Supplementary Materials: Evolutionary Conservation of *pou5f3* Genomic Organization and Its Dynamic Distribution during Embryogenesis and in Adult Gonads in Japanese Flounder *Paralichthys olivaceus*

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Table S1. The Genbank accession numbers or Ensembl IDs of the POUV proteins analyzed in Figure 1C.

Species	Genbank Accession No./ Ensembl IDs	Species	Genbank Accession No./ Ensembl IDs
Acipenser sinensis	AEK81554.1	*Pan troglodytes*	NP_001238970.1
Anolis carolinensis	ENSACAP00000017001	*Ornithorhynchus anatinus*	NP_001229656.1
Bos taurus	NP_777005.1	*Oryzias latipes*	NP_001098339.1
Carassius auratus	AET79963.1	*Oreochromis niloticus*	XP_003444455.1
Danio rerio	NP_571187.1	*Pagrus major*	BAH08689.1
Gadus morhua	ENSGMOP00000005053	*Paralichthys olivaceus*	KJ522774
Gasterosteus aculeatus	ENSGACP00000023125	*Rattus norvegicus*	NP_001009178.1
Homo sapiens	NP_002692.2	*Takifugu rubripes*	XP_003965650.1
Labeo rohita	ADC96616.1	*Tetraodon nigroviridis*	ENSTNIP00000016222
Latimeria chalumnae	XP_005994419.1	*Xenopus tropicalis*	ENSXETP00000008656
Mus musculus	NP_038661.2	*Xiphophorus maculatus*	XP_005799711.1

Table S2. The Ensembl IDs of the analyzed sequences in Figure 3B.

Species		Ensembl IDs
Human	*Homo sapiens*	ENST00000259915
Cow	*Bos taurus*	ENSBTAT00000028122
Mouse	*Mus musculus*	ENSMUST00000025271
Stickleback	*Gasterosteus aculeatus*	ENSGACT00000023169
Tilapia	*Oreochromis niloticus*	ENSONIT00000004857
Zebrafish	*Danio rerio*	ENSDART00000065817

