



SUPPLEMENTARY MATERIAL 4. Maximum-likelihood phylogeny of *Cottus* based on rhodopsin haplotypes ($n = 68$ derived from 482 sequences). Inset, amino acid (AA) phylogeny. Species complexes are colored. Numbers on the right indicate the candidate species (and in one case, the form), associated with each clade. Dots (gray, >90%; black, >95%) denote ultrafast bootstrap support.