

Takifugu_rubripes-_cox1_sequence.seq	TAT AATCGGAGCCCCAGACATGGCCTTCCCCGAATGAACAACATAAGCTTCTGACTGCTTCCCCCATCC	70
TrSSCs-cox1_sequence_.seq	TAT AATCGGAGCCCCAGACATGGCCTTCCCCGAATGAACAACATAAGCTTCTGACTGCTTCCCCCATCC	70
Consensus	t a t a a t c g g a g e c c c a g a c a t g g c c t t c c c c g a a t g a a c a a c a t a a g e t t c t g a c t g e t t c c c c a t c c	
Takifugu_rubripes-_cox1_sequence.seq	TTCTCTCTTCTGCTCGCATCCTCTGGAGTAGAAGCGGAGCGGGTACGGCTGAACCTGTTTACCCACCCG	140
TrSSCs-cox1_sequence_.seq	TTCTCTCTTCTGCTCGCATCCTCTGGAGTAGAAGCGGAGCGGGTACGGCTGAACCTGTTTACCCACCCG	140
Consensus	t t c c t c t t c t g e t c g a t c c t c t g g a g t a g a a g c e g g a g e g g g t a c g g g e t g a a c t g t t t a c c c a c c c c	
Takifugu_rubripes-_cox1_sequence.seq	TAGCAGGAAATCTTGCCACGCAGGGGCTTCTGTAGACCTCACCATCTTCTCTCTTCATCTTTGCAGGGGT	210
TrSSCs-cox1_sequence_.seq	TAGCAGGAAATCTTGCCACGCAGGGGCTTCTGTAGACCTCACCATCTTCTCTCTTCATCTTTGCAGGGGT	210
Consensus	t a g c a g g a a a t c t t g c c c a c g c a g g g g e t t c t g t a g a c c t c a c c a t c t t c t c t t c a t c t t g c a g g g g t	
Takifugu_rubripes-_cox1_sequence.seq	CTCCTCTATTCTAGGGGCAATCAACTTCATCACAACCATCATTAACATGAAGCCCCAGCAATCTCACAA	280
TrSSCs-cox1_sequence_.seq	CTCCTCTATTCTAGGGGCAATCAACTTCATCACAACCATCATTAACATGAAGCCCCAGCAATCTCACAA	280
Consensus	c t c c t c t a t t c t a g g g g c a a t c a a c t t c a t c a c a a c c a t c a t t a a c a t g a a g c c c c a g c a a t c t c a c a a	
Takifugu_rubripes-_cox1_sequence.seq	TACCAACACCTCTTTTCGTGTGAGCCGTTTTAATTACTGCTGTACTTCTCCTGCTTCCCTTCCAGTCC	350
TrSSCs-cox1_sequence_.seq	TACCAACACCTCTTTTCGTGTGAGCCGTTTTAATTACTGCTGTACTTCTCCTGCTTCCCTTCCAGTCC	350
Consensus	t a c c a a a c a c c t c t t t t c g t g t g a g c c g t t t t a a t t a c t g e t g t a c t t c t c e t c t c c c t t c c a g t c c	
Takifugu_rubripes-_cox1_sequence.seq	TTGCAGCAGGGATTACAATACTTCTCACTGACCGAAACCTAAATACAACCTTCTTTGACCCAGCAGGAGG	420
TrSSCs-cox1_sequence_.seq	TTGCAGCAGGGATTACAATACTTCTCACTGACCGAAACCTAAATACAACCTTCTTTGACCCAGCAGGAGG	420
Consensus	t t g c a g c a g g g a t t a c a a t a c t t c t c a c t g a c c g a a a c c t a a t a c a a c c t t c t t t g a c c c a g c a g g a g g	
Takifugu_rubripes-_cox1_sequence.seq	AGGAGACCCCATCTTGTACCAACACTTATTCTGATTCTTTGGACACCTGAAGTCTACATTCTAATTCTCT	490
TrSSCs-cox1_sequence_.seq	AGGAGACCCCATCTTGTACCAACACTTATTCTGATTCTTTGGACACCTGAAGTCTACATTCTAATTCTCT	490
