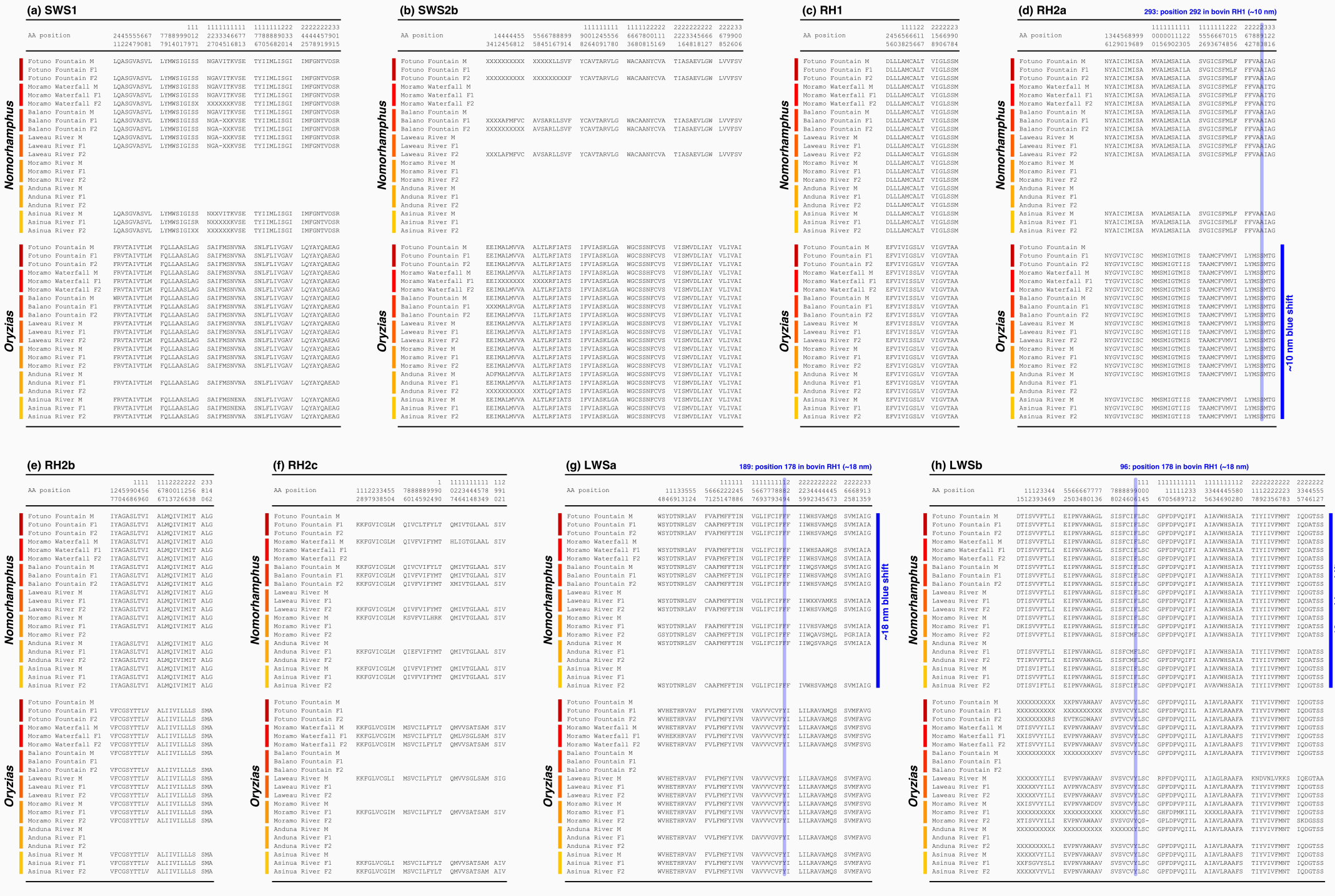

Figure S3 Amino acid sequences estimated from the RNA-Seq consensus sequences of opsin genes of each wild individual of *Nomorhamphus* and *Oryzias* from the seven local populations. (a) SWS1, (b) SWS2b, (c) RH1, (d) RH2a, (e) RH2b, (f) RH2c, (g) LWSa, and (h) LWSb. We found that SWS2a was lost from the *Oryzias* genome. The spectrum tuning sites were predicted for each opsin by aligning its amino acid sequences with the amino acid sequences of the bovine RH1.