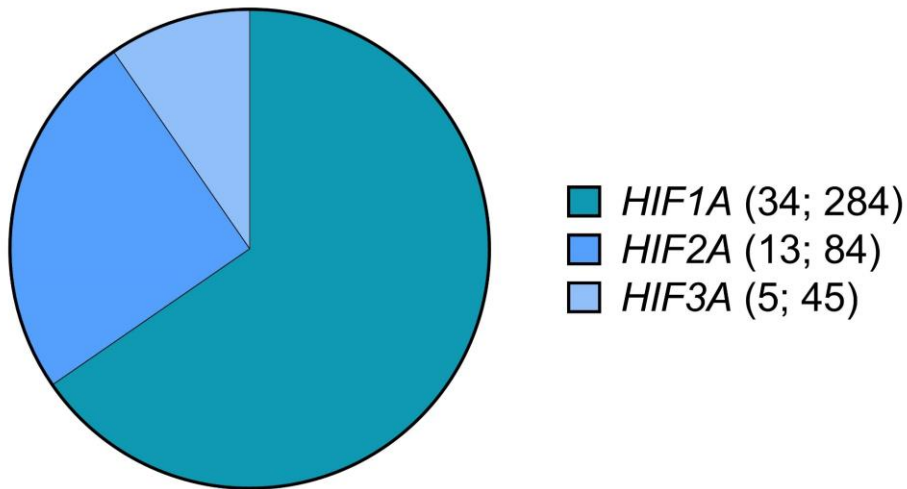


Figure S1. Summary of **(A)** *HIF*A genes and **(B)** tissues sampled in studies reviewed here. In each panel, the wedges represent the proportion of studies examining each *HIF*A gene or tissue. The number of studies and the number of discrete sampling points are shown in parentheses (studies; samples). For panel **(A)**, all forms of each gene are combined (ancestral and teleost-specific duplicates). For panel **(B)**, “Other” represents one sample each from spleen, swim bladder, and testis.

A



B

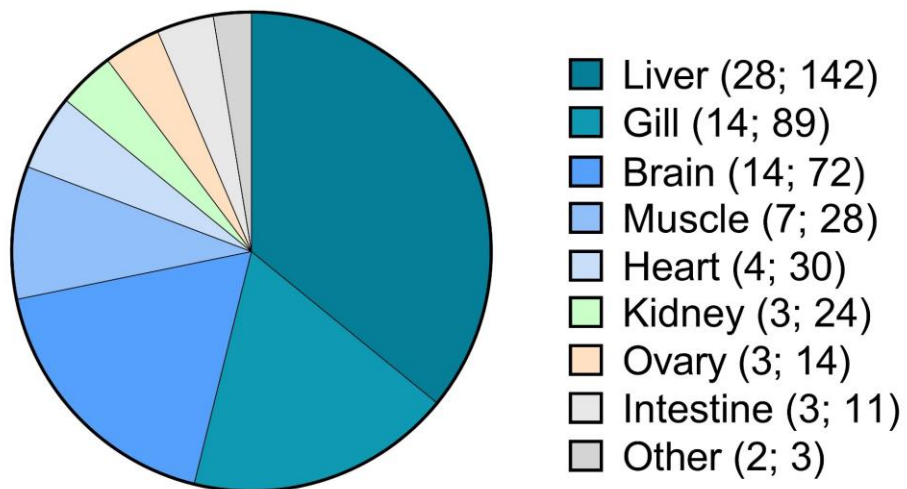


Figure S2. Results of generalized linear mixed effect model analysis of the effects of cumulative oxygen deficit on the predicted frequency of **(A)** *HIF2A* and **(B)** *HIF3A* mRNA increases during hypoxic exposure of fishes. The effect of COD was not significant for *HIF2A* ($P = 0.296$) or *HIF3A* ($P = 0.749$). See Tables S6 and S7 for complete statistical outputs.

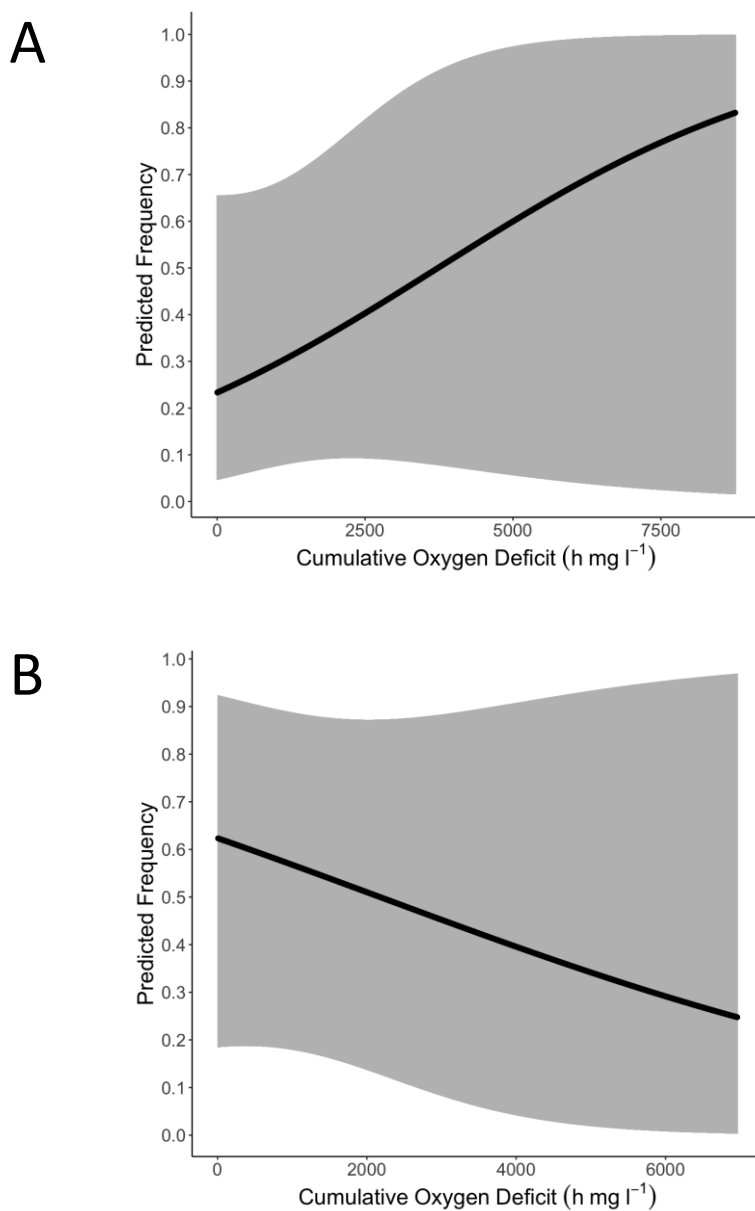


Figure S3. Results of generalized linear mixed effect model analysis of the effects of methods reporting on the predicted frequency of **(A)** *HIF2A* and **(B)** *HIF3A* mRNA increases during hypoxic exposure of fishes. Models included the number of essential MIQE criteria as a fixed effect and study as a random effect. The effect of MIQE score was not significant for *HIF2A* ($P = 0.127$) but it approached statistical significance for *HIF3A* ($P = 0.0547$). See Tables S9 and S10 for complete statistical outputs.

