

Supplemental Figures

Sp box

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AssP1 : ...MSNQQGEMAAVESGGGYSQKRNTNS.QDSQQPSPLALLAATCSRIDTPGENDSTTD...QQ..QD : 60
AmSP1 : ....MSERNEMAAMGEGDGDGRKKRNTKTDQDAQPPSPPLALLAATCSRIDENDAAE.....QQ : 54
CaSP1 : ..... : -
DrSP1 : ..... : -
KmSP1 : ...MNNQQGEMAAVESGGGFSQKRNTNS.QDSQQPSPLALLAATCSRIDTPGENDSPAD...QQ..QN : 60
LcSP1 : .....MAAVESGGGFSQKRNTNS.QDSQQPSPLALLAATCSRIDTPGENDSPSD...QQ..NQ : 52
OnSP1 : ...MSNQQGEMAAVESGGGFSQKRNTNS.QDSQQPSPLALLAATCSRIDTPGENDSPADQHQQ..NQ : 62
OlSP1 : ...MSNQQGEMAAVESGGGFSQKRNTNS.QDSQQPSPLALLAATCSRIEPPGENDSSAD...QHQTQQ : 62
PnSP1 : .MSDRQQNEMAALVENDGDFRKKRNSNAEREAQPPSPPLALLAATCSRMDENDAAD.....QQ : 57
SsSP1 : MKLTNNQDEMAAMVESGGGFLOKRNTNTGDSQQPSPLALLAATCSRIDTPGESDSGSE...QQ..LD : 64
SfSP1 : ..MSDQQQDEMAALVEGGGGFLOKRNSNTGDSQQPSPLALLAATCSRIDTPGEGEGTSD...QQ..QQ : 62
ScSP1 : .....MAAVESGGGFSQKRNGNS.QDSQQPSPLALLAATCSRIDTPGENDSPSD...QQ..NQ : 52

AssP1 : ..QLELN....QGVFTSSANG.WQVVSINVQASSGSNTI.TTDSSGVMTGDDG...KSR..QVLSPSST : 116
AmSP1 : LQV..HRNDLTHTQVSHATNG.WQIVSQGVQTTTASGNN.ISQKIVQ.D.....KNQ..T..... : 102
CaSP1 : ..... : -
DrSP1 : ..... : -
KmSP1 : ..QLEIN....QSVFTSSANS.WQDVPPGVQASSGSNTV.TTDSSGLMTGGDN.SKGR..QGLSTSAA : 118
LcSP1 : QQQLDIN....QGVFTSSANG.WQVIPLSIQTSSGTNTI.TTDSSGVMTVGDG.GKGR..QVLSPSV. : 110
OnSP1 : QQQLDLN....QAVFTSSANS.WQVNPLSVQASSGSNTV.TTDSSGVMMSGDL.IKNR..QVLSPA.. : 119
OlSP1 : ..QQLKIN....QI.FTSNANG.WQVPLSLQTTAGCNTTTT.TTDSTGVMTGGE...KSR..QVLSTSEA : 118
PnSP1 : NLLQDHRTEHQSQASHTTNG.WQIIPLAGQGTGVSGNI.IKSGSLTED.....KSR..H..... : 108
SsSP1 : LS.....QAQLTQTANGSWQIIPVSLGSSSGSNTI.TTDTTGMVMTAGDSGKNRGQQ..... : 115
SfSP1 : NQLLDIN....QAQLTQTANG.WQIIPVSVQSSSSSNTV.TTMASGQAAPVGDAGKNR..... : 115
ScSP1 : QQQLDLN....QGVFTSSANG.WQVIPLSVQASSGTNTI.TTDSSGVMTGDDP.GKSR..QVLSPSV. : 110

