Supplementary information, Figure S1



Fig. S1 Purification and characterization of the GABA_B heterodimer and GABA_B-G_{i1} complex. a Schematic diagram of the heterodimeric GABA_B receptor. b Schematic diagram of constructs used in this study. Δ cc represents the coiled-coil (c-c) domain is removed. Δ C represents the entire C-terminus after TM domain in GB1 or GB2 is truncated. c Size-exclusion chromatography profile and SDS-PAGE gel of the purified antagonist-bound GABA_B receptor. d Negative staining EM analysis of the purified inactive GABA_B receptor shows the clear density for VFT and detergent micelles. e G protein pull-down analysis of the different truncations (GB1-GB2, GB1 Δ cc-GB2 Δ cc, and GB1 Δ C-GB2 Δ cc) of GABA_B receptor. SDS-PAGE gel showed that GB1 Δ C-

GB2 Δ cc exhibits a greater efficiency in complex formation among these constructs and were selected for further structural study. f Dose-response curve of baclofen-induced BRET changes in the Gai sensors for the wide-type and GB1 Δ C-GB2 Δ cc construct of GABA_B receptor (GABA_B Δ cc), showing that GABA_B Δ cc exhibits similar pharmacology to that of wild-type receptor. g Size-exclusion chromatography profile and SDS-PAGE gel of the purified agonist/PAM bound GABA_B–Gi1 complex using GB1 Δ C-GB2 Δ cc construct. h Negative staining EM visualization of the purified GABA_B-Gi1 complex showing clear density for VFT, detergent micelles and Gi1 protein.