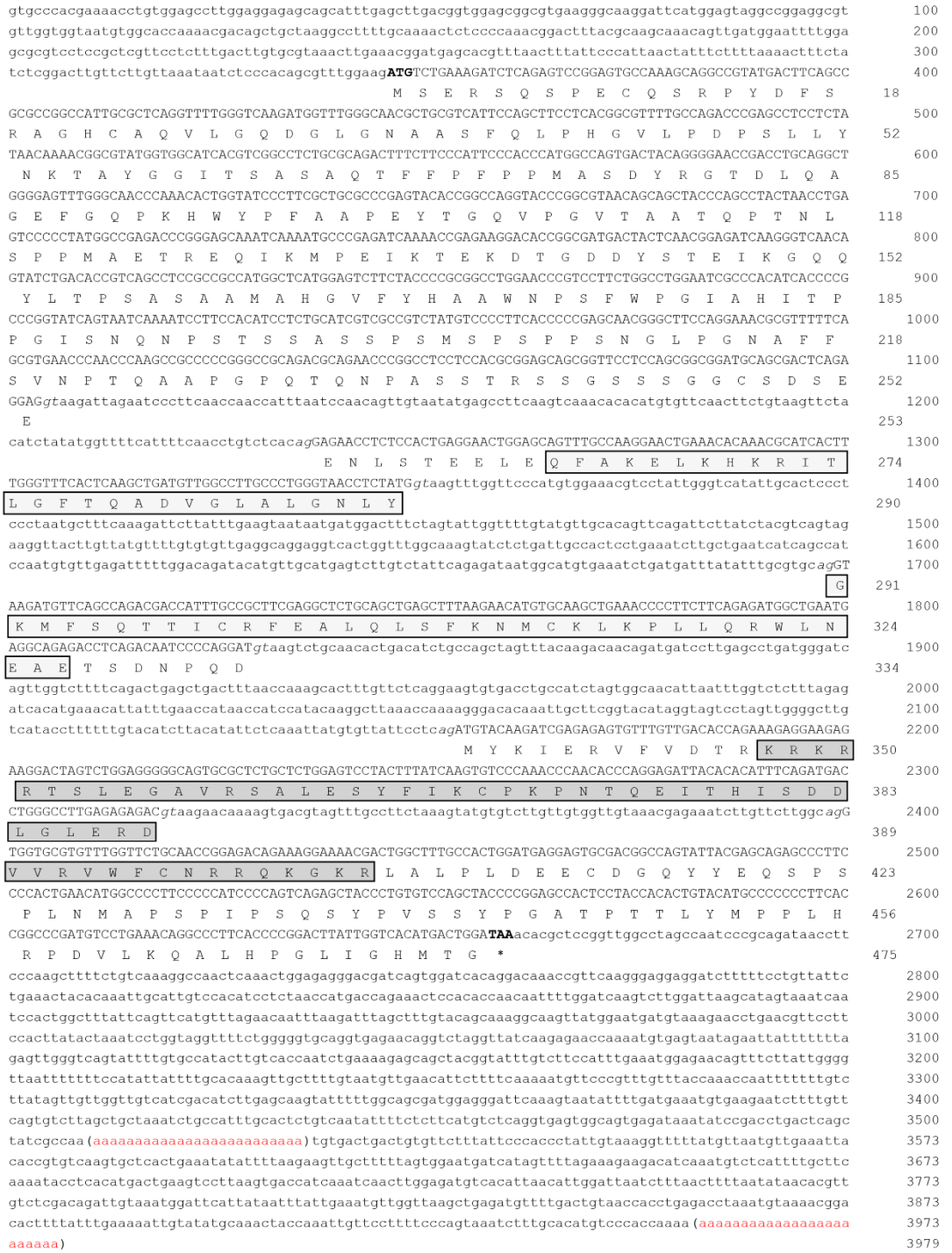

Figure S1. Nucleotide and protein sequences of Japanese flounder *pou5f3* gene (accession number: KJ522774). Coding sequences (CDS) are denoted in uppercase letters, whereas the UTRs or introns are denoted in lowercase letters. The deduced amino acids are indicated in one-letter code and exhibited below the coding regions. The GT/AG intron/exon boundaries are shown in italic and the start and termination codons are highlighted in bold. The POU-specific domain and POU homeodomain are shadowed with light and dark gray boxes, respectively. The red letters indicate the poly (A) tails of the two isoforms of *Popou5f3* transcripts.

