Diagram

Description automatically generated

A

B

A. japonica FP-FABP --MVEKFVGTWKIADSHNFGEYLKAIGAPKELSDGGDATTPTLYISQKDGDKMTVKIENG

A. bicolor bicolor FP-FABP --MVEKFVGTWKIAESHNFGEYLKAIGAPKELSDGGDATKPTLYISQKDGDKMTVKIENG

A. australis FP-FABP --MVEKFVGTWKIADSHNFGEYLKAIGAPKELSDGGDATTPTLYISQKDGDKMTVKIENG

A. mossambica FP-FABP --MVEKFVGTWKIADSHNFGEYLKAIGAPKELSDGGDATTPTLYISQKDRDKMTVKIENG

G. zonipectis FP-FABP --MLEQFVGKWTIAESKDFGKYLEAIGAPTSLSEAGDNTQPKLEISQKDGNKMTVDIDNG

K. hyoproroides FP-FABP --MFEDFLGTWKCIDSQNFGAYLAAIGAPPVLSERADATRPTVHFN-RDGDKLSLKVEHG

K. n. sp. FP-FABP --MFEDFLGTWECIDSQNFGAYLAAVGAPPVLSDRADATRPTVYFN-RDGDKLSLKVEHG

H. sapiens FABP-7 --MVEAFCATWKLTNSQNFDEYMKALGVGFATRQVGNVTKPTVIIS-QEGDKVVIRTLS-

G. zonipectis FABP-7 like --MVDAFCATWKLLDSQNFDDYMKAIGVGFATRQVGNVTKPTIIIG-KDGDKMFVKTLS-

D. rerio FABP-7 --MVDAFCATWKLVDSQNFDEYMKSLGVGFATRQVGNVTKPTIVIS-HEGDKVVIKTLS-

K. hyoporoides FABP-7 like --MVDAFFGTWKLVDSQNFDEYMKALGVGFATRQVGNVTKPTVIIG-QDGDKVFVKT-Q-

D. rerio FABP-3 --MADAFIGTWNLKESKNFDEYMKGIGVGFATRQVANMTKPTTIIS-KEGDVFTLKTVS-

A. japonica FABP-3 MVIMEPFLGTWHLKTSENFDEYMKELGVGFATRKIGNTTKPTLIIA-ADGDKFQVKTQS-

D. rerio FABP-10 --M--AFSGTWQVYAQENYEEFLRAISLPEEVIKLAKDVKPVTEIQ-QNGSDFTITSKT-

A. japonica FP-FABP PPTFLDTQVKFKLGEEFDEFPSDRRKGVKSVVNLVGEKLVYVQKWDGKETTYVREIKDGK

A. bicolor bicolor FP-FABP PPTFLDTEVKFKLGEEFDEFPSDRRKGVRSVVNLVGEKLVYAQKWDGKETTYVREIKDGK

A. australis FP-FABP PPTFLDTQVKFTLGEEFDEFPSDRRKGVRSVVNLVGEKLVYLQKWDGKETTLVREIKDGK

A. mossambica FP-FABP PPTFLDTEVKFKLGEEFDEFPSDRRKGVRSVVNLVGEKLVYLQKWDGKKTTLVREIKDGK

G. zonipectis FP-FABP PPTNYQVQVKFTLGEEFDEKTSDGRKGIKTTVTYEDNKLVYTQRWDGKKAVTYRQVVDGT

K. hyoporoides FP-FABP PPPLKDVLLSFKLGEEFDEHPTDGRK-CKTLVTFEGDKLLYLQKWDGKETVVVREIRDGN

K. n. sp. FP-FABP PPPLKDVILSFKLGEEFDEHPTDGRK-CKTLVTFEGDKLLYLQKWDGKETVVVREIRDGN

H. sapiens FABP-7 --TFKNTEISFQLGEEFDETTADDRN-CKSVVSLDGDKLVHIQKWDGKETNFVREIKDGK

G. zonipectis FABP-7 like --TFKNTEISFKLGEEFDETTADDRN-CKSVISMEGDKLVHVQKWDGKETKFVREIQDGK

D. rerio FABP-7 --TFKNTEISFKLGEEFDETTADDRH-VKSTVSLEGDNLVQVQRWDGKETKFVREIKDGK

K. hyoporoides FABP-7 like --TF-NTEISFKLGEEFDETTADDRN-CKSVV-MEGNSLVHVQ-WDGKETKFVREVQDGK

D. rerio FABP-3 --TFKSTEINFKLGEEFDETTADDRK-VKSVITLDGGKLLHVQKWDGKETTLLREVSDNN

A. japonica FABP-3 --LLKSTEINFKLGEEFDETTADDRK-VKSVVKLEDGKLVHLQKWDSKETSLVRAVDGNK

D. rerio FABP-10 --PGKTVTNSFTIGKEAEITTMDGKK-LKCIVKLDGGKLVCRT----DRFSHIQEIKAGE

A. japonica FP-FABP LVVTLTMGDVVAVRSYRRATE-----

A. bicolor bicolor FP-FABP LVVTLTMGDVVSVRSYRRATE-----