AssP1 : ....Q.G..QQLOQQQYVVAQAPSVPGQQVLTITISGVV...PNIQYQVIPQFQTVDDGQPLHFAH...AQ : 172
AmSP1 : IVTSGV...QQQQQQQYIVASAPSIQGGQLLTITISGVM...PNIQYQVIPQFQTVDDGQQLQFAQ...TT : 162
CaSP1 : ..... : 25
DrSP1 : ..... : 20
KmSP1 : AVSSQ.G..QQPQQQQYVVAQAPSVPGQQVLTITISGVM...PNIQYQVIPQFQTVDDGQPLHFAH...AQ : 178
LcSP1 : AVSTQ.G..QQQQPQQYVVAQAPSMQGGQVLTITISGMM...PNIQYQVIPQFQTVDDGQTLQLAH...AQ : 170
OnSP1 : ..ASSQS.QQQQQQQYVVAQAPSMQGGQVLTITISGVM...PNIQYQVIPQFQTVDDGQTLHFTH...AQ : 178
OlSP1 : AVCSQ.AQQQQQQQYVLAQAPSVTGGQVLTITISGMM...PNIQYQVIPQFQTVDDGQQLHFAA...PQ : 179
PnSP1 : VVSTGA..GAPPQQQFIVASAPSIQGGQVLTITISGVM...PNIQYQVIPQFQTVDDGQQLQFAQ...TS : 168
SsSP1 : VLTSVSS.GHQGGQQYVLSSAPSIQGGQVLTMSGQQVSMVPMNIHYQVIPQFQTVDDGQHLQFAQAGVQQ : 182
SfSP1 : AVSTASG.GQQGQQQFVVASAPTIPGGQVLTITISGVV...PNIQYQVIPQFQTVDDGQQLQFTQ...QD : 176
ScSP1 : AVASSAG.QHQQPQQYVVAQAPSMQGGQVLTITISGVM...PNIQYQVIPQFQTVDDGQSLQLTN...TQ : 171

AssP1 : QE...SAAAGT.GQQFQIVSSPNGQQIIT.AAT.NRAGAAGNIITMP.SVLOGAIPIQNITLGNVQLQN. : 232
AmSP1 : QDAS....AAGTGQLQLVSSPNGQQIITATSA.GQNTGAGNITVP.GLLQQAIPLQN...LALGNTVL : 222
CaSP1 : APEV....STA.GQFQIVTSPSGNQQIIT.AAP.SRAS..GNITVP.GLFOQAIPLQN...SLSGAVL : 81
DrSP1 : QLQA....AQD.MSGQLLVSSPGGQQIIRAAG.....S..GNITVP.GLFOQAIPLQNLS....AVL : 70
KmSP1 : QD...S.AAGQ.GQQFQIVSSPNGQQIIT.AAT.NRAGAAGNIITMP.SVLOGAIPIQNITLGNVQLQ. : 237
LcSP1 : QEATVS.GAAP.GQQFQIVSSPNGQQIIT.AAT.NRAGAAGNIITMP.GLLQGAIPIQNITLGNVQLQ. : 232
OnSP1 : QESAVP.ATAGPGQQFQIVSSPNGQQIIT.AAS.NRAGAAGNIITMP.SLIQGAIPIQNITLGNVQLQ. : 241
OlSP1 : QE..SGIT.GQ.GQQFQIVSSPNGQQIIT.AAAANRTGTSGNIITMP.SVLPQAIPIQSISLGNVQLQ. : 240
PnSP1 : HDAS....AAGPGQLQLVSSPGGQQIITAPT.SQSTGAANITVP.GLLQQAIPLQN...LALGNTVL : 228
SsSP1 : DPNA....AGA.GQFQIVSSPNGQQIIV.....RAGSGGNITMPAGLLQQAIPLQN...LGLNSVL : 237
SfSP1 : SSAT....AAA.GQFQIVSSPGGQQIIT.ATT.SRAAGAGNIITAMP.GLIQQAIPLQN...LGLNIQ. : 233
ScSP1 : QDSTVS..AAGTGQQFQIVASPNNGQQIIT.AAA.NRPGAMGNIITMP.SLLOGAIPIQNITLGNVQLQ. : 234

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AsSP1 : ..QPQFL..ANMPVSLNGNITLV..PVSTGVTGGDANS...GETS..GNQLIQQSP..QPVS....SNNGT : 286
 AmSP1 : P..SQTQF..LANVPM..SLNGGITLLPVSAQAAGAKADDGTS..GVC...Q..QVV..QQA....IVS... : 273
 CaSP1 : P..NQAQF..LTNMP..NANITLLPVGSV.....SDA..NAGGAPQQ....LLQ... : 119
 DrSP1 : P..NQTFQF..LANVPL..NANITLLPVGFGPVG.....GDTHTA....VAA... : 106
 KmSP1 : ..NQPFQF..LANMPVSLNGNITLLPVSTGATGGDANGN..GDTG..GNQLIQQ..QSKQPVVS....SNSGA : 295
 LcSP1 : ..NQPFQF..LANMPVSLNGNITLLPVSTGASGTGDANS..GGDTG..GNQLI..QSQHPVS....SNS... : 287
 OnSP1 : ..NQPFQF..LANMPMSLNGNITLLPVTAGAA..GGDTNGGGEAG..GNQLM..QQQQQPV..VSSNSEA... : 298
 OlSP1 : ..NQPQI..LANMPVSLNGNITLLPVSTGATGGDANCA..GDGG..CHQQVEN..QTQQPVVS.....SGA : 295
 PnSP1 : N..NQTFQF..LANMPVSLNGSITLLPVSAAGAAAGAKSDDVTS..GTSGVSQ..QLLHAQQA....VAA... : 284
 SsSP1 : QNNQGFQF..LANMPGLLNGNITLLPVSAASGSEGDGGSN.....Q..QLMQQVVS....TS... : 286
 SfSP1 : ..NQAQF..LANMPVSINGNITLLPVATGTTGGGGDAAGV..G..SGSSQ..QLLQPPAS....SAG... : 287
 ScSP1 : ..NQPFQF..LANMPVSLNGNITLLPVSTGTTGTGADANGGGDAG..GNQLV..QQQLQNAVSSNSNT.. : 294

