

Mikalsen SO, Tausen M, í Kongsstovu S. Phylogeny of teleost connexins reveals highly inconsistent intra- and interspecies use of nomenclature and misassemblies in recent teleost chromosome assemblies.

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All data in this Supplemental Information have been collected and curated manually. Human errors and inconsistencies cannot be excluded. We would be grateful if detected errors and major inconsistencies are reported to us (sveinom@setur.fo).

Suppl. Fig. 1. Human (*Homo sapiens*) connexins.

The chronology of the sequences are according to the Greek nomenclature. Both the Greek nomenclature and the size nomenclature are indicated, and the GenBank accession number is given for each entry.

Yellow: Conserved domains as defined by Cruciani and Mikalsen (2007)

Green: Conserved cysteine codons (cysteine signature)

Grey: 15 nt added at the ends of the conserved domains

Turquoise: Splice site.

Other colors are explained where necessary.

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Suppl. Fig. 2. Mouse (*Mus musculus*) connexins.

The chronology of the sequences are according to the Greek nomenclature. Both the Greek nomenclature and the size nomenclature are indicated, and the GenBank accession number is given for each entry.

Yellow: Conserved domains as defined by Cruciani and Mikalsen (2007)

Green: Conserved cysteine codons (cysteine signature)

Grey: 15 nt added at the ends of the conserved domains

Turquoise: Splice site.

Other colors are explained where necessary.

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Suppl. Fig. 3. Opossum (*Monodelphis domestica*) connexins.

Yellow: Conserved domains as defined by Cruciani and Mikalsen (2007)

Green: Conserved cysteine codons (cysteine signature)

Grey: 15 nt added at the ends of the conserved domains

Turquoise: Splice site.

Other colors are explained where necessary.

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Suppl. Fig. 4. *GJC1like* and *GJA9* connexin sequences from other marsupials and platypus

Yellow: Conserved domains as defined by Cruciani and Mikalsen (2007)

Green: Conserved cysteine codons (cysteine signature)

Grey: 15 nt added at the ends of the conserved domains

Turquoise: Splice site.

Other colors are explained where necessary.

>Sh-GJC1like-XM 003761914 *Sarcophilus harrisii*

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Suppl. Fig. 5. Zebrafish (*Danio rerio*) connexins.

Yellow: Conserved domains as defined by Cruciani and Mikalsen (2007)

Green: Conserved cysteine codons (cysteine signature)

Grey: 15 nt added at the ends of the conserved domains

Turquoise: Splice site.

Other colors are explained where necessary.

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 claims it to be a part of the exon. Splice site.

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Suppl. Fig. 6. Japanese pufferfish (*Fugu*; *Takifugu rubripes*) connexins.

Yellow: Conserved domains as defined by Cruciani and Mikalsen (2007)

Green: Conserved cysteine codons (cysteine signature)

Grey: 15 nt added at the ends of the conserved domains

Turquoise: Splice site.

Other colors are explained where necessary.

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This record has been removed from GenBank as a result of genome annotation process (July 2019). This sequence gives a 100% identical hit with gjb1like-XM_029847578, which is an erroneous identification (remark as of Oct 31, 2019). The reason for the erroneous identification could be that "gja3like" and "gjb1like" are closely located in the genome.

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>Fr-gja5like-XM_011603067 Modified. The prediction and/or sequencing/assembly does not seem to be correct in cysteine-encoding signature area of the second extracellular loop. Underlined+italics: 13 nucleotides removed. ■: added nucleotides to keep the open reading frame to follow the general pattern of connexins. without these Ns, the sequence must probably be regarded as a pseudogene. Splice sites.

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or an assembly error.

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>Fr-gjcl-45-XM_003964814 Modified according to prediction in Ensembl (which has omitted other parts of the sequence).

In July 2019 this sequence was made obsolete, and replaced by XM_029836267 (and other transcription variants). There is only one nucleotide difference between our modification of XM_003964814 and the new XM_029836267, marked in purple. As we have used the accession number XM_003964814 in all analyses (which were done before July 2019), for the purpose of this manuscript we keep the obsolete accession number.

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>Fr-gjel-XM_011611785 This prediction is probably erroneous with regard to the first exon. We have replaced this with the more likely first exon, which is separated from exon 2 by a approx 235 nt intron. Red font: Our suggested modification for exon 1. Splice site

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Suppl. Fig. 7. Green spotted pufferfish (*Tetraodon nigroviridis*) connexins.

Green spotted pufferfish, *Tetraodon nigroviridis* (Tn)

Assembly: TETRAODON 8.0, March 2007.

Genebuild: May 2010.

Database version: 98.8

As far as possible, the names of the sequences are taken from the Ensembl predictions. Where there is a prediction (although we might have modified it) without a name, we include NN (no name) as a prescript, use the most common name of the ortholog sequence (usually from zebrafish), and end the name with an abbreviated Ensembl gene prediction number. Where there is no prediction in Ensembl and no predicted (or experimentally found) sequences in GenBank with a name, we include NP (not predicted) as a prescript, and use the most common name of the ortholog sequence (usually from zebrafish).

The Ensembl gene abbreviation is done as follows: ENSNIG00000015676 = G15676.

Yellow: Conserved domains as defined by Cruciani and Mikalsen (2007)

Green: Conserved cysteine codons (cysteine signature)

Grey: 15 nt added at the ends of the conserved domains

Turquoise: Splice site.

Other colors are explained where necessary.

>Tn-NP-gja1 This sequence is predicted by Ensembl as an intron in the gene ENSNIG00000007253 enah. Note that this sequence was included in our previous analyses (Cruciani and Mikalsen, 2007) as Tn13946001.

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>Tn-NN-cx39.9-G08981 Underlined: Sequence not included in Ensembl transcript prediction, but we consider it as a likely part of cds.

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 CGTTTGAAGGCGCCCTGCTGCGAACTTACGTCTTCAACATCATCTTCAAGACCCTGTTT
 GAAGTGGCCTTTATTGTAGCTCAGTACTTCTCTATGGTTTCGAGCTCAAGCCGATGTAC
 ACCTGCACCGCTGGCCTGCCCAACATGGTGAACTCGTACATCTCTCGACCCACTGAG
 AAGACGGTCTTCATCTCTTCATGCTGGCGGTGGCTTGCATCTCTCTGCTGCTCAACCTG
 GTGGAAATGTACCATCTGGGATTACCAAGTGCCACCAGGCGCTTCGGTACAGGCGATCA
 AAGACCAGAAAACAGTCTCCCAAGGCCCTCCACGAGCCCGTCATGCCCTTTGTTCCCAGT
 TACAATACTACACCGGTACCCCTGCAGTGCCGGAGCCGTTTCCGACCGACTCCAAGTAC
 AGCGTGACAGAGCCCGCTTACAGCCCTACAGCAATAAGGTCGTCTACAAGCAG
 AACAGGGACAACATGGCTGTGGAGAGGAAGGGAAAAACCCGAGGACGAGGTCGTGATGGAG
 AGGAAACCCACCTGCCCTGCCTTTGAGGGGTCTGCTGACAGTCAGCGCAGAAACAGTCAG
 TCAAGCAAGCACAGCAAGAGCAGACTGGATGACCTAAAGATCTAA

>Tn-cx39.4-G09223 Underlined: Sequence not included in Ensembl transcript prediction, but we consider likely as a part of cds. Red font: One nucleotide is removed here relative to the genomic sequence. Ensembl predicts a 4 nt long intron here (cgagcgaAGCCaacttt), where upper case letter is the predicted Ensembl intron, and **g** is the nucleotide that we have removed.

ATGTCAGAGAGGTGACTGGTCTTCTGGAGAACCTGCTGGAGGAGGGCCAGGAGTACTCG
 ACAGGCATCGGCCGTGTCTGGCTCACCGTGTCTTCTCTTTTCGATGCTTGTGCTGGGA
 GCATCTGCAGAGTCGGCCTGGGATGACGAGCAAGCCAACTTTGTCTGCACACGAATCAG
 CCTGGCTGCACACGCTGTGTACGACAAAGCCTTCCCATCTCCCACTTCCGCTACTTT
 GTCCTCCAGGTCATATTTGTGTCCACGCCGACCATTCTTCTACTTCGGATACGTCGCTTTG
 AGAGTCAGAAGGATCAAAAAAGACGCAGAGGAAGGTTTGTATAGAGGAAGTGTAAAAAAG
 ACAACAGTCACTCAGAGGAAGCGAGGAAAAGCGGGAGGGCTGAAGAGGAAGCTCCCGAG
 GCACCTCGGCTGAAGGCGAGACTGCTGTGTGCAACGCCCTCAGCATCTTCTTAAAGGTC
 CTCCTGGAGGTTGGCTTCATGTGAGGCTGTATTTTCTCTACAATGGCTTCTACATCGCA
 GCAAAGTTTCGAGTGTACAGGAACCCTTGTCTCACACGGTGGACTGCTTCGTCTCACGG
 CCCACGGAGAAGACCCTTCTCGTGTATACACTCAGGTCGTCTCCGGCGTCTCCCTGCTC
 CTCAACCTGCTGGAGCTGCTCCACCTTCTCCAGCTTGCCATCACTCACCGGCTGGAGAAA
 CATTACCACGGTCTGTATGGAGACTACCTCCCCCGCAGAGCAGGGGACTGCGGAAGCT
 GCACGAATCCAAATGGAGGCTCGCAGTCCGGTAAGACAGGGAGCGACACTCACCTTCCA
 ACCCAGTGTGAGATGGAGGAGTCTGCCAATCCCTGCCAGAGTTTCGGAGAAGCAGGCATA
 GAACCAGGCATGAACCGCTCATCTGGAGAGACTGGGAACAGCCTCCTCCCACTTATGTG
 ACCTGCATCAAAGCCTCGAGGATGATGCATTACCCAGAGCCCATCACAAAAAACACACA
 GTCCACACCTCCAAAAACACCAAGGCCGCTCAGAAGGGACATTCCAAACTCAGGCATTAC
 GTCTGA

>Tn-GJA5-G02166 Underlined: Sequence not included in Ensembl transcript prediction, but we consider it as a likely part of cds.

ATGGGTGACTGGAGCTTCTGGGGAACCTTCTAGAAAGAGTCCAGGAACACTCCACCTCG
 GTCGGGAAGGTCTGGCTCACCCTCTTCATCTTCCGATCCTGGTGTGGGCACGGCC
 GCCGAGTCGTCTGGGGCGACGAGCAGAGCGACTTCTCTGACACCCAGCAGCCCGGT
 TGCACCAACGCTGTGTACGACAGCGCCTTCCCCATCGCCACATCCGCTACTGGGTGCTG
 CAGATCGTCTTCGTCTCCACGCCCTCCCTCATCTACATGGGTACAGCCATGCACACCGTG
 CGCCGGGAGGAGAAACAGCGCGGAGGAGCAGGAGGAGGGAGGCGAGGGGGAGCGC
 GGAGACAGCTTGGAGGAGAAGGAGTTCTCCAGCAGAAGGAGAGCGAAAAGGCTCCGGCG
 TCCGAAGGGAGCAGCCGCTGCGCCTGAGAGGAGCCCTGCTGCAGACCACATACTCAGC
 ATCCTGATCCGCACGGTGATGGAGGTGACCTTCATTGTGTGTCAGTACCTGATGTACGGG
 GTCTTCTCAACGCCCTGTACCTGTGCAAGGCCTGGCCCTGTCACCAACCTGTCAACTCG
 TACATGTCCAGGCCACGGAGAAGAAGCTTTCATCGTCTTCATGCTGGTGTGGCCGGC
 GTGTCCCTGCTGCTCTCGTGTGGAGCTTACCACCTCGGCTGGAAGAGCCTCAAAAGG
 TGTCTGCGCCAAAAGCTGATGGAAAAGAGCAGCCGAGGACTGTGGCGGTGGCGGTGTGCG
 GCGGCCCTGGAGCCCAACAGTCCGCTCAGCCTTCTGTTTCTGACGCGCGCCCCAGAT
 TTCAGCCAGTGGCTGGCAGTCTCAGGTTCCATCAACGCCATCGCCTCCATGGCCTCCAC
 CCCTTACGCAACAGGATGGCGCTGCAGCAGAACTCGGCCAACTTGGCCACCGAGCGGCAT
 CACAGCTCCGACAACCTGGAGGACGAGGCGGACTTCTGAGGATCCGATACGACCAGCTG
 CCCTCGGAGCTGCCCCGAGCTGCTGCGCGTGCCCCCTCTGCACTGTGGCTTCATCAGG
 GACAAACGGCGCCTGAGCAAGACCAGCGGAGCAGCAGCAGACCTCGCCACGATGACCTT
 GCAGTGTAA

>Tn-NN-gja5-G09857 Underlined: Sequence not included in Ensembl transcript prediction, but we consider it as a likely part of cds.

ATGGCAGACTGGAGCCTACTGGGAACTTCTGGAGGAGGTGCAGGAGCACTCCACCTCT
 GTTGGAAAGGTGTGGCTGACCATCCTGTTATCTTCCGTATCCTCGTGTGGGACCGCC
 GCCGAGTCATCCTGGGGAGACGAGCAAGAAGATTTCAACTGTGACACCGAACAGCCAGGC

TGC GAGAACGTTTGT TACGACCGAGCCTTCCCAATAGCGCATATACGATACTGGGTGCTG
CAGATTGTGTTTGTGTCCACGCCAGCCTGATCTACATGGGCCACGCCATGCACAGGGTT
CGCAGGGAGGAGAAGAGGAGGAACAGGGAGGAGGAAGGTGGGGAGGGGAGAGGTGGAGAG
GAGGACCCAGGAGGAGGAGGAAGAGGAGGAGATGACGGCAGAGAAGAAGATAAGAAAGGA
GGGAAAGAAAGTGGCGGACCAAGGAGAGAAGGAGAGCGGAGGTCTGTGTGCGCTTGAGGGGA
GCGCTGCTGCAGACC TATGTACTGAGTATACTGATACGAAGCATCATGGAGGTGGTGT
CTCAGTCTCCAGTATTTCTGTACGGGATCTTCTCACTCCCCTGTATGTC TGC GAGGCC
TGGCCG TGT CCACATCCGGTGAAC TGT TATGTCTCCAGGCCAACAGAGAAAAACGTGTTT
ATTGTGTTTCATGCTGGCTGTTTCTGCCGTCTCTCTGGTTCTCAGCGTGCTCGAGCTGCAA
CACCTGGCCTGGAGGCACTGCTGCAGGAAGGCGGTAGCTGCTAATGAGGCCTCTCTGGGC
CGACAGCTCTCCTTGTCTCCTCCACCACCATCAACCCACCTCCAGACTTCAGCCAGTGC
ATGATGGGCTCGACACACTTCTACCTCTGGCTTTCCCCAGCCACCACCTGGTGCACCAA
CAGAACTCCGAGAACATGGCCACCGAGAAGCACAAAATCGCCGCCGCGCTCGAAGAGGCC
ACCCTCCTCCAGATGGGCTGCTACTCGCACGGATGGCAAAGAGCAATCCAGCCAGATC
CAGGAGGACGCCTACCTCAGGAAGGACAATAACTGCTACGGGCCCGGAGGCAGGAAGATG
AGCTGTCCGAGATTGAGAATGGGGGCTCCGACAGGCTGCTGCTTTGCCCCGGCGGGGCT
CTCAGTCAGAAGGACAAGCGGAGGTTTACGAAAACCAGCGGCACCAGCAGCCGAACAAGA
GCGGACGACCTGTTCGGTTTAA

>Tn-gja8a-G13937 Underlined: Sequence not included in Ensembl transcript prediction, but we consider it as a likely part of cds.

