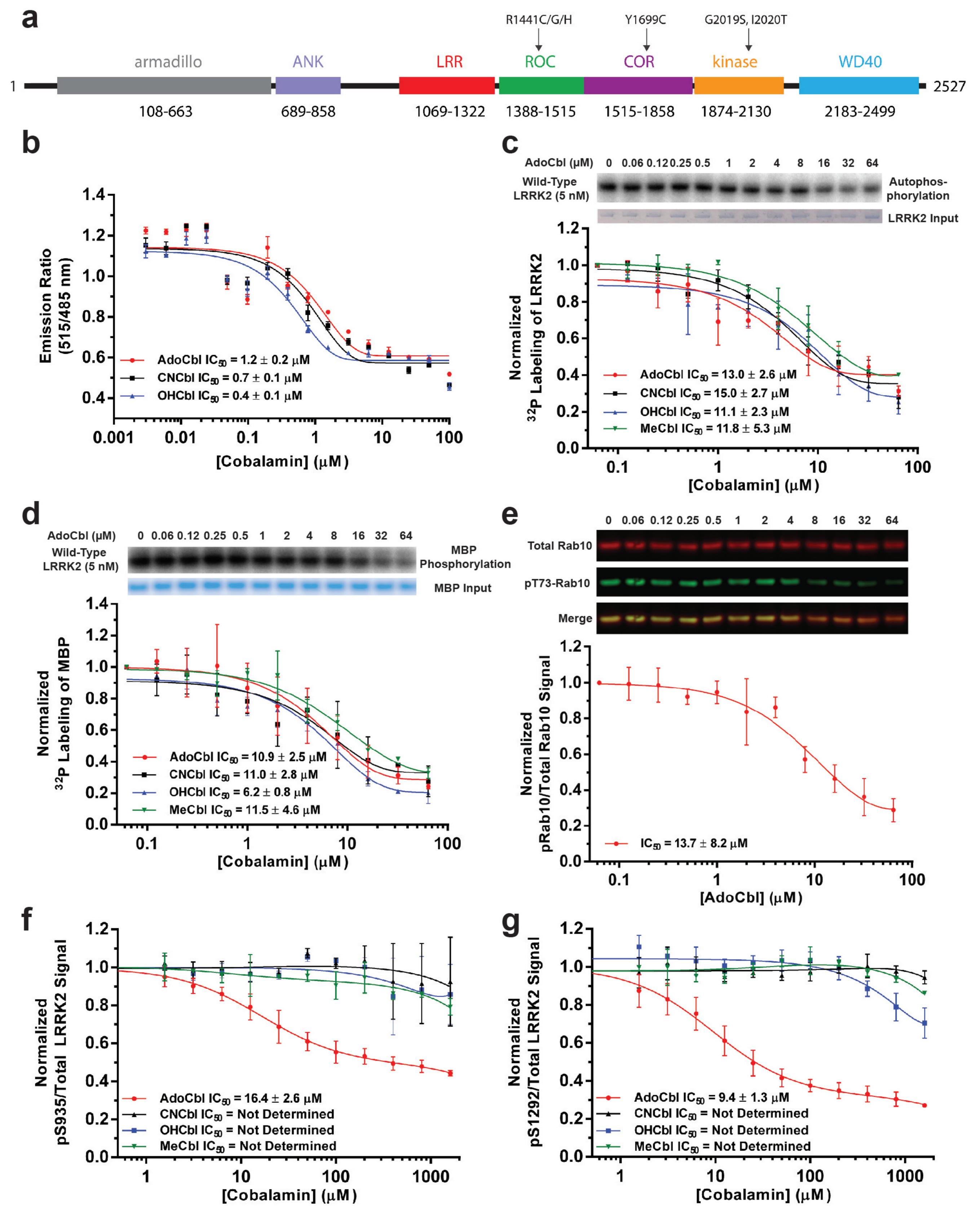
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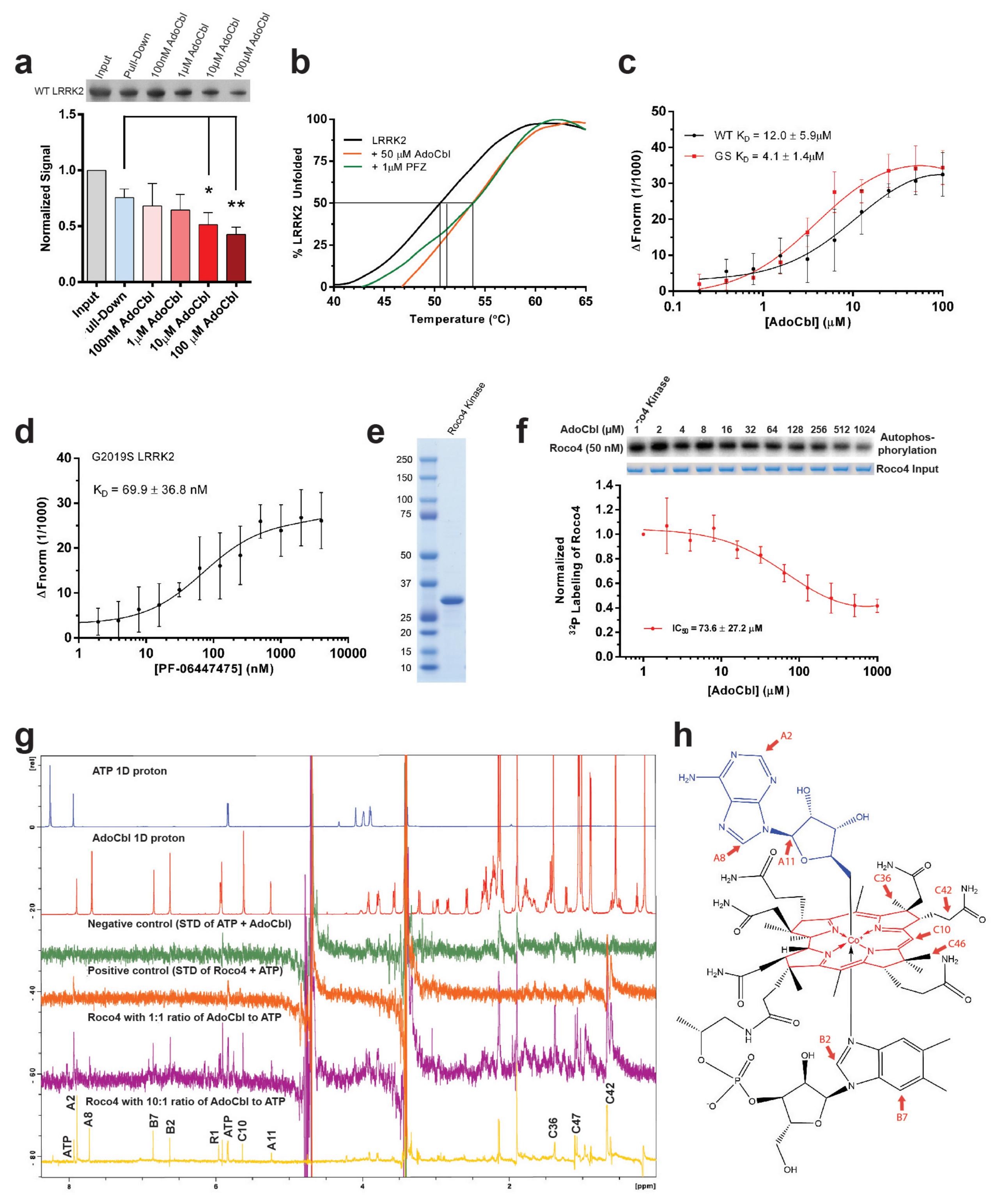
Fig. 6. AdoCbl rescues deficits in *Drosophila* visual physiology induced by the dopaminergic expression of human *LRRK2-G2019S*. (a) Outline of the retinal neural network of *Drosophila*, with three main neuronal layers: photoreceptors, lamina neurons and medulla

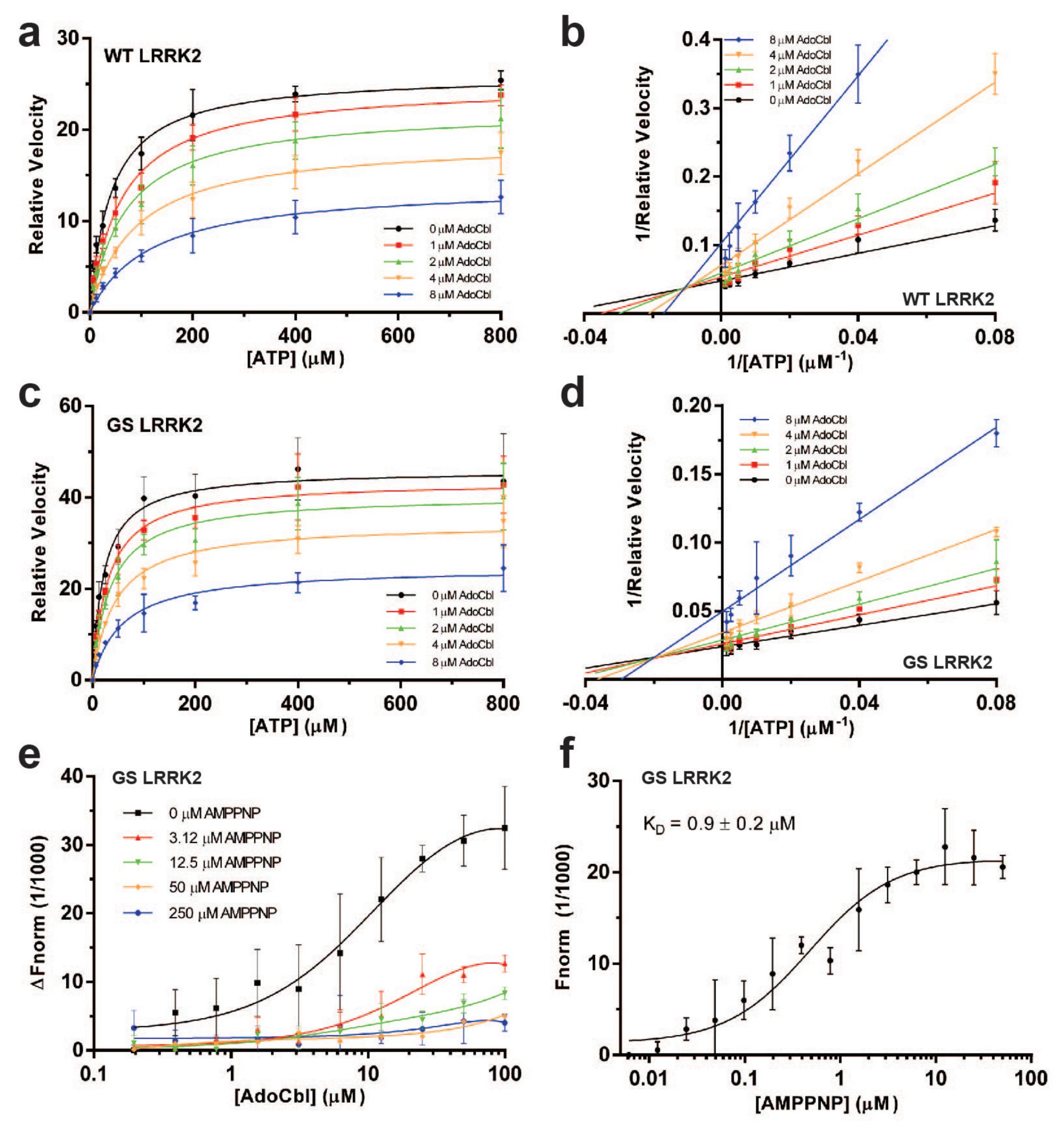
1327	neurons (Modified after Afsari et al ³¹). (b) Contrast response functions (CRFs) for the
1328	photoreceptors, lamina neurons and medulla neurons show that the dopaminergic expression of
