

# **Comparative genomic organization and tissue distribution of FABPs**

**Report: Yuru Zhang**



# Fatty acid-binding protein (*fabp*) genes of spotted green pufferfish (*Tetraodon nigroviridis*): comparative genomics and spatial transcriptional regulation

Aruloli Thirumaran and Jonathan M. Wright

Genome, 2013

## Comparative genomic organization and tissue-specific transcription of the duplicated *fabp7* and *fabp10* genes in teleost fishes

rossMark

Manoj B. Parmar and Jonathan M. Wright

Genome, 2014

<sup>c</sup> Department of Aquaculture, Faculty of Fisheries, Atatürk University, 25240 Erzurum, Turkey

OPEN ACCESS Freely available online

2013

PLOS ONE

## Phyletic Distribution of Fatty Acid-Binding Protein Genes

Yadong Zheng<sup>1,2</sup>, David Blair<sup>3</sup>, Janette E. Bradley<sup>1\*</sup>

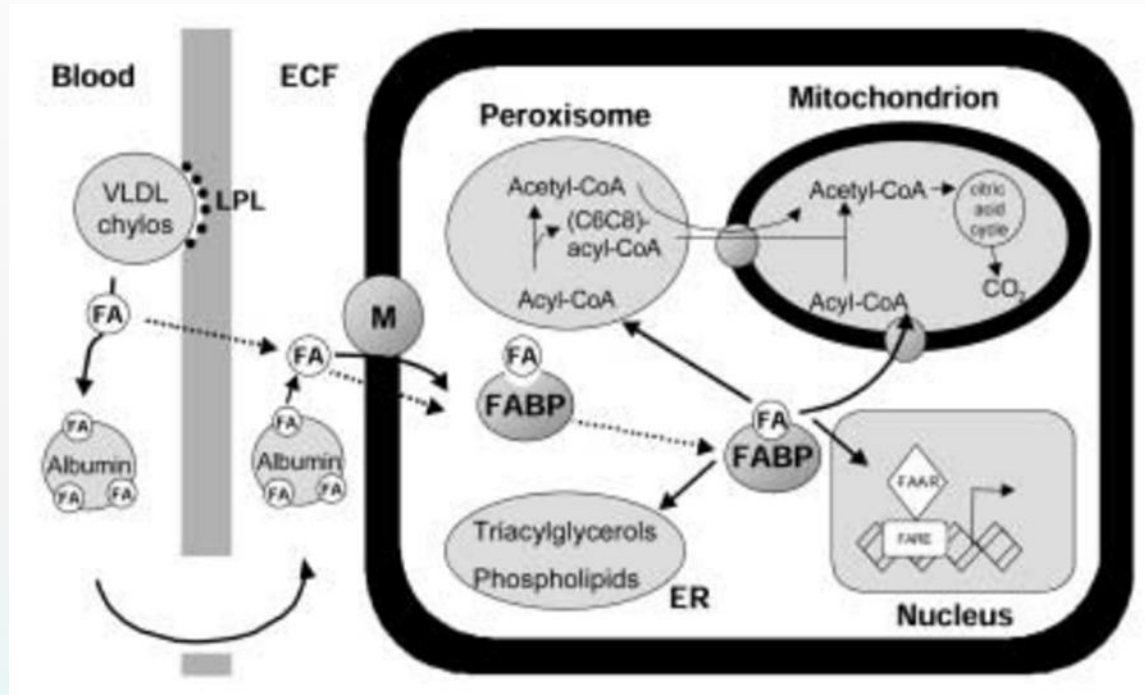
1 School of Biology, University of Nottingham, Nottingham, United Kingdom, 2 State Key Laboratory of Veterinary Etiological Biology, Key Laboratory of Veterinary Parasitology of Gansu Province, Lanzhou Veterinary Research Institute, CAAS, Lanzhou, Gansu, China, 3 James Cook University, Townsville, Queensland, Australia

# Content

- ◆ **1, Background**
- ◆ **2, FABPs in invertebrate species**
- ◆ **3, FABPs in teleost fish**

# 1 Background

## 1.1 The role of FABPs



Schematic representation of the role of FABPs in FA uptake and intracellular FA trafficking.













































----Zimmerman, *Cell Mol Life Sci*, 2002

Intracellularly, FAs are bound by FABPs, which are considered to be important carriers for intracellular FAs.

They increase FA solubility and facilitate transport of FA from the plasma membrane to sites of FA oxidation (mitochondria, peroxisomes), to sites of FA esterification into TGs or phospholipids, or to the nucleus, possibly for regulatory functions.

# 1.2 FABPs type

## Protein Domains:

1. Muscle fatty acid binding protein (m-fabp) [50848]
  1. [Human \(Homo sapiens\) \[TaxId: 9606\]](#) [50849] (5)  
  2. [Cow \(Bos taurus\) \[TaxId: 9913\]](#) [50850] (1)  
2. Intestinal fatty acid binding protein [50851]
  1. [Rat \(Rattus norvegicus\) \[TaxId: 10116\]](#) [50852] (11)    
*SQ P02693*
  2. [Human \(Homo sapiens\) \[TaxId: 9606\]](#) [50853] (3)  
3. Brain fatty acid binding protein [63809]
  1. [Human \(Homo sapiens\) \[TaxId: 9606\]](#) [63810] (3)  
4. Epidermal fatty acid binding protein [50854]
  1. [Human \(Homo sapiens\) \[TaxId: 9606\]](#) [50855] (2)  
5. Adipocyte lipid-binding protein, ALBP [50856]
  1. [Mouse \(Mus musculus\) \[TaxId: 10090\]](#) [50857] (17)  
  2. [Human \(Homo sapiens\) \[TaxId: 9606\]](#) [110275] (4)    
*SQ P15090*
6. Fatty acid-binding protein homolog 1 [89366]
  1. [Flat worm \(Echinococcus granulosus\) \[TaxId: 6210\]](#) [89367] (1)  
7. Fatty acid-binding protein [50858]
  1. [Tobacco hornworm \(Manduca sexta\) \[TaxId: 7130\]](#) [50859] (1)  
  2. [Desert locust \(Schistocerca gregaria\) \[TaxId: 7010\]](#) [50860] (1)  
8. Cellular retinoic-acid-binding protein (CRABP) [50861]
  1. [Human \(Homo sapiens\), CRABP-II \[TaxId: 9606\]](#) [50862] (12)  
  2. [Cow and mouse \(Bos taurus\) and \(Mus musculus\), CRABP-I, identical sequences \[TaxId: 9913\]](#) [50863] (3)  
9. Cellular retinol-binding protein II (CRBP) [50864]
  1. [Rat \(Rattus norvegicus\) \[TaxId: 10116\]](#) [50865] (9)  
  2. [Zebrafish \(Danio rerio\) \[TaxId: 7955\]](#) [75000] (2)  
10. Cellular retinol-binding protein III [63811]
  1. [Human \(Homo sapiens\) \[TaxId: 9606\]](#) [63812] (1)  
11. Liver fatty acid binding protein [50866]
  1. [Rat \(Rattus norvegicus\) \[TaxId: 10116\]](#) [50867] (4)  
  2. [Human \(Homo sapiens\) \[TaxId: 9606\]](#) [141464] (8)    
*SQ P07148 I-127*
12. Liver basic fatty acid binding protein, LB\_FABP [89368]
  1. [Chicken \(Gallus gallus\) \[TaxId: 9031\]](#) [89369] (5)    
*SQ P80226*
  2. [Argentine common toad \(Bufo arenarum\) \[TaxId: 38577\]](#) [89370] (1)  
  3. [Axolotl \(Ambystoma mexicanum\) \[TaxId: 8296\]](#) [141465] (2)    
*SQ P81400 I-125*
13. Cellular retinol-binding protein IV [82157]  

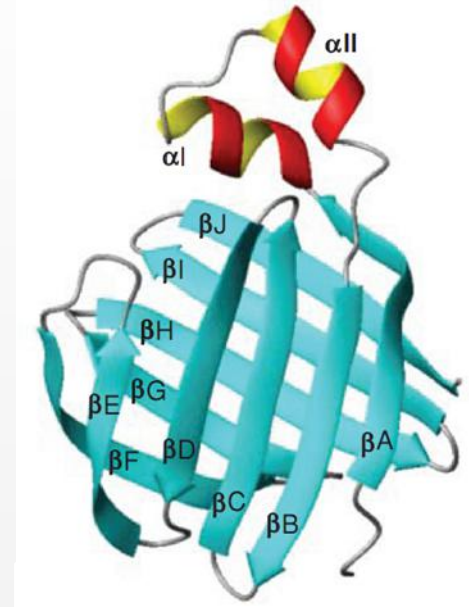
Fatty acid binding protein-like Family in Scop Database

