

**Supplementary Materials:**

>GCLC

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>GR

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>Nrf2

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**Fig. S1.** Nucleotide sequences of *Megalobrama amblycephala* *GCLC*, *GR* and *Nrf2*.

>GCLC

MAPKKNKAAKSKADINEMTIMVEDSPTKINGLNTLLECGNGFSCISTEV  
EYMLVEMDERHEKVRLVLNGKDVLETLQEKGEKINPNHPTLWRPEYGSYM  
IEGTPGQPYGGTMSEFNTVEDNMGKRRREASSVLSQNQTLLTVTSFPRLG  
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VMALSAASPFYRGFVSDIDCRWGVISASVDDRTREERGLEPLKNNKFRIN  
KSRYSIDSYLSCCGEKYNDIELTIDEEINKQLLDAGIDKLLAQHIAHLF  
IRDPLSLFQEKIHLDDENESDHFEVQLTDFENSAYVVFIVLLTRVILSYK  
LDFLIPLSKVDENMKVAQKRNAVQEGMFYFRKDVFKGCNPVLDPPSTAQN



GVSEASDGEEFTLMSIDTIINGKVDENMKVAQKRNAVQEGMFYFRKDVF  
KGCNPVLDPPSTAQNGVETEVS DGEEFTLMSIDTIINGKEGVFHLIPML  
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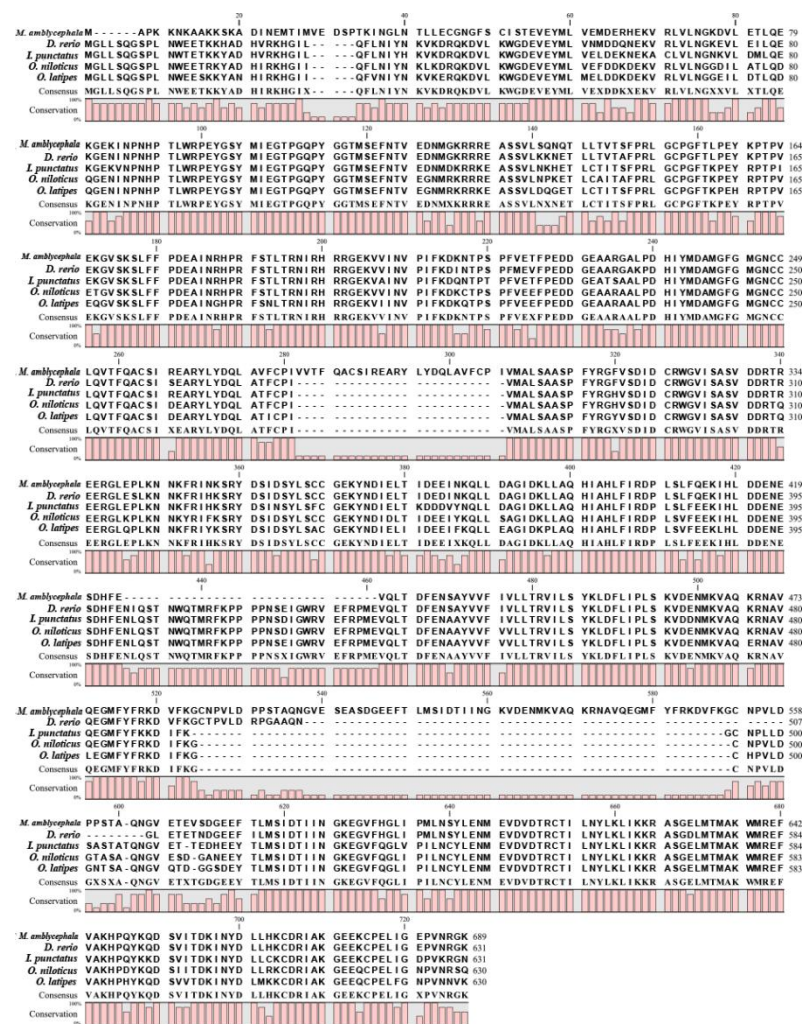
>GR