AsSP1 : SYMTESESTIIT..QTT...SSYGI..TQKNSNGSGS..GTFQ..QNPASSLGIPIQPDNRAE.....QQPQ : 341
 AmSP1 : TATEYHTSATSTTTQAVM..SCSGVSRANTVTGNTFQTTVGITP...IQAIQSDNPDGKQQQQQQQQQT : 338
 CaSP1 : STTAAYCTTSTSTQTTAPGGVLTLAQSNITSEPGKTFQNTSGD...GPKVSQAQIVI.....QP : 175
 DrSP1 : PPQGPEFCSIASSTRATAAVGIATLAQSR.....PAASDGQKG.....QP : 147
 KmSP1 : GYMTSASTVTT..QAT...SSYGI..TQTQKNSG..SVTGTTFQ..QNPTTSLGVPIQPDNRDG.....QQPQ : 351
 LcSP1 : GYMTSASTIIT..QAS...TSYGM..TQTQNTNGVMTGTFQHNAATSLGVPIQPDNRDG.....QQPQ : 343
 OnSP1 : GYMTSASTVTTQT..S...SSYGV..TQKNSNGAVTGTTFQ..QNMASSLGVPIQPDNRDR.....GQPQ : 354
 OlSP1 : GYMTNVSTVTT..Q..T...TSYGI..TQTQKNSGSGTGSFQSQSPS..SVGVAVQPENRNG.....QQPQ : 349
 PnSP1 : PVTAHYHSSSTTTSTTQVMTSCSGVSSQSNM..TGATFQTTAA...GISVQSENDRDGK.....QP : 340
 SsSP1 : ..GYTYTNSTTTTQTGTSYGGMTOQTOSTNGFQNSGGGIPIQ...PDNRD..... : 332
 SfSP1 : GTGFYTNITTTTTSQAATSYGGGTQAQSSSVGGNGFQSSGG...GASGQSDNRDG.....QN : 343
 ScSP1 : GYMTSASTVTT..T..S...SSYGM..TQTQNSNVAMTGTTFQ..GNTGSSLSVPIQPDNRDG.....QQPQ : 349

AsSP1 : QIL.....IQSPQVIQGGAPLQTIQASTVTSAGGVFAAPTLSQEGQLNLQIM..PNTGPILLR : 398
 AmSP1 : QQPQI.....LIQPQQLFQGTSTLQAIQPA.....SGQVFATQTLSDGLQNLQM..IPNNSILLR : 394
 CaSP1 : QQVLQS.....VSA.....GGQVFATQSLSDGLQNVQIQTIANGSPILIR : 216
 DrSP1 : QMLIQGVQQGAUSA.....PGQVFTTQTLSDGVQNVQIQTIASGSPILIR : 193
 KmSP1 : QIL.....IQPQQVIQGGTSLQTIQASAVATAGGVFAAPTLSQEGQLNLQIM..PNTGPILLR : 408
 LcSP1 : QIL.....IQPQQVIQGGTPLQTIQAGTVATAGGVFAAPTLSQEGQLNLQIM..PNAGPILLR : 400
 OnSP1 : QIL.....IQPQQVIQGGAQIQTQAGTVAATGGQVFTPTLSQEGQLNLQIMP..NTGA..ILLR : 410
 OlSP1 : QIL.....IQPQQVIQGGTSLQTIQ.....AGQVFFAAPTLSQEGQLNLQIM..PNTGPILLR : 400
 PnSP1 : QQHPQV.....LIQPQQLFQGAAPALQAIQSG.....GGQVFFAHTLSQEGQLNLQIQTIIPNSTILLR : 398
 SsSP1 : .QLQOI.....LIQPQQLIQGGTSLQTIISA.....GGQVFATPTLTQDALQNLQIQTIIPNTSPILLR : 388
 SfSP1 : QQPQI.....VIQPQQLQSGHSLQTIQTGAIST..GGQVIAAQTLSQDALQNLQIQAIPTSPILVR : 405
 ScSP1 : QIL.....IQPQQVIQGGAPL...QAGTVATAGGVFAAPTLSQEGQLNLQIM..PNTGPILLR : 403