1329	<i>hLRRK2-G2019S</i> (<i>DA</i> \rightarrow <i>G2019S</i>) flies have a much bigger response than either the <i>DA</i> \rightarrow
1330	<i>hLRRK2</i> or the <i>DA</i> \rightarrow <i>G2019S</i> which have been fed 2.5 µM AdoCbl. (c) Dose-response curve
1331	for the effect of AdoCbl on the $DA \rightarrow G2019S$ flies, shows a 50% reduction in phenotypes by
1332	250-500 nM AdoCbl, with almost complete rescue by 2.5 μ M AdoCbl. (d) There is no effect of
1333	2.5 µM AdoCbl on flies with dopaminergic expression of kinase-dead hLRRK2-G2019S-
1334	K1906M (DA \rightarrow KD). (e) The visual response of flies with wild-type dLRRK2 is reduced by
1335	2.5µM AdoCbl. (f) Applying 2.5 µM AdoCbl to $dLRRK^{-}$ transheterozygote flies (in which the
1336	drosophila LRRK2 homolog has been knocked out) has no statistically significant effect. Data
1337	represents the mean (\pm s.d.) and the numbers in brackets are the number of flies tested. In (c),
1338	statistical analysis from Tukey Post-hoc tests on the first principal component of a PCA, which
1339	accounted for 88% of the variance (Supplementary information, Fig. S9). (d-f), analysis by
1340	MANOVA. n.s. not significant; *** $p < 0.001$). Boxes correspond to the median +/- quartiles.
1341	Dots indicate data from individual flies. dLRRK ⁻ genotype: dLRRK [^] e03680/dLRRK [^] ex1; wild
1342	<i>type</i> genotype: w^a/w^1118.