ATGGGTGACTGGAGCTTCTGGGTAATATTTTAGAGGAAGTGAACGAGCACTCTACGGTG
ATCGGCCGGGTGTGGCTCACGGTCTCTTCATCTTCCGCATCCTCATCTGGGCACGGCG
GCAGAGTTTGTGTGGGGGACGAACAGTCAGACTATGTC TGC AACACGCAGCAGCCTGGC
TGT GAGAATGTGTGC TATGATGAGGCCTTCCCCTATCTCCACATCCGCTGTGGGTGCTG
CAGATCATCTTTGTGTCCACGCCGTCTCTGGTGTACGTGGGTACGCTGTGCAC CACGTC
CACATGGAG GAGAAGCGCAAGGAGCGGGAGGAGGCAGAGCTCAGCCGGCAGCAGGAGCTG
AGCGAGGAGCGCCTCCCTTGGCCCCCGACCAGGGTAGCGTCCGCACCACCAAGGAGACC
AGCACCAGGGGAGCAAGAAGTTCGGCTGGAGGGC ACCCTGCTGAGGACC TACATCTGC
CACATCATCTTCAAGACGCTGTTTGAAGTGGGCTTCGTGGTGGGCCAGTACTTCTGTAC
GGCTTTTCGCAATTCTGCCGCTGTACAAA TGC AGCCGCTGGCCC TGC CCAACACGGTGGAC
TGC TCGTGTCCCGACCCACCGAGAAGACCGTCTTCATCATCTTCATGCTGGCTGTGGCC
TGCGTCTCTCTCTTCTCAACTTTGTGGAGATTAGTCACTTGGGCCTG AAGAAGATTTCG
TTTGTCTTTTCGCAAGCCGCTGCCGGCCCCGGCCAGGGCGAGGGCTCGGCCCGCTCCCG
GCCCCGGGCAAGAGTCTGCCCTCCCTCGCCGTGCCCTCCATGCAGAGAGTGAAGGGGTAC
AGGCTGCTGGAGGAGGAGAAAGCTCCCCCAATAACTCACCTCTACCCACTGGCCGAGGTG
GGCATGGAGGCCGGCAGAGGGAGCCCCCTTCCAGGGACTAGAGGAGAAGCCGGAGGAG
GTGCTGCCCATGGAGGACATCTCCAAGGTGTACGACGAGACTCTGCCCTCTACACCCAG
ACCACCGAGACTGGGGGGGTGACACTACACGAGGAGGAAGAGGTAGAGGTAGAGGAGGAG
CAGCCAGCCGAAGCAGAGAAGGAGGAGGTGGTTGTGAGGGAGGAGGCAGAGGAGGTGGTG
AATGTGAGGGGGCCAGAGCCGCGGAGGCCCCGATACGATAGAAGACACCCGACCGCTG
AGCCGACTGAGCAAAGCCAGCAGAGGCCAGGTGAGATGATCTGACGGTATGA

>Tn-GJA9-G06130 As predicted by Ensembl

ATGGGAGACTGGAACCTCCTCGGAGGGATTTTGGAGGAGGTGCACATTCACTCCACCATG
GTGGGGAAGATCTGGCTACCATTTCTGTTTATTTTCCGCATGCTAGTCTCGGCGTGGCG
GCGGAGGACGTGTGGAAACGACGAGCAGGCTGACTTCATC TGC AACACCGAGCAGCCGGGA
TGC AGGAACGTGTGC TACGACCGGGCTTTTCCATCTCCCTCATTTCGCTACTGGGTGCTG
CAGGTTATTTTCGTGTCTCTCCCTCGCTGGTTTACATGGGCCACGCTCTGTAC AGACTG
CGGGCCCTG GAGAAAGCGCGGCAGAGGAAGAGAGCGCTGCTCCGGAAGGAGCTGGAGATG
GTGGGCGTGGATTTGGCCGAAGCTAGGAAGAGGATGGAGTGTGAGGTGAAGCAGCTGGAC
CAGGCCAGGCTGAACAAAGCCCCGCTCAGGGGATCCCTGTTACGCACG TACGTGGCCAC
GTTCTCACTCGCTCCGTTGTGCAAGTGGCCTTCATGACGGGCCAGTACCTTCTTTACGGA
TTTCACTCTACCCGCTTTTCAAG TGC GAGCGGGATCCT TGT CTAATGCCGTGGAC TGT
TATGTCTCCAGGCCACAGAGAAAAGCCTTTTCATGGTCTTCATGCAATGCATCGCCGCC
ATTTCCCTCTCTCTGAACATTTTGGAGATCGTGCATCTGGGTAC AAGAAGATTAAACGG
AGCATCTTGGATCTTTGCCGTTACGGGATGAACTGGAGGAGACTTTGCTGTTAAGGAC
AAAAGAGAATCTGTGCACAGTTGTGCACCGCTGCGGCCCGGAAGATGACCATTAACGTTT
TCACCGCGGATGACAACGTGCTGCAGGGAACGGGGCGTCCAAACAATATCGCGCCAACG
GTTCTTCTCTTCTGAGCGAGGCGTCCACTCAACTGGATCTGGAGGAATCCAGATGTGCG
TCCCAGCGTCCAAAAGACTGCAGCTGCGTGTGACCGCGCGGCTGGTGAAGCGCCGCTCG
CCCTCCGTCGTTTCTCCAGAGCGGGAAAGCAGAGCAGCGGAAGTGGCAGCCCGGATTGT
CCAAGACGCCACCAAGCCGGCACACGGATCCACCTTCCCCGCGCTGCCGGCGAACGCC
CCCAGGAGGCTTGGAGGCTCGTTTCTTCAATGCGCCACAGTCTTGGAGGGGAAAAGC
TCTGACACCGACTCACGCGAGAGCGCCAGGGAGAGCAGCGAACCGCAGGGAAAACCTGGC
GCCTGCCGCCACAGCCTCAGCTCTGCGGCAGAGTACCCGACGACTCCAGCGCGGGGTCC
GTGCACAGCCCCAGGCTGCCTTCTTCTGCTGCAAAACATCAATAACAAGCAAAACCAGC
AGCGGTGCGGCTCCAGATCTGCAAAATTTAA

>Tn-cx52.9-G05726 Underlined: Predicted as intron in Ensembl transcript. If this intron is used, the 3'-tail is extended.

ATGGGAGACTGGAATTCCTTGGAGGAATCTTGGAGGAGTCCACATTCACCTCCACCATG
GTGGGCAAGATCTGGCTGACCATCCTGTTTCATCTTCCGGATGCTGGTGTGGGGGTCGCC
GCAGAGGACGTGTGGAATGACGAGCAGTCCGATTTTCATCTGCAACACGGAGCAGCCCGGC
TGTTCGCAACGTGTGTACGACACAGGCCTTCCCCATCTCCCTCATCCGATACTGGGTGCTC
CAGGTGATTTTTGTGTCTCCCTTCTTTGGTCTACATGGGTACGCCATTTATCAGCTA
CGAGCTCTGGAGAAGGAGCGCCACTGCAAGAAGGTGGCGTTGCGCCGGGAGATGGAAGCG
GTGGATGCGGAACCTGGTGGAGGCGAGGAAGAGAATCGAGAAAGAGATGAGGCAGCTGGAG
CAGGGCAAACCTCAACAAAGCCCCCTGAGGGGCTCCCTGCTGTGTACTTACGTGGCCAC
ATCGTAACTCGCTCGGTGGTGGAGGTCAGCTTCATGATGGGTGAGTACATCCTGTACGGA
CACCCTCTGAAACCTCTTTACAAGTGGGAGAGAGCCGTCCCGAACGTGGTGGACGCG
TTCGTGTCCAGACCCACGGAGAAGACGGTTTTTCATGATGTTTCATGCAAGCCATTGCTTGC
ATCTCCCTCTTCTCAGTCTCCTTGAGATTATCCACCTGGGATTTAAGAAGGGTGAAGAA
GGGCATCTTGGACTTTTACCCGCATCTGAAAGAGGACCCGGATGA

>Tn-cx52.6-G03863 Underlined: Not included in Ensembl prediction

ATGGGGGACTGGAATTTATTAGGAAGCATTTTAGAAGAAGTCCACATTCATTTCGACCATC
GTGGGAAAAATCTGGCTGACCATTTCTTTCATTTTCCGAATGCTTGTCTTGGCGTTGCG
GCTGAGGACGTCTGGGACGACGAGCAAAGCGAATTTGTTTGCATACGGAGCAGCCCGGG
TGCAAAAACGTGTGTACGACACAGGCCTTCCCCGTCTCCCTGATCCGTTACTGGGTCTTG
CAAATCATCTTCTGTCTCTCCCGTCACTAGTCTACATGGGACATGCGCTGTATCGCCTG
AGGACTCTGAGAAAGAGAGACACAAGAGGAAAGCCTGCCTGAAGGCTGAGCTGGAGGGC
ACAGACCCTGTCCAGGAGGACACAGGAGGATTGAGCGAGAATCAGAAAGCTAGATGAA
CAGAAGAGGGTGAGGAAAGCTCCTCTAAGGGGCTCCTTGTCTGCGCACAACGTCCTCCAT
ATCTTAACCAGATCTGTTGTGGAGGTGGCTTTTATTATAGGACAATGTGCTCTGTACGGG
CTCGGGTGTGCGCCCTGTACCGATGTTACAGACCGCCAACGCAACACCGTCGACGCG
TTTGTCTCTCGGCCTACAGAGAAGAATGTTTTTCATGGTTTTTCATGCTGGTTATCGCTGGC
GTTTCGTTGGCGCTCAACATTTCTGGAGATCTTGCATCTGGGTGTGAAAAGGATTAAACAA
AGTTTGTATGGATATAAATACAGAGACGACGAGAGCGTGTGTCTGCTCCAGAAAAACTCC
ACCGTGCAGCAAGTTTGCCTTCTTGTAGTTCTTCCCCTCAGAGGCTGGTGCAGCTGACC
CAAGTCACTTGTCTCCGCTCTGCCCAACACTAATGCGACGAGTCTGTCCCATCAGAACCAG
GAAGGTCGCGAAACGCCAACAGCATCCCTCACACGCGTGCCTGCCATCCAGGGTGTG
CAGCAGTGGCACCGCGCGAGCAGCATCGCCTTTTCGGGACTGAGGAAGCCGTCGTGCAGC
AGCGAGGAATCCAGCGAGCCTCACGTGAAGCCCCAGTACGCCGGCCCTCGAGCCACGCTC
GTGGCCAGCCACATGGAGATCCCGCGGCCCTAAAGAACCAGCAGGAAGCAGAGCAGA
GTCACGATTTATAAAGAGCTCAGTGACATGAGCGACTCTGCCGAGAGCGAGCCCCACCTC
CCAGCCCGCAAATGTAGCTTTATGTCTCGGGGCTGTGCGACGGAAGCTGTCCAACCCA
TCCGACAGCGCCGACAGCCGAGCGGAACAGACTCGGAAGCCAGCACCTCAACCAATCA
GAGAGCTCAGTGGTGACCCACCGCTCCAGCCAGTGGCAGAAGGATGTCCATGGTTAGT
GGGCCGGGTTTCAATTTTCCACCACAAAACCTAGACACACGTGA

>Tn-cx34.5-G19149 Underlined+italics: Ensembl ENSTNIT00000022585 predicts a 63 nt long insert here. Splice sites.

ATGGGGGAATGGGATTTGCTGGGCGCCTGCTGGATAAAGTGCAGACTCACTCCACGGTT
CTGGGCAAGATTTGGCTACGGTGCTCTTCGTCTTCCGCATCCTGGTGTGCAGACGGCT
GCCGACAAAGGTGTGGGGGACGAGCAATCGGACTTCATCTGCAACACTCAGCAGCCAGGC
TGCGAGAACGTGTGTACGACCTGGCTTTCCCCATCTCCACGTCCGCTTCTGGTTTCCTT
CAGATCATTTGCCATAGCGACGCCAAAGCTGCTCTACCTCGGCCACGTCTTCAACGCTGT
GTGTTTCTCAGGAGCTACAAAGTTCCCAAGTACGTCAAAGGCTCGGGCAAGATCAGCATC
CGCGGGCGCCTCCTCCGAGTTACACCTTCCACCTGATGGCCATGATCATCCTGGAAGGC
GCCTTCATCGCCAGCCAGTACCTCCTCTTTGGCTTCGCTCTGGAGACGCGCTACGTGTGT
GAGCGCCACCCCTGCCCCACAAGGTGGACTGCTTCCCTGTCCAGGCCACGGAGAAGTCG
GTCATCATCTGGTTTATGCTGGTGGCGGCGGTGCTCTCCCTGGCCCTCAGCCTGGCCGAG
CTCTTCTACCTGGGCTCAAGGCCACAGGGAGTGCATGGCCAGGAGGCAGGACTACACG
GTGACGCGCGTACGCGCGCCGCTTTTCGGGGAGAAAAGCCTTCAAATCTCCGATGAGATG
ATCCGAACTGCATCAACCTGGAGCTGGAGCAGCTTAAAGAAAAGAAGGTCCGGAGGGTC
GCCGGGGGGCCGAGGAGGTGCCAGTGTGCCCCGCCCGGCAACAGGAACAAGGGAGAG
GTCCACATCTGA

>Tn-cx32.3-G19150 No modifications. This sequence corresponds to the predicted transcript ENSTNIT00000002345.

