

Supplementary Materials:

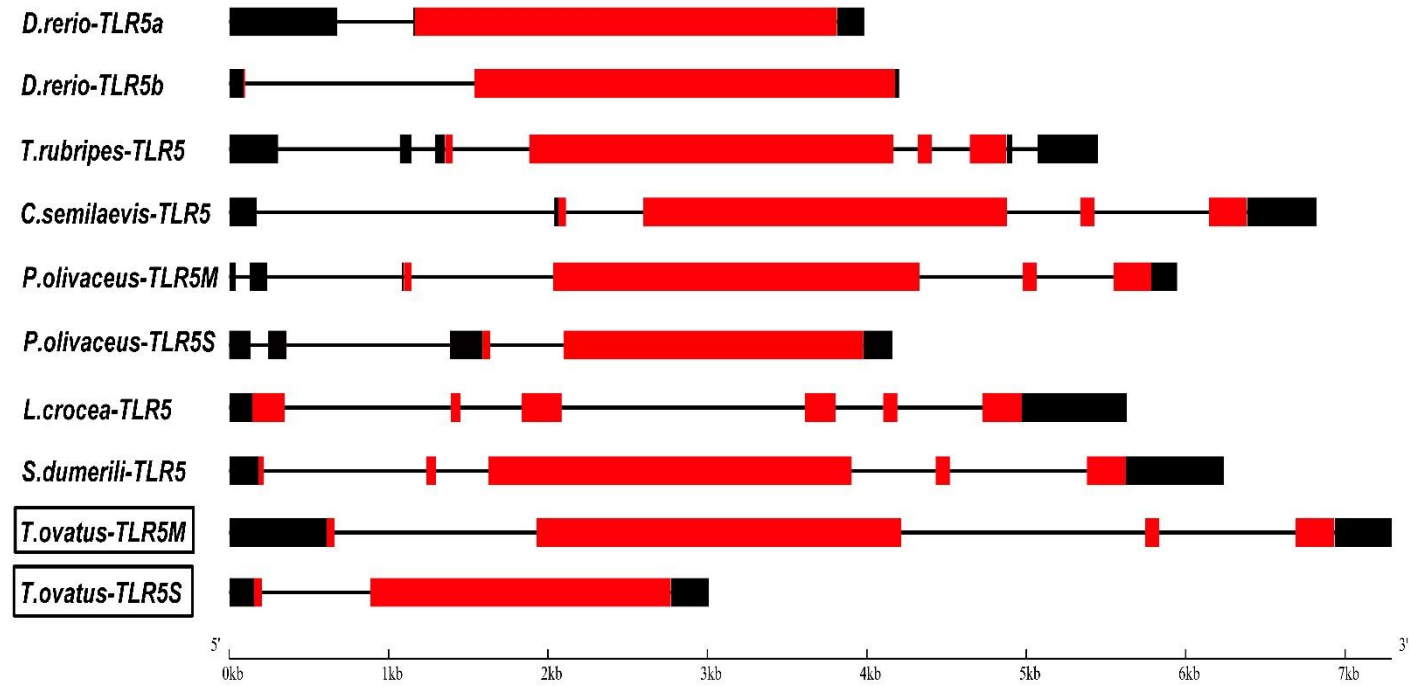


Figure S1. Comparison of the exon-intron organization of the *TLR5*. The boxes and bars represented the exons and introns, respectively. The boxes in black represented the UTR. The boxes in red represented the CDS. The *TLR5* sequence No. of each species: *D. rerio* (NC_007131.7); *T. rubripes* (NC_018905.1); *C. semilaevis* (NW_007585113.1); *P. olivaceus* (TLR5M: NW_017859659.1; TLR5S: NW_017860348.1); *L. crocea* (NC_040021.1); *S. dumerili* (NW_019174280.1).

Figure S2. Analysis of the promoter sequences of *ToTLR5M* (A) and *ToTLR5S* (B). Nucleotide sequence of 5'-flanking regions of two *ToTLR5s*. The predicted transcriptional start site was expressed in a box and defined as +1; the predicted transcription factor binding sites were underlined. The box showed the transcriptional start site.

Table S1 The amino acid sequences in various species used for domain structures.

TLR	Species	Accession Number
TLR5	<i>Homo sapiens</i>	AAI09119.1
	<i>Mus musculus</i>	AAI25248.1
	<i>Gallus gallus</i>	ACR26275.1
	<i>Danio rerio</i>	AAI63198.1
	<i>Cyprinus carpio</i>	BAU98383.1
	<i>Takifugu rubripes</i>	AAW69374.1
TLR5M	<i>Trachinotus ovatus</i>	MT596697
	<i>Coregonus maraena</i>	CEF90216.1
	<i>Epinephelus coioides</i>	AIS23536.1
	<i>Miichthys miiuy</i>	ALJ55566.1
	<i>Paralichthys olivaceus</i>	BAJ16367.1
TLR5S	<i>Trachinotus ovatus</i>	MT596698
	<i>Ictalurus punctatus</i>	AEI59667.1
	<i>Epinephelus coioides</i>	ACV04459.1
	<i>Miichthys miiuy</i>	ALJ55567.1
	<i>Paralichthys olivaceus</i>	BAJ16368.1