

Supplementary Materials

Comparison of Structural and Physicochemical Characteristics of Skin Collagen from Chum Salmon (Cold-Water Fish) and Nile Tilapia (Warm-Water Fish)

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1 MFSFVDIRLA LLLSATVLLA RGQGEDDRTA GSCTLDGQYY NDRDVWKPEP
51 CQICVCDSTG VMCDVICED TSDCPNPVIP HDECCPICPD DGFQEPKVEG
101 PQGDRGAKGE PGAPGFPNGD GTPQCPGLPG PPGPPGPPGL GGNFSPQMSG
151 GFDEKSGGGM **SMPGPMGPMG PRGPPGPPGS SGPQGFTGPP GEPGEAGSSG**
201 **PMGPRGPAGP** PGKNGDDGES GKPGRPGERG ASGPQGARGF PGTPGLPGIK
251 GHRGFSGLDG **AKGESGPAGP KEGGASGEN GAAGAMPGRG** LPGERGRAGP
301 **NGAAGARGND** GAAGAAGPPG PTGPAGAPGF PGPGGAKGEV GAQGARGGEG
351 PQSGRGEAGN PGAPAGPAGLA GNGADGNPG TKGAPGSAGI AGAPGFPGR
401 GPPGPQAGG APGPKNTGE **VGANGAKGEA GAKGESGPAG VQGPAGPAGE**
451 **BGKRGSRGEP** GAAGARGAPG ERGGPSRGF PGSDGAAGPK GGPGERGGAG
501 VAGAKNTGE **PGRNGEPMGP GSKGMTGSPG SPGPDGKTGP SGAGGQDGRP**
551 **GPPGPVGARG QPGVMGFPGP KGAAGEGKGP GERGVMPGG AVGAPGKDGD**
601 VGAPGAPGVA GPSGERGEGG AGPPGPFQGL SGPQGAIGET GKPGEQGLPG
651 EGGAPGSAGS RGDGRFPGER GAPPSGSPG ARGSPGSAGN DGAKEAGAA
701 GAPCGGQPPG LQGMGERGA GGLPGLKDR GDQGVKGADG AGKDGVRGM
751 **TGPIGPNGPA GSPGDKETGE APGAVGPSGA** RGAPGERGES **GAPGPAGFAG**
801 **PPGGDGQPGA KGEAGDNGAK** GDGAQGPAG PTGAPGPQP AGNTGAKGAR
851 **GAAGPPGATG FPGAAGRVGP** PGPSGNSGPP GPPGPGKKEG QKGNRGETGP
901 AGRPGELGAA GPPGAQGEKG **QPGGDGPNPG SGTTPGQIG GQRGIVGLPG**
951 **QRRGERFPGL AQGLGEPKQ GPGGPSGERG PPGPMGPPL AGAPGEPGRE**
1001 **GTPGNEGSSG** RDGAAGPKGE RGESGVAGAS GAPGPPGAPG SVGPAGKSGD
1051 **RGESGPAGPA GIAGPAGPRG PSGPAGARGD** KGEAGEAGER GMKGHRGFTG
1101 **MQGPPGPSQ SGESGPAGAS GAPAGRGPSG** SAGAAGK**DCM** **SGLPGTIGPP**
1151 **GPRGRSGEMG** PSPPGPPGPG PGPPGPPGGG FDMGFIAQPX QEKAPDPFRH
1201 FRADDANVMR DRDLEVDTTL KSLSQIENI RSPEGTKKNP ARTCRDLKMC
1251 HPDWKSGEYW IDPDQGTQD AIKVCNMET GETCVYPTA XIPKKSUYTS
1301 KNIKEKHHVW FGEAMTDGFQ FEYSGESSA QDVNIQLTFL RLMATEASQN
1351 IITYHCKNSIA YMDQSGNLK KSLLLQGSNE IEIRAEGNSR FTYSVTEDGC
1401 TSHTGAWGKT VIDYKTKTTS RLPIIDIAPM DVGAPNQEFQ IEVGPVCFI

A

1 MFSFVDNRIL LLLAVTSFLA SCQSGPTGEK GPRGDRGPQG RNRDCKDGL
51 PGVAGPPGPP GLGNFAAQF DGK**GSMDPG** **GPMLMGSRG** PNGPPGSPGP
101 QGFTGHAGEP GEPQQTGSIQ ARGPSGSACK PGEDGNNGRP GKPGDRGGPG
151 TQARGFPPT PGLPGMKGHR **GYNGLDGRKG** ESGSGGAKGE TGAHGANPN
201 GPAGSRGLNG ERGR**AGPAGP** **AGARGADGST** GPAGPAGPLG AAGPPGFPGA
251 PGPK**GEIGGA** **GANGSPGPQG** GRGEPGTNGA VGPVGPVGNP GNNINGAKG
301 AAGLPGVAGA PGFPGPGRGP GPQGPQGSGT **ARGLGGDPGP** **SCQKGDGSAK**
351 **GEPGHSQVQG** **AAGPAGEEGK** **RGSTGEVGAT** **GPAGLRGARG** GAGTRGLPGL
401 EGRGGPI**GMP** **GARGATGPAG** IRGAPGDAGR **AGESLTCAR** GLPGNSGQGG
451 **PPKKEGPSGA** **AGLDGRTGPP** GPTGPRRQPG NIGFPGPKGP GGEAGK**GGDK**
501 **GPTGATGLRG** GPGADGNNGA PGPAVGVGNA GEKEGQPSG APGFQGLPGP
551 AGPAGEAGKP GNQGMHGDQ LPPGAPVKGE RCNSGPAGSA **GSQAIGARG**
601 PAGTPGPDGG KGEPCSVGIA GPGHQQPGG MPGERGAGGT PGPKGEKGE
651 **GHRGLEGNMG** **RDGARGAAGP** **SGPPGPSGAN** **GEKESGSFG** **PAGPAGLRGP**
701 SCER**EGGPA** **GPPGFAGPPG** **SDGQSGPRGE** KGPAGKGDV GPAGPSGPAG
751 QSGPSGASGP AGPPGGR**GDA** **GPSGLTGFPG** **AAGR**VGGPG AGISGPPGSA
801 GPAGKDGPRG **LRGDSGPAGP** **QGEHQIGIPS** **GIAGDKPTG** ESGPPGAPGT
851 AGPQVLGPS GFVGLPGSRG **DKGLPGGPA** **VGEPGLRGA** **GASGPRGPAG**
901 **NIGMPGMTGT** **QGEAGREGSP** GNDGPPRPG TAGFKDRGE PGSPGALGSS
951 GQPGPNPSG AVGRPGNRGE **SGPTNGGPPV** **GAAGARGAPG** PAGPRGEKGG
1001 ACEKDRGMK GLRG**HGGLQG** **MPGPNGPSGE** **TGSAGITGPA** **GPRGPAGPHG**
1051 **PPGKDGRRAG** **HGAIGPVGHR** GSPGHLGPAG PPGSPGLPGP AGPAGGGYDQ
1101 SGGYDEYRAD QPSLRADYE VDATICSLNS QIENLLTPEG SKKNPARTCR
1151 DIKLSHPEWS SGFYWIDPNQ GCIAADAIAH CDFSTGHTCI HPHPESTARK
1201 NWRSSSENK HWFWGETING GTEFAYNDET LSPQSMATQL AFMRLLANQA
1251 TQNTITYHCKN SVAYMDGENG NLKKAIVLLQ SNDVELSAEG NSRFTFNVLE
1301 DGCTRHTGQW SKTVIEYRTN KPSRLPILDI APLDIGGADQ EFLDIGPVC
1351 FK

B

Figure S1. Primary structure identification of type I collagen. (A) *Oncorhynchus keta* type I collagen α 1-chain; (B) *Oncorhynchus keta* type I collagen α 2-chain. The matching peptide is marked in red and bold, and the central triple helix domain Gly-X-Y triplet is marked in gray shading.

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1 MFSFVDLRL LLSAAVLLV RAQGDDRTG KSCTLDQVVF ADRDVKPEP
51 CQICVDSGT VMCDVICED TTDCPNPIIP HDECCPICPD DGFQEPQTEG
101 TVGARGPKGD RGLPGPPGRD GMPGQPLPG PPGPPGPPGL GGNFSPQMSG
151 GYDEKSPAMP VPGPMGPMGP RGPPGPPGSS GPQGFTGPPG EAGEPGSPGP
201 MGPRGPAGPP GKNGEDGESG KPGRPGGERGP PGQGAARGFP GTPGLPGIKG
251 HRGFSGLDCA KDDTGPAGPK GEAGTPGENG TPGAMPPRGL PGERGRAGAT
301 GAAGARGNDG AAGAAGPPGP TGPAGPPGFP GGPGAKGDAG AQGGRGPEGP
351 AGARGEGCNP GPAGPAGPAG NPGSDGAPGA KGAPGAAGVA GAPGFPGRG
401 PSGPQAAGA PGPKNGTEA GAPGSKGEAG AKGEAGAPGV QGPFPGE
451 GKRARGEPPG AAGARGPGE RGAPGGRGFP GSDGPAGPKG ATGERGAPGL
501 VGPKGATGEP GRTGEPGLPG AKGMTGSPGN PGPDGKIGPS GAPGDGRPG
551 PPGPGGARQG PGVMGFPGPK GAGEAGCKPG ERGTMGTPGP AGAPCKDGDV
601 GAQGPPGPAG PAGERGEQGP AGSPGFQGLP GPQGAIVGETG KPGEQGVPE
651 AGAPGPAGAR GDRGFPGERG APGAIGPAGA RSPGASGND GAKGDAGAPG
701 TPGAQPPGL QGMPGERGAA GLPGLRCNRG DQPKGADGT PGKDGPRLT
751 GPIGLPGPAG SPDGKEPGA QGPVGPSPGAR GPPGERGEAG PPGAGFAGP
801 PGADGQPGAK GEPGDNAGAK DSGPPGPAGP TGAPGPQGPV GNTGPKGARG
851 PAGPPGATGF PAGAARGVGP GPAGNAGPPG PPGAGKEGP KGNRGETGPA
901 GRPGELGAG PPGPPGEKGS PGADGAPGSA GIPGPQGIAG QRGIVGLPGQ
951 RGERGFPGLA GPVEGPCKQG PSGPSGERGP PGPMGPPGLA GAPGEPGREG
1001 TPNGEAAGR DGAPGPKDR GESGPAGAPG APGPPGAPGP VGPAGKTGDR
1051 GETPGPAGPAG AAGPGPPRGP AGAPGLRGDK GETGEAGERG MKGHRGFTGM
1101 QGPPGPPCTS GESGPAGAG PAGPRGPPSGA AGAPGKDGVG GLPGPTGPPG
1151 PRGRSGEMGP AGPPPGPPGP GAPGAPGGGF DLGMVQFQE KAPDPFRMYR
1201 ADDANVLRDR DLEVDTLKS LSQIEQIRS PDGTRKNPAR TCRDLKMCHP
1251 DWKSGEYWD PDQCTQDAI KYVCNMETGE TCVSPTQREV AKKNWYISK
1301 IKEKKHWFGE EAMNEGFQFE YGSEGLPED VNTQMTFLRL MSTEASQNT
1351 YHCKNSVAYM DAAANLKKKA LLLQGSNEIE IRAEGNSRFT YSVLEDGCT
1401 HTGTWGTVI DYKTSKTSRL PIIDIAPMDV GAPDQEFGE VGPVCFI

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A

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1 MFSFVDTRIL LLLAVTSYLA SCQFAGPKGP RGRGPPGPN GKDLPGPPG
51 PAGPPGPPGL GGNFAAQYDG VKAPDPGPGP MGLMGPPRGP GPPGASGPQG
101 HTGHAGEPGE PGQAGAVGPR GPPGPPGKAG EDGNNGRPKG PGDRGAPGPQ
151 GARGFPPTGP LPGMKGHRGY TGLDGRKKGEP GAAGPKGEPG AHGAAGSPGL
201 AGARGLPGER GRPGPAGPAG ARGADGNAGP TGPAGPLGAA GPPGFPGGPG
251 PKGETPGVGA TGPSGPQCSR GEPGPNAGV PVGSPNGPA NGLNAGKAA
301 GTPGVAGAPG FPGPRGGPGP QGPQGAAGPR GLAGDPGIQG VKGDSGPKGE
351 PGHSGPQGP GPQGEEGKG PTGEIGATGL AGARGARGAP GSRGMPGAEG
401 RTGPVGMPGA RGATGAAGPR GPPGDAGRAG EPGAAGLRGL PCSPGSSGPP
451 GKEGPAGPSG QDGRSGPGP SGPRGLSGNI GFPGPKPSG EPKPGERGA
501 TGPTGLRGPP GPDGNNGATG ATGVAGGPE KGEQPSGPSP GFQGLPGPAG
551 PTGEAGKPGD RGIPGEPGAA CNAGAKERG NPGACSAGP QGIGPRGPA
601 GAPGPDGGKG EPGPAGVAG PGHQAGAGMP GERGAGTPG PKGEKGEPGH
651 KGPDGNPGRD GPRGLAGPAG PPGTGANGD KEGGSFGPA GPAGPRGPSG
701 ERGEVGPAGA PGFAGPPGAD QGAGARGERG PSKAKGEVPG SGLAGPAGQS
751 GPAGPAGGG PPGARDNGP PGLTGFPAA GRVGAAGPAG IVGPPGPAGP
801 SGKDGPRGRP GDPGSPGSPG EPGIIGPPGL AGEKPSGES GPPGSPGAPG
851 TSGPLGLQGF VGLPGSRGDR GAPGCAGGVG EPCRLPAGP PGARGAPCNI
901 GLPGMTGPQ EAGREGSPGN DGPPGRPGAA GLKDRGEPEG SAGTTGLAGA
951 PGPAGPTGAA GRPGNRGEAG PSGPSGAVP AGARGASGPA GPRGEKVAG
1001 DKGERGMKGL RGHPLQGMPP GPSGPPGDTG AAGAHGPSGP RGPAGPHGPV
1051 KDGRGPGAH TMCAPGARGP NGYSGPVGPP GPPGLPGPPG PAGGGYDVSG
1101 GYDEYRADQP ALRAKDYED ATIKSLNTQI ENLLTPEGSR KNPARTCRDI
1151 KLSHPDWSSG FYWIDPNQGC TNDAIKVCD FTRETCTIYA HPESIARKNW
1201 YRSTENKKHV WFGETINGGT EFTYNDETLS PQSMATQLAF MRLLSNQASQ
1251 NITYHCKNSV AYMDGESGL KKAVVLQGSN DVELRAEGNS RFTFSVLEDG
1301 CTTHTGEWSK TVIEYRTNKP SRLPILDIAP LDIGGADQEF GLDIGVPCFK

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B

Figure S2. Primary structure identification of type I collagen. (A) *Oreochromis niloticus* type I collagen α 1-chain; (B) *Oreochromis niloticus* type I collagen α 2-chain. The matching peptide is marked in red and bold, and the central triple helix domain Gly-X-Y triplet is marked in gray shading.

Sequence alignment of type I collagen α1-chain between CSSC and NTSC. The same amino acid is marked with red shading.

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1      10      20      30      40      50      60
CSSCa1 MFSFVDRLALLLSATVLLARQGEDDRTAGSCTLDGQYVNDRDVWKPEPCQICVCDSGT
NTSCa1 MFSFVDRLALLLSAVLLVRAQGEDDRAGKSCCTLDGQVFAARDVWKPEPCQICVCDSGT

70      80      90      100     110     120
CSSCa1 VMCDEVICEDTSDCPNFWIPHDECCPICPDDGFOEPKVVEGPGQGRGAKGEPFPAAGFPGNQ
NTSCa1 VMCDEVICEDTIDCPNFWIPHDECCPICPDDGFOEPQTEGTVGARGPKGDRCLPAGFPGRD

130     140     150     160     170     180
CSSCa1 GEPGQPLPGPPPPPPPPGLGGNFSQMSGGFDEKSGGMSMPGPMGPMGPRGPPPPPGS
NTSCa1 GEPGQPLPGPPPPPPPPGLGGNFSQMSGGVDEKSEAMPVPGPMGPMGPRGPPPPPGS

250     260     270     280     290     300
CSSCa1 PCTPGLPGIKGHRGFSGLDCAKGESGPAGPKGEAGASGENGAAGAMGPRGLPGERGRAGP
NTSCa1 PCTPGLPGIKGHRGFSGLDCAKGDTPGAGPKGEAGTTPGENGTPGAMGPRGLPGERGRAGP

310     320     330     340     350     360
CSSCa1 NGAAGARGNDGAAGAAGPPGPTGPAGAPGFPFGPGGAKGEVGAQGARGGEGFQSGRGEAGN
NTSCa1 NGAAGARGNDGAAGAAGPPGPTGPAGPPGFPFGPGGAKGDAGAQQGRGPEGPACARGEPGN

370     380     390     400     410     420
CSSCa1 PGPAGPAGLAGNNGADGNGPKGAPGSAIAGAGFPFGPRGPPGPQGAAGAPGPKNGTGE
NTSCa1 PGPAGPAGPAGNPGSDGAPGAKGAPGACVAGAGFPFGPRGPPSGPQGAAGAPGPKNGTGE

430     440     450     460     470     480
CSSCa1 VGANGAKGEAGAKGESGPAVQVGFAGFAGEEGKRGSRGEFGAAGARGAPGERGGPGSRGF
NTSCa1 VGANGAKGEAGAKGESGPAVQVGFAGFAGEEGKRGSRGEFGAAGARGAPGERGGPGSRGF

490     500     510     520     530     540
CSSCa1 PGSDGAPGPKGATGERGAPGLVGPKGATGEPGRNGEPGMPGSKGMTGSPGSPGPDGHTGP
NTSCa1 PGSDGAPGPKGATGERGAPGLVGPKGATGEPGRNGEPGLPGAKMTGSPGSPGPDGHTGP

550     560     570     580     590     600
CSSCa1 SGAGGQDGRPGPPGFGVARGQPGVMGFPKGAAGEGKPGERGVMGPGGAVGAPGKDG
NTSCa1 SGAGGQDGRPGPPGFGVARGQPGVMGFPKGAAGEGKPGERGVMGPTGPAVAPGKDG

610     620     630     640     650     660
CSSCa1 VGAPEGAPGVAGPSGERGEQAGGPPGFQGLSGFQGAAGETGKPGEGQLPGEAGAPGAS
NTSCa1 VGAPEGAPGVAGPSGERGEQAGGPPGFQGLSGFQGAAGETGKPGEGQLPGEAGAPGAS

670     680     690     700     710     720
CSSCa1 RCDRGFPGERGAPGSGPSGARGSPGASGNDGAKGAGAGAPGSGGPPGLQGMPPGERGA
NTSCa1 RCDRGFPGERGAPGSGPSGARGSPGASGNDGAKGAGAGAPGSGGPPGLQGMPPGERGA

730     740     750     760     770     780
CSSCa1 GLPLGIRGDRDQGVKADGAGGKDGVRGNTGPIGNGFAGSPGDKGEGTAPGAVGPGSA
NTSCa1 GLPLGIRGDRDQGVKADGTEGKDGVRGNTGPIGLGFAGSPGDKGEGTAPGAVGPGSA

790     800     810     820     830     840
CSSCa1 RGAPGERGESGAPGPAGFAGPPGDGQPGAKGEAGDNGAKDGGAGQGPAGPTGAPGPQGP
NTSCa1 RGAPGERGESGAPGPAGFAGPPGADGQPGAKGEAGDNGAKDGGAGQGPAGPTGAPGPQGP

850     860     870     880     890     900
CSSCa1 AGNTGAKGARGAGFPFGATGFPGAAGRVGPPGPGSGNSGPPGPPGPGCKEGQKGNRGETGP
NTSCa1 AGNTGAKGARGAGFPFGATGFPGAAGRVGPPGPGAGNAGPPGPPGPGCKEGQKGNRGETGP

910     920     930     940     950     960
CSSCa1 AGRPGELGAAGPPGAQGEKGPFGDGPNGPSGTGPGQGIAGGORGIVGLPGQGERGFPGL
NTSCa1 AGRPGELGAAGPPGPPGEKGPFGDGPNGPSGTGPGQGIAGGORGIVGLPGQGERGFPGL

970     980     990     1000    1010    1020
CSSCa1 AQQLGEPGKQGPFGPSGERGPPGPMGPPGLAGAPGEPGREGTPGNEGSSGRDGAAGPKGE
NTSCa1 AQQLGEPGKQGPFGPSGERGPPGPMGPPGLAGAPGEPGREGTPGNEGSSGRDGAAGPKGE

1030    1040    1050    1060    1070    1080
CSSCa1 RGESGVAGASGAPGPPGAPGSGVPAGKSGDRGESGPAGPAGTAPGAPGRGSPGAPGARGD
NTSCa1 RGESGVAGASGAPGPPGAPGSGVPAGKSGDRGESGPAGPAGTAPGAPGRGSPGAPGARGD

1090    1100    1110    1120    1130    1140
CSSCa1 KGEAGEAGERGMKGHRGFTGMQGGPPGSGSGESGPAGASGPAGPRGPGSSAGAGAKDGM
NTSCa1 KGETGEAGERGMKGHRGFTGMQGGPPGSGSGESGPAGAGAPAGPRGPGSSAGAPGKDG

1150    1160    1170    1180    1190    1200
CSSCa1 SGLPGFPGPPGPRGRSGEMGPGPPGPPGPPGPPGPPGGGGFDLGFVQFOEKAPDPFRH
NTSCa1 SGLPGFPGPPGPRGRSGEMGPGPPGPPGPPGPPGPPGGGGFDLGFVQFOEKAPDPFRM

1210    1220    1230    1240    1250    1260
CSSCa1 FRADDANVRDRDLEVDITLKSLSQQIEIRSPGTGKNPARTCRDLKMCNCHPDWKSGEYW
NTSCa1 FRADDANVRDRDLEVDITLKSLSQQIEIRSPGTGKNPARTCRDLKMCNCHPDWKSGEYW

1270    1280    1290    1300    1310    1320
CSSCa1 IDPDQGCTQDAIKVYCNMETGETCVVPTFAXTPKKSNWTSKNIKEKKHVNFGEAMTDCGQ
NTSCa1 IDPDQGCTQDAIKVYCNMETGETCVVPTQREVAKKNNWTSKNIKEKKHVNFGEAMNDCGQ

1330    1340    1350    1360    1370    1380
CSSCa1 FEYGSEGSAAQDVNIQTFLRLMTEASONITYHCKNSTAYMDQSSGNLKKSLLLQGSNE
NTSCa1 FEYGSEGSLEQDVNIQTFLRLMTEASONITYHCKNSTAYMDAAAAGNLKKALLLQGSNE

1390    1400    1410    1420    1430    1440
CSSCa1 IEIRAEGNSRFTYSVTEGCTSHTCWGTVIDYKTKTSRLPIIDIAPMDVGAPNREFG
NTSCa1 IEIRAEGNSRFTYSVTEGCTSHTCWGTVIDYKTKTSRLPIIDIAPMDVGAPDREFG

CSSCa1 EVGPVCFLL
NTSCa1 EVGPVCFLL

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Figure S3. Sequence alignment of type I collagen α1-chain between CSSC and NTSC. The same amino acid is marked with red shading.

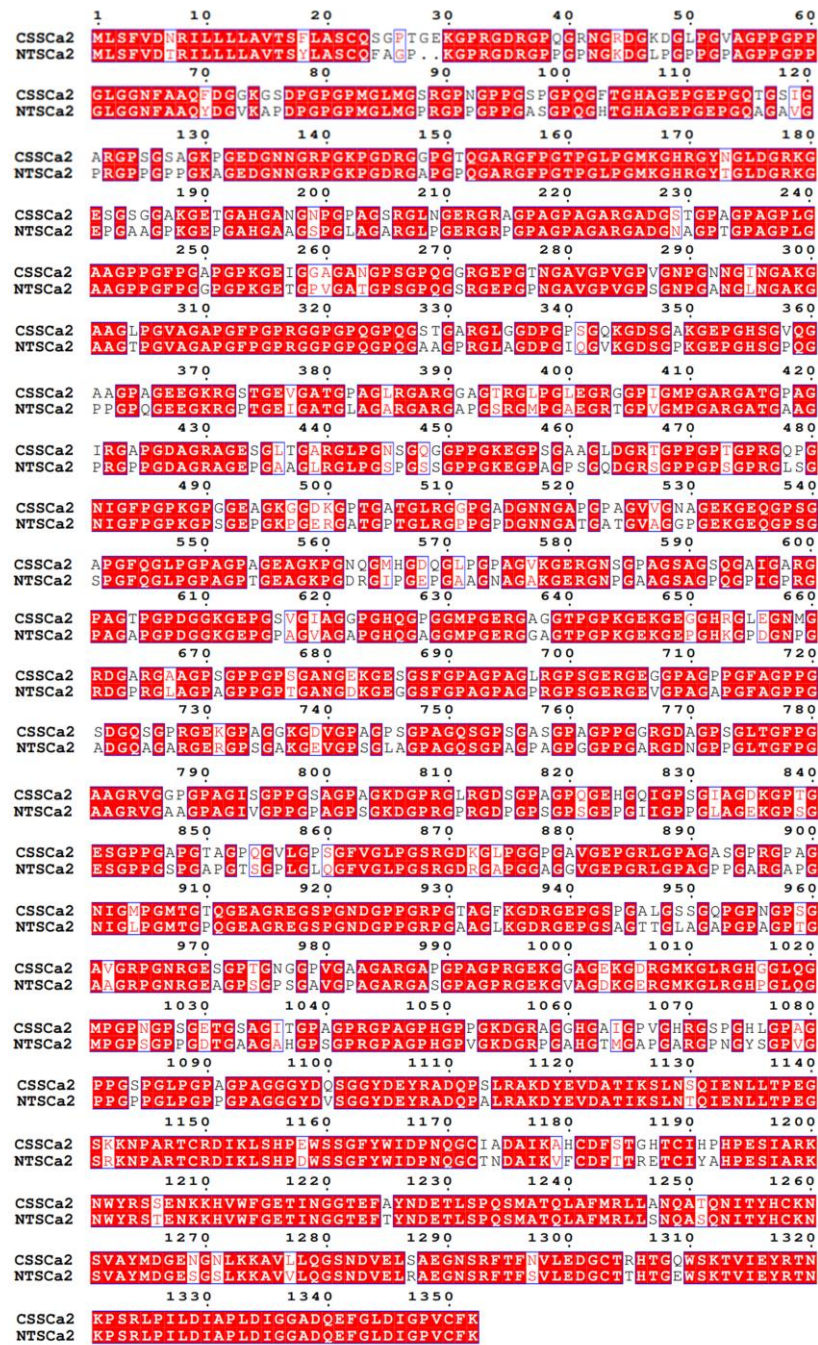


Figure S4. Sequence alignment of type I collagen α2-chain between CSSC and NTSC. The same amino acid is marked with red shading.

Table S1. LC-MS/MS identification of $\alpha 1$ and $\alpha 2$ chains.

Protein	Accession no.	Score	Mass (Da)/PI	Peptide hits	Coverage (%)	Protein description
CSSC $\alpha 1$	XP_035626829.1	1996	137955/5.53	28	30%	Collagen alpha 1(I), (<i>Oncorhynchus keta</i>)
CSSC $\alpha 2$	XP_035651756.1	1219	127004/9.24	28	30%	Collagen alpha 2(I), (<i>Oncorhynchus keta</i>)
NTSC $\alpha 1$	BAL40987.1	527	138225/5.64	18	21%	Collagen alpha 1(I), (<i>Oreochromis niloticus</i>)
NTSC $\alpha 2$	BAL40988.1	906	126856/9.18	22	25%	Collagen alpha 2(I), (<i>Oreochromis niloticus</i>)