Supplementary information, Figure S10

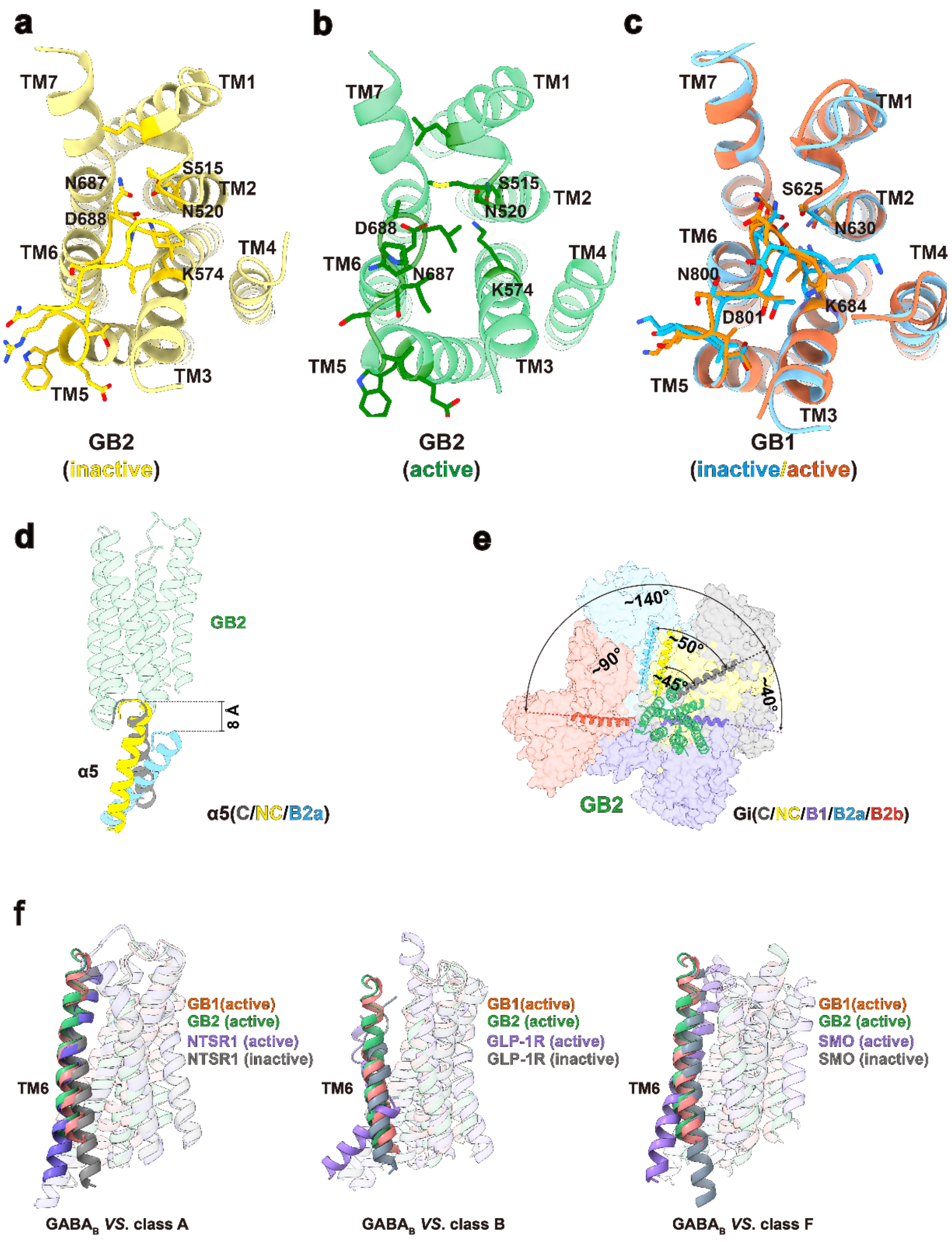

Fig. S10 Conformation of ICL3 in inactive and active GABA$_B$ structures and the α5–receptor interface in GABA$_B$–G$_{i1}$ complex. a-c Interactions of the ICL3 with other residues of TM domain in GB2 inactive (**a**), active state (**b**) and GB1 in both states(**c**). **d** Comparison of the $G\alpha_{i1}$ α5-helix binding position between GB2 (B2a state) and the NTSR1–Gi1 protein complex in canonical (C; PDB code: 6OS9) and noncanonical (NC; PDB code: 6OSA) states. The position of α5-helix from GABA_B–Gi complex in different states show around 8 Å downward movement compared with that of NTSR1–G_{i1} complex. Structures were aligned by the TM domains and only GB2 TM domain is shown for clarity. Color usage for α5: C state, grey; NC state, gold; B2a state, cyan. **e** Orientations of the Gi protein when coupling to GABA_B and NTSR1 receptors. Rotation of Gi protein are measured by the αN domains. Color usage for G proteins: C state, grey; NC state, gold; B1 state, purple; B2a state, cyan; and B2b state, red. **f** Comparison of the active GB1 and GB2 TM domains with the inactive and active structures of class A GPCR NTSR1 (PDB code: 4BUO and 6OS9 for inactive and active states, respectively), class B GPCR glucagon-like peptide-1 receptor (GLP-1R; PDB code: 5VEW and 6B3J for inactive and active states, respectively) and class F GPCR Smoothened receptor (SMO; PDB code: 6JKV and 6OT0 for inactive and active states, respectively), showing the positions of TM6 helices of GB1 and GB2 subunits are similar to that of the representative class A, B and F GPCR in the inactive state.