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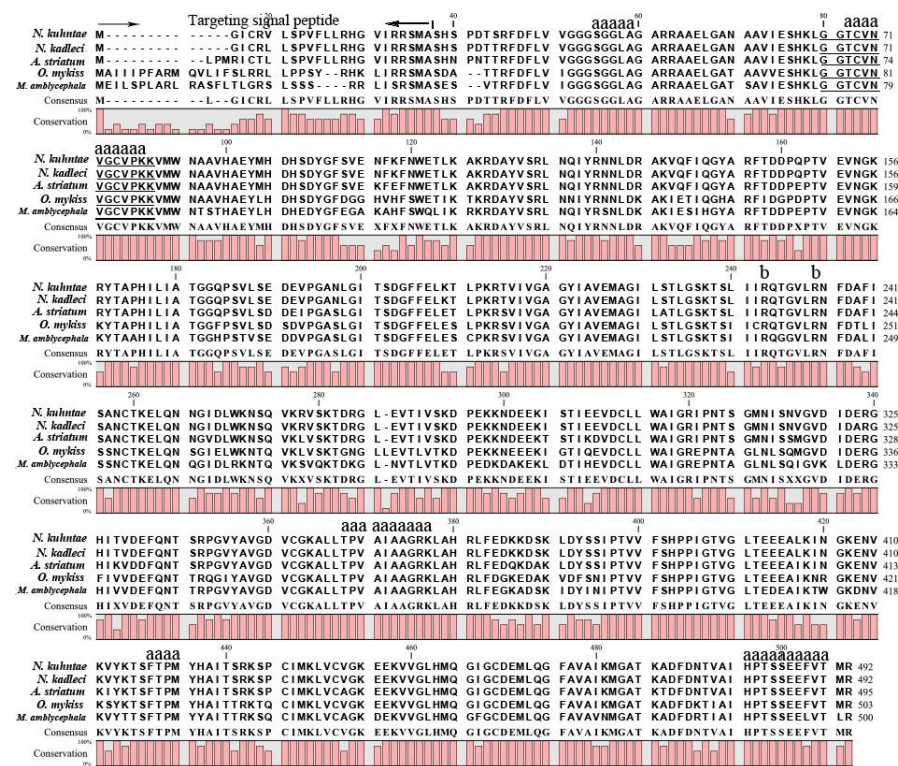
>Nrf2

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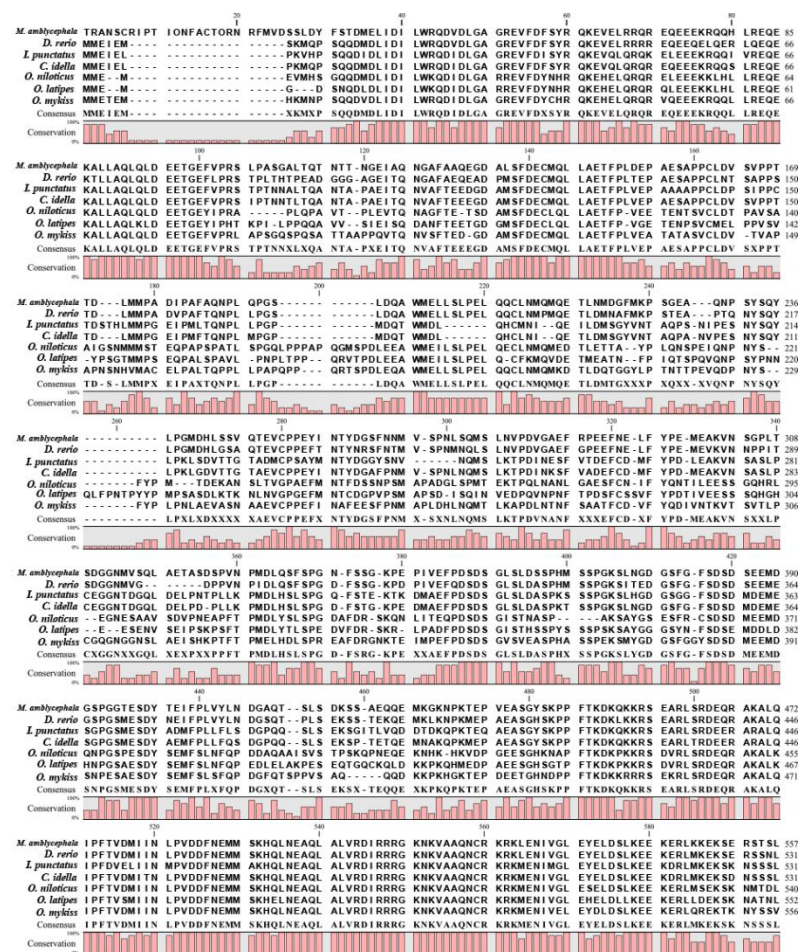
**Fig. S2.** Amino acid sequences of *Megalobrama amblycephala* GCLC, GR and Nrf2.