AsSP1 : TVGPNGQVSWQTIHQNPAGAQTILAPVQSLPQLG....QTQGG..TGAGTVP..V..QIENLQITINLN : 457
 AmSP1 : TVGPNGQVSWQTVQLQSPAGAQTILAPVHSLPQLTQTGTTAT.TMQ.....LPGLQTI : 446
 CaSP1 : TVGPNGQVSWQTLQLOSPANTQITLAQ.....PGT..LSGLQITINLN : 256
 DrSP1 : TLGADGQVSWQTLQLOSPA..QITLAPTGAAG.....PVQLSGLQITINLN : 237
 KmSP1 : TVGPNGQVSWQTIQIQSPAGTQITLAPVQSLPQLG....QPQGG..AGAVPVS..TMQIPSLQITINLN : 468
 LcSP1 : TVAPNGQVSWQTIQIQSPAGPQITLAPMQSLPQLG....QAQGAAAGGVSVN..TVQIPGIQITINLN : 462
 OnSP1 : TVAPNGQVSWQTIQIQSPAGTGAQTILAPVQSLPQLG....QTQGTAAAGGVVPVN..TVQIPGIQITINLN : 472
 OlSP1 : TVGPNGQVSWQTIQIQSPAGTGAQTILAPVQSLPQLG....QAQGN..TGAGAVPVNTLQIPGIQITINLN : 462
 PnSP1 : TVGPNGQVSWQTVQLQSPAGAQTILAPVPSLPQLAQTG..TAT.TMQ.....LPGLQTI : 449
 SsSP1 : TVGLNGQVSWQTLQLOSPAGTQITLAPM...QGLSQLG..QAQ..GGTM.....QLPGLHTINLN : 441
 SfSP1 : TLGPNQVSWQTLQLOSPAGAQTILAPVQSLQPLPQLA..QAQ..AGSAGGVSVN..PVQIPGIQITINLN : 469
 ScSP1 : TVGPNGQVSWQTIQIQSPAGTQITLAPVQSLPQLG....QAQGAAAGGVSVN..TVQIPGIQITINLN : 465