1343	

Fig. 7. AdoCbl prevents LRRK2-G2019S induced neurotoxicity and rescues deficits in
dopamine transmission in LRRK2-PD mouse models. (a) Quantification of percent apoptotic

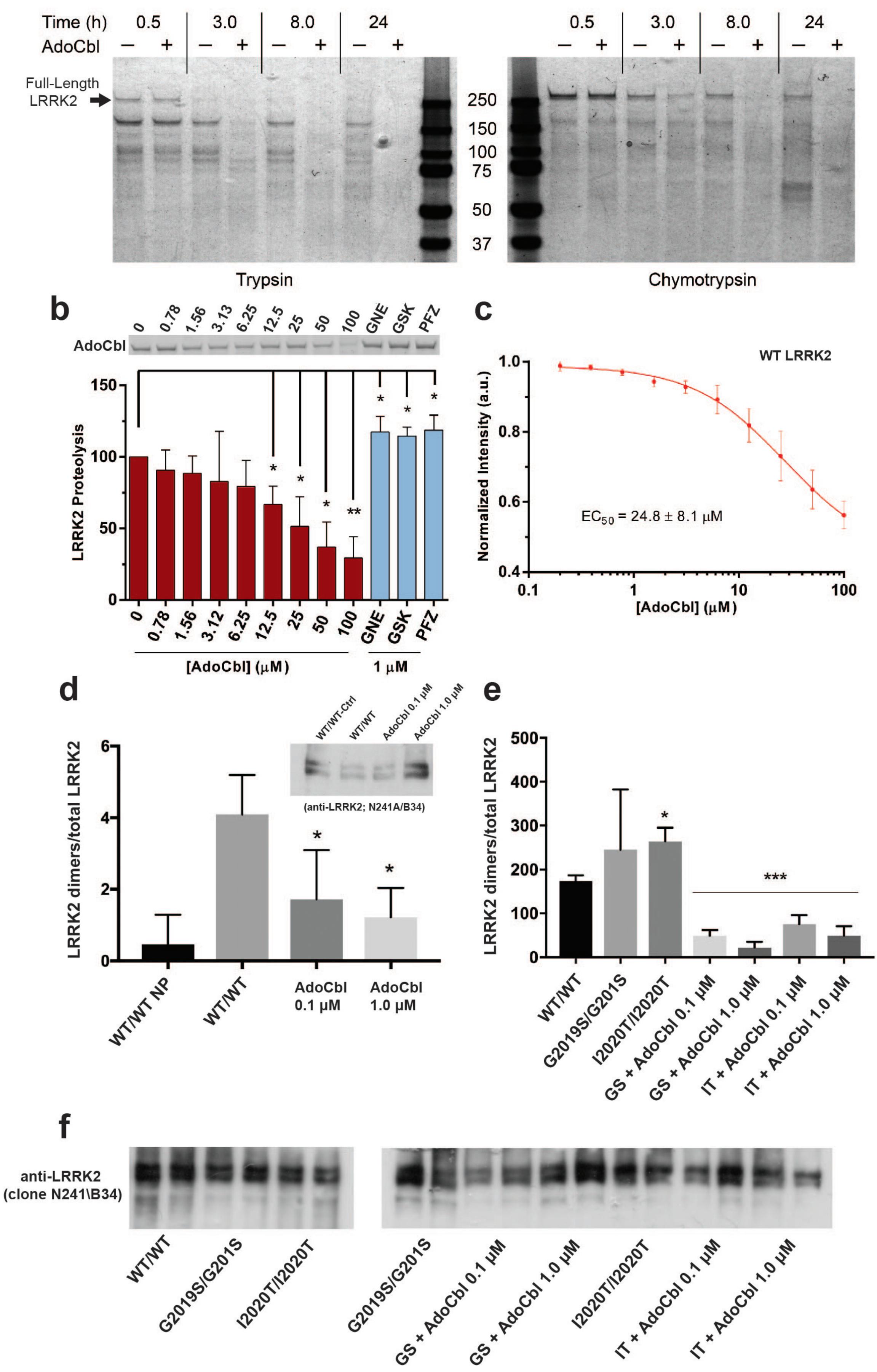
1350 neurons after LRRK2 overexpression and treatment with MLi-2 or AdoCbl. Cortical neurons were co-transfected with LRRK2 and a GFP reporter. Transfected neurons displaying apoptotic 1351 