**Fig. S3.** Multiple alignment of GCLC amino acid sequences of *Megalobrama amblycephala*, *Danio rerio* (AAI64554.1), *Ictalurus punctatus* (AHH41791.1), *Oreochromis niloticus* (XP\_003441171.1) and *Oryzias latipes* (XP\_023819156.1). Dashes indicate alignment gaps.



**Fig. S4.** Multiple alignment of GR amino acid sequences of *Megalobrama amblycephala*, *Oncorhynchus mykiss* (CCX35037.1), *Nothobranchius kuhntae* (SBR05132.1), *Aphyosemion striatum* (SBP18818.1), and *Nothobranchius rachovii* (SBR93084.1). Dashes indicate alignment gaps. Targeting signal peptide location is marked above (between the first two arrows). (a) glutathione binding residue; the redox-active disulfite bridge is underlined; (b) conserved arginine residues for NADPH binding.



**Fig. S5.** Multiple alignment of Nrf2 amino acid sequences of *Megalobrama amblycephala*, *Danio rerio* (NP\_878309.1), *Ictalurus punctatus* (AHH39733.1), *Ctenopharyngodon idella* (AKL60850.1), *Oncorhynchus mykiss* (XP\_021452898.1), *Oreochromis niloticus* (XP\_003447344.1), and *Oryzias latipes* (XP\_004081819.1). Dashes indicate alignment gaps.

**Table S1. The information of *GCLC* amino acid sequence alignment**

Species	pI	M <sub>w</sub> (kDa)	Number of amino acids	Number of Arg (R)	Number of Lys (K)	Identities with <i>MaGCLC</i> /%
<i>Megalobrama amblycephala</i>	5.32	78.15226	689	36	48	
<i>Danio rerio</i>	5.73	72.41573	631	36	45	77
<i>Ictalurus punctatus</i>	5.76	72.46966	631	33	48	73
<i>Oreochromis niloticus</i>	5.42	72.18121	630	38	40	73
<i>Oryzias latipes</i>	5.27	72.12107	630	33	41	70

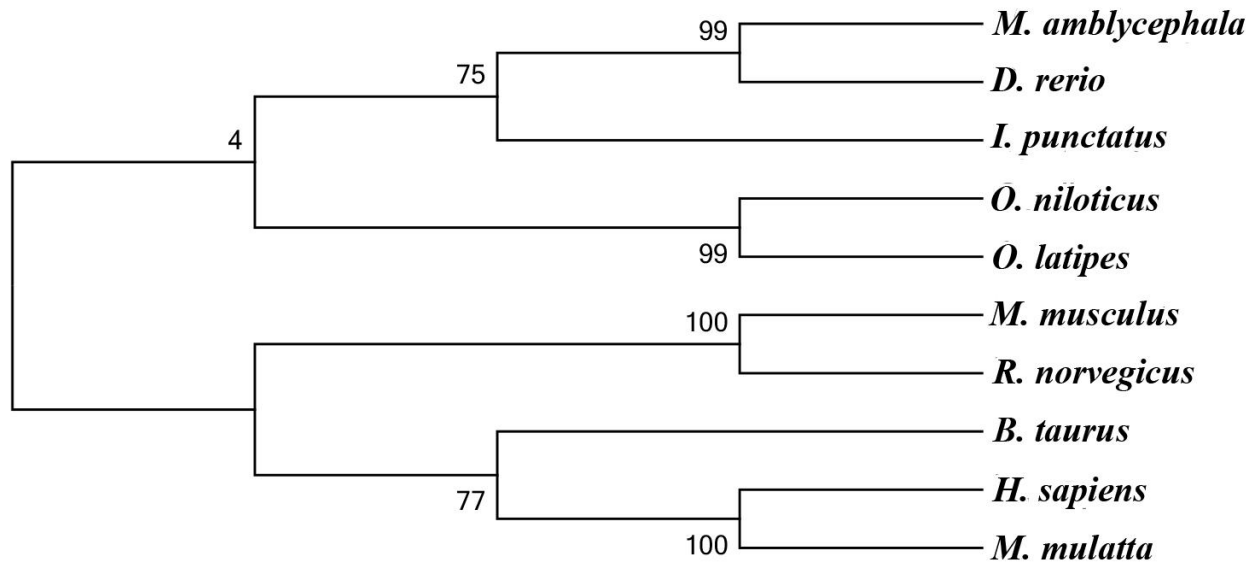
**Table S2. The information of *GR* amino acid sequence alignment**