A. australis FP-FABP LFVTLTMGDVVSVRSYRRASE-----

A. mossambica FP-FABP LVVTLTMGDVVSVRSYRRATE-----

G. zonipectis FP-FABP LVTKLTYGDVVSVRKYKRINV-----

K. hyoporoides FP-FABP VVATLSHEGVVALRVYKKVAGPTALE

K. n. sp. FP-FABP VVATLSHEGVVALRVYKKVAGPTA--

H. sapiens FABP-7 MVMTLTFGDVVAVRHYEKA-------

G. zonipectis FABP-7 like MVMKLTFEDILAVRTYEKA-------

D. rerio FABP-7 MVMTLTFEGVQAVRTYEKA-------

K. hyoporoides FABP-7 like LVMKLTFEDVLSVRTYEKA-------

D. rerio FABP-3 LTLTLTLGDIVSTRHYVKAE------

A. japonica FABP-3 LTLTLTFGNVVSTRHYEKAE------

D. rerio FABP-10 MVETLTVGGTTMIRKSKKI-------

**S2 Figure.** **(A)** Phylogenetic tree of fluorescent and nonfluorescent FABPs, rooted to the midpoint. Fluorescent proteins are shown in green. Input data statistics: 14 sequences with 146 amino-acid sites. Number of constant sites: 24 (= 16.4384% of all sites). Number of invariant (constant or ambiguous constant) sites: 24 (= 16.4384% of all sites). Number of parsimony informative sites: 91. Number of distinct site patterns: 143.

The consensus tree was constructed from 1000 ultrafast bootstrap trees (Hoang et al., 2017).

**(B)** Alignment of all sequences shown in the phylogenetic tree. Amino acid sequences were aligned using MAFFT v7.487 with the L-INS-i Iterative refinement method and default parameters (Hofacker et al., 2002; Katoh et al., 2002, 2005; Katoh and Toh, 2008; Tabei et al., 2008; Katoh and Frith, 2012; Kuraku et al., 2013; Katoh and Standley, 2016; Yamada et al., 2016; Rozewicki et al., 2019). The best model of substitution was selected using ModelFinder (Kalyaanamoorthy et al., 2017).

Sequences used for the tree and alignment are as follows: *Anguilla japonica* FP-FABP (UnaG, Accession P0DM59.1), *Anguilla australis* FP-FABP (Accession BAP76194.1), *Anguilla bicolor* *bicolor* FP-FABP (Accession BAP76195.1), *Anguilla mossambica* FP-FABP (Accession BAP76197.1), *Gymnothorax zonipectis* FP-FABP (GymFP, Accession PRJNA718586), *Kaupichthys hyoproroides* FP-FABP (Chlopsid FP I, Accession PRJNA192511), *Kaupichthys n. sp.* FP-FABP (Chlopsid FP II, Accession PRJNA223153), *Homo sapiens* FABP-7 (Accession NP\_001437.1), *Danio rerio* FABP-3 (Accession NP\_694493.1), *Danio rerio* FABP-7 (Accession NP\_571680.1), *Danio rerio* FABP-10 (Accession NP\_694492.1), *Anguilla japonica* FABP-3 (Accession BAA92241.3), *Kaupichthys hyoproroides* FABP-7 like (Accession PRJNA192511), *Gymnothorax zonipectis* FABP-7 like (Accession PRJNA718586).