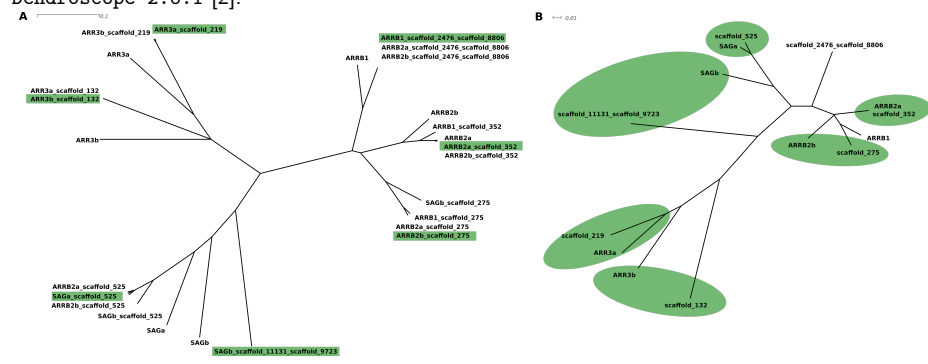


Additional file 2 — Phylogenetic tree of arrestin annotations from Scipio

Figure 1 Phylogenetic tree of arrestins as annotated by Scipio in pufferfish together with query orthologs from zebrafish. Scipio was run in sensitive mode (modified options: max_assemble_size=50000, min_score=0.1, exhaust_align_size=50000, region_size=90000). The alignment and neighbor joining-tree on protein level were built with Clustal Omega 1.2.1 [1] on all columns of the alignment (A) and on all columns that did not contain any gaps (B). The alternative solutions of Scipio on the same genomic unit may slightly differ in dependence on the query paralog it was retrieved with (indicated by first part of the node label). The zebrafish paralogs are denoted as *SAGa,b*, *ARRB1*, *ARRB2a,b* and *ARR3a,b*. The solution proposed by the EMS-pipeline is highlighted in green. *ARRB1* is situated on scaffold.2476_scaffold.8066. Due to long branch attraction, missing data and sequence divergence, zebrafish and pufferfish orthologs do not always form monophyletic groups. This makes inference of paralog-to-contig assignments based on the phylogenetic tree difficult. The trees were edited and displayed with Dendroscope 2.6.1 [2].



Author details

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