Species	pI	M <sub>w</sub> (kDa)	Number of amino acids	Number of Arg (R)	Number of Lys (K)	Identities with <i>MaGR</i> /%
<i>Megalobrama amblycephala</i>	8.24	54.24798	500	26	34	
<i>Oncorhynchus mykiss</i>	8.43	54.72796	503	24	35	81
<i>Nothobranchius kuhntae</i>	8.43	53.69451	492	25	34	77
<i>Aphyosemion striatum</i>	7.99	54.02797	495	24	34	80
<i>Nothobranchius kadleci</i>	8.57	53.664.53	492	25	34	79

**Table S3. The information of *Nrf2* amino acid sequence alignment**

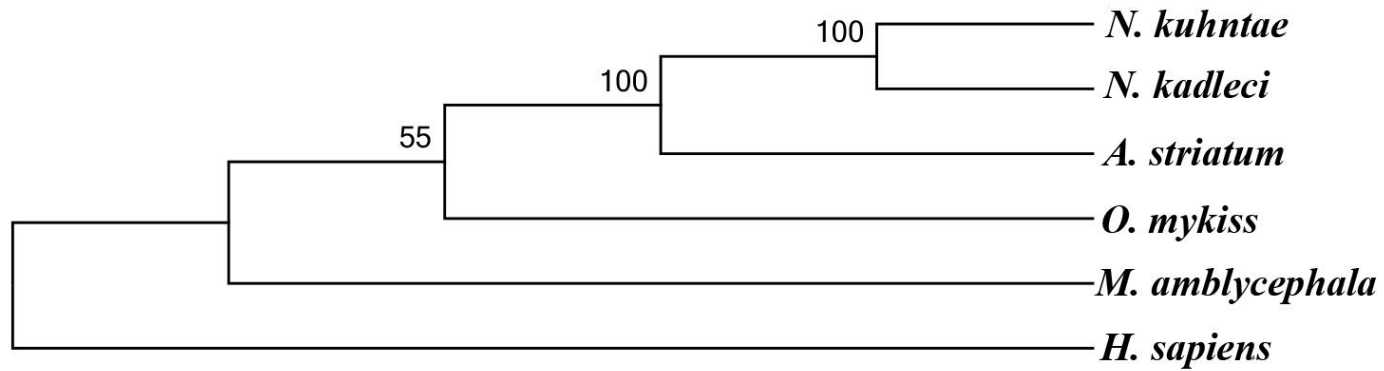
Species	pI	M <sub>w</sub> (kDa)	Number of amino acids	Number of Arg (R)	Number of Lys (K)	Identities with <i>MaNrf2</i> /%
<i>Megalobrama amblycephala</i>	4.52	65.9294	590	25	32	
<i>Danio rerio</i>	4.53	65.88785	586	24	33	83
<i>Ictalurus punctatus</i>	4.49	65.51239	586	20	37	74
<i>Ctenopharyngodon idella</i>	4.46	65.91587	586	23	35	66
<i>Oncorhynchus mykiss</i>	4.71	69.26243	613	28	34	61
<i>Oreochromis niloticus</i>	4.61	67.20991	597	24	35	56
<i>Oryzias latipes</i>	4.71	68.47255	605	23	40	53