nuclear morphology were counted 48 h after transfection using DAPI. Apoptotic neurons were 1352 1353 defined as those having condensed fragmented chromatin comprised of two or more apoptotic bodies. Data represents the mean $(\pm s.d.)$ from n = 3 biological replicates of triplicate coverslips. 1354 Significance was measured by one-way ANOVA. (b) Quantification of pS1292/Total LRRK2 1355 after brain slice tissue from LRRK2-G2019S BAC-transgenic mice were treated with AdoCbl. 1356 One mouse brain provided enough slices to test each treatment condition one time. Three mouse 1357 1358 brains were used in total, resulting in three biological replicates. Data are the mean $(\pm s.d.)$ and significance was measured by one-way ANOVA (c) Voltammetric traces of striatal DA release 1359 evoked at 2-min intervals from G2019S, or (e) R1441G, and WT controls after 2 h treatment 1360 1361 with control vehicle (water), or with 300 µM AdoCbl. (d) Summary of DA release sustainability for G2019S mice (n = 9 sites) or (f) R1441G (n = 10 sites) compared to WT controls. Data are 1362 expressed as the mean (± s.d.) and were analyzed by two-way ANOVA with *Bonferroni's post* 1363 *hoc* analysis. For all figures, * $p \le 0.01$, ** $p \le 0.001$, *** $p \le 0.0001$. 1364