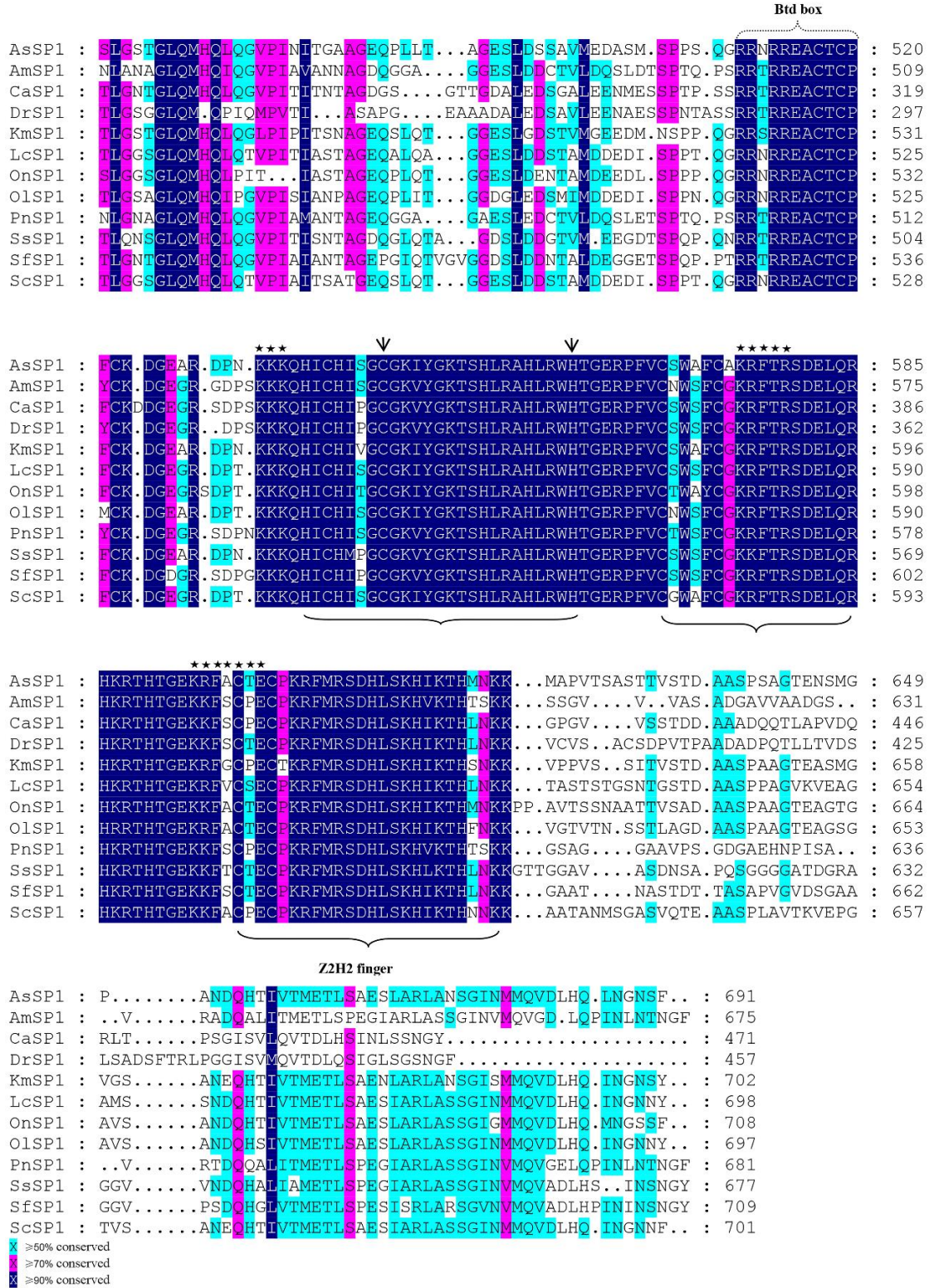


Figure S1. Alignments of the deduced full-length amino acid (aa) sequences of Sp1 from *S. canaliculatus* (ScSP1) and other fish species (*L. crocea*, LcSP1, XP_010730401.1; *S. salar*, SsSP1, XP_013989519.1; *A. striatum*, AsSP1, SBP16265.1; *A. mexicanus*, AmSP1, XP_007248419.1; *K. marmoratus*, KmSP1, XP_017264015.1; *O. niloticus*, OnSP1, XP_019214905.1; *O. latipes*, OlSP1, XP_004068725.1; *P. nattereri*, PnSP1, XP_017548304.1; *S. formosus*, SfSP1, XP_018597836.1; *D. rerio*, DrSP1, AAH67713.1). The black and gray boxes indicate identical and similar aa residues, respectively. The solid-line and dotted-line brackets indicate Sp and Btd boxes, respectively. The solid

braces denote zinc finger domains. The pentagrams and arrows indicate potential phosphorylation sites and Zn binding sites.

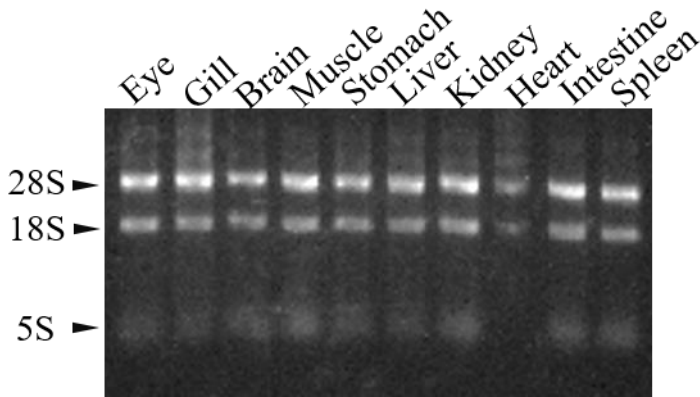


Figure S2. RNA integrity assay for eye, gill, brain, muscle, stomach, liver, kidney, heart, intestine and spleen of rabbitfish (*S. canaliculatus*), related to Figure 3.



Figure S3. Alignment of *fads2* promoters among rabbitfish (*S. canaliculatus*) and other fish species. The numbers indicate sequence positions relative to possible transcription start site, related to Figure 8.