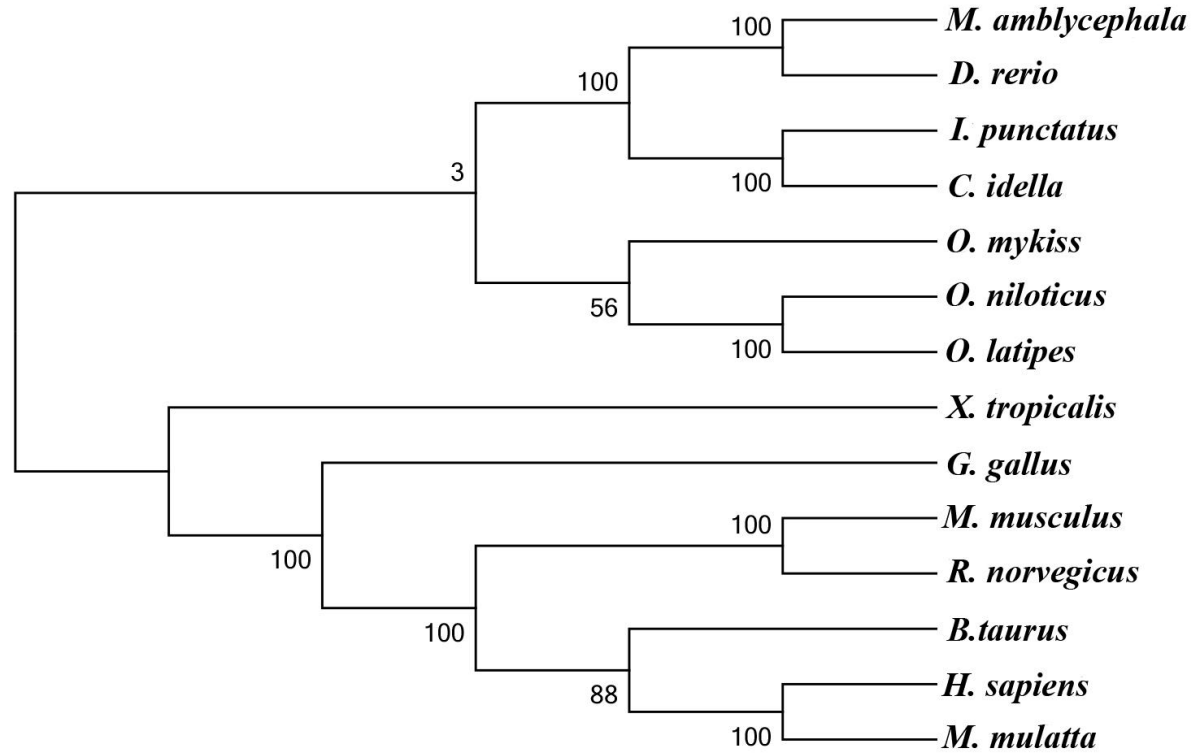


**Fig. S6.** Neighbor-Joining (NJ) phylogenetic tree was constructed using MEGA7.0.21, showing the relationships among protein sequences of GCLC of various fishes and mammals. Numbers at the branches indicate bootstrap probabilities inferred with 1000. The GenBank accession numbers for the mammals sequence are as follows: *Bos taurus* (NP\_001077143.1), *Mus musculus* (NP\_034425.1), *Homo sapiens* (NP\_001489.1), *Rattus norvegicus* (NP\_036947.1) and *Macaca mulatta* (NP\_001248036.1).





**Fig. S7.** Neighbor-Joining (NJ) phylogenetic tree was constructed using MEGA7.0.21, showing the relationships among protein sequences of GR of various fishes and mammals. Numbers at the branches indicate bootstrap probabilities inferred with 1000. The GenBank accession numbers for the mammals sequence are as follows: *Homo sapiens* (AAH69244.1).



**Fig. S8.** Neighbor-Joining (NJ) phylogenetic tree was constructed using MEGA7.0.21, showing the relationships among protein sequences of Nrf2 of various fishes and mammals. Numbers at the branches indicate bootstrap probabilities inferred with 1000. The GenBank accession numbers are as follows: *Bos taurus* (NP\_001011678.2), *Mus musculus* (NP\_035032.1), *Homo sapiens* (NP\_001138884.1), *Rattus norvegicus* (NP\_113977.1), *Macaca mulatta* (NP\_001244536.1), *Gallus gallus* (NP\_990448.1) and *Xenopus tropicalis* (NP\_001007490.1).