We thank the editor for the opportunity to resubmit our revised manuscript, “Comprehensive, structurally-informed alignment and phylogeny of vertebrate biogenic amine receptors.”

**Response to the Associate Editor**

Of the two revision options recommended by the associate editor, we have opted to address the following,

b) alternatively, you could weaken your assertions pertaining to tree and alignment quality. In particular, specifically drop claims of "high-quality" sequence alignment (several occurrences) and change your statement "our phylogeny reveals that only two ligand-based receptor classes, mAChR and TAAR, are truly monophyletic." into "our phylogeny indicates that ...".

Accordingly, we have removed the all instances of the phrase “high-quality” from the paper, and we have written the mAChR/TAAR sentence per the editor’s recommendation.