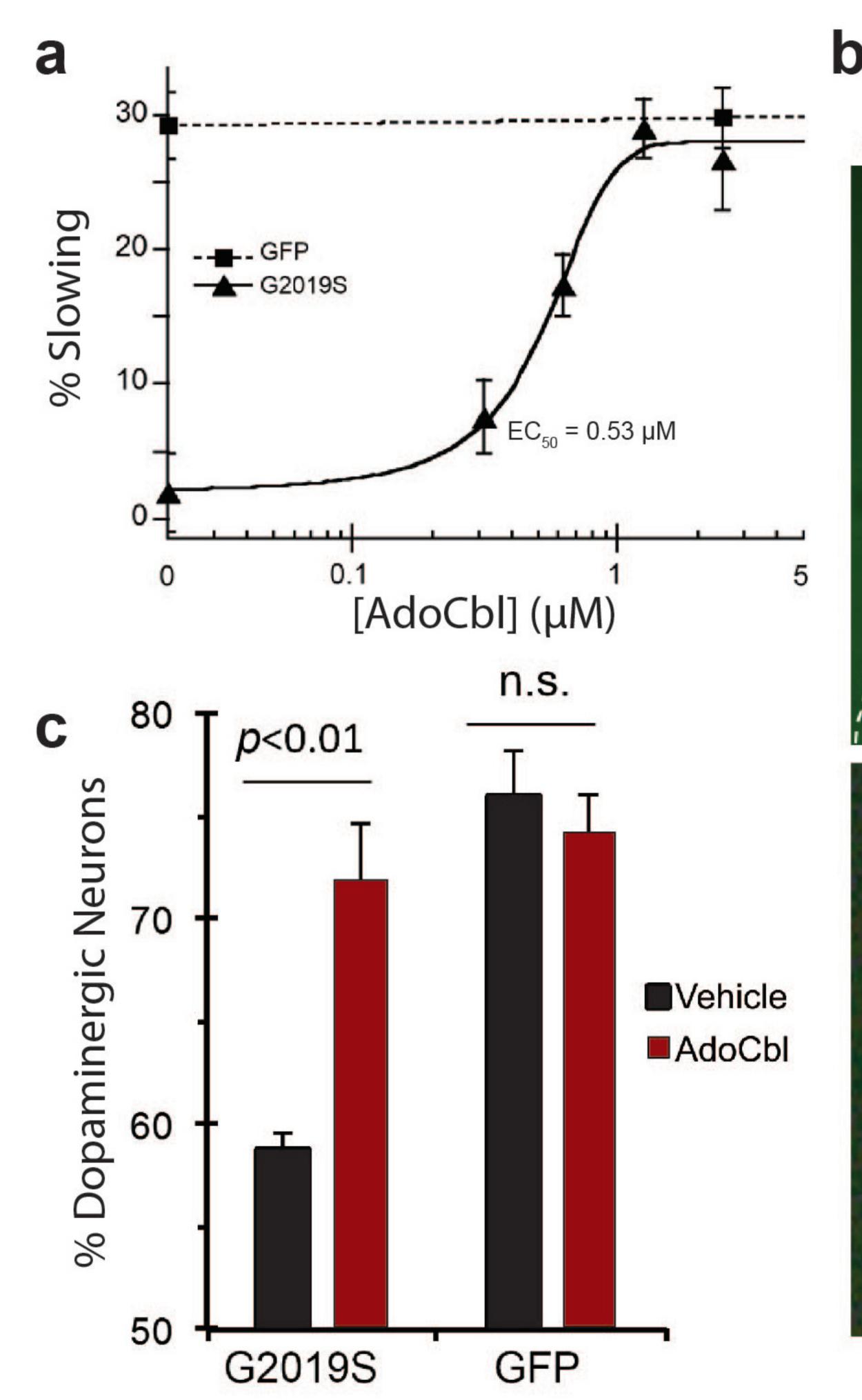




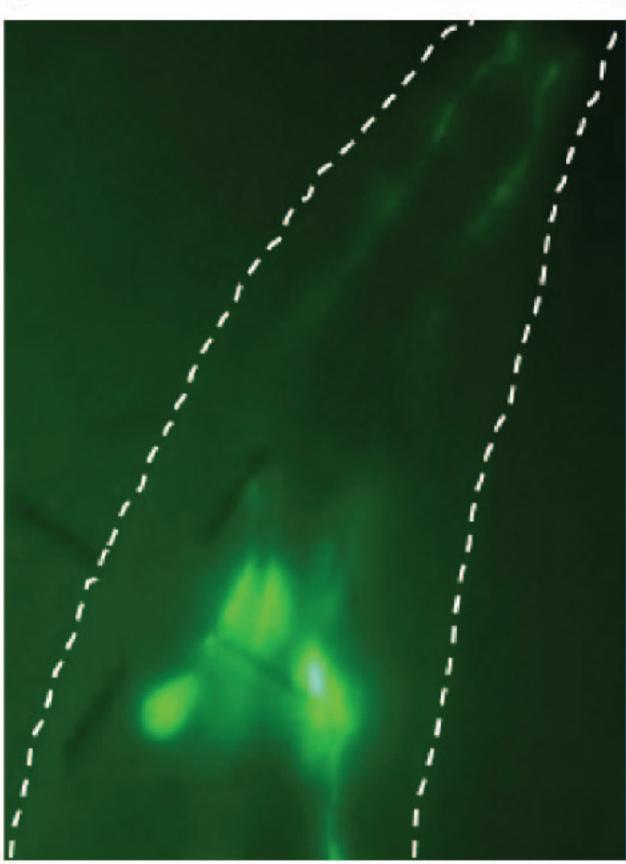
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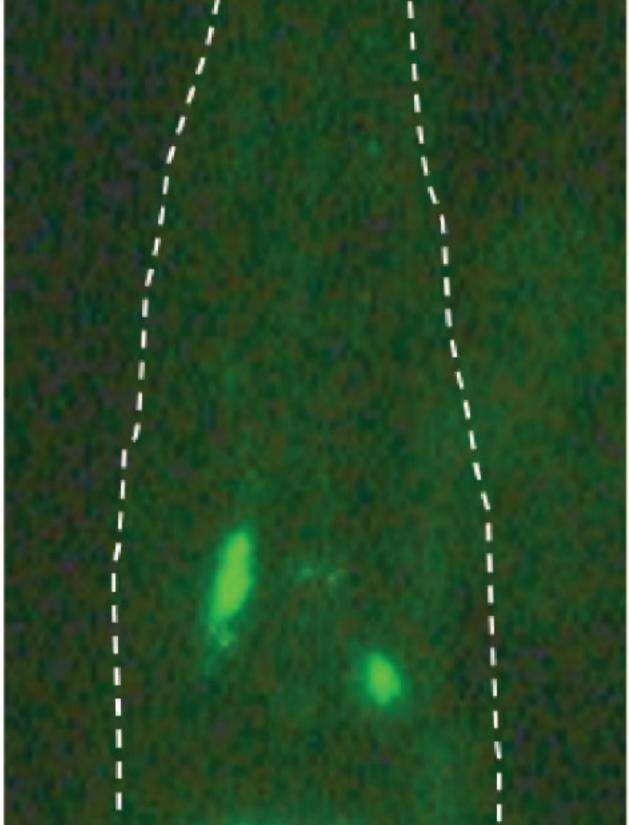


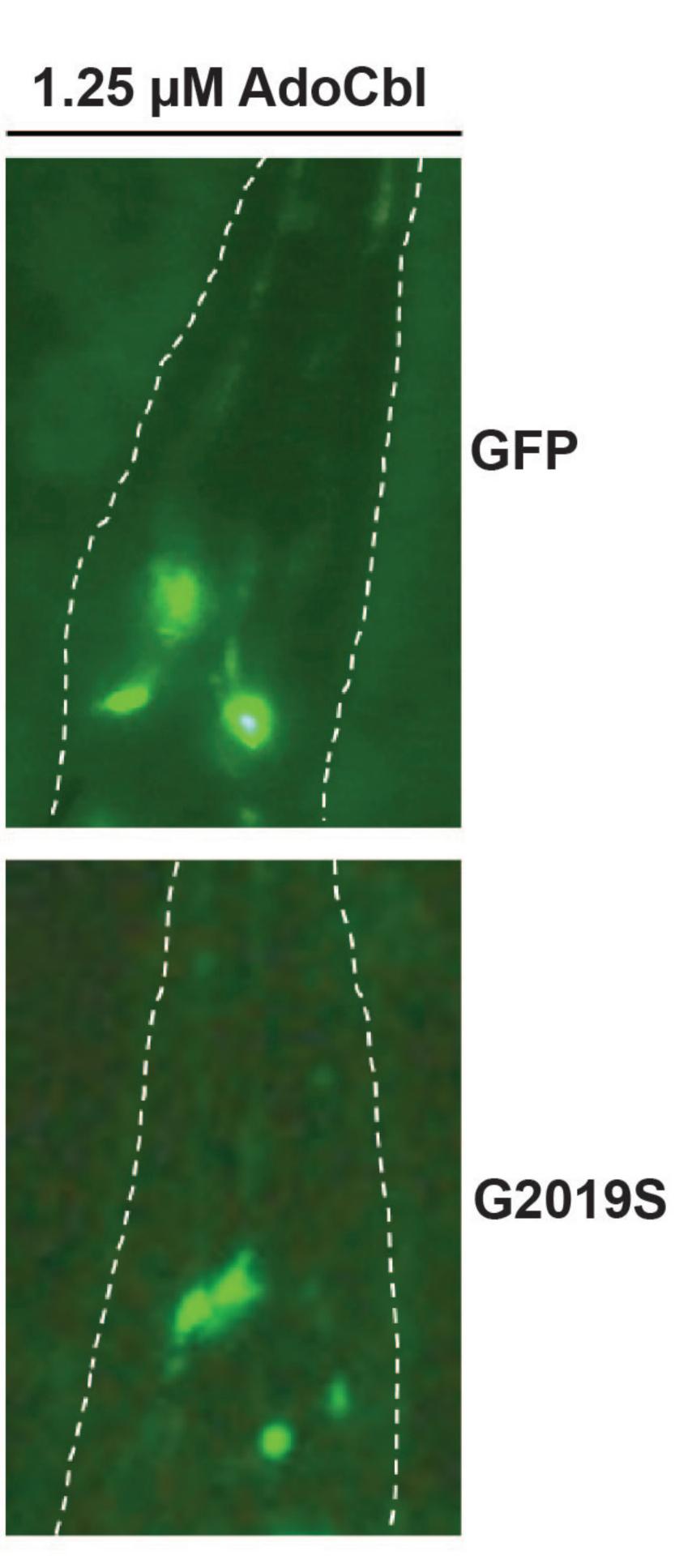


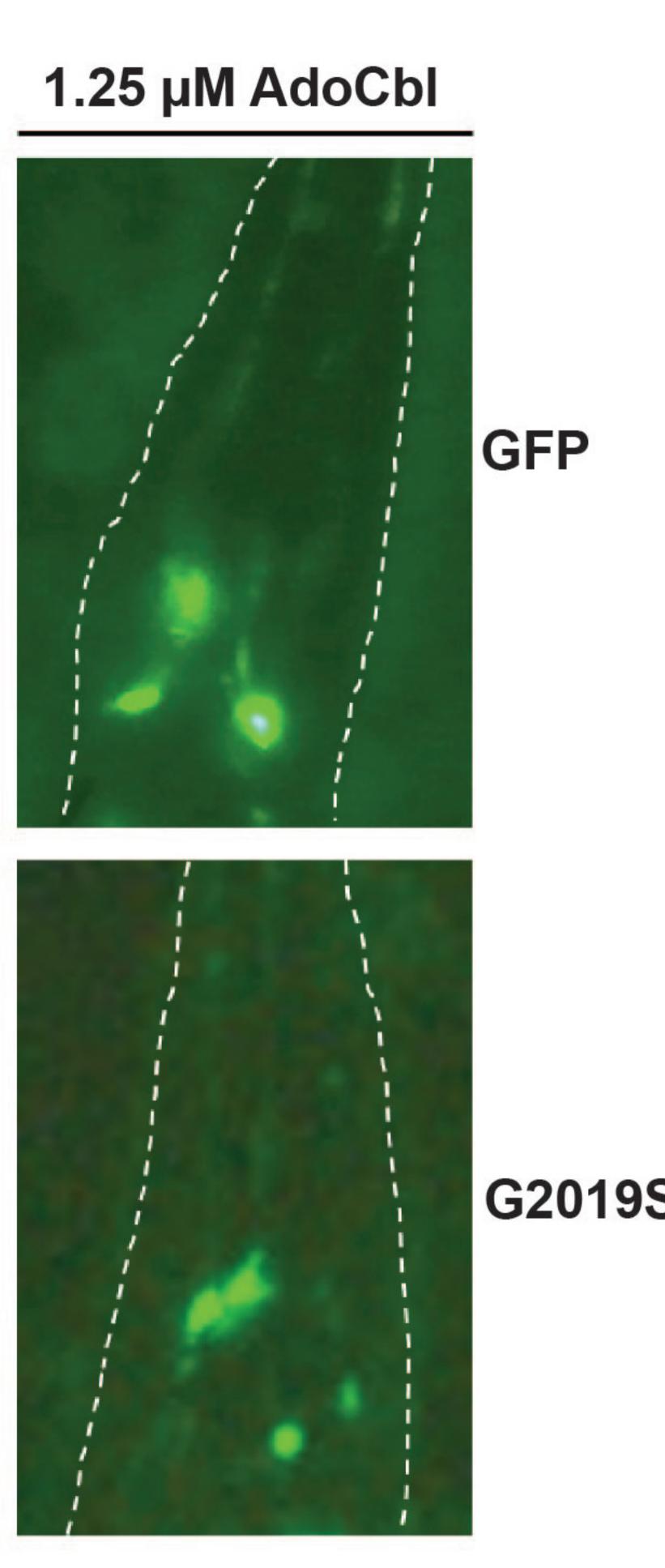


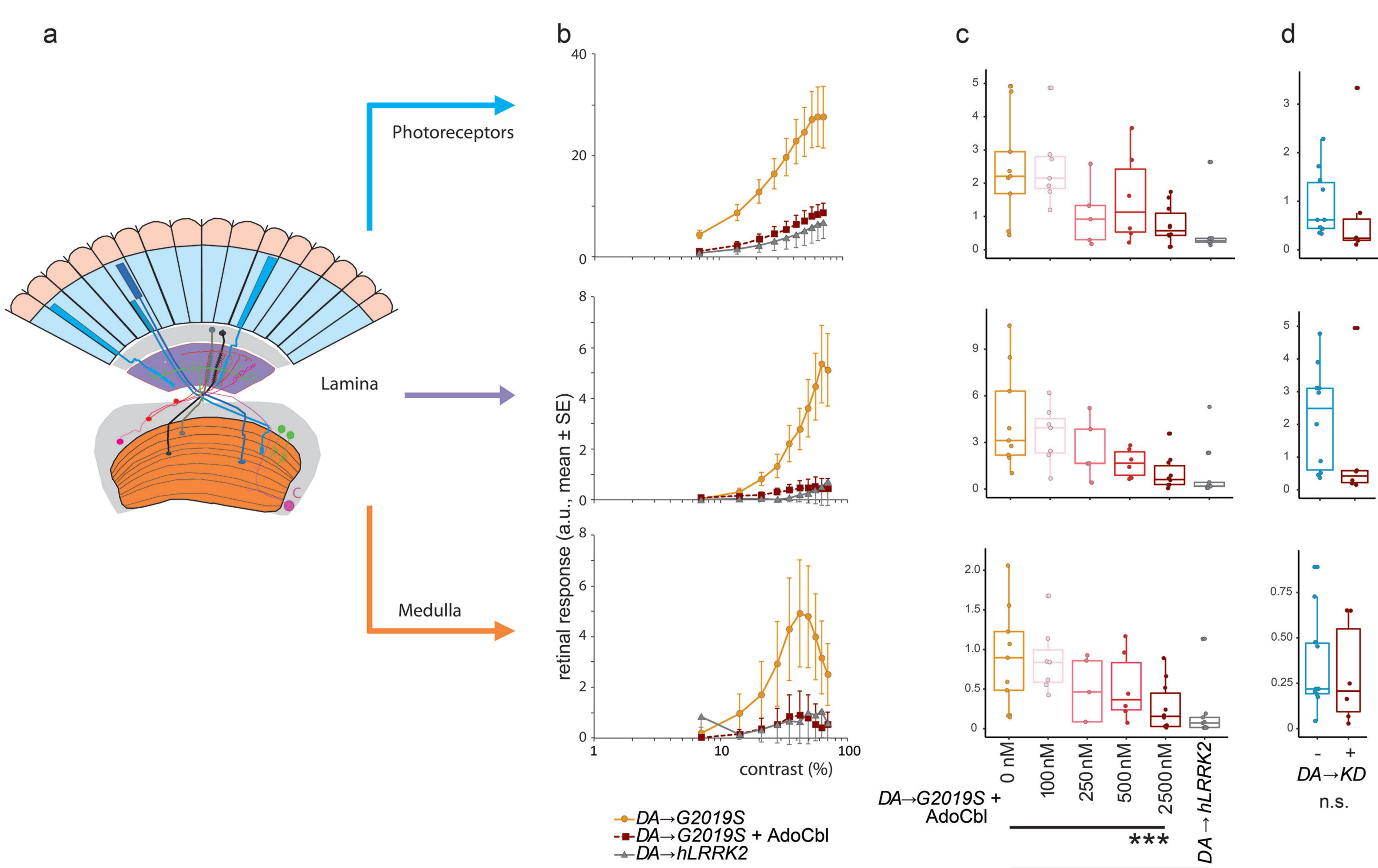
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