ATGGGAGACTGGGGATTTCTGTCTCTTGGTGGACAAAGTCCAGTCCCACTCCACCATC
ATCGGGAAGATCTGGATGAGCGTCTCTTCTCTGTTTCAGGATCATGGTCTTGGGCGCCGGC
GCCGAGAGCGTCTGGGGCGACGAGCAGTCCGGGTTTCATCTGCAACACTCAGCAGCCCGGT
TGCGAGAACGTGTGTACGACTGGACCTTCCCCATTTCCACATCCGCTTCTGGGTCTCTC
CAGATCATCTTCTGTCTCACGCCGACGCTGGTGTACCTGGGCCACGCCATGCATGTCATC

CACCAGGAGAATAAGCTGAGGGAGAAGCTGCAGAGCCCCGGCGGGAGCCGCTTGCTCAAG
 GTGCCCAAGTACACCGACGAGAAGGGGAAGGTGAAGATCAAGGGGAACCTGCTGGGGAGC
 TACCTGACCCAGCTGGTCTTCAAGATCCTCATCGAGGCGGCCTTCATCGTGGGGCCAGTAC
 TACCTGTATGGCTTCATCATGGTGCCGATGTTCCCTTGGTCCAAGAAGCCCTGGTCCCTTC
 ACCGTGGAGTGGCTACATGTCCCGCCCCACCGAGAAGACCATCTTCATCATCTTCATGCTG
 GTGGTGGCCTGGCTCTCGCTGCTCCTCAACGTCATCGAGATGCTCTACCTCCTGTGCACC
 AGGCTCAAAATGCGCCTCCAGATCGCGGACGAGAAGCTGACGTGGGCCAGAGCCCCGCC
 GGCTGTGGCCCCGAAATGGCCGACGGCGGAGGACGCGCTCCATCAGAACCGGATCAAC
 CTGGAGCAGGAGCGTGCCAGAGCGTCGGCGGGAGCCTGGACGGCGCCAAGGAGGAGATG
 AAGCTTCTGCATCACAACCTGA

>Tn-NN-gjb1-G08980 Note that our sequence is only a minor part (the 3'-end) of the predicted Ensembl transcript

ATGAAGTGGGGAACCTTTTACGCCCTCATCAGCGGCGTGAACAGGCACTCAACGGGCATC
 GGAAGGTTTGGCTCTCCGTCATCTTCTGCTTCCGAATCCTGGTGTGGTGGTGGCTGCC
 GAGAGCGTCTGGGGCGATGAGAAGTCGGGCTTCACCAGCAACACCCAGCAGCCCGGCAGC
 AACAGTGTCTGGCTACGACCACTTCTTCCCATCTCGCACATCCGCTGTGGGCTCTGCAG
 CTGATCTTGGTCTCCACCCCGGCCCTGCTGGTGGCCATGCACGTAGCCACAGACGCCAC
 ATCGACAAGAAGATCCTGAAGAGGGCGGCCGCTGGCACACCCAAAGACCTGGAGCAGATA
 AAGAACCAGAGGTTCCAGATCACTGGAGCTCTGTGGTGGACGTACATGATCAGCATCATC
 TTCAGGATCGTCTTTGAGGTGGCTTTCTCTACATCTTCTACCTGATTTATCCAGGTTTC
 AAAATGGTGGTCTGGTCAAGTGTGACTCTTACCCTTGGCCCCAACACCGTGGATGGT
 GTGTCCAGACCCACTGAGAAAACCATATTTACAGTGTTCATGCTGGGGGTCTCGGGGGTG
 TGGCTGCTTCTGAACCTGGCGGAGGTGGTCTACCTCATCGGCAGGCCTGCAGACAGTGC
 ATCCGAGGCTCTGAAGAAACCTCCAAAGTCCCCTGGATCAGTCAAAAATGTCTCTTAC
 AGGCAAAATGAGATCAACGAACGTACTGGACCATCCCTCAGGTCAAAGTTCAGTGTG
 ACCAAAAAGAAGCCAGCTGA

>Tn-cx27.5-G11825 Note that the predicted Ensembl transcript extends another 42 nucleotides on the 5'-end

ATGAAGTGGGCATCGTTCTACGCCCTGCTCAGCGGCGTGAACAGACACTCCACGGGCATC
 GGCCGCATCTGGCTCTCCGTCATCTTCTGCTTCCGCATCCTGGTCTGGTGGTGGTGGCTGCA
 GAGAGCGTGTGGGGAGACGAGAAGTCGGGCTTCACCAGCAACACCCAGCAGCCCGGCAGC
 AACAGCGTCTGGCTACGATCACTTCTTCCCATCTCCACATCCGCTCTGGGCTCTCCAG
 CTCATCTTGGTCTCCACTCCGGGCCCTGCTGGTGGCCATGCACGTGGCTCAACCGCCGCCAC
 ATCGACAAGAGGCTCTACAAGCTGTGAGGGCGCACCAATCCCAAAGACCTGGAGCAGATT
 AAGACCCAGAAAATGAAAATCACAGGCGCACTCTGGTGGACATACGTATCAGCCTGCTT
 TTCCGCGTTATCTTTGAGGTGACCTTTATGTACCTGTTCTACATGATCTATCCTGGTTAC
 AAGATGATCCGGCTGGTGAAGTGTGACTCGTACCCCTGGTCCCCAACACGGTGGACGGT
 GTCTCCAGGCCCCACAGAGAAGACTGTTTTACCGTCTTCATGCTGGCTGTGTCAGGGGTT
 TGTATTTTGGTCAACATTCGCGGAGGTGGTCTTCTTGGTGGGGAGGCCTGCGGTAGGCAT
 TTACAGCACGCTGGAGACTCCGCTGTGGGAACCTGGATCCAGCAAAAACCTCTGCTTCCTT
 TAG

>Tn-NN-cx28.9-G19153 **Splice site.** Two 100% identical predictions are located approx. 10000 nt apart (G19153 and G19151).

ATGGGAGAGTGGGGTTTTCTGTCTCTCTGCTGGACAAGGTCCAGTCTCATTCCTCCGTC
 ATCGGAAGGTCTGGCTCAGCGTGCTCTTCATCTTCAGGATCATGGTCTGGGAGCTGGA
 GCTGATAAGGTTTGGGGCGACGAGCAGTCCAATATGATTGGTAACACCAAGCAGCCCGGC
 TGTAAAAACGCTGGCTACGACACCGCTTCCCCATCTCGCACATTGCTTTCTGGGTCTC
 CAGATCATCTTCGTCTCCACGCCACGCTGGTCTACCTGGGACACGTCTCTGCACGTCATC
 CACAAGGAAACAAGATGAGAGAGTACATGAAGACGCACACTCAGAGCAACCTGGCCAAA
 TACCCCAAGTACACCGACGAGAAGGCCACGTGGAGATCCGGGGCAACCTCCTGGGCACC
 TACATGACCTCCATCGTTTTCCGCATCTTCTGGAGATCGCCTTCATCGTGGGGCCAGTAC
 TACCTGTACGGCTTCATCATGGACCCCAAAGTGGTCTGGTCCCCGGGCCCTGGCCCTTC
 ACCGTCGAGTGGCTACATGTCTCGTCCACCGAGAAGACCATCTTCATCTCTTCATGCTC
 GCGGTCTCTTGGCGCTCGCTGCTTAACGTGGTGGAGATCTGCTACTTGGTGTGCTCC
 CGCTCGAAGAAAAGAGCCAAGACGCCCGCGCTCCGCGCTGCTCATTACCCACGGTTC
 ACCAGCGAAAGCAAAGCCTGA

>Tn-NP-cx30.3 Note that this sequence was included in our previous analyses (Cruciani and Mikalsen, 2007) as Tn29165001.

ATGCTTGGGGCGCACTTATTAGTAAGCTGGGTGGTGTCCACGAATACTCCACGACCTG
 GGAAGGTCTGGCTTTCTGTCTCTTCTCCTCTCCGCATCGGTATTCTGGTGTGGCCACC
 GAGAAAGTCTGGGGAGACGAACAGTCCAGCTTTACGAGCAACACAGCAGCCCGGCAGC
 AAAAACGCTGGCTACGATCACTTCTTCCCGGTTTACACATCCGCTTGTGGTGGCTGCAG
 CTGATCTTTGTGTGACCCCGGCCCTTCTGGTGACCATGTACGTGGCTTACAGAAAACAT
 AAAGATGAGAAAAATTGTTTAGACTCCAAGGACAGTGAGACGGGGAAGGAGGAAGAGACG

GGAAAAAAGGTTAAAAAAGAGGAACAAAAAAGCGTCTGCCCATCACAGGTCCTATGTGG
 TGGATCTACACCAGCAGCTTGTCTCTCAGACTGCTCTTTGAGGGGGGCTTCATGTACGCT
 CTGTACTTCATCTATGATGGCTTCCAGATGCCACGTCTGCTCAAGTGTGAGCAGTGGCCT
 TGC CCCAACAAAGGTGGACTTGC TTCGTCTCCAGGCCGACGGAGAAAAACGGTCTTCACCATC
 TTCATGGTGGCTCGTCCGTCAATTTGTATGGTTCTTAATTTTGCCGAACATCATCTACCTA
 ATTGGCAAGGCCCTCTTTAAGAGAAGTAGTGGGGGGAAAAAATGCACATATAGAATTAAAC
 TCCAACCAGAATACCATGCTTTTGGAGAAAAATTAA

>Tn-cx30.3-G01258 Underlined: Sequence not included in Ensembl transcript prediction, but we consider likely as a part of cds.

ATGTCTTGGGCCGAACTTTATAAGCGGCTGGGCGGCGTCAACAAACACTCCACCAGCCTG
 GGGAAAGTCTGGCTTTCTGTCTCTTCATCTTCCGCGTCTCTATTCTGGTTCTGGCCGCC
 GAGAAAGTCTGGGGAGACGAACAGTCCGACTTTACGTGC AACACACAGCAGCCGGGC TGC
 AAAAACGTC TGC TACGATCACTTCTTCCCGGTTTACACATCCGCTTGTGGTGCCTGCAG
 CTGATCTTTGTGTGCGACCCCGGCCCTTCTGGTGACCATGTACGTGGCCTACAGAAAACAA
 ACAGATTGGAAAAAAGGTTTAGCCTCCAAGGACAGTGAGACGGGGGAAGGAGGAAAAAGTG
 GAGAAGGGCGGTGAGAAGAATGAGGAGGAAATACTCATATTGCTTGAAGAGGGGGAAAGT
 AATTTCAGTCCCCGAGAACAGTAAGAAAAGTGAAGGAGGAAAAATACGACAGAGTTAAAGAAT
 GATAAGGACAATGAGAAGAAAAAGGGGAAAAAAGAGGAACAAAAAATGAGCGTCTACCC
 ATCACAGGCCCTCTGTGGTGGATCTACACCAGCAGCTTGTCTTCAGACTGCTCTTTGAG
 GGGGGCTTCATGTACGCTCTGTACTTCATCTATGATGGCTTCCAGATGCCACGTCTGGTC
 AAGTGTGAGCAGTGGCCTTGC CCCAACAAAGGTGGACTGC TTCGTCTCCAGGCCAACGGAG
 AAAACGGTCTTCACCATCTTCATGGTGGCCTCGTCCGTCATTTGTGTGGTTCTTATTTTT
 GCCGAACCTTTTTTACCTATTGAC AAGGCCCTCTTTAAGAGAAGTACCATAGAATTAAAC
 TCCAACCAGAATACCATGCTTTTGGAGAAAAATAAAAAATAAAGTTCTGTAA

>Tn-cx30.3-G15674 Underlined: Sequence not included in Ensembl transcript prediction, but we consider likely as a part of cds. N: Nucleotide added to keep reading frame.

ATGTCTTGGGCCACACTTTACAGTCAGCTGGGCGGCGTCAACAAACACTCCACCAGNCTG
 GGGAAAGTCTGGCTGTCTGTCTCTTCATCTTCCGCGTCACTATTCTGGTTCTGGCCGCC
 GAGAAAGTCTGGGGAGATGAACAGTCCGACTTTACGTGC AACACACAGCAGCCGGGC TGC
 AAAAACGTC TGC TACGATCACTTCTTCCCGGTTTACACATCCGCTTGTGGTGCCTGCAG
 CTGATCTTGGTGTGCGACCCCGGCCCTTCTGGTGGCCATGTACGTGGCCTACAGAAAACGT
 GGAGATAAGAGAACTGTCTGGCCTCCGCGGGGATGAGAAGGTGAAGGAGGCAGACCTG
 CAGACCTGAAGACGAAGCGTCTGCACATCACAGGCCCTCTGTGGTGGACC TACACCAGC
 AGCTTGTCTTCAGACTGCTCTTTGAGGGGGGCTTCATGTACGCTCTGTACTTCATCTAT
 GATGGCTTCAGAGATGCCACGTCTGGTCAAGTGTGAGCAGTGGCCTTGC CCCAACAAAGGTG
 GAC TGC TTCATCTCCAGGCCGACGGAGAAAACGGTCTTCACCATCTTCATGGCGGCCCTCG
 TCCGCCCTTTGTATGGTTCTTAATATTGCTGAACCTCGTCTACCTGATTGTC AAGGCTCTC
 GTGCGGTATATCAGCCAGGTCCAAGCAGCGGAAACAGAGATACGCTCGGGAGAACTTCCAC
 CGGGATCACATGCTTCTGAGAACAAAGAAGAATGAGAACATGTTTCTCAGACCCAACA
 AGCAACAGAACCATGTGTTGA

>Tn-NN-cx30.3-G10340 Underlined: Sequence not included in Ensembl transcript prediction, but we consider it as a likely part of cds. Splice sites.

ATGTCTTGGGCTGCTCTGTACAGCCAGCTGGCTGGAGTAAACCGCCACTCCACCAGTCTG
 GGGAAAGTCTGGCTCTCTGTCTCTTTATTTTCCGAGTCATGGTTTTGGTTGTGGCTGCT
 GAGAGCGTTTGGGGGGATGAACAGTCCGACTTCACCTGT AACACCCTACAGCCTGGC TGT
 GAGAACGTC TGC TACGATCAGTTCTTCCCTGTCTCCACATCCGGCTCTGGTGTCTTCAG
 CTTGTCTTTGTTTTCCACCCAGCGCTCCTGGTGGCGATGTACGTGGCCTACCGGAACCAC
 GGCGATAAGAAGAAGCTCTACAGAAATTCTGGAAGAGTTGGGATCTTGAGCACGGAAGGT
 CCAGAGGAGCAGCTGGAGAGCCTCAGGAGCAGGAGGCTGCCATATCTGGCGCTCTCTGG
 TGGACGTACGCCTTCAGCCTTCTGTTCAGGCTCCTGTTTGAAGGAGGTTTCA TGTACGCC
 CTCTACGTGATTTACGACGGTTTCCGGATGCCACGCTTGGTGC GG TGC GACCAGTGGCCG
 TGC CCCAACCTAGTGGACTGT TTCATCTCACGGCCGACAGAGAAAACAGTCTTCACCGTT
 TTCATGGCCACCTCATCATCTGCATGCTCCTCAACGTGGCAGAGCTCGCATATCTT
 GTTGGCAAGGCTGTGCACAA GCGCACCAGCAGGAGTAAAGAGACGTGAAGAGAGAAAGTGAG
 AGAAGACTGGTGTGTTTGACAGGAGAGCGGTAAGCAGGGTGGAGGCTGCCTGGACTAAT
 GCTGCTGCTGAGGTGGGAGGAGGAATTAGGAGGAGGATCTCATCCTTCCACCTGCTGG
 ATTATGAGCTTCTCTCATGGTGC GTTACGTCCATGTGGGAAAGACTGCAAAACAGGAAAA
 CTGGCATATTTCAGAAATGATTATAGTCAGTATTGTTGTAAAATTGTTGTAA

>Tn-cx35.4-G16899 As predicted by Ensembl.

ATGGACTGGAAGACCTTCCAAGCCCTCCTCAGCGGGGTGAACAAGTACTCCACCGCGTTT
 GGGAGGGTCTGGCTGTGGTGGTGTTCGTGTTTACGGGTGATGGTGTACGTGGTGGCGGCG
 GAACGCGTGTGGGGCGATGAGCAGAAAGACTTCGAT TGC AACACCAAGCAGCCGGGC TGC
 GCCAACGTC TGC TACGACTACTTCTTCCCATCTCCACATCCGCTGTGGGCCCTGCAG

CTCATCTTCGTCACCTGCCCGTCCTTCCTGGTGGTCATGCACGTGGCGTACCGGGATGAG
 CGCGAGCGCAAGTACAGGGCCAAGCACGGCGATGAAAGCAAGCTGTACACAACACGGCC
 AAGAAACACGGCGGCCCTGTGGTGGACCTATCTGCTGAGCCTGTTTGTGAAGACGGGCATC
 GAGGTGGCCTTCTCTACATCTCCACCTCGTCTACGACAGCTTCTACCTGCCGAGGCTG
 GTCAAGTGGGAGGTGGCGCCCTGGCCCAACCAGGTGGACTGGCTACATCGGACACCCCACT
 GAGAAGAAGGTCTTCACATACTTCATGGTTGGCGCCTCGGCCCTCTGCATCGTCCTCAAC
 ATTTGCGAGATCATTTATCTCATCTCCAGCGCATTGCGCGGTGCGCCAACAAGCACAGG
 AGGCACCATCGCAATCCGGCCGTACACCTCCAGACGAGAACAACAATGGACGACCCCT
 TTCAGCAACCACAAAGCCATGGAGCCCAAGCCAGGGCTGAAGGAAAGGCCCCCGTCCTTT
 AACACCGCCTCCAAGTTCCTCATATAACATGGACAGCTTCCGGATGGCCGACAAGATCCGA
 GCCTCCGCCCCCAATCTGTCTTCATGA

>Tn-cx28.6-G08925 Grey font: Intron? Underlined: Sequence not included in Ensembl transcript prediction, but we consider likely as a part of cds. **Splice site.**

ACTTTCCAGCGGGCTGGACCAACATAAGCTACGACCACATCTTCCCATCTCCACATC
 CGCCTGTGGGCGCTGCAGCTGATTTTCGTCACCTGCCCGTCGCTGATCGTGATGGCTCAC
 GTCAAAATTCGCGAAGGGAAGAGGCCAAGTACGTGGAGCAGCACCACGGCTCCCACCTC
 TACAGCAACCCCTGGCAAGAAGAGAGGCGGGCTGTGGTGGACCTATCTCCTCAGTCTGATC
 CTCAAAGCCGGATTGATGCTTCTTTTACCTCCTGTACAGAATCTATCACGGTTAT
 GATCTGCCCAATTATCGAAAATGCTCGCTGGAACCGTGTCCCAACACGGTGGACTGCTTC
 ATCAGCCGTCCACGGAGAAAAAGATCTTCATGCTCTTCATGGTCTGCTCCAGCGCTCTT
 TGCATTTTCATGTGCATCTGCGAAATGTTCTATCTCGTCGGAACACGCATCGCCAAACGG
 GTGCAGAGCCACCGCAGAAACAAGCAGATTCTGTTTGTGTGACCAGCAGAACTGACCAAC
 ATGGTTCCACCCAGATCCAGTATCGGGAGACTGACCCACCCCTGACGGGCAGTCAGCTG
 AGCCTGGGCAGAAAGGACAAGGTACAGGAGGAGGCGGTGACAACGACCTGTAA

>Tn-cx30.9-G09221 Underlined: Sequence not included in Ensembl transcript prediction, but we consider likely as a part of cds. **Splice site.**

ATGAAGTGGTCTGCCCTGGAGGCCCTGCTCAGTGGGGTCAACAAGTATTCACCTGTGTTC
 GGACGCGTCTGGCTGTCCATGGTCTTCGCTCTCCGCGTGATGGTGTTCGTGGTGGCGGCT
 CAGAGGTGTGGGGTGACGAGCAAGGACTTTGTCTGCAACACAGCGCAGCCGGGCTGCG
 AACACGCTCTGCTACGACAGCATCTTCCCATCTCACACATCCGCGCTGTGGGCCCTGCAG
 CTCATTTTCGTCACGTGCCCGTCGCTGATGGTGGTGGGGCACGTCAAGTATCGGGAGAAG
 AAAGATTCCAGTACAGACCTCACACCAGGGAAGCATCTGTACGCCAATCCTGGAAAG
 AAGCGCGGAGGGCTGTGGTGGACCTACCTGGTAGTCTGATTTTCAAGGCCAGCTTTGAC
 GCTGGTTTCTGTACATCCTCTACACATCTACGATGGTTACGACATGCCCCGCTGTCC
 AAGTGTTCCTGGAGCCGTGGCCCAACACGGTGGACTGCTTCATATCCCGGCCACCGAG
 AAGAAGATCTTCAACCTCTTCATGGTGGTCTCCTCTGCCATCTGCATCCTGATGTGCATC
 TGTGAGATGATCTACCTCATCTGCAAGCGCATCAGTAACTCATTAAGAGAAGGAACGAG
 GCAGAGAGGAGGCTGTTTGTCTCAGCAGCAGAGATGACGCGCTGGCACCACCGAGGTCA
 GAGCTGAGGTCCAAATCGCCGATCAGGTTGGATCCAACAGCCTCAATCCAAGATCTTGGC
 GCCATCGCTGAGGACAAGCAACCGCCTGAGAAACAACAGGTACACAGCGTAG

>Tn-cx34.4-G16900 Underlined: Sequence not included in Ensembl transcript prediction, but we consider likely as a part of cds.

ATGAAGTGGGATTCCTCCAGGGCCTCCTCAGCGGGGTGAACAAGTACTCCACCGCCTTC
 GGCCGAGTGTGGCTCTCCATCGTCTTCTCTTTCAGGGTCATGGTGTTCGTGGTGGCGGCG
 GAGAAGGTCTGGGGCGACGAGCAGAAGGACTTCAAATGCAACACGGCTCAGCCTGGTGGC
 CACAACGCTCTGCTACGACTACTTCTTCCCGTGTCCACATCCGGCTGTGGGCCCTGCAG
 CTCATCTTCGTCACCTGCCCTCTCTCCTGGTGGTGTGACGCTGGCGTACCGGGAGGAC
 AGGGAAACGGAACACAGGCTAAATTCGCGGAAAACTGCCACCGTATTTACCAGAACAAC
 GGAAGAAGCGCGGAGGCGCTGTGGTGGACCTACGTCCTCACTTTGGTCTTCAAAATCGCC
 GTAGACGCGCTCTTCGTCTACCTTCTCTACACATCTATGAGGGCTACGACTTCCCCTTG
 CTCATCAAGTGGCAGCAGAAGCCCAGCCCAACATAGTGGACTGCTTCATCGCTCGCCCC
 ACCGAGAAGCGCATCTTACCATCTTCATGGTGGTACCAGCCTGGTCTGCATCTTCCTC
 TCCCTCCTGGAGATCTCTACCTGGTGGGCAGCGCTGCCACGAGTGTTCAGGGCCGTT
 CACGACTCCCACCGCATCGTACCCGCCCATCTCCAGCGGAACCAACATGATGGAGTCC
 CGGGTCGAAAAACAGCCCCGAAAGTCTGGCGCCCTTGTACAACCTCTGCCAAAGCGGAC
 AGCCGGACAGCCAGGACTCTGCCAGACTCTGAAGTTACCTGA

>Tn-cx28.8-G19193 Underlined: Sequence extended in 3'-direction until stop codon.

ATGAAGTGGAGCTTTCTGGAGAACATCCTCAGTGGGGTGAACAAATACTCCACAGTCATT
 GGGCGCGTCTGGCTCTTTGTGGTGTTCCTCTTCAGGATCTTGGTGTACGTCTGAGCGGCC
 GAACAAGTGTGGAAGGAAGAGACGAAGGAGTTCTGTGCAACACCCGTACGCCCGGCTGGC
 GAGACCACCTGCTTCAACCACTTCTTCCCTGTTTCGACGGCGCTCTCTGGGCCATGCAA
 CTCATCTGGTGTCTACCCCATCTCTGCTAGTGGCCCTGCATGTGGCATATAGGGAACAC
 CGAGAGGCCAAGCACAAAGAAAAAAGTGTACCAGGACAAGCGACCATGACGGGGGATTG
 CTTTTCACTTACATCGCCAGTCTCATTTTAAAGACGGCGTTCGAGGTGGGCACCCTGCTG

GTGTTTCTACTACGTCTACAACGGTTTTGAGCTTCCGGCGCTGCTCCGCTGCGGACCAGAGT
 CCCGCGCCAAACGTAGTGGACTGTTTTCATCGGCAAAGCCACCGAAAAGAGATTTTCCTC
 TACATCATGGCCTGCACATCTATCCTCTGCATCGTTTTGAATGTCGTTGAGCTTATTTAC
 ATCGTATGGGAAGCAAGTCGTTAAATACGTCATCCAGCATTACAATCCTGTGGAGAAGAGA
 CCTCCCTCTGGCAACCAGACACAAAGTGTCCAACGTCAATGGATATGTCTCTGTTGACCAC
 GTTGGAAATGAAGAAGACAGCCCAAAAGACTAAACCATTAG

>Tn-NN-gjc1-G00149 Underlined: Sequence not included in Ensembl transcript prediction, but we consider likely as a part of cds.

ATGAGCTGGAGTTTCCCTGACTCGCCTGTTGGAAGAAATTCACAACCATTCCACGTTTGTG
 GGCAAGATCTGGCTCACTGCTGGTTGTCTTCCGCATCGTGCTGACGGCGGTTGGCGGC
 GAGTCCATCTACTACGATGAGCAGAGCAAGTTTGTGTGCAACTCGGGCCAGCCGGGC
 GAGAACGTCGCTACGACGCCTTTGCTCCGCTGTCGCATGTCCGCTTTTGGGTGTTCCAG
 ATCATTTCTGGTGGCCACCCCTTCGCTCATGTACCTGGGATATGCCGTCAACAAAATCGCT
 CGCACAGAGGAGCAGTGGGTGGGATGGGAGTGAGGGGATGTTTCGCAGAGGAAGCTCAAG
 AGAAAGCTGTATCTGGCAGACAGAAAGCAGCACAGAGGCATTGAAGAAGCTGAGGATGAC
 CAAGAGGAAGACCCCTATGATCTATGAAATGGCAGAAGTGGGAGCGACTGCAGTGAAGAA
 ACAAAGGCAATGTTGTGTTGGAAGATTAAGGTCAAGGTCCGCCACGATGGACGCCAGCGT
 ATCAAAGAGGATGGTCTGATGCGTATTATGTCTTTCAGCTCCTGGCCCGCTGCTTGCTG
 GAGGTGGCTTTCTTGTGCGGGCAGTACGCCCTGTACGGATTTCGCTGTTCCCCCTACCTAT
 GTCGCTTCTCAGCTGCCCTGCGCCCCACAGCGTGGACGCTTCGCTGTCCCGCCCACTGAG
 AAGACCGTCTTCTCATCATTATGTACATCGTCTCCCTGCTCTGTCTGATGCTCAACATC
 TGGGAGATGCTTACCTGGGCATCGGCACCATCTGCGAGATCATTTCGTTCCCGGCGGGTC
 CCCGAGGAGGAGCTGTACGGCTGACACAAGCGAAAGAGCCCCAGCCAGAGAGGATTAC
 AGCAGCTACCTTTCTCTGGAACGCGCCATCAGCTCCGCTGGGTACAAACATCACAAATC
 AAGCCCCAATGGTGCCGGCAGAACGCCACGATCAACCCCTACCGGTACCGACCTCACC
 AGCGCGAAGATGGCATGCCGACAAAACACGCTAACATCGCGCACGAGGAGCAGCAACAG
 TACAACAATAACGACGAAAACCTTCGCAGAGCCGGGATGGGAGATGACCGCACGCTTCC
 CATCACTCTCAGAACAGACTGGAGATGGACGCGTCAGCCACAGCCAGCCGAGGGCCAA
 AACACAACAAGCCTACCGCGACCGCAAAACACCGCCAGGCCTCCAAACATGCGTCCGGC
 AAGGCTGACGCAGACCGAGCGCAGCAGCACCAGCAACACCAGCAAAATACGGAGTCATC
 AAAGGCTCCGAGTGGATCTGA

>Tn-NN-gjc1-G05345 Underlined: Sequence not included in Ensembl transcript prediction, but we consider likely as a part of cds.

ATGAGCTGGAGCTTCCCTACGCGGCTGCTGGAGGAGATCCACAACCACTCCACCTTCGTG
 GGGAAAGTGTGGCTCACCGTGCTCATCGTCTTCCGCATCGTCTCACCGCCGTGCGGGGA
 GAGTCCATCTACTACGACGAGCAGAGCAAGTTTCGTGTGCAACTCGGGACAGCCGGGC
 GAGAACGTCGCTACGACGCCTTCGCGCCGCTGTCCCACGTCCTGCTTCTGGGTTTTCCAG
 ATTATCTCTGGTGGCCATGCCCTCCCTCATGTACATGGGCTACGCCATCAACAAGATCGCC
 AGGCTGAGGAAGCCAAAGGAGGCGGGGCTCGGCGGCCATCAGGACGGGAGGCGGAGGC
 TACACGCACAGAAAGCCCAGGAAGATCTGTTTCGGAGCGCGGCAGCACCGGGGCATCGAG
 GAGACCGAGGAGGACAGGAGGACGACCCCATGATCTACGAGGTCCCGAGGTGGAGCCC
 CCCAAGAGGCCCGGGGACCCGCTGCAGCCACGCCAGCCAGACCCAAAGTCCGGCACGACGGG
 CGCAAGCGGATCAGAGACGAGGGCCTGATGCGGGTTTACGTGCTGCAGCTGGTGACCCGT
 ACCGTGCTGGAGGCGGGCTTCTCGCCGGCCAGTATCTGCTCTACGGTTTCCGCGTGATG
 CCCGTGTTTCGTGTGCTCGGGGAGACCGTGCCTCCACAGCGTGGACTGCTTCGTGTGCGGC
 CCCACGGAGAAGACCATCTTCTGCGCATCATGTACGGCGTCACCGTCTTTGCTCTGCTC
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 CGGCGCGCCCCCGCCAGGACGATGAGTACCAGCTGGGCTTGTGGGCGCAACGGAGCC
 GTGGAGGGCTCCGTGCGGGGCACGGCCCCGAGGCGGGTTCCGAAGGAGGGGTGGGCGGT
 GACGGGGCCGCGGACTACGTGGGCTACCTTTCTCGTGGAAACACGCCGTCCGGCTCCGCCC
 GGCTACAACATCTGTGGTCAAACCCGAGCAGATGCCCTACACGGACCTGAGCAACGCCAAG
 ATGGCGTGCAAGCAGAACCGGGCCAACATCGCCAGGAGGAGCAGCAGCAGTTTGGTAGC
 AACGAAGACAACCTTCCCCACGGGGGAGAAAGCCGCGTGGCTTTGAACAAAGACATGATC
 CAGCAGGCTCACGAGCAGCTGGAGGCGGCCATCCAGGCCTACAGCCAGCAGCACCAGGCC
 GAGGTGACGTGGGGGACAACAGGACGACAAACCCAAAGCAACATCATCCAGGCGCAG
 CCGCTGCTGCAGCGGCAGCCTCAGAAGGAGCGCAAGCATAGATTCAAGCACGGGAAAGGA
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 CCTCCGTGTGGATTTAG

>Tn-cx47.1-G08482 As predicted by Ensembl

ATGAGCTGGAGCTTCCCTACACGCTCTCTGGAAGAGATCCACAATCATTCCACATTTGTG
 GGGAAAGTGTGGCTGACAGTGCTCATCATCTTCCGCATGTGCTCACGGCAGTCGGAGGC
 GAATCCATCTACTCGGACGAGCAGACGAAGTTTCACTGCAACCAAGCAGCCGGGC
 GATAACGTAAGCTACGATGCCTTCGCCCTCTCTCGCACGTCCGTTTTTGGGTTTTCCAG
 ATCATCATGATCTCCACCCCTTCCGTCATGTACATGGGCTATGCTATTTCATAGATAGCG
 CGGAGTTCGGATGAAGAGCGCAGAAAGCTCCACAGGCTTCGCAAAAGCCCCCACCACAT

TCCAGATGGAGAGAGAACCATCACCTGCAGGGCGTCTTAGAGGAGGACGAAGACGACGAC
GCTGAGCCCATGATCTATGAGGATACGCTAGAGGTTCAAGATGCCAAACCAGGACCAGGG
AACAGCGGTAGCAAAAACCCACCGAAATATGACGGCCGTCGAAAAATTATGCAGGAAGGT
CTAATGAGGATCTATGTCCTTCAGCTGATGTCAAGAGCTGTTTTTGAATTCCTTCCTT
GCTGGACAGTACCTCCCTGTATGGTTTTTCGTGTCAAGTCCATCATATGTAATGCAACAGGATC
CCGTGCAACACAGGGTGGACATGTTTCATCTCAAGACCCACAGAAAAAACTATTTTCCTC
CTGATTATGTACGTGGTGAAGCTGTCTCTGCTCTGCTAAACGTCTGTGAGATGCTTCAC
TTGGGAATCGGTACTTTCCGGGACACCTCCGCCTGAAGAGGAACAGGGGCCGACAGTCA
TCCTACGGCTACGCTTTTCTCGCAATATCCACAGCGTCTCCTCCAGGGTACAACCTTGTG
ATGAAAACAGACAAACCAAGCAGGATTCCTAACAGCCTTATTGCCCATGAGCAGAACGTG
GCCAATGTAGCTCAGGAGCACCAGTGCATCAGCCAGACGAGAACATCCCTCTGACCTT
GCGAGCCTACACGGCACCTAAGAGTTGCTCAAGAACAGCTCGATATGGCTTTTCAGACT
TACCAAAACCAAAACAAACAGCAGACGTCCAGAACCAGTAGTCCAGTGTCTGGAGGCACC
ATGGCAGAACAAAACAGAGTCAATGCAGTTCAAGAGAAGCAGGGCGCAAGGCCAAAATCA
GCCACAGAGAAGGCCACGACCGTGGTAAAAAATGGAAGAGCTCTGTCTGGATTAG

>Tn-NN-cx43.4-G02041 Nearly identical to G02430/G02447. Splice site.

ATGAGCTGGAGTTTTCTGACGCTCTGCTGGACGAGATCTCCAACCACTCCACCTTCGTG
GGGAAGATCTGGCTGACCATTTTGATCATCTTCCGCATCGTGCTGACGGCCGTCGGCGGT
GAGACCATCTACTACGATGAGCAGAGCAAATTTGTTTGCACACGCAGCAGCCCGGATGC
GAGAACGTGTGCTACGACGCCTTCGCCCGCTCTCCACGTACGATTCTGGATCTTCCAG
GTGATCCTGATCACCACCCCCACCATCATGTACCTGGGCTTCGCCATGCACAAAGATCGCA
CGCATGAACGACAGCGAGTACCGCGTCGTCCGGAAGCCAAGAAGAAGATGCCCATAGTG
AACC CGGACCGCGGACTACGAGGAGGCGGAGGACAACGGCGAGGAAGACCCCATGATC
GCCGAGGAGATTGAACAGAGAAGCCTGACAAAGCGGAGAAGGGCCCCGAGAAAAAGCAT
GATGGCCGACGGCGAATCCAGCGTGACGGCCTGATGAAGGTCACGTGTGCCAGCTGCTG
TGGCGCTCTTCCTTCGAGGTGCGCTTCCTCTTTGGCCAGTACGTCTCTACGGCTTCGAA
GTGCACGCGTCTACGTGACACCGCTCGCCGTGCCCCACACGGTGGACTGCTTTCGTG
TCGCGCCCCACAGAGAAGACCATCTTCTGTCTGGTCAATGTATGTGGTGTCTTCTCTGC
CTGTCTCTCACCCTCTTTGAAATGCTCCACTTGGGGATCGGGCGCTCCGCGACACCTTC
CGCAGGGCGTCCGCTCTCAACAGCGGGGCCCTCGTCTGACGGCCCCACGTAGCATCGCC
ACGGCGCCGCGGGGTACACGCTACCATGAAGAAGGAGAAATTGAAAGGACGGCTGAGG
GACTCGCCCATGGGCGACTCCGGGAGGAGAGCTTCGGTGACGAGGGTCCCTCATCCCGG
GAAC TGAGCGGCTGAGGAGGCACCTGAAGCTGGCCAGCAACACCTGGACCAGGCCTAC
CAGGTTGAGGACAGGAGCCCCCTCGCGGAGCAGCAGCCCCGAGGTGAACACGGCCGCGCAG
ACGGCCCGCGGAGCAGAACCGACTCAACTTTGCCCAGGAGAAGCAAGGAGAACCAGCGAG
AAAGGTAAAGAAATGCTCAGGCGCCATCAGATGGAGGTGCGGCGACTATTACAGGTGGTG
GTTTTGGCCAGCAGGACGCGTTTTTCAGAGGCGTCTCTGTCTGCTGTTAG

>Tn-cx43.4-G08887 Underlined: Sequence not included in Ensembl transcript prediction, but we consider likely as a part of cds.

ATGAGTTGGAGCTTCCTCACCCGCCTGTTGGACGAGATCTCCAACCACTCCACCTTCGTG
GGCAAAATCTGGCTCACCTCCTCATCGTCTTCCGCATCGTCCTGACGGCCGTCGGCGGC
GAGTCCATATACTACGATGAACAGAGCAAATTTGTGTGCACACAAACAGCCCGGTGCG
GAGAACGTGTGCTACGACGCGTTTGCGCCGCTGTGCGACATCCGCTTCTGGGTGTTCCAG
GTGATCATGATCACCACGCCCCACCATCATGTACCTCGGCTTTGCCATGCACAAAGATCGCC
CGGATGGACGACAACGACTACCGGCCCGCGCCAGGAAGAGGATGCCAATCGTCAGCCGC
GGCGCCAACCGGACTACGAGGAGGCGGAGGACAACGGCGAAGAAGACCCGATGATTCTA
GAAGAGATCGAGCCAGAAAAGGAGAAGGAGACCGCGGAGAAGCCGGGCAAAAAGCACGAC
GGCCGGCGTCCGATCAAGCGCGACGGTCTGATGAAAGTTACGTGTTCCAGCTGCTGTG
CGCGCCATCTTTGAAGCCTCCTTCTGTTTCGGGCAGTACATCCTCTACGGGCTGGAGGTG
GCGCCCTCGTACGTTTGCACGCGCTCCCCGCCCCACACGGTGGACTGCTTTGTTTCC
CGTCCCACCGAGAAAACCATCTTCTGCTCATCATGTACGCCGTGAGCGCGCTCTGCCTG
CTCTTCACCGTGTCTGGAGATCTTCCACCTCGGCATCAGCGGCTCCGGGACTGCTTCTGC
GCCCCGCGGCCCCGCCCCACCCCCCGTCACTCGGCCCTGGCCAGCCAGAGGTCTCTC
ATCTGCCGCCAGCCGTCCGCTCCTCCGGGGTACACACGGCCCTGAAGAAGGACCCCTTC
GGGAAAGCTGGGCTTCAGGGACAACCTGGGGGACTCCGGCCGGGAATCCTTCGGGGACGA
AGCTTCGTCCCGGGAAGCTGGAGAGGCTGCGCAAGCACTGAAACTGGCGCAGCAGCACCT
GGACATGGCCTACCAGAACGAGGAAAGCAGCCCCCTCGCGCAGCAGCAGCCCGAGTCCAA
CGGCACCGCGGCGGAGCAGAACCGACTGAATTCGCCAGGAGAAGCAGAGCGACAAAG
TGA

>Tn-NN-gjd2*2-G11801 Splice site. As predicted by Ensembl.

ATGGGGGAATGGACCATTTTGGAGCGTTTGCTGGAAAGCGGCTGTCCAGCAGCACTCCACT
ATGATCGGAAAGGATCTGCTGACAGTGGTGGTGATCTTCCGCATCCTAATAGTGGGCATA
GTGGGTGAGAAGGTGTACGAGGACGAGCAGATCATGTTTCATCTGCACACCATGCAGCCC
GGCTGCACACAGGCCGTGCTACGACAAGGCTTCCCCATCTCACACATCCGCTACTGGGTT
TTCCAGATCATCTTGGTGTGTACGCCAAGCCTGTGCTTCATCACGTATTCCGTTTCAC

TCTGCCAAAGCGCGTGACCGAAGCTACTCCCTGCTGCATCCGTACATGGATCACCATGGT
CACGGTCACCACGGTCGCCATCACGACCACACGCTCGCAAGATCCACTCGCGCTACATA
AATGGTATTCTGGTGCATCTTGAGAGCAGTAAGGAAGACCACGACTGCCTGGAGGTCAAG
GAAATCCCCAATGGACCCCGGGACTCCCTCCGACACACAAGAGTGCCAAAGTCCGGCGG
CAGGAAGGTATTTCCCGTTTCACGTCATCCAGGTGGTGTTCGCAATGCGCTGGAGATA
GGCTTCTTGGCAGGCCAATACTTTCTGTATGGCTTCAACGTTCCAGGGATGTTTGAGTGC
GATCGCTACCCCTGTGTGAAGGAGGTGAGTGTACGTATCCCGTCCCACAGAAAAGACT
GTGTTTCTGGTCTTTATGTTTGCCGTCACTGGCATTGTGTGCTGCTCAACCTGGCGGAG
CTCAACCACATCGGCTGGAGGAAGATAAAGACGGCCATCCGAGGGGTGCAGGCCCGGAGG
AAGTCCATCTGTGAACTGCGTAAGAAGGATGTGTCTCACCTGTCCCAGGCCCGAACCTG
GGCAGGACCCAGTCCAGTGAGTCAGCTACGTCTGA

>Tn-gjd2b-G17236 Splice site. As predicted by Ensembl.

ATGGGGGAATGGACTATACTAGAGAGGCTCCTGGAGGCTGCTGTCCAGCAGCACTCTACT
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GGCTGCAACAGGCGGTGACGACAAGGCGTTCCCCATCTCGCACATTAGATACTGGGTG
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TCGGCCAAGCAGAAGGAGCGGCGCTACTCCACCCTCTATCTGACCCTCGATAAGGATCAA
GATTCACTGAAACGCGACGAGAGCAAAAAGATAAAGAACCATTGTGAACGGAGTACTT
CAGAACACGGAGAATCCACCAAAGAAGCCGAACCGGACTGTTTGGAGGTGAAAGAGATC
CCCAATTTCGGCCATGAGAAGTGCAAAGTCCAAAATGAGGCGCCAGGAAGGCATCTCCAGG
TTCATCATCATCCAGGTGGTCTTCAGAAACGCGCTGGAGATCGGCTTCCTGGTGGGCCAG
TACTTTCTGTACGGATTCAACGTGCCGTGGTGTACGAGTGCAGCCGCTACCCCTGCATC
AAAGACGTCGAGTGTGTCTCCAGACCCACGGAAGAAGACGGTGTTCCTGGTGTTCATG
TTCGCCGTGACGCGGCTTCTGCGTGGTGTGAACCTGGCCGAGCTCAATCACCTGGGCTGG
AGGAAAATCAAGACGCGCGTGCAGGCCGCGGGAAGTCCATTACGAGATC
CGAAACAAGGACCTGCCGAGGATGAGCGTGCCCAACTTCGGACGCACTAGTCCAGTGAC
TCCGCGTACGTGTAG

>Tn-NN-gjd2-G14329 Corresponds to transcript ENSTNIT00000017564. Splice site.

ATGGGAGAATGGACCATCCTAGAGCGCCTCCTGGAGGCTGCGGTGCAGCAGCATTCTACT
ATGATTGGGAAGGATCCTGCTGACAGTGGTGGTGTATCTCCGTATCCTGATCGTGGCGATC
GTTGGGAGACGGTGTACGAGGATGAGCAGACCATGTTTCATCTGCAACACTCTGCAACCA
GGCTGCAACAGGCGGTGACGACAAGGCGTTCCCCATCTCCACATCCGCTACTGGGTCT
TTCCAGATCATCTGGTGTGCACTCCAGTCTCTGCTTTATCACTTACTCCGTCCACAG
TCAGCTAAGCAAAAGGACCGTCTGCTACTCCTTCTCTATCCCATTATGAAAGGGACTAC
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GGCGATGGCGGAGGAGGAAAGGAAGAACCAGACTGCCTGGAGGTGAAGGAGATCCCCAAC
GCCCCGCGGGGCTCACTCATGGCAAGAGCTCCAAGGTTGCGCGCCAGGAAGGCATCTCC
CGCTTCTACGTCAATCAAGTGGTCTTCCGAAACGCCCTGGAGATCGGATTCTTGGCAGGC
CAGTACTTCTCTACGGCTTTCAGCGTGCTGGGATTTTCGAGTGCAGCCGCTACCCGTGT
CTGAAGGAGGTGGAGTGTACGTGTCCCGGCCACCGAGAAGACGGTGTTCCTGGTGTTC
ATGTTTCCGGTGAGCGGCATCTGCGTGGTGTCTAAACCTGGCTGAGCTCAACCATCTGGGG
TGGCGCAAGATCAAGCGGCCATCAGGGGTGTCCAGGCCCGCAGGAAGTCCATCTGCGAG
ATCCGGAAGAAGGACATGGCGCACCTCTCCAGCCGCCAACCTGGGCCGTACGCAGTCC
AGCGAGTCGGCCTACGTGTGA

>Tn-cx36.7-G03401 Underlined: Sequence not included in Ensembl transcript prediction, but we consider likely as a part of cds

ATGACGGAATGGACCTGCTGAAACGCCCTCCTGGATGCCGTCCATCAGCACTCCACCATG
ATTGGCCGCTGTGGCTGACTGTGATGGTTCATCTTTAGGCTGCTGGTAGTTGCTGTGGCA
ACGGAGGACGTGTACACGGACGAACAGGAGATGTTTGTGTGCAACACGCTGCAGCCGGGG
TGCTCGACCGTCTGCTACGACGCCTTTGCGCCCATCTCGCAGCCGCGCTTCTGGGTGTTT
CACATCATCAGCGTGTCCACGCCGTCGCTCTGCTTCATCATCTACACGTGGCACAACTG
TCCAAGGTCCACAGCGCTGCTCAAAGGCACCCACGCGGCGCTGGCCAGCCGCTCGGCCAA
GACGTCGGCCAAGCGCAAGGAGGTCTGGGAAAGGAGGCGGGAAGGCAGGTGGCGAC
CGGGAGGTGTACCTTCCAAGCTGCAGCTCGGACAGCTGCTCCGTCTCTCCACAAGCAC
CTCGGCCACAGCCTGGTGGACATTTTAGACGGCGTCGCGCCCGTAGTTTGCGAAACGGA
GACCCGCGACCTCCAGGCCCATCCAAGCTTACACCTTTAAAGACGGAAGCTCGGAGGGT
CTGGCGGTCTCTGGAGGATTTCTGTCCAAATGCTACATCTTCCACGTGTGTCTACGCGCA
GCTCTGGAGGTGGGATTTGTGCGCGCCAGTGGAACTGTTCGGATTGCAGGTGCCTGTC
CGCTTTTGTGTACCTCTCTGCGCCGCAACAGCCCGTGGACGTGTACGTCTCCAGGCCG
ACGGAGAAGACCATATTCCTGATCTTCATGTTTGTGTGTGGCGTCTTCTGTATCTTCTCT
AACTGCTGGAACCTCAATCACCTGGGCTGGAAGAAGATCAGGCAGGCGGTGCGGCTGAAG
GAGGACGAGGCGCCCTGGCAGGCCTGCGCGGGGATAGGACGCGGATACCAGACCATCCCT
CCGGTCAGCCCTTCGCCCAAGTCTTCGGGTATGAACGGCACCGCCCTCCGCCACTTTG
GACGTGGCGATGGGCCACAAACCGAGTGGGGCTGCGTGGTCAACTGTGCGGCACCCGA

GGGTGCGGAAAGGTCAAAGGAGAGAGGAAACACAAGGAGCTGAGAGGGTTCAAGCAGAGC
AGCGCAGAAGTCTGGATCTGA

>Tn-GJD3-G12849 Underlined: Sequence not included in Ensembl transcript prediction, but we consider likely as a part of cds.

ATGGGGGAGTGGGGCTTCCTCGGTGGACTCTTCGACAGCCTCCAGGCTCACTCGCCCATG
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GCCAGCGACCTGTTTGAGGACGAGCAGGAGGAGTTTGCCTGCAACACTCTCCAGCCGGGC
TGCAAGCAGGTGTGTTACGACATGGCCTTCCCCATCTCGCAGTACAGATTCTGGGTCTTT
CACATCGTGTCTCATCGCCACGCCTTCGCTACTCTTCCTCGTTTACACCATGCATCATCAC
AACAAGAGCAAACTGCAAATTCAATCCCAGGTACAGGGAAGACGTGCGTTGAGGAGGCTC
TATATTCTCAACGTGGTGTTCGGATTCTGGCCGAGGCCGCCTTCCTGGTGGGCCAGTGG
CTGCTCTATGGCTTCAAGGTGGAGGCCAGTTCCCCTGCAGCCGCTTCCCCTGCCCTAC
ACCGTGGACTTGCTTCACCTCGCGTCTCGAGAGAAGACCATCTTCCTCTGCTTCTACTTC
GTCATCGGGGCCATAGCCGCCCTCTTCAGCTGTGCGGAGCTCTTCCACATCTCTGTGAAG
TGGTTCTGCGCCGGCCCGAGCCCTCGAAGACAGAGGACTCGGGCATCAGCGATAACCTT
CTCAACGTGAAGCAGGAGGAAGGGATCAAAAAGGAGAAGCAGCAGGAGAAGAAGCAGCAA
GCTCCCGACAGCAGAAGGCTGAAGAGAGGATCGGTGAGGAGCAGCTCCAGCAGGAAGAGC
TCCGGCGGCCTCCACAGGCACATCAGTGGCAAATACGTGAGCAGCAGGACTTTGATGGTG
TGA

>Tn-NN-cx39.2-G01238 Underlined: Sequence not included in Ensembl transcript prediction, but we consider likely as a part of cds.

ATGGGAGACTGGTCCATCTTGGCCGCTTCTTAACCGAAGTTCAAAATCATTCCACGGTC
ATTGGCAAGATATGGCTGACCATGCTGCTCATCTTCCGCATCTTGCTGGTAGCACTGGTG
GGCGACGCGGTGTACAGTGACGAGCAGTCTAAGTTTACCTGCAACACCCTCCAGCCTGGA
TGTAACAACGTCTGCTATGACACCTTTGCTCCCGTCTCGCACTTGCGCTTCTGGGTCTTT
CAGATTGTTCTTGTCTCCACACCTTCTATTTTCTACATCGTCTACGTCTTACAAAAGATC
ACCAAGAATGAAAAGTTAGAGGTGAAAAAGGTTGTAGTGATACCACGGTCTCCTACACCA
TTCAAAGGGGGGGAGGATCGAGGAGGAGATAAAGAGGCAATGCTGGAGACTGGTGGCCCT
TATAACCCAACCTATAACAATGAGGAGTGGAGCTCTCAGGAGGATGAGTGTGAGGAGAGG
AGCCAGCTGAATGAGGAAATGAAAGAGGTGCGAAAAGACCCGACCCAGCTCTCCAGTCAA
GTGTTACTCATTTACATCATCCATGTTCTGCTGCGCTCCATCATGGAGATCATCTTCCTC
ATTGGACAGTATTACCTCTTTGGATTTGAGGTGCCACATCTTTTCCGCTGCGACACCTAC
CCGTGTCCAAACAGAACCAGTGCTGCTTTGTCTCTCGAGCCACGGAGAAGACCATCTTCCTG
AACTTCATGTTTATAGCTCAGTCTTGGGTGCTTCATCTTGAACATCGTGGAGCTGCATTAT
CTCGGCTGGATTTATATTTTCAGAGTGTGCTGCTCTCTGCATGCTGCACGTGCTGCAAGTCC
AACAGAGACCCGGTTCAGCAGGTGGAGTTGTATTTCGGACAACAACCCACTGCTGCTGGAG
CTCAAGCATTCACTGCGGGGCAGGGTCTGCTGTCAGGCCACCTCTGCCGTGACACGGGAC
AAAAGCAGCAGCGTCCCAAATCAGGCCCCAGCTATCTCTTTTGAAACAGACTCCACACTG
GAGTGCACTTTCGAAGCGGAACCCAGATGAAAAGGAACGCACTAAGGCAAGACTGCACAAA
ATCGGAAGAGGCCAAAAGTCATGGCTGTAA

>Tn-NN-gjd4-G07977 Ensembl prediction as pseudogene. Underlined: Sequence not included in Ensembl transcript prediction, but we consider likely as a part of cds. Exon 1 is missing.

GGTAAGACCTGGTGGACTCTGCTGCTGGGTTTGCGCCTGAGCGTCTGCTGCTGCTGGGC
TTACAGCTCTTCAGCGACGAGCAGGAGCGCTTCGTCTGCAACACCATCCAGCCGGGCTGC
TCCAACGTGTGCTTCGACGCCTTCGCTCCCGTGTCCGTCTTCCGCCTCTGGCTCCTCCAC
CTCGTCTCTGGCTCTTCCCCATCTGCTCTTTGCCACCTACGTGATGCACCGGCTTCTG
ACCGCTCCGGGTTCCCTCTGGCTCGTCCCAGGGAAGTGTCCCTTGCGCGGGAGCCAGCTC
CAGGAGCCCGGAGGAGCGCGCTTCTACTGCGCGTACGTCCCGGTGGTGGTGGTCCGGATC
CTTCTGGAAGTTGTTTTCGGGGCCGGCCAGTTTCACCTCTTCGGTTTGTCCTTTCCAAAG
AGCTTCTCTGTGCTACAGGCCCCCTGCACCTCGGGGTGGAGTGCTACATCTCCAGACGC
ACCGAGAAGTCCCTCATGCTCAGTTTCATGTTGGGCGTGGCCTCGCTCTCCATCCTGCTG
AGTTTGTGTTGATCTGCTGGGCTCCGTGAAGGCGATGGTGAGCTGGAGGAGGAGGAGGAG
ATGCTGGCGGAGGAGATGATCAAAGGAGAAACAAGCAGCGTGATTACGGCGACGACCATG
GCTGAAGACAGCGATAAAAGCCCCGAGTCCAACAGTCCCAGCAGCAGAGATGCTCAGGTG
GACACACCTCCCACTCCCAACAGCACTCCAGCACCTCCTCGGTGGTCTCCACAGCCGG
GTCGGACCCCCGCTGTCCCTCGGCCGTGACAGGGAACCACTGAGGGACCCAGCACCAGTG
GGGGGAGGAAGCCGGCCAGTACGGTCCAGCCGGGACAACCTCGGGCCAACAGTCTGAC
GGCGAGGCTCCAGACAGACGAGCCTGGGTTTGA

>Tn-GJD4-G08724 Ensembl predicts another exon 1 and another splice site. Underlined: Sequence not included in Ensembl transcript prediction, but we consider likely as a part of cds. Splice site.

ATGGCGGGATCAAGTACCTGTGAGGTCATCTTCATCTCTGTCAATCACAGCATCCCGCTG
ATG**GG**GAAAGTGTGGCTCATAGTGATGATCTTTCTCCGTATCCTGACCCCTCCTTTTTGCC
GGATACCCCTCTACCAGGACGAGCAGGACCGATTTCGTGTGCAACACCATCCAGCCTGGA
TGTGCCAACGTC**TGC**TACGACCTGTACTCCCCGTCTCCCTCTTCCGCTTCTGGCTGGTC
CAACTCATCACTTTGTGTCTTCCCTACATCGTCTTTGTCACTACATCATCCAC**AAGGTC**
TCAAATGACCTCTGCGCACACCTGAACTCCTCGGGCCAGGTCAGAACCTCGCGGCTGTTT
CAGATCCAGCAAGAGGCACCTGGTGAGAAGATGGCGCCTGAGAGGGGATCGGCTCGG**TGC**
TTCACAGGAGCCTTATATCCTCCACCTGATGTTCCGAACCTTGCTGGAGGCAGGATTTGGA
GCTGCTCATTACTATCTCTTCGGTTTTCAACATCCCCCGGAGGTTCTG**TGT**CAACACCCA
CCG**TGC**ACCACCCAGGTGGAC**TGC**TACGTGTCCAGACCCACCGAGAAGACTGTGATGCTC
AGCTTCATGCTCGGCGTGGCCGTCTGTCCTTTTTTTAAACGTTTTTGGATTTTATTAGC
GCCATCAAG**CGCTCTGT**CACCAAGAAGGGCAAAAAGAAGTTGATGGTAGGGAAGATTTAT
GAGGAGGAGCAGTGCTTCCTGTCAACGGGTGCGGCCTCCGGACCAACAGACCCAAACCAC
TCGGTGGGTAAACAGAATCTAGAGGTGGAGGCTCAGGCGGGCGGTTTCCGGAAGAGGCAC
AACAGCAAGGGTTCTTGCGCAGGGGTTGCTGTCCCTGTAGGGCAAGATCCACCCTCTCTC
GACCGTTCTTCATCCTTTCACGTTCACTTGGACCTCCAGGGTCCAACACAAATGGGAAC
AATGGCTACTCCCTTCCACAGGAGGATGTTTCAGAAAACAATGGCAGCGACGTGGCCCTC
TGCCCCCAGAGTCCATGGGGACACCTAGATCCATTTCGAGTTAGCAAACGAGGTCGATTA
AAACCTCCTCCTCCACCTAGGCGAGATCTGGGTTTCGTCTCCAAGTGGGCCGGCGGGGCC
CCTGGGGACATTTAGCAATCTGTACCAGAAGGGTCGGCCAATTCACACTGGTAGAGCTG
TCCAACGCAGAGCTACGGACCAGTGAAGACGGGCAAGACAAAAGGTCAGAGTGGGTCTGA

Suppl. Fig. 8. Three-spined stickleback (*Gasterosteus aculeatus*) connexins.

Stickleback, *Gasterosteus aculeatus* (Ga)

Assembly: BROAD S1, Feb 2006.

Genebuild last updated: May 2010.

Database version: 98.1.

As far as possible, the names of the sequences are taken from the Ensembl predictions. Where there is a prediction (although we might have modified it) without a name, we include NN (no name) as a prescript, use the most common name of the ortholog sequence (usually from zebrafish), and end the name with an abbreviated Ensembl gene prediction number. Where there is no prediction in Ensembl and no predicted (or experimentally found) sequences in GenBank with a name, we include NP (not predicted) as a prescript, and use the most common name of the ortholog sequence (usually from zebrafish).

The Ensembl gene number abbreviation is done as follows: ENSGACG00000004089 = G04089.

Yellow: Conserved domains as defined by Cruciani and Mikalsen (2007)

Green: Conserved cysteine codons (cysteine signature)

Grey: 15 nt added at the ends of the conserved domains

Turquoise: Splice site.

Other colors are explained where necessary.

>Ga-cx43-G04089 As predicted by Ensembl, but 1 A exchanged with N to avoid unexpected stop codon)

ATGGGGGACTGGAGCGCTCTGGGCCGTCTCCTGGACAAGGTCCAGGCCCTACTCCACCGCC
GGCGGCAAAGTCTGGCTGTGGTCTCTTCATCTTCCGCATCCTGGTCTGGGCACGGCG
GTGGAATCCGCCTGGGAGACGAGCAGTCCGCCCTTCAAATGCAACACCCAGCAGCCCGGT
TGTGAGAACGTGTGCTACGACAAATCCTTCCCCATCTCCACAGTCCGCTTCTGGGTCTCT
CAGATCATCTTCGTGTCCACGCCCACGCTCCTTACCTGGCTCACGTCTTCTACTTGAAC
CGGAAGGAGCAGAAGTTCAACAGGAAGGAGGAGGAGCTCAAGGCCGTGCAAAACGATGGC
GGCGACGTTGACATCCCGCTGAAGAAGATCGAGATGAAGAAGCTGAAGTACGGCATCGAG
GAGCACGGCAAGGTGAAGATGAAAGGGGCCCTGCTCAGAACCACATAGTCAGCATTTTC
TTCAAGTCCATGTTTCGAGGTGGGCTTCTGGTGATCCAGTGGTACATCTACGGGTTTCAGC
CTCTCTGCGGTCTACACCCTGAGAGGGACCCCTGCCCACACCGGGTAGACTTCTTCTG
TCGCGTCCCACGGAGAAGACGGTGTTCATCATCTTCATGCTGGTGGTGTCCCTGGTGTCC
CTGATGCTCAACCTCATTGAGCTTTNATACGTCTTTTCAAGAATATCAAAGATCGCGTGA
AGNNNNN

>Ga-GJA3-G01367 Our modification. Underlined: Introns predicted by Ensembl are included as part of exon.