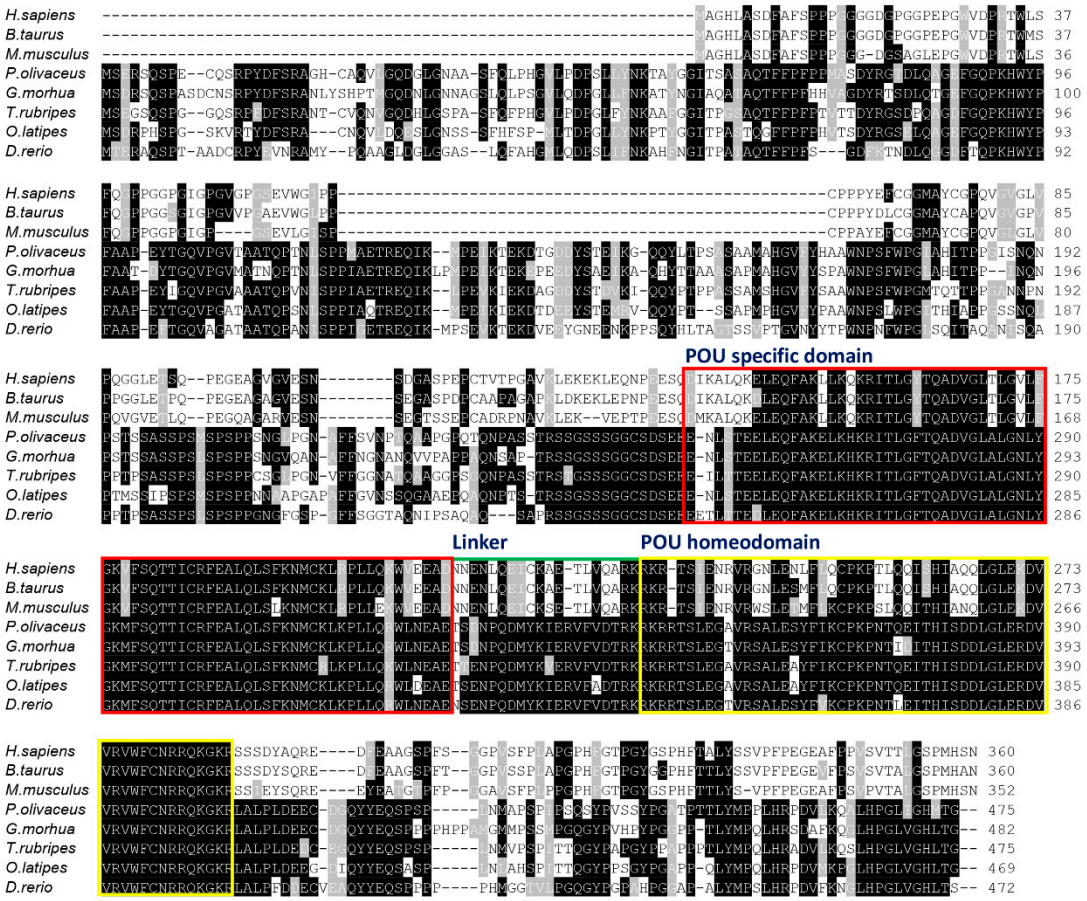

Figure S2. Comparison of the full-length amino acid sequences of Japanese flounder Pou5f3 protein with other vertebrate orthologues. Identical and similar residues are highlighted in black and gray, respectively. POU specific and homeodomains are indicated with red and yellow frames, respectively. The linker regions between two domains are shown by green line. The alignment is generated with ClustalW and shaded with BOXSHADE 3.21. The hyphens (−) indicate gaps that were inserted to maximize sequence similarity.

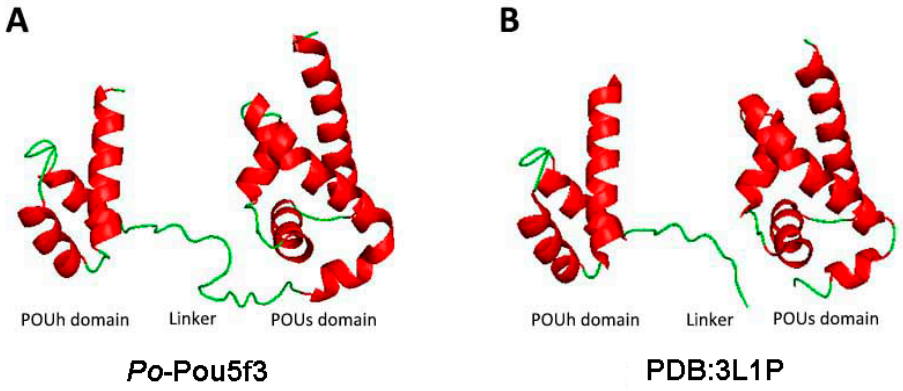

Figure S3. The predicted three-dimensional model of *Po*Pou5f3 POU domain based on *M. musculus* Pou5f1 (PDB ID: 3L1P) by homology modelling method using SWISS-MODEL online server. The α-helices and loop regions are shown as red and green ribbons, respectively.