Consensus	a g g a g a c c c c a t c t t g t a c c a a c a c t t a t t c t g a t t c t t t g g a c a c c c t g a a g t c t a c a t t c t a a t t c t c	
Takifugu_rubripes-_cox1_sequence.seq	CCTGGCTTCGGAATAATTTACACACATCGTAGCCTACTACTCGGGCAAAAAAGAACCTTCGGCTACATGG	560
TrSSCs-cox1_sequence_.seq	CCTGGCTTCGGAATAATTTACACACATCGTAGCCTACTACTCGGGCAAAAAAGAACCTTCGGCTACATGG	560
Consensus	c c t g g c t t c g g a a t a a t t t c a c a c a t c g t a g c c t a c t a c t c g g g c a a a a a g a a c c a t t c g g c t a c a t g g	
Takifugu_rubripes-_cox1_sequence.seq	GCATGGTCTGAGCCATAATGGCCATCGGTCTTCTTGGTTTTATTGTATGAGCCCACCACATGTTACAGT	630
TrSSCs-cox1_sequence_.seq	GCATGGTCTGAGCCATAATGGCCATCGGTCTTCTTGGTTTTATTGTATGAGCCCACCACATGTTACAGT	630
Consensus	g c a t g g t c t g a g c c a t a a t g g c c a t c g g t c t t c t t g g t t t t a t t g t a t g a g c c c a c c a c a t g t t a c a g t	
Takifugu_rubripes-_cox1_sequence.seq	CGGCATGGACGTAGACACCCGAGCCTACTTTACCTCTGCCACAATAATTATTGCCATCCCAGACAGGAGTC	700
TrSSCs-cox1_sequence_.seq	CGGCATGGACGTAGACACCCGAGCCTACTTTACCTCTGCCACAATAATTATTGCCATCCCAGACAGGAGTC	700
Consensus	c g g c a t g g a c g t a g a c a c c c g a g c c t a c t t t a c c t c t g c c a c a a t a a t t a t t g c c a t c c c a c a g g a g t c	
Takifugu_rubripes-_cox1_sequence.seq	AAAGTATTTAGCTGACTTGCAACCTTGCATGGAGGATCAATTAAATGAGAAACCCCTATACTATGAGCCC	770
TrSSCs-cox1_sequence_.seq	AAAGTATTTAGCTGACTTGCAACCTTGCATGGAGGATCAATTAAATGAGAAACCCCTATACTATGAGCCC	770
Consensus	a a a g t a t t t a g c t g a c t t g c a a c c t t g c a t g g a g g a t c a a t t a a t g a g a a c c c c t a t a c t a t g a g c c c	
Takifugu_rubripes-_cox1_sequence.seq	TCGGCTTCATCTTCTATTTACAGTGGGTGGCCTAACCGGAATTGTCCTAGCCAATTATCCCTAGACAT	840
TrSSCs-cox1_sequence_.seq	TCGGCTTCATCTTCTATTTACAGTGGGTGGCCTAACCGGAATTGTCCTAGCCAATTATCCCTAGACAT	840
Consensus	t c g g c t t c a t c t t c e a t t t a c a g t g g g t g g c c t a a c c g g a a t t g t c c t a g c c a a t t c a t c c c t a g a c a t	
Takifugu_rubripes-_cox1_sequence.seq	CGTATTACACGACACCTACTACGTAGTTGCCATTTCCTACTAC	883
TrSSCs-cox1_sequence_.seq	CGTATTACACGACACCTACTACGTAGTTGCCATTTCCTACTAC	883
Consensus	c g t a t t a c a c g a c a c c t a c t a c g t a g t t g c c a t t t c c a c t a c	

**Supplementary Figure S1. Sequence of *cox1* gene of *T. rubripes* and TrSSCs.** The *cox1* PCR product was 883 bp in length. The sequence alignment analysis showed 100% similarity between the sequences from TrSSC and that from tiger puffer fish (Genbank accession number: AJ421455).