ATGGGCGACTGGAGCTCTCTGGGCCGCTGCTGGAGAACGCTCAGGAGCACTCGACGGTG
GTCGGCAAGGTGTGGCTGACGGTCTCTTCATCTTCCAGATCCTGGTGTGGGCGCGGCG
GCCGAGGAGGTGTGGGGGACGAGCAGTCCGACTTCAACGCAACACGACGAGCCCGGC
TGCAGAGAACGTGTGCTACGACGAGGCCCTTCCCCATCTCGCACATCCGCTTCTGGGTGCTG
CAGATCATCTTCGTGTCCACGCCCACCTCATCTACCTGGGCCACGTGCTGCACATCGTC
CGCATGGAGGAGAAGCGCAAGGAGAAGGAGGAGGACGCGCGCAAGGCCAGCAGGATCCGA
GAGGAGAAAGAACTCCTTTGTAGGAACGCTGCGGACTCGGAGGAGGCGGGGGACGGGGC
GCCAAGAAGGAGAAGCCGCCAATCAGGACGAGCAGCGCAAGATCCGCATCCGGGGCGCG
TTGCTGCGCACCTACGTGTTGAACATCATCTTCAAGACCCTGTTTGAAGTGGGCTTCATC
CTGGGGCAGTACTTCTGTACGGCTTCCAGCTCAGGCCGCTGTACAAGTGGCGCCGCTGG
CCGTGCCCCAACGCGGTGGACCTTTCATATCCCGGCCACCGAGAAGACCATCTTCATC
GTGTTTATGCTGGTGGTGGCCTGCGTGTCTCTCTGCTGAACCTGTTGGAGATCTATCAC
CTGGGCTGGGAAGAAGGTCAAGCAGGGCATGAGCAGCAGTCCCCGCCCTCCACGAGTCG
CCGCGCCGCGTCAACCTCGCGCAGCCCGAGTGCTCCCGGACTGCCCGCCCGCGGCTCGGC
CGCCCCCGGACTACACGACGCTGACGGCGGGCAGCGCGCCTTCTGCGCGCCGCGGGC
CTGGCGGCGGCGGAGTTCAAGGCGGGCGGACTCCGGCGGGAGGAGCCGCTCCGCCGC
CCCCCACCCTCCGCCCTACTACGTACGACAGCAACAACAACCAACCAACCGCTGGCC
ACGCAGCAGAACTGGGCCAACCTGGCCACCGAGCAGCAGACCCGGGAGATGAAGGCCGCC
GCCGCCCGCGCCCCCTCTCTCTGCTCCAGCAGCAGCGGCAAGAGCGGCAGCAGCGG
CCCGTGGATGCCGCGGCGCCCCCCCCAGCAGCAACGTCTGCAGCAACGTGACTCCACC
GCCGCCGCTCCAGCAGCAGCAGCAGCAGCATCGCTCCAGCGCGGCGAGCTGGAGG

GGGGGCAAGAGCGGGCAGGAGGAAGGTCACGCCACCAACACCCTCCACCACCACCGTGA
 GATGCACGAGCCCCCGCTGACCGACCATCGGCGGCTCAGCCGGGCCAGCAGACCAGCAGC
 GTCAGGGCGAGGCCGAGCGACCTGGCCGTCTGA

>Ga-NN-gja3-G14074(2) Our modification. There are two connexins (wrongly) fused into one Ensembl prediction. The other sequence is Ga-NN-cx30.3-G14074(1). Underlined: Exons predicted by us. Splice site.

ATGGGTGACTGGAGCTTCTTGGGCGGCTGCTGGAGAACGCTCAGGAACACTCCACTGTG
 ATTGGAAAGGTGTTGGCTGACCGTTCTCTTCATCTTCCGCATCTTGGTGCTTGGCGCAGCG
 GCCGAAGAGGTTTGGGGCGACGAGCAGTCCGACTTCACCTGTAACACCCAGCAACCCGGT
TGCGAGAACGCTTGCTACGACGAGGCCCTCCCATCTCCACATCCGCTTTTGGGTGCTG
 CAGATCATCTTTGTCTCCACGCCGACCTCATCTACCTGGGCCATGTGCTGCACATCGTC
 CGCATGGAGGAGAAGCGGAGGGAGAGGAGGAGCTCCGGAAGGCCGGGCGGCACCAG
 GAGGACCACGATCCGCTCTATCACCTCGGAGCCGCTGATGGGGGAGGAAAGAAAGAGAAG
 CCGCCAAATCCGCGATGAGCACGGGAAGATCCGCATTCCGCGGGGCACTGCTGAGGACCTAC
 ATCTTCAACATCATCTTCAAGACTCTGTTTGGAGTTGGCTTCATCTGGGACAGTACTTC
 CTGTACGGCTTCCGCTGAGGCCGCTCTACAAGTGTGGCCGCTGGCCCTGCCTCAACACC
 GTGGACTGCTTCATCTCCAGGCCCACTGAAAAGACAATCTTCATCATCTTCATGCTGGTG
 GTGGCTGTGTCTCCCTGCTCCTCAACCTGCTGGAGATCTACCACCTGGGCTGGAGAAG
 GTCAAGCAGGGGCTCTCAACGAGTTCGCCCCCGCGGGGAGTCTCCGCGCTGATCGGG
 GACGAGCCCGGGGACCCGAGACGATCCGCGAGCAGACGTACCCGCGGACGCTCGACTGT
 TTGCCCGGTGACGCCACCGTGAACGTGGCAGGGGTCCGGGCTGAAGAGGGAGGAGCCTAC
 AGTTCGACCGAAGCCTGCGCACCAGTGGTGCCCGCCAGATTCAAGATGGACGCCGCTTG
 TTCCACCACGACGACTTCCTGTTGGACTCGCTGCCTACGTCTTTTACGCCGGGAAAGGG
 AGTGACGGGTGCCGCGAGCAGCGGATGGAGACGGAGCAGAACTGGAGCAACATGTGCTG
 GAGCTCCACAATCGGGAAGGGAAGGAATCCTCCTCCGCTCCTACCCGCTCTCCCTCT
 CCTCCACATCCGCTCTTCTCTCCCGAGAGGATACCGCCCCGCCACTTCCACACGGG
 GAGCAACACTCCACGTTTCTTACACTTCCGCGTCACACCCCCCTGTCTCCGCTCGCACCT
 GAAGAGCGCGCGGCGGACGAGGACACGTCCCCCTCATACGGCCCTCCACGACAACCTTACC
 GTGGTTATCAAGGCGGAGATGCATCCGCTCCCACTTCTGCCACGAGAGACGTCCCAAAG
 CCCAGTCGGTCCGGCAAGAGCGGCGGTGTCCGAGCTCGCCCCGACGACCTGGCAGTGTAG

>Ga-NN-cx39.9-G20329 Our modification. Underlined: Intron predicted by Ensembl is included as part of exon.

ATGGGGGACTGGAATTCGCTGGGGAAGCTGCTGGAGAGCGCCAGGAGCACTCAACCGTT
 GTGGGCAAGTTTGGCTGACAGTCTTGTTCATTTTCCGCATCCTGGTGCTGGGATCCGCC
 GCTGAGAAGGTTTGGGGCGACGAGCAGTCGGGCTTCACCTGCGACACCAAGCAGCCCGGT
TGTCAGAACGCTTGCTACGACAAGACCTTCCCCATTTCCTCATATCCGCTTCTGGGTGTTG
 CAGATCATCTTTGTCTCCACGCCAACGCTCATTTATCTGGGCCACATCCTTCACCTGGTC
 CGCATGGAGGAAAAGGAGGTGCAGAAAGAAAAGGACCTCGCCACCGACGAGGAAATGCAC
 GAGCAGTTACACGCGACCAAAGCCAAGAGGCCTCGGTCAAAGACAAACAGGGCCACGTG
 CGCTTAAAGGGGCACTTTTGCGAACCTACGTCTTCAACGTCATTTTAAAGACCTGTTT
 GAGGTGGCTTTTATCGTCGCCCAGTACTTCTGTACGGTTTGGAGCTAAAGCCCATGTAC
 ACCTGCGACCGCTGGCCTTGCCTTAACATGGTGAACTGCTACATCTCTCGACCCACCGAG
 AAGACCATATTTCATCTGTTTCATGCTGGCCGTGGCCTGCGTCTCCTTGCTGCTCAACCTG
 GTGGAATGTACCATCTAGGCTTCAAAAGTGCCACCAGGGCCTCAGTTACAGACGGGCG
 CGGGCTGCTCGCGAGGCTCCGAAGGCCTTAAACGAGGCTGTCGTGCCGTACGTACCCGAC
 TACAGCTTCTTTTCCGGTCACGCCGCGGTGCCTAGTCTTTCCCCGTGGACTCAAAGTAC
 AGCGCGGACGCGCCCAACGCCGCTACAGCCCTACAACAGCAAAGCGGTTCAACAGCAG
 AACAGAGACAACATGGCCGTGGAGAGAAAAGGCAAACCAGAGGGAGACGAGGCGAAGGAG
 AGCAAAATCTCAGGCCCCGTTTCTGAGTTGCCCGGCGAACATCAGCGCAGAAACAGTCAG
 TCAAGCAAACACAGCAACAACAAGAGCAGGCTGGATGACCTGAAGATCTAG

>Ga-NP-cx39.9 This sequence is predicted by Ensembl as a part of an intron in vma21 (vacuolar H⁺-ATPase homolog) (G18298).

ATGGGCGACTGGAACCTGCTGGGAAAGCTTCTGGAAAAGGCCAGGAGCACTCCACCGTG
 GTGGGGAAGGTGTGGCTACCGTGCTGTTTCATCTTCCGTATCCTGGTCTCAGTGCCGCC
 ACAGAGAAGGTGTGGGGCGACGAGCTGTGGGCTTCACCTGCGACACGAAGCAGCCGGGC
TGTGAGAACGCTTGCTACGACGTCACTTCCCCATCTCTCACGTCCGGTTTGGGTGCTG
 CAGATCATCTTCGTGTCCACGCCGACGCTGATCTACCTGGGGCACATCCTGCACCTGGTG
 CGGATGGAAAGAAAAGGACCAGCAGAAAGAGCTCGCTCAGCATTCGGACAAGCAGGCCCTT
 GTTGGCGATGGTAAGCAGAAGAAAGCTCTGGTGAGGGACAATAAGGGTCGAGTGCGCCTG
 CAGGGGAGCTCTTGGCTACAATATGTGTTAATGTGGTCTTCAAAACCTGTTGAAGTG
 GGTTTTCATCGTGGCCCACTCTTGTACGGCTTCGAGCTGAAGCCCATGTACACGTGT
 GACAGACCGCCCTGCCCCAATGTGGTCAACTGCTACATTTCACGTCCCACGGAGAAAACC
 ATCTTCATCATCTTCATGCTGGGAGTGGCTAGCGTGTCTCTGCTCCTCAACCTCGTAGAG
 ATCTACCACTGGGCTTCAACAAGTGTGCCAGGGCATACCTTCAGGCGACGCCATCGG
 TTCTCCAGGGGGCTCCCCAAGGAGCCAGCGGGGCCGCGGTGCCGTACGCGCCGAGTTAC

GACGACTACTTCCACCAAGTCCAGCCGGCCTACCCGCCGTACCCAGCTACGACCTCCAC
 CCTCTGTCCGAGGGCACCAGCCGCCCTTCCACCCCTACCACAGCAAGCGGCCTACAAG
 CAGAACTCTGACAACCTTGGCGGTGGAAGGAGCGGTGGCAAACAGAGGAAAGTGACCCA
 AAGGGTAAAAAGGGAGCCGGGTGGCCCCGGGTGCCCCCGGGTCGCCCCCGGGTCC
 CCTACGAGGCCAGGCCAGGCCGACGCGCAACACAGCAACAACAAGACTAGAATAGAC
 GATCTTCAGATATGA

>Ga-cx39.4-G07433 Our modification. Underlined: Exon extended in both direction until initiation and stop codon.

ATGTCCAAAGCTGACTGGTCTTACCTACAGCACCTGCTGGAGGAGGGCCAGGAGTATTCG
ACGGGCATCAGCCGCTTGGCTTACCGTGCTCTTCTGTTTCGCATGCTGGTCCTGGGC
ACCGCCGCTGAATCCGCTGGGACGACGAGCAAGCCGACTTTGTCTGCAACACGCTGCAA
CCCCGGCTGCACAGCTGTGTGCTACGACAGGGCCTTCCCATCTCCCACTTTTCGCTACTTT
GTCCTCCAAGTCATCTTCGTCTCCACGCCGACCATCTTCTACTTTGGATATGTGGCCATA
ATGGCCGGGAAAGACAAGCAGAAAGAAGAAGATGGGAAGGAGGCGGAGGAAGGCGGT
GGTGGAGGTAGAAGTGGAGGGAGAGCATCAGAAAGGGACGATGACAATGTGACCAGAGAC
AATGCCCAGAGAAGGAGAACTAGGGGGCGGTGGCAGAGGTAGGCGAGCTGAGAGGGAC
CCACCTGCCGCTCCTAAACTGAAAGGAAGGTGCTGTGCGCATATGTGTTACGATCCTG
TCCAAAGTGCTCCTGGAGGTTCGCTTCATCGTAGGGTTGTGGTTCTCTACGATGGCTTC
TACATTGCAGCGAAGTTTGAGTGCACCTGGTCCCCTGTCCCCACACCGTGGACTGCTTT
GTGTCCAGGCCACGGAGAAGACCATCTTACCATCTACACCCAGGTGATTGCTGGCATC
TCCCTGCTCCTCAACCTCGCCGAGCTCCTTCAGCTCGCCGTCTCCACCGGCTGGCGAAG
TACTACCGTACCCAGACCCAGGACCACCTTCCTCGATCCAAGCAGGTACCGGCTAGACAG
GAGGCGGCTTCCGAACCTCCGCCGATTATCCAGGCCCTACAATGCAGGGGGTCATGTC
AACCCCCCGGGCCGGGAGGCTCCATGCTACGCCACACCTTGTGAGAGCTACGGGGAC
CTGGGGATCGAGGTGCGGTGGGGTCCCAGGGAGGTGGGAGTGACCTGCTTCCAGTTAT
GTGAATGCATAGGGGCTATGAAGACCCACTGCCAAAAGTCCATTATAAGGCACACCCA
AAGCTCCTTGGGAAAAAGACTAAGGGTGTCCATAAGGAACACTCGGGGAGAAGCATTAC
GTATGA

>Ga-GJA5-G03669 Our modification. Underlined: Introns predicted by Ensembl are included as part of exon.

ATGGGGGATTGGAGTCTCCTGGGGAATTTCTAGAGGAGGTCCAGGAACACTCTACCTCG
GTCGGGAAGGTCTGGCTACCGTCTCTCATCTTCCGCATCCTGGTGCTGGGCACGGCG
GCCGAGTCGTCTGGGGCGACGAGCAGAGCGATTTCTCTGTGCGACACCCAGCAGCCCGGC
TGCACCAACGTGTGCTACGACAGCGCCTTCCCCATCGCCACATCCGCTACTGGGTGCTG
CAGATTGTTTTTGTCTCCACGCCGTCCCTCATCTACATGGGCCACGCCATGCACATTGTG
CGCCGGGAGGAGAAGCAGCGGAGGGTGGAGCAGGAGGAGAGGGAGGAGAGGGGGGAAGGG
GGAGAAGACCTGGGGGGGAGAAGGAGTACCTCCAGCAGAAGGTGAGCGGGAGAATGGTG
GCGTCTGACGGGACCGGCCGTGTTGCGCTGAAAGGGGCGCTGCTGCAGACGTACATCCTG
AGCATCATGATCCGCACGGTGATGGAGGTGACATTTGTGCTGGTGACATGATCTAC
GGGGTGTTCTCAGGGCGTTGTACCTGTGCAAGTCTTGGCCCTGCCCCAACCCCGTCAAC
TGCTACATGTCCCGGCCACGGAGAAGATGTCTTCATCGTCTTTATGCTGGTGGTGGCC
GGCGTGTCCCTGCTGCTCTCCGTGCTGGAGCTCTACCACCTCAGCTGGAAGGGCGCCAGG
AGGTGTTTACGCAAGAAGAGGATGGAGAAGAGCAGCCACAAAGCTGTGACGGCGGCCGTC
TCCGCGGCTTGGAGCCCAACAGCCCCCACTGCCCCCGGCTCCTGCACCCCGCCTCCT
GACTTCAGCCAATGCCTGGCGGCTCGAGCTCCATGGACCCCATGACCTCTATGGCCTCG
CACCCCTTCAGCAACAGGATGGCGCTGCAACAAACTCCGCCAACCTGGCCACGGAGCGG
CACCACAGCTGCGACGACCTGGAGGATGAGAAAGACTTCCAGAGGATGCGATTGACACG
GCGCCCCAGAGGTGCCACACAGCTGCTCTCCCTCGCCGCTGCTGCACTCCGGCTACACG
AAGGACAAACGCCGCTGAGCAAGACCAGCGGCACACAGCCGGCTCGGCAGGACGAC
CTGGCAGTGTAG

>Ga-NN-gja5-G11699 Our modified prediction, including the removal of two nt in first conserved domain (between lower case letters). Underlined: Introns predicted by Ensembl are included as part of exon. Note that also a part of an Ensembl predicted exon is considered as intron by us (at splice site 2). Splice sites.

ATGGCGGACTGGAGCCTGCTGGGAAACTTCTGGAGGAAGTGCAAGGAGCACTCGACCTCC
GTTGGCAAGGTGTTGGCTGACCGTCTCTTCATCTTCCGCATCCTGGTGCTCGGGACGGCC
GCCGAGTCTTCTGGGAGACGAGCAGGAGGACTTCAACTGCGACACCGAGCAGCCGGgc
TGCGAGAACGTTTGCTACGACCGAGCTTTCTCATCGCCACATACGATACTGGGTGCTG
CAGATcgTGTTCGTGTCCACTCCCAGCCTCATCTACATGGGCCACGCCATGCACACCGTC
CGCATGGAGGAGAAGAGGAGGAGCCGGGAGGAGGAGGACGGGGACGGGGGGAGAGGCAG
GAGGACCCGGGAGGGGGCGGAGGGGATGGAGGAGGAGAGAAACACGGGAGGAAAGGAGAG
AAGGACAGAGGAAAGGAGGAAAGCAGAGACGGTCAGGCGGACGGTCGAGTGCGTCTGAGG
GGCGCGCTGCTGCAGACGTACGTCTGAGCATCCTGCTGCGGAGCGTCATGGAGGTGGTG
TTCTGCTCCTCCAGTACTTCATGTACGGCGTCTTCTCAACCCTCTGTATGTCTGCAAG
GCCTGGCCGTGTCCTCATCCAGTGAACTGTTACGTCTCCAGGCCGACGGAGAAGAAGTC

TTCATAGTGTTCATGATGACCGTGTCCGCCGTCTCCCTGCTCCTCAGCGTGCTCGAGCTG
CATACCTTGGCGTGGAGACACTGCTGCAGGTACGCGCGCTCACAGCGAAGGCCGTCCT
CTAGCCAACGCCTCGCTGGCCCCGTGAGTCTCTGTGCCCCCCCCGCTGCCGCCACCCCT
CCCCCGGAGTTCAACAGTGCCTGATGGGCTCCTCCCACTTCTGCCGCTCCCTTTCCCC
AACCACCGCCTCGCCGACCCAGCAGAACTCCGACAACATGGCCGCCGAGAGAACAATAATG
GCCGTGCCGCCGAGAGGAGGTGACCTCTCCAGATGAGCCGCTACTCACCCGCGTGG
CCCCGCCGCCGCCGCGGTGAGATCCAAGATGGCGGATACCTGAGGACCGCGACGGGGAG
ACGGGCGGGGGTACAGGACCGACGAGGTTTACGAGGACGAGCGGAACGAGCAGCCGG
ACCCGAGCCGACGACCTCTCGGTTTAG

>Ga-gja8a-G03667 No modifications.

ATGGGTGACTGGAGCTTTCTGGGTAATATTTTAGAGGAAGTTAACGAGCACTCTACGGTG
ATCGGCCGGGTGTGGCTCACGGTGTCTTCATCTTCCGTATCCTCATCTGGGCACGGCG
GCGGAGTTTGTGTGGGGCGATGAGCAGTCTGACTATGTCTGCAACACGCAACCGGGA
TGTGAAAACGTGTGCTACGACGAGGCCCTCCCATCTCCACATCCGCTGTGGGTGCTG
CAGATCATCTTCGTGTCCACGCCGTCTCTGGTGTACGTGGGTACGCCGTGCACCATGTG
CACATGGAGGAGAAGCGCAAGGAGCGCAGGAGGCGGAACCTAGCCGGCAGCAGGAGCTG
AGCGAGGAGCGTCTCCCCCTGGCACCAGGAGGCGAGCTCCGACCCCAAGGAGACC
AGCACCAGGGCAGCAAGAAGTTACGGCTGGAGGGCACCTGCTGAGGACCTACATTTGC
CACATCATCTTCAAAACACTGTTTGTAGGTGGGCTTCGTGGTGGGACAGTACTTCTGTAC
GGCTTCCGCATCTTCCGCTGTATAAAAGCAGCCGCTGGCCCAGCCCAACACGGTGGAC
TGTTTTGTGTCCCGGCCACGGAGAAGACCGTCTTCATCATCTTCATGTTGGCCGTTGCC
TGCGTCTCGCTCTTCTCAACTTTGTGGAGATCAGTCACTGGGCCGTGAAGAAGATCCGC
TTCGTTTTCCGCAAGCCGGCCCCCGGCTCAAGGGGAGGCGACGGCCCCCTGCCG
CCACCAGGAAAGAACTTGCCCCCTCTGGCTATGCCAGCCCTTCAAAGAGCGAAGGGTTAC
AGGCTGTGGAGGAGGAGAAAGCTCCCATGACTCAGCTCTACCCGCTCACCGAGGTGGGC
ATGGAGGCTGGCAGAGGGCCCCACCTTCTGGGGCTGGAGGAGAAAGCGGAGGAGGTG
CTGCCAATGGGGGGCATCTCTAAGGCGTACGACGAGACTCTGCCCTCCTACGCCAGACC
ACCGAGACGGCGGGGGTGACGCTACGCCAGGAGGCCGAGGAGGTGCAGCCGGCAGAGGCA
GAAGCAGAGAGATGGAGAAGGGTGGGATGAGGATCTGGAGGTAGAGGAAGCGGGGAAC
GGGGAGGGGTAAATCCAGAGGAGACAAGGATGGAGGTACGGATACGATAGAAGACACC
AGACCGCTGAGCCGACTGAGCAAAGCCAGCAGCAGGGCCAGGTACAGACGATCTTAACGTA
TGA

>Ga-GJA9-G13675 Our modification. Underlined: Intron predicted by Ensembl is included as part of exon.

ATGGGCGACTGGAACCTTCTCGGCGGGGTTTGGAGGAGGTGCACATCCATTCCACCATG
GTGGGCAAGATCTGGCTCACCATCCTTTCATCTTCCGCATGCTGGTCTCGGCGTGGCG
GCGGAGGACGTGTGGAACGACGAGCAGGCGGACTTCGTGTGCAACACCGAGCAGCCGGC
TGCAGGAACGTGTGCTACGACCACGCGTTCCCATCTCCCTCATCCGCTTCTGGGTGCTG
CAGGTCTCTTTGTGTCTCTCCCTCGCTGGTGTACATGGGCCACGCGCTCTACAGGCTG
CGGGCGCTGGAGAAGGCCCGGCAGAAGAAGAGCGCTGCTGCGGAAGGAGCTGGAGCTG
GTCGACGCGGAGTCCGCGGAGGCCAGGAAGAGGATCGAGCGGAAGTGAAGCAGCTCGAC
CAGGCAAGCTGAACAAAGCCCCCTGAGGGGCTCGCTGCTGCGAACCACGTGGCGCAC
GTCTTCAACCCGCTCGGTTGTGGAAGTGGCCTTCATGACAGGCCAGTACGTCCTTTACGGC
TTTCACTCCACCCGCTCTTCAAGTGCAGCGGACCCCTGTCCTCAATGCCGTGGACGTG
TATGTGTCCAGACCGTCAGAGAAAAGTGTCTTCATGGTGTTCATGCAATGCATCGCGGCC
ATATCCCTCTTCTGAACCTCTTGGAGCTCACGTACCTGGGCTACAAGAAGGTCTATGCAG
GGCATCTTGGACCTTTACCTCACTTGCAGGACGAACCCGATGACTACTGCGCCAACAAG
TGCAAAAAGAATCTGTTGTGCAAAATATGCACCAGCGTACCCGAAGGTGACGGTTGCC
TCCGCACCTGTGACTACAACCTCTTGTGGAGAGGTACCCGAACCTCCTCAGACCTCCA
TCTTTTCTCCCTCATCGGAGCGAGCAGACCCACCAGCAGTATTTGGAGGATCCCCCGCAC
GGCAAGAGGACGGAGGAATCCAGACTCTCAAAGAAGGCCGACTCAAACCTCAGCCCCG
GAGACACCGGAAGAGTCCAGCTCAGGATCCAGGGACAACCCAGGCCGCTTCTTCCAAC
GGCAAGACGCCAGTGGACAGACGGCCGCGAGACCTGCAGATCTGA

>Ga-cx52.9-G02230 Our modification. Underlined: Intron predicted by Ensembl is included as part of exon.

ATGGGAGACTGGAACCTTCTTGGAGGGATCTTGGAGGAGGTGCACATCCACTCCACCATG
GTCGGCAAGATCTGGCTCACCATCCTGTTTCATATTCCGGATGCTGGTGTGGGCGTCGCG
GCGGAAGACGTGTGGAACGACGAGCAGTCCGACTTCGTGTGCAACACCGACCGCGGC
TGCCGCAACGTGTGCTACGACCAGGCCCTCCCATCTCCCTCATCCGCTACTGGGTGCTC
CAGGTCTTTTCTGTCTCTCGCCCTCCCTGGTGTACATGGGCCACGCCATCTACAGCTG
CGGGCTCTGGAGAAGGAGCGGCACCTGCAAGAAGGTGGCCCTCCGTCGCGAGCTGGAGGCG
GTGGACGCGGAGCTGGTGGAGGTGCGGCGGAGGATTGAGAGGGAGATGAAGCTGCTGGAG
CAGGGGAAGCTCAACAAGGCTCCTCTGAGGGGCTCTCTGCTGTGCACCACCTGGTCCAC
ATCGTCACGCGCTCAGTGGTGGAGGTGAGCTTCATGGTGTGTGAGTACTTCTCTACGGA
CACC GGCTGAACCCGCTCTACAAGTGTGAGCGGGAGCCGTGCCCAACGTGGTTCGACGTG

TTCGTCTCCAGGCCACCGAGAAGACGGTGTTCATGGTGTTCATGCAGGGGATCGCCTGC
 ATCTCGCTCTTCTCAGCCTCCTGGAGATCATGCACCTGGGATTCAAGAAGCTCAAGAGG
 GGCATCTGGACTACTACCCGCACCTGAAGGCCGACCTCGACGAGTACTACGTGGACAAG
 TCGAAGAAGGACTCGGTGGTGCATCAGGTGTGCGTGGGCACGTCCGTGGGTGCGAAGACC
 ACCATCCCCACGGCGCGTGTGGGTACACGTTGCTGTTGGAGAAGCAGGGCAACGGGCC
 GCCTACCCTCTCCTCAACGCCTCCTCTGCCTTCGTCCCGATCAAAGGGGACCCTGTGCA
 AAGCCGACCTCCACAAGGACGGCAAGGAGGGCGTCCCGAGCCCCACGGAGCAGAACAGC
 AACTCCAACAACACGAGCAGCAGACGCGCTCCCTCCTTCAGACAAACAGGAGGAGCCG
 GAGGAGCAGTCTTCGCCCCCTCTGGAACGCATGGGGTGCACCAGCTCCGAGTATCCGACC
 CTCCCCGTGGCCTCATCGTGCACACGATGTGAGGAGCTGCGAGGAAGTCGCGGAGGGTC
 AGTCCACCGTGGAACTGCTCCACGCTGGTGGAAAGGCAACGGGTGCGACACGGGAGACTCC
 TATCAAGGGAACAACGGCGGGAAGCCGCTGGCGGCTGCGTGGACCCCGAGCGAGGGTG
 CTCTCCAAATCAGACACGAAGAGGCCGAGCAGGCCTCAGAGCCCGGACTCCGCAGGGGAG
 CTGAGCTCAGTGTCTCGACACAGCCGCGAGAGCAACAGCCCCGTCCAGCCTCTCCAGC
 CGCCGCTGTGACGGGTGAGCAGCAACGGCAGCAGAAGGGCCCCAACTGATCTGCAGATA
 TGA

>Ga-cx52.6-G06243 Our modification. Underlined: Intron predicted by Ensembl is included as part of exon.

ATGGGCGATTGGAACCTATTAGGGAGCATCTTAGAAGAGGTCCACATTCACTCCACCATC
 GTGGGAAAGATCTGGCTCACCATCCTTTCATCTTCCGCATGCTGGTGTGCGCGTGGCC
 GCCGAGGACGTGTGGGACGACGAGCAGACCGAGTTCGTCTGCAACACGGAGCAGCCCCGGC
 TGC AAGACCGTCTGCTACGACACGGCTTCCCCATCTCCCTCATCCGCTACTGGGTGCTG
 CAGGTCACTCTTCGTGTCTCCTCCCGTCCCTGGTCTACATGGGCCACGCGCTGTACCGCCTG
 AGGACCCCTGATAAGGAGAGGCACAGGAAGAAGGCCTCCCTAAAAGCCGAGCTGGAGGGG
 ACGGACCCCGTCCAGGAGGACCACCGTAGGATCGAGCGGGAGCTCAGGAAGCTGGACGAG
 CAGAAGAAGGTGAGGAAGGCGCCCCCTCAGGGGCTCGCTGCTGCGCACCACGTTTTCCAC
 ATCCTGACACAGGTCCGTGCTGGAGGTGGGCTTCATCATTGGCCAGTGCCTCTGTACGGC
 ATCGGGCTGTCTCCCTCTACAAA TGC GAGCGGTGTCCT TGC CCAACAGCGTGGAT TGT
 TