Supplementary information, Figure S4

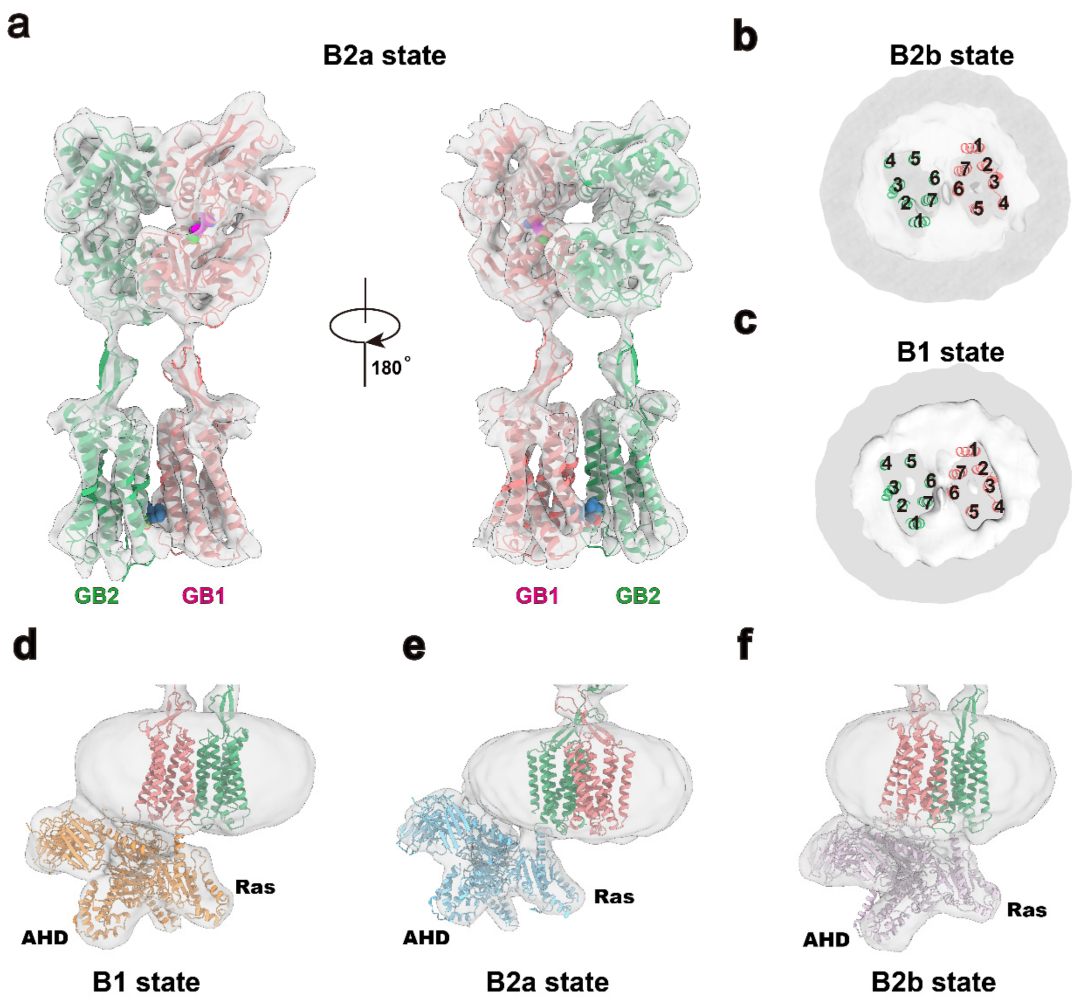

Fig. S4 Fitting of the active GABA$_B$ structure into the cryo-EM density maps of GABA$_B$–G$_{i1}$ complex in B2a, B2b and B1 states. a Side views of the active GABA$_B$ structure derived from the high-resolution density map against cryo-EM map of GABA$_B$–G$_{i1}$ complex in B2a state. **b-c** Cut through of bottom-up views of the active GABA$_B$ structure derived from the high-resolution density map against cryo-EM map of GABA$_B$–G$_{i1}$ complex in B2b state (**b**) and B1 state (**c**), respectively. The model of GABA$_B$ receptor was rigid-body docked into the density. **d-f** Rigid body fitting of the G$_{i1}$–scFv16 structure from the activated-CB2–G$_{i1}$ complex (PDB code: 6PT0) into the cryo-EM density maps, revealing that most regions of the G_{i1}–scFv16 structure in a good agreement with the cryo-EM densities in B1 state (**d**), B2a state (**e**), and B2b state (**f**).