**Table 1** Fatty acid-binding protein multigene family

Gene	Protein	Name	Alternate names	Tissue/cell expression
<i>FABP1</i>	FABP1	Liver FABP	L-FABP	Liver, intestine, pancreas, kidney, lung, stomach
<i>FABP2</i>	FABP2	Intestinal FABP	I-FABP	Intestine, liver
<i>FABP3</i>	FABP3	Heart/muscle FABP	H-FABP	Heart, skeletal muscle, brain, kidney, lung, stomach, testis, aorta, adrenal gland, mammary gland, placenta, ovary, brown adipose tissue
<i>FABP4</i>	FABP4	Adipocyte FABP	A-FABP	Adipocyte, macrophage, dendritic cell
<i>FABP5</i>	FABP5	Epidermal FABP	E-FABP	Skin, tongue, adipocyte, macrophage, mammary gland, brain, intestine, kidney, liver, lung, heart, skeletal muscle, testis, retina, lens, spleen
<i>FABP6</i>	FABP6	Ileal FABP	Il-FABP	Ileum, ovary, adrenal gland, stomach
<i>FABP7</i>	FABP7	Brain FABP	B-FABP	Brain, glia cell, retina, mammary gland
<i>FABP8</i>	FABP8	Myelin FABP Myelin P2	M-FABP My- FABP	Peripheral nervous system, Schwann cell
<i>FABP9</i>	FABP9	Testis FABP	T-FABP	Testis, salivary gland, mammary gland
<i>fabpP10a and fabpP10b</i>	Fabp10a and Fabp10b	Liver basic FABP	Lb-FABP	Liver of teleost fish
<i>fabpP11a and fabpP11b</i>	Fabp11a and Fabp11b	–	–	Liver, intestine, muscle, brain, heart, eye, swim bladder, gills, kidney, skin, ovary and testis of teleost fish
<i>FABP12</i>	FABP12	–	–	Retinoblastoma cell from human. Retina, testicular germ, kidney and cerebral cortex from rodents

(Hertzell and Bernlohr 2000; Kim 2006; Smathers and Petersen 2011; Parmar et al. 2012; Bayir et al. 2015)

# 1.3 FABPs gene and protein structure



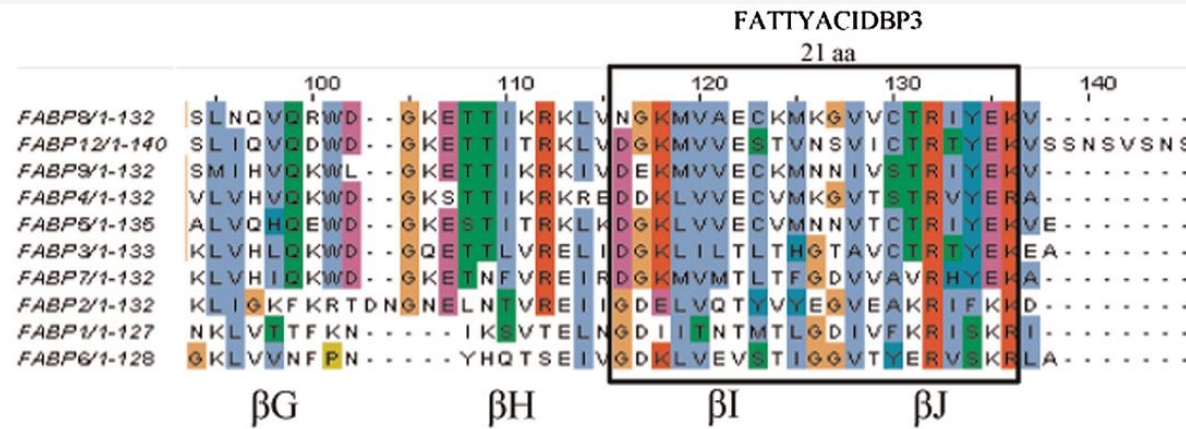
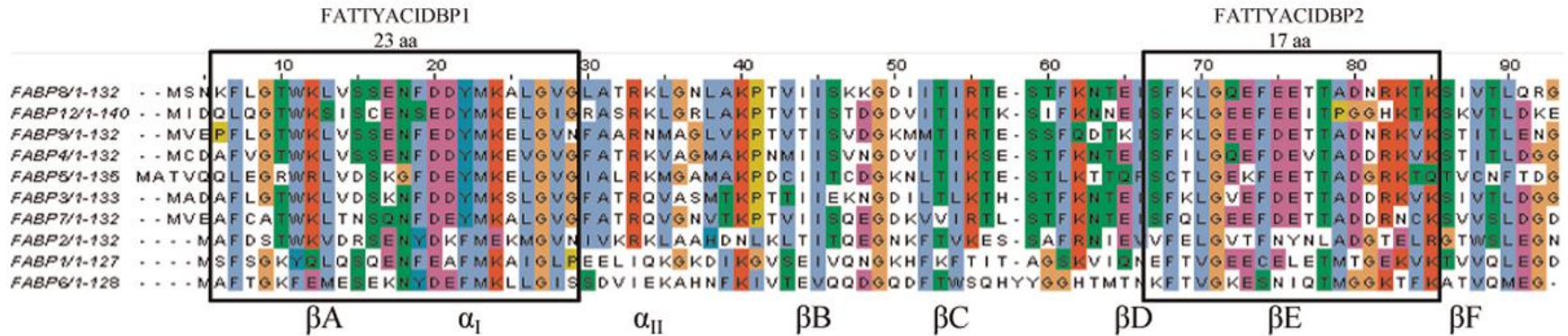
- ◇ Protein: 126–134 amino acids
- ◇ 10 anti-parallel  $\beta$ -strands
- ◇ Bind non-covalently **hydrophobic ligands** mainly fatty acids

- ◇ Gene structure:



---Esteves, A. and R. Ehrlich, *Comp Biochem Physiol C Toxicol Pharmacol*, 2006

# Conserved motif in proteins



---Rebecca L Smathers, human genomics, 2011

The divergence of protein sequences :20%-70%

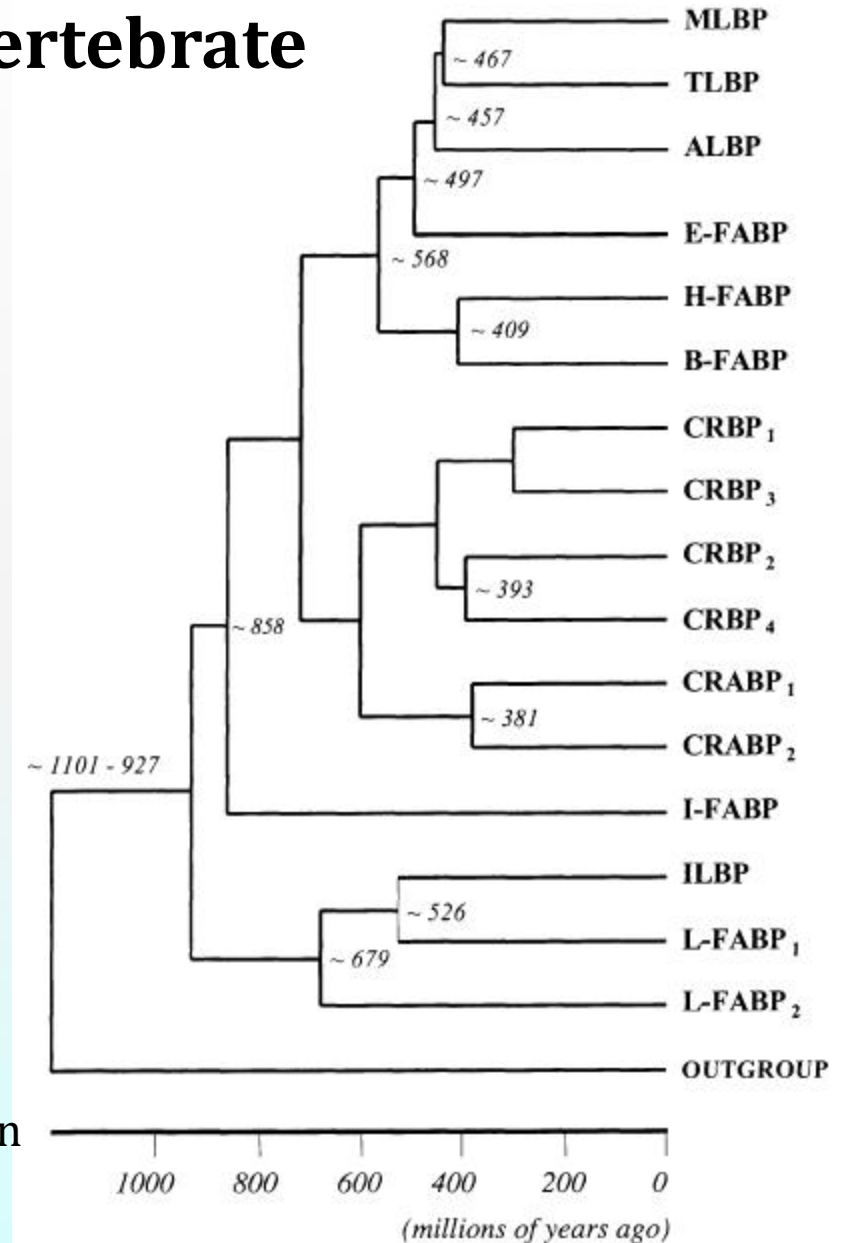


# 1.4 FABPs evolution in vertebrate

**iLBP arose through duplication and diversification of an ancestral gene, the common ancestor arose after divergence of animals from fungi and plants.**

----Schaap and van et al., Mol Cell Biochem,2002

Gene duplication times are shown in million s of years ago



# 2 FABPs in invertebrate species

Species for which genome databases were searched	Num. loci found in genome drafts	Length <sup>a</sup>	Evidence		Alternative splicing Data origin <sup>c</sup>
			b		
<b>Cnidaria</b> 腔肠动物门					
<i>Nematostella vectensis</i>	/	/	/	/	JGI
<i>Hydra magnipapillata</i>	/	/	/	/	Metazome
<b>Placozoa</b> 扁盘动物门					
<i>Trichoplax adhaerens</i>	5	120~178	1/5	No	JGI NCBI
<b>Annelida</b> 环节动物门					
<i>Capitella teleta</i>	7	135~167	7/7	No	JGI NCBI
<i>Helobdella robusta</i>	3	119~143	3/3	No	JGI NCBI
<b>Mollusca</b> 软体动物门					
<i>Lottia gigantea</i>	7	132~163	7/7	No	JGI NCBI
<b>Platyhelminthes</b> 扁形动物门					
<i>Schmidtea mediterranea</i>	3	123~168	2/3	No	SmedGD NCBI
<i>Schistosoma mansoni</i>	2	132, 133	2/2	Yes	GeneDB NCBI
<i>Schistosoma japonicum</i>	1	130	1/1	No	GeneDB NCBI
<i>Echinococcus granulosus</i>	5	124~143	2/5	No	NCBI Sanger
<i>Echinococcus multilocularis</i>	5	124~143	4/4	No	Sanger
<b>Nematoda</b> 线虫动物门					
<i>Caenorhabditis elegans</i>	9	135~165	9/9	Yes	NCBI
<i>Pristionchus pacificus</i>	4	118~163	4/4	No	NCBI WormBase WUGSC
<i>Heterorhabditis bacteriophora</i>	3	133~164	3/3	No	NCBI WUGSC
<i>Trichinella spiralis</i>	3	133~143	3/3	No	NCBI WUGSC
<i>Haemonchus contortus</i>	0 <sup>d</sup>	133~164	4/4	No	Sanger NCBI
<i>Strongyloides ratti</i>	4	132~165	4/4	No	Sanger WormBase
<i>Brugia malayi</i>	3	130~180	3/3	No	NCBI

34 invertebrate species from 8 phyla

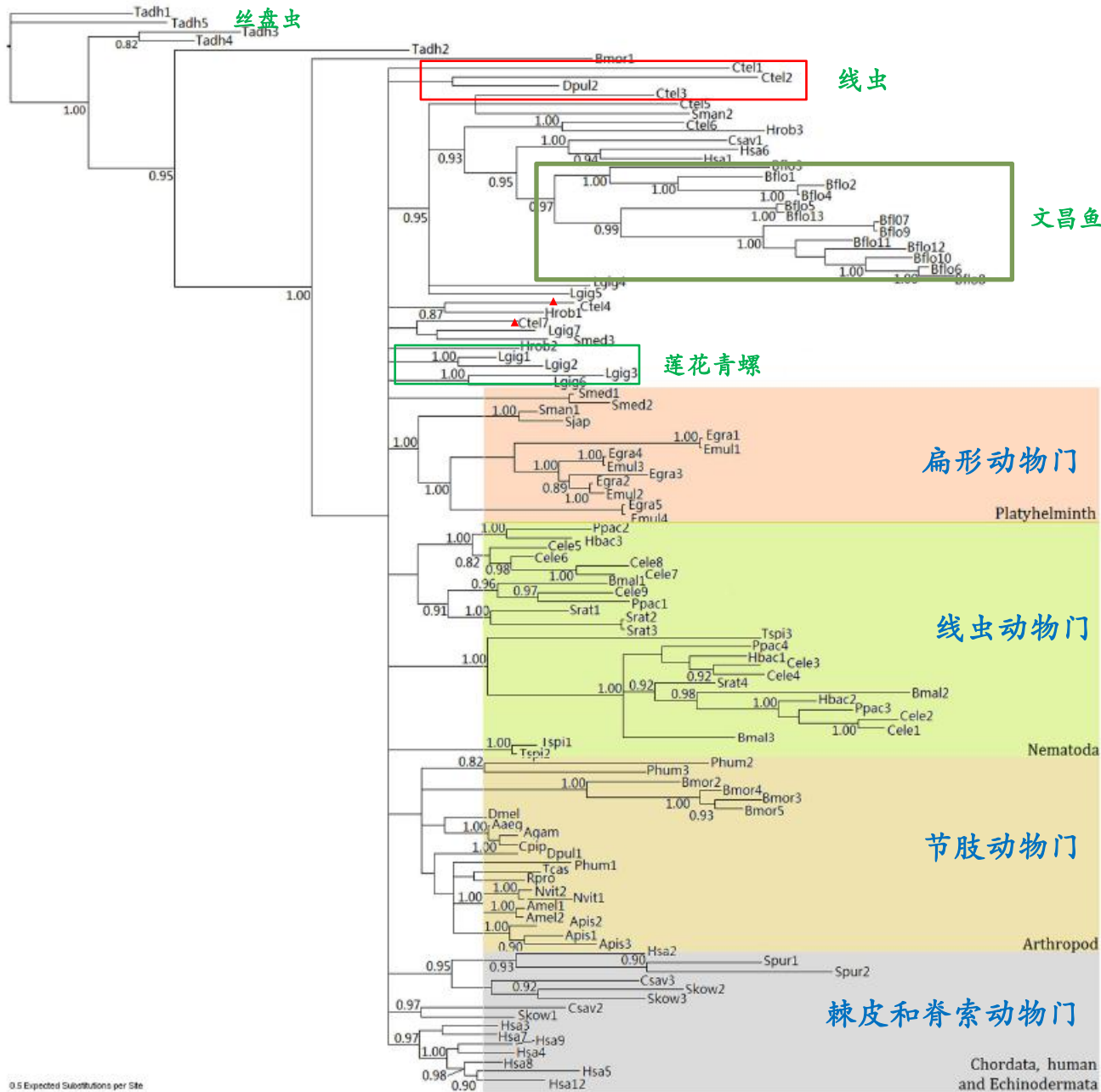
-----Yadong Zheng, plos one, 2013

## 2.1 Distribution and features of FABP genes in invertebrates

Species for which genome databases were searched	Num. loci found in genome drafts	Length <sup>a</sup>	Evidence		Alternative splicing Data origin <sup>c</sup>
			b		
<b>Arthropod 节肢动物门</b>					
<i>Daphnia pulex</i>	2	130, 131	2/2	No	wFleaBase NCBI
<i>Pediculus humanus corporis</i>	3	132~135	0/3	No	NCBI VectorBase VectorBaseFlyBase
<i>Bombyx mori</i>	5	95~142	4/5	No	SilkDB
<i>Tribolium castaneum</i>	1	136	1/1	Yes	NCBI
<i>Nasonia vitripennis</i>	2	132	2/2	No	NCBI
<i>Acyrtosiphon pisum</i>	3	135, 136	3/3	Yes	NCBI
<i>Apis mellifera</i>	2	132, 133	2/2	Yes	NCBI
<i>Drosophila melanogaster</i>	1	130	1/1	Yes	NCBI FlyBase
<i>Anopheles gambiae</i>	2	131	1/1	No	VectorBase NCBI
<i>Aedes aegypti</i>	1	132	1/1	No	NCBI
<i>Culex pipiens quinquefasciatus</i>	1	132	1/1	No	NCBI
<i>Rhodnius prolixus</i>	1	134	1/1	No	NCBI VectorBase
<b>Echinodermata 棘皮动物门</b>					
<i>Strongylocentrotus purpuratus</i>	2	130	2/2	No	NCBI JGI
<b>Chordata 脊索动物门</b>					
<i>Branchiostoma floridae</i>	15	135~151	7/14	No	JGI NCBI
<i>Ciona savignyi</i>	3	127~133	3/3	No	Broad NCBI
<i>Saccoglossus kowalevskii</i>	3	132~138	3/3	No	Baylor NCBI Metazome

-----Yadong Zheng, plos one, 2013

## 2.2 Phylogenetic analysis of invertebrate FABPs



Extraordinary gene expansion was observed in amphioxus via gene duplications.

A Bayesian tree of FABPs.

## 2.3 Diversity of FABP gene structures across invertebrates

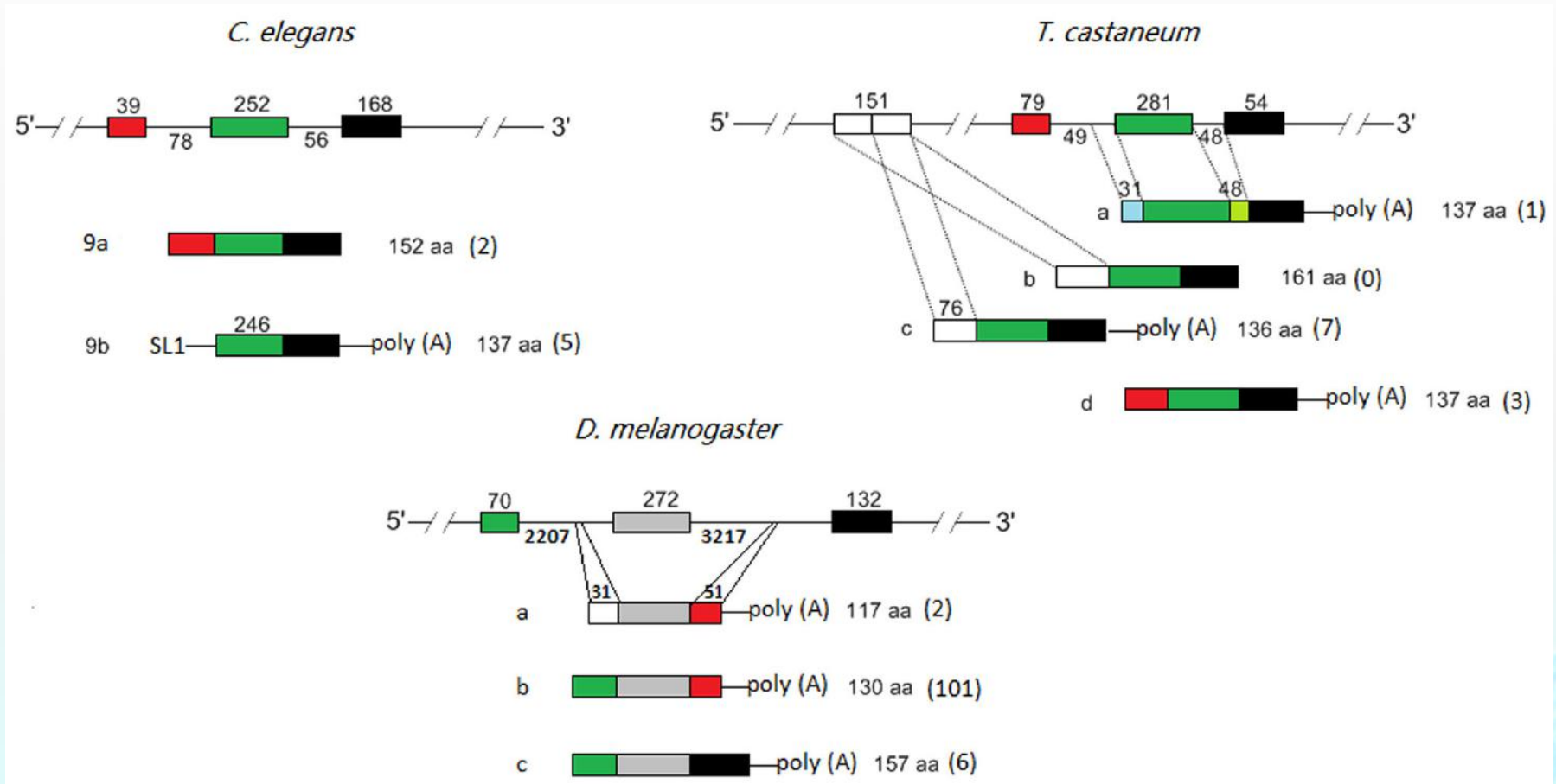
**Table 2.** FABP genomic structures in invertebrates.

Species <sup>a</sup>	Number of exons					
	6	5	4	3	2	1
<b>Placozoa</b>						
<i>Trichoplax adhaerens</i> 丝盘虫	1	1	3			
<b>Annelida</b>						
<i>Capitella teleta</i>			7			
<i>Helobdella robusta</i>			2			
<b>Mollusca</b>						
<i>Lottia gigantea</i> 青螺	1	7				
<b>Platyhelminthes</b>						
<i>Schmidtea mediterranea</i> 涡虫	1	2				
<i>Schistosoma mansoni</i>		2				
<i>Schistosoma japonicum</i>			1			
<i>Echinococcus granulosus</i>				3	2	
<i>Echinococcus multilocularis</i>				3 <sup>b</sup>	2	
<b>Nematoda</b>						
<i>Caenorhabditis elegans</i>		1	4	4		
<i>Pristionchus pacificus</i>	1	2				
<i>Heterorhabditis bacteriophora</i> 异小杆线虫	2	1				
<i>Trichinella spiralis</i>		3				
<i>Strongyloides ratti</i>				1	3	
<i>Brugia malayi</i>		2	1			

Species <sup>a</sup>	Number of exons					
	6	5	4	3	2	1
<b>Arthropod</b>						
<i>Daphnia pulex</i>			1	1		
<i>Pediculus humanus corporis</i>				1	2	
<i>Bombyx mori</i>			4	1		
<i>Tribolium castaneum</i>				1		
<i>Nasonia vitripennis</i>				2		
<i>Acyrtosiphon pisum</i>				3		
<i>Apis mellifera</i>			1	1		
<i>Drosophila melanogaster</i>				1		
<i>Anopheles gambiae</i>					2 <sup>b</sup>	
<i>Aedes aegypti</i>					1	
<i>Culex pipiens quinquefasciatus</i>					1	
<i>Rhodnius prolixus</i>						1
<b>Echinodermata</b>						
<i>Strongylocentrotus purpuratus</i>					1	1
<b>Chordata</b>						
<i>Branchiostoma floridae</i>			12 <sup>b</sup>	3		
<i>Ciona savignyi</i>			2	1		
<i>Saccoglossus kowalevskii</i>			1			3
<b>Total</b>	1	6	52	22	16	14

b. Each of these species has two different loci that encode identical FABPs at the amino acid level.

## 2.4 Alternative splicing in invertebrate FABP genes



In each group, an annotated FABP gene is placed above the variants that are indicated by a, b, c or/and d; the number of ESTs is shown in the brackets.

# 3 FABPs in teleost fish



**Jonathan M. Wright**

Professor

Email: [J.M.Wright@Dal.ca](mailto:J.M.Wright@Dal.ca)

Department of Biology, Dalhousie  
University, Canada

## Biography

Research interests of my laboratory include:

(I) Expression of genes coding for fatty acid and retinoid (vitamin A derivatives) binding proteins in adults and embryos of the zebrafish. Zebrafish serves as a model system for vertebrate development as many of the genes and the developmental processes they control are similar, or the same, in zebrafish and humans. As such, studies in zebrafish can provide valuable insights into developmental processes and disease of humans.

(II) Localization of cloned genes to fish chromosomes to determine the structure and evolution of chromosomes.

## Research Interests

- Gene regulation
- Gene structure
- Gene function
- Zebrafish
- Development
- Fatty acid
- Retinoid binding proteins

# FABPs study protocol

Specific genes in specific fish



Gene identification in fish



Sequence alignment, phylogenetic analysis, and conserved gene synteny



FABPs expression in different tissue

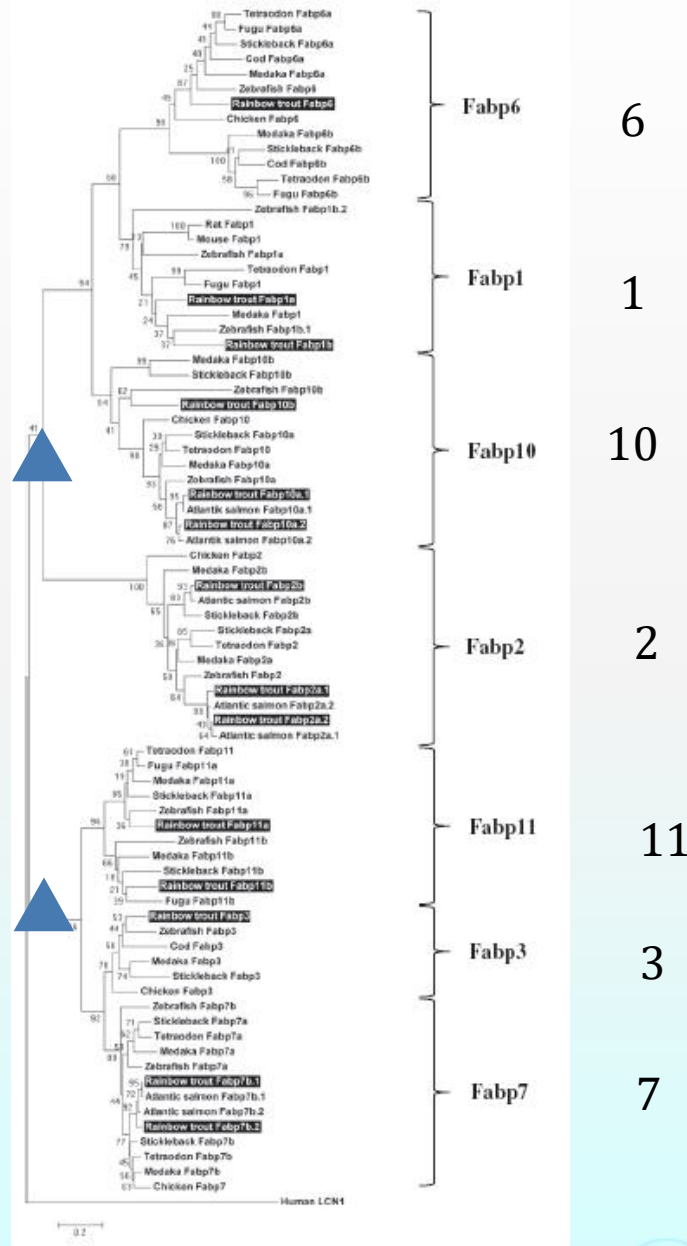


# 3.1 Fabps type and evolution in teleost fishes

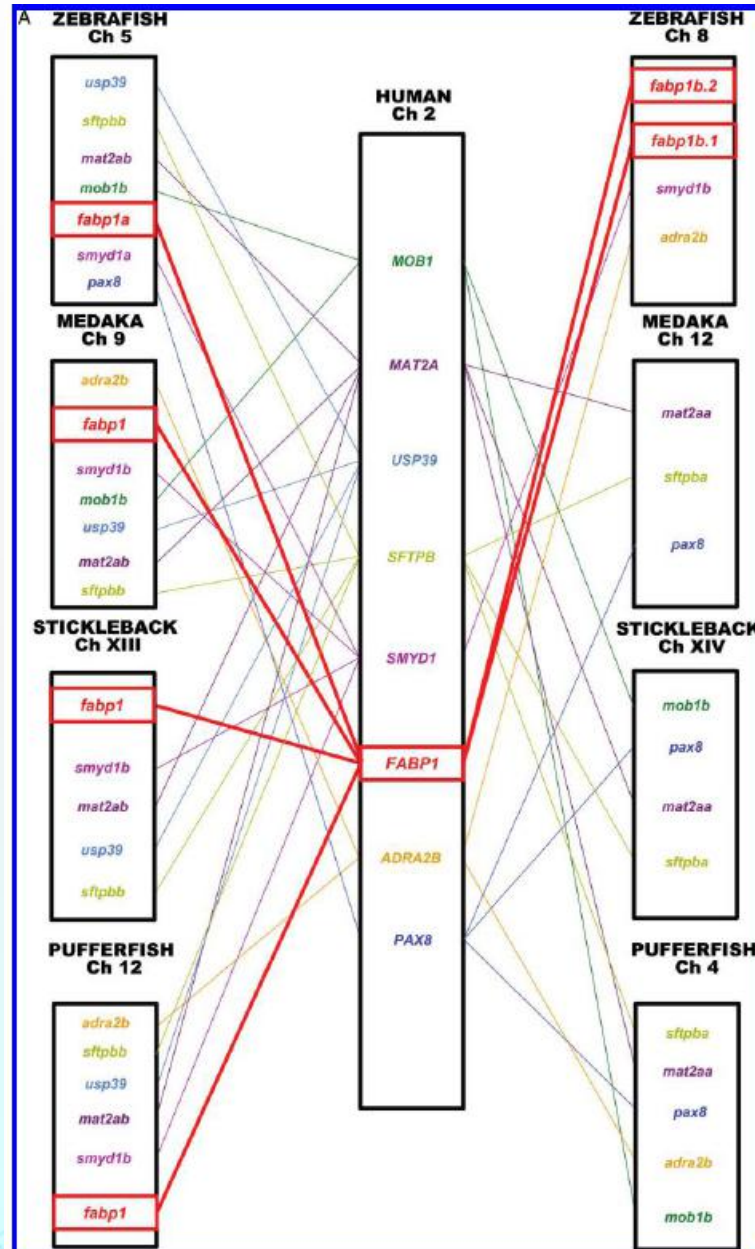
	<i>Fabp1</i>	<i>Fabp2</i>	<i>Fabp3</i>	<i>Fabp6</i>	<i>Fabp7</i>	<i>Fabp10</i>	<i>Fabp11</i>
<b>Zebrafish</b>	1a,1b.1, 1b.2	2	3	6	7a,7b	10a,10b	11a,11b
<b>Atlantic salmon</b>	?	2a.1,2a.2,2b	?	?	7b.1,7b.2	10a.1,10a.2	?
<b>Medaka</b>	1	2a,2b	3	6a,6b	7a,7b	10a,10b	11a
<b>Three-spined stickleback</b>	?	2a,2b	3	6a,6b	7a,7b	10a,10b	11a
<b>Green spotted pufferfish</b>	1	2	3	6a,6b	7a,7b	10	10a,10b
<b>Rainbow trout</b>	1a,1b	2a.1,2a.2	3	6	7b.1,7b.2	10a.1,10a.2, 10b	11a,11b

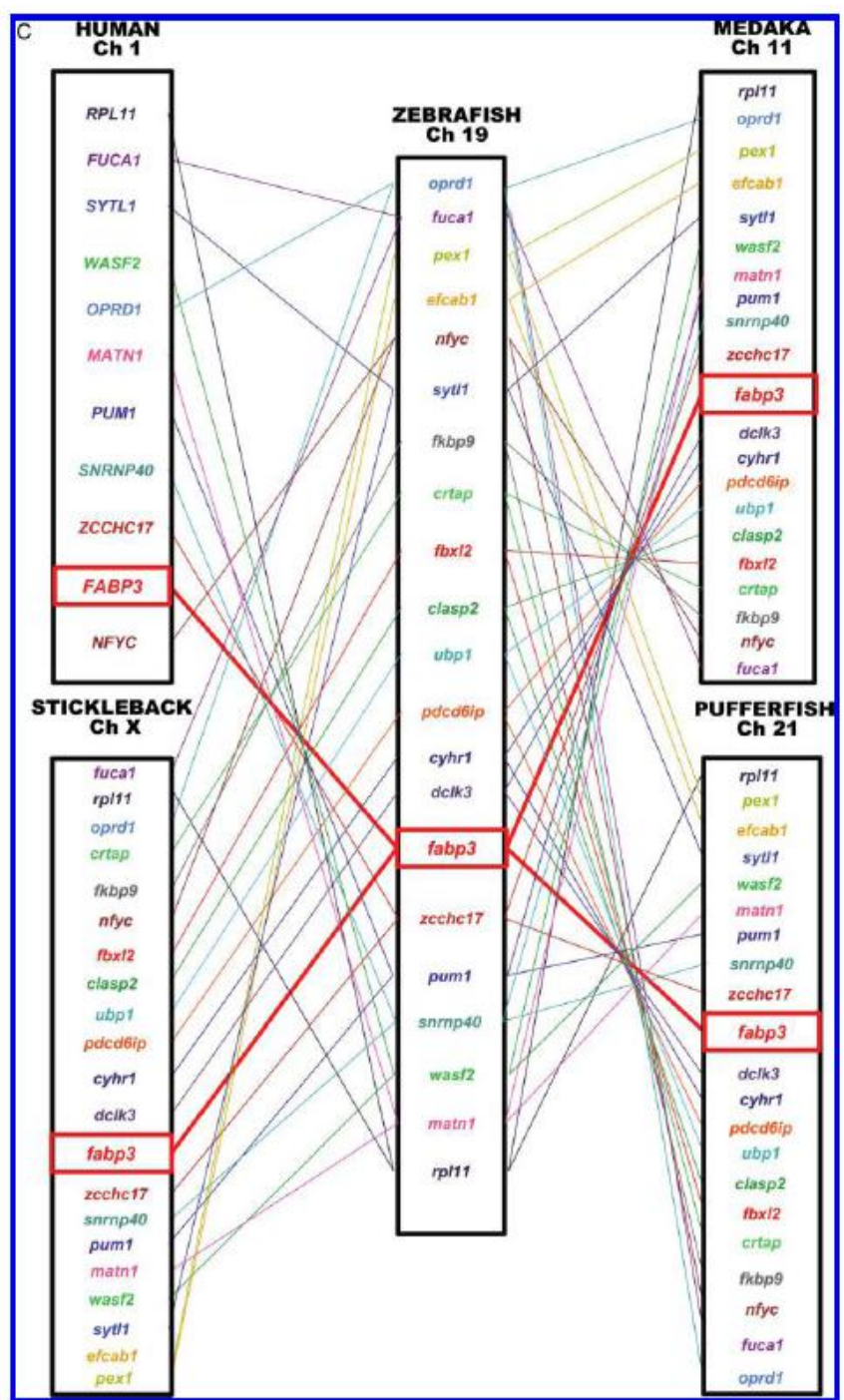
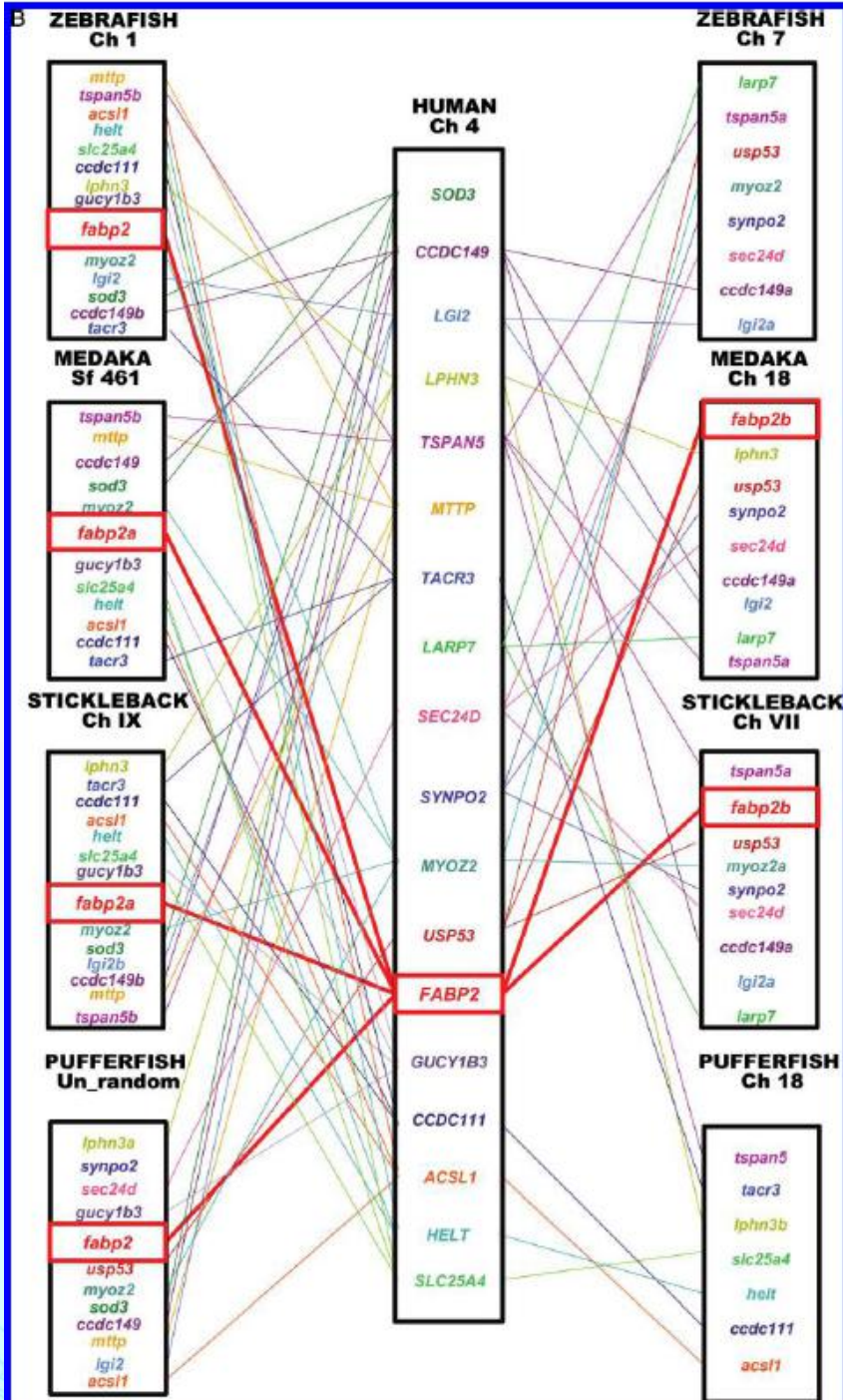
# Phylogenetic relationship of teleost fishes

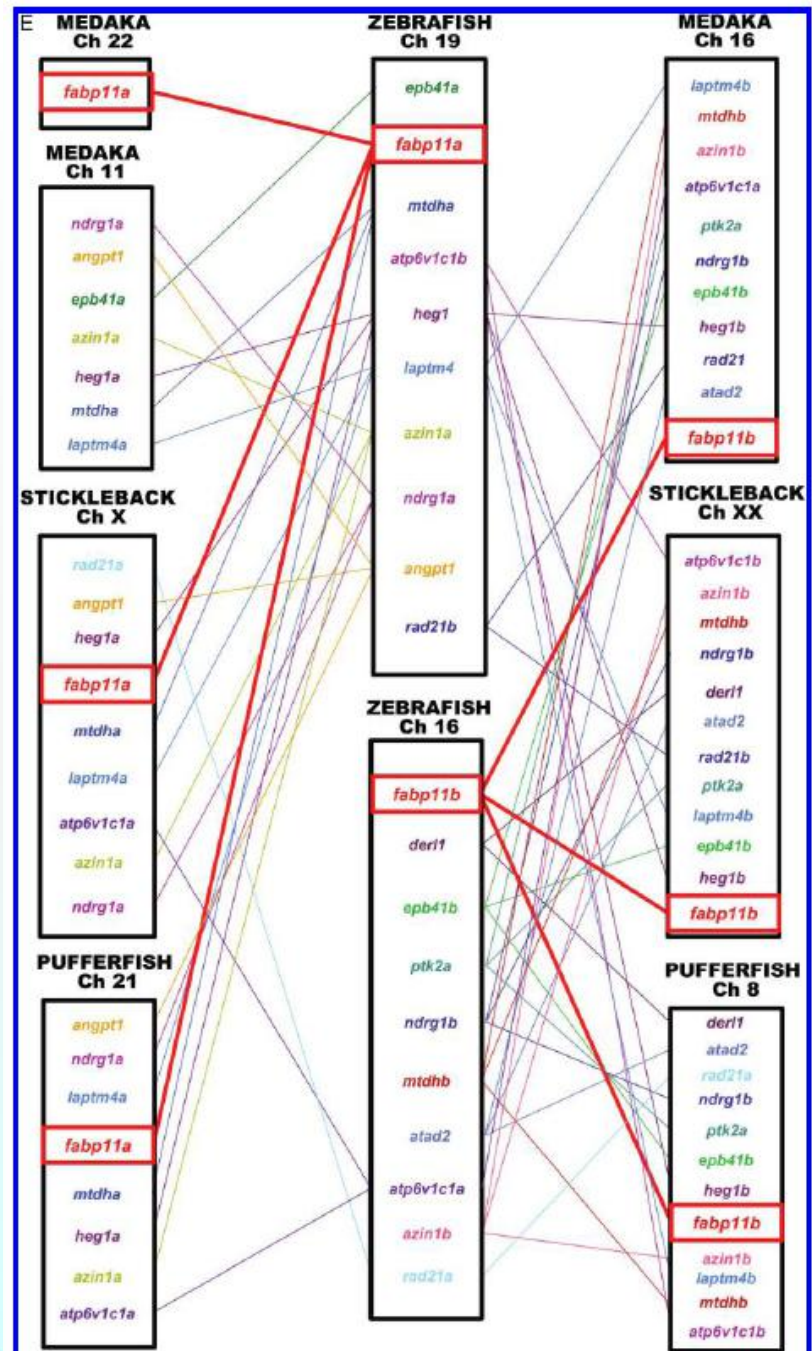
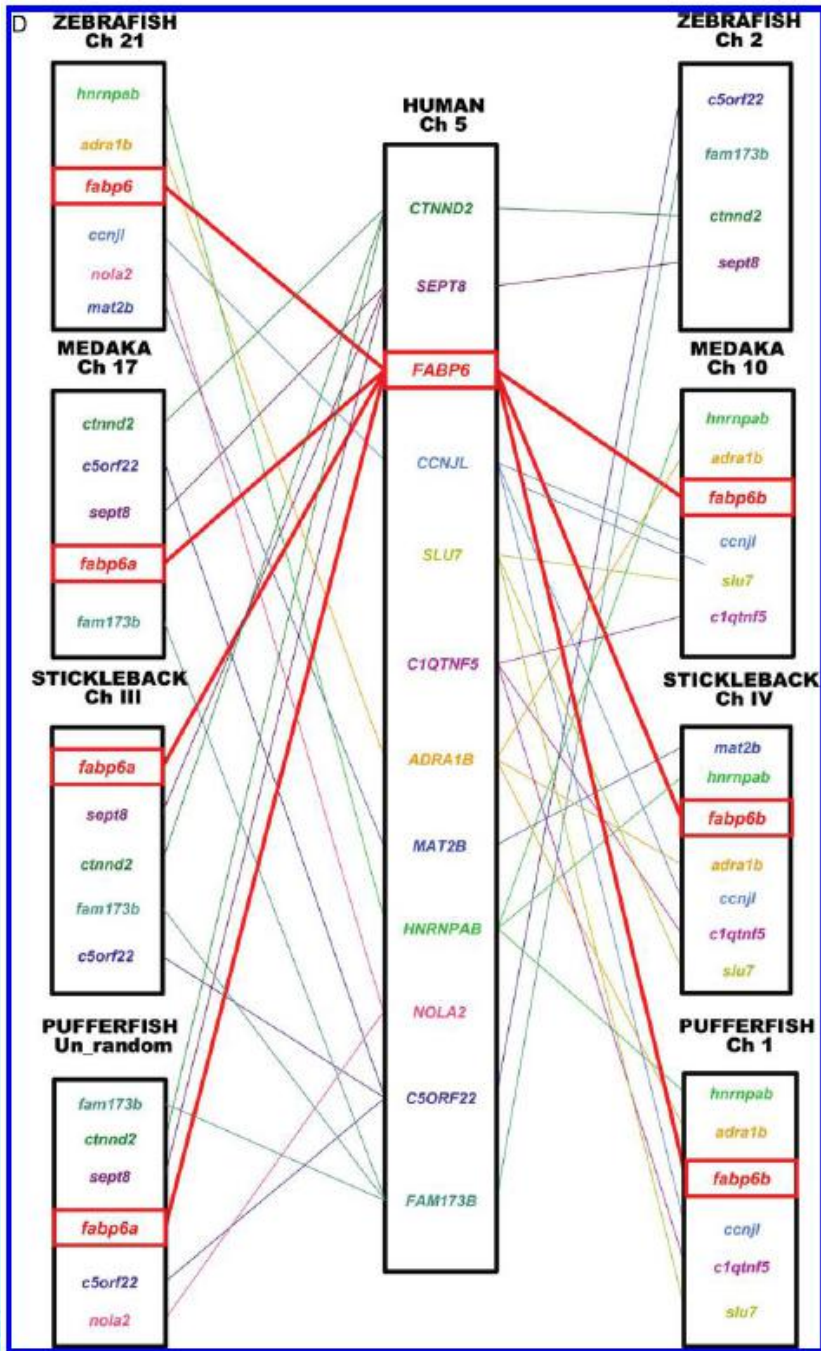
The NJ tree of Fabps from teleost fishes and tetrapods

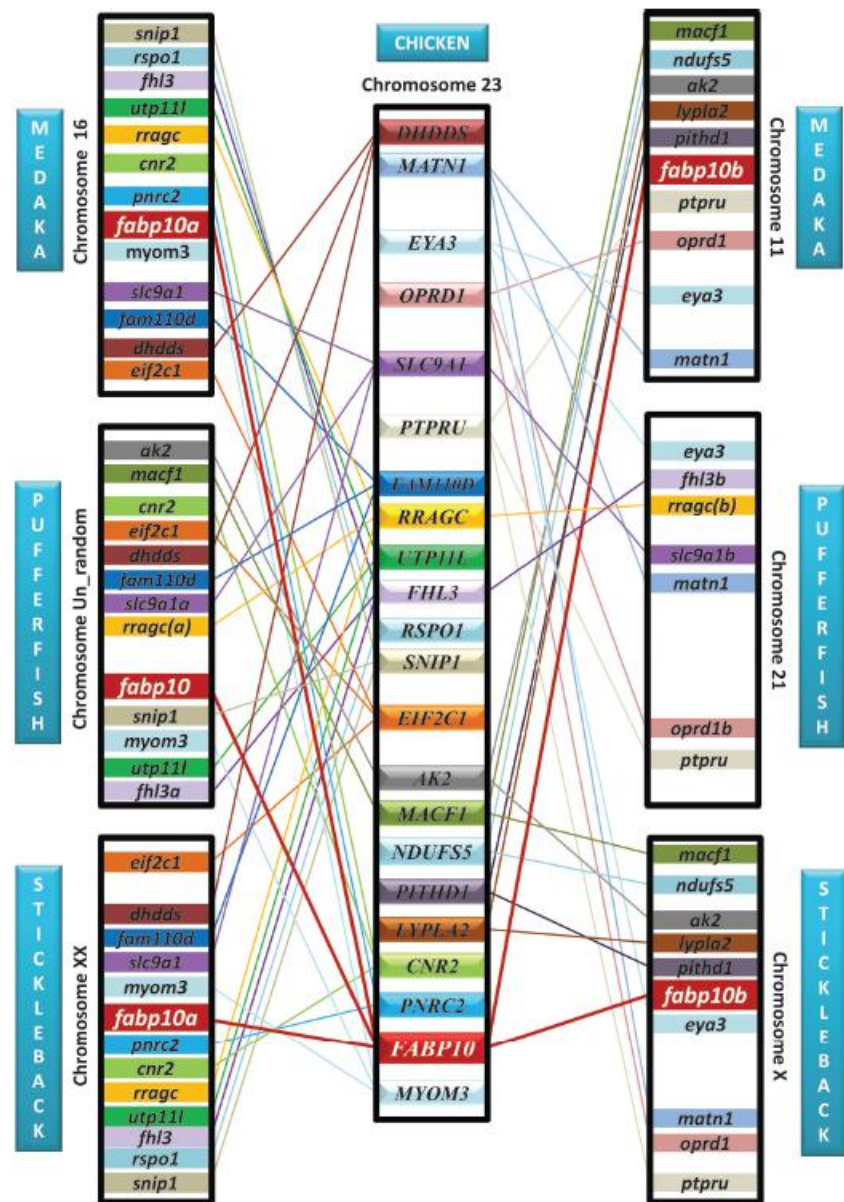
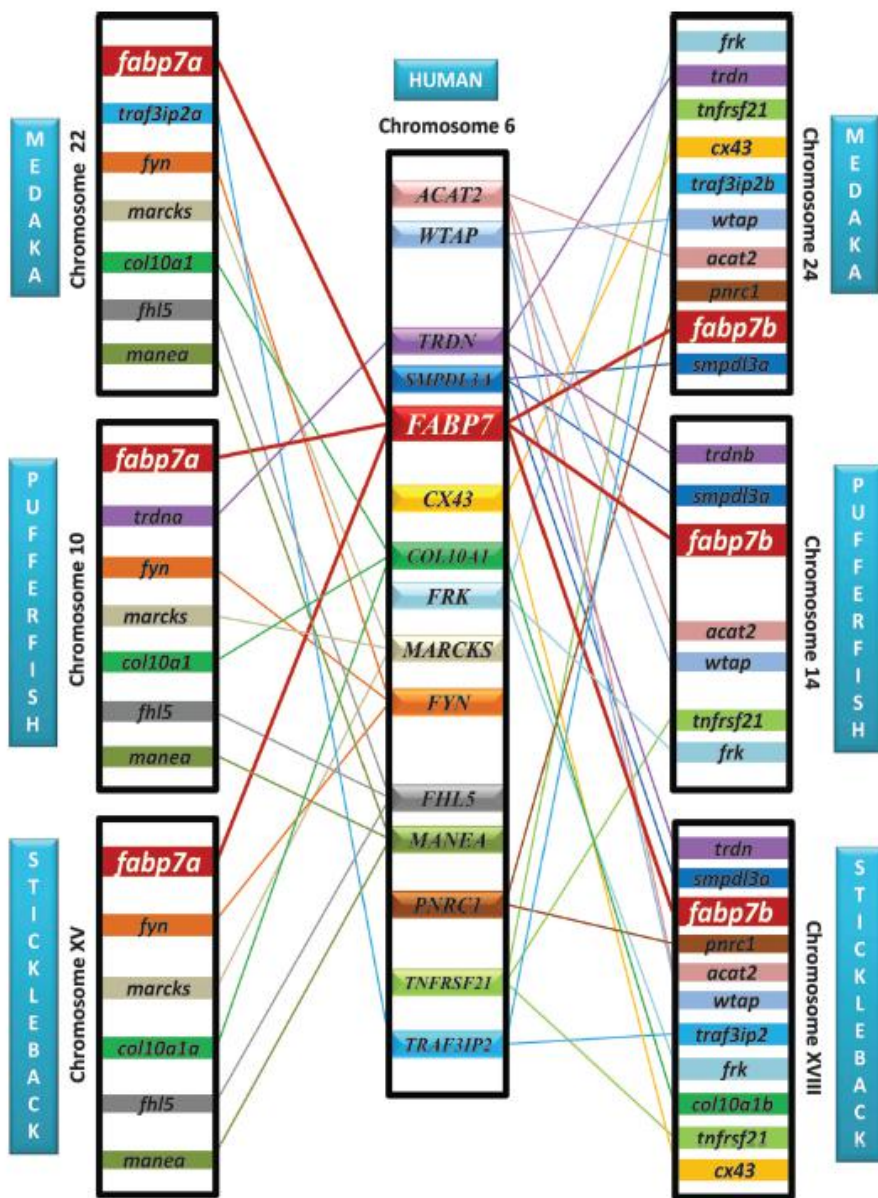


# 3.2 Conserved gene synteny analysis

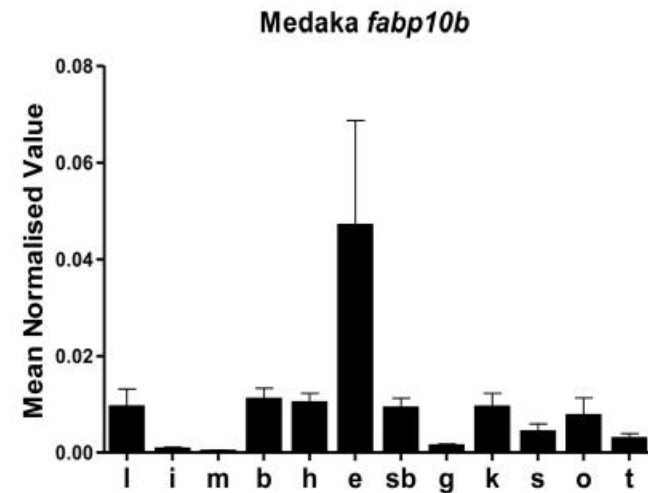
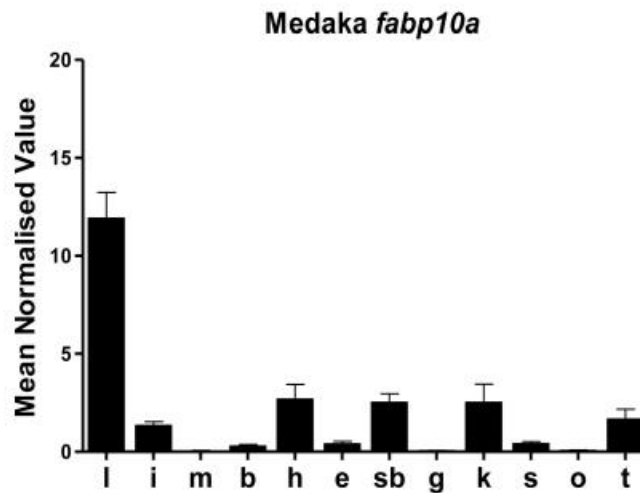
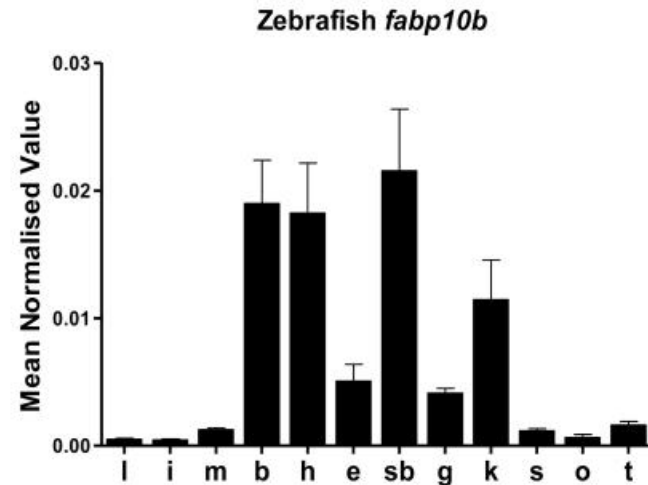
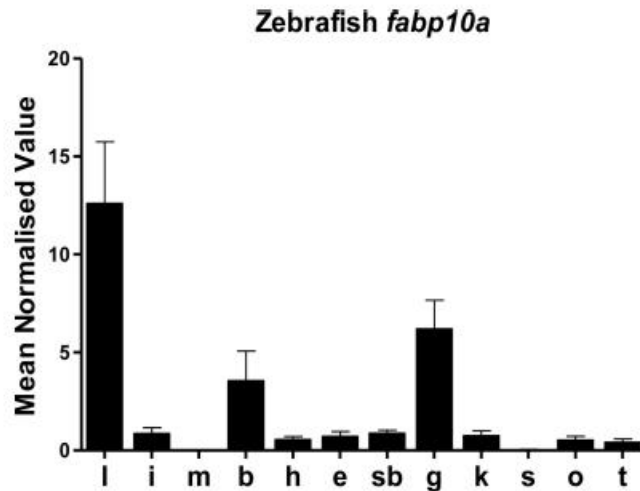








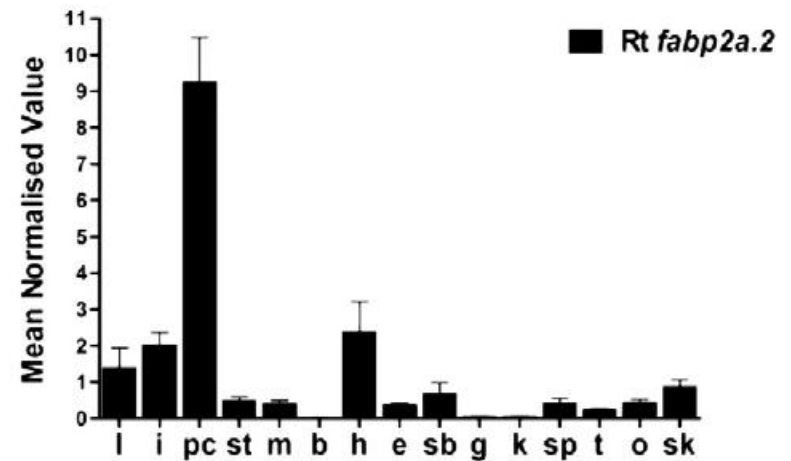
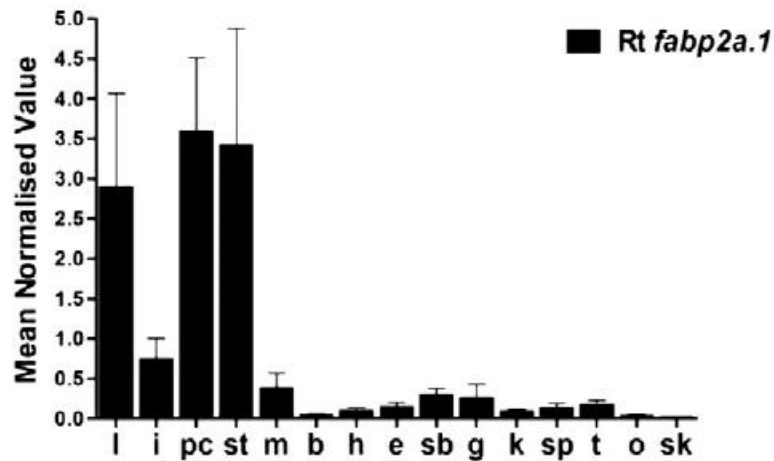
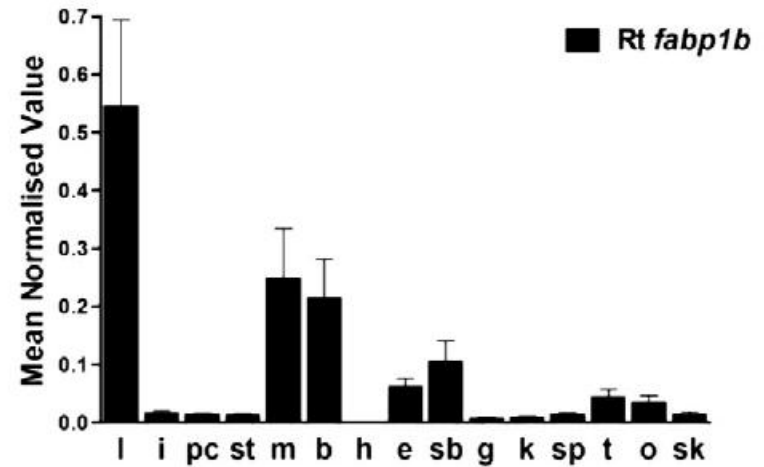
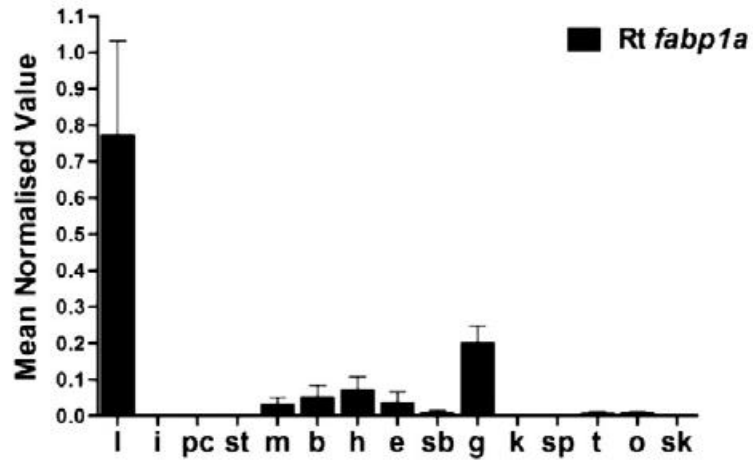
# 3.3 *fabps* expression in different tissue



Three-spined stickleback *fabp10a*

Three-spined stickleback *fabp10b*

Same *fabp* in different fish



Different *fabps* in specific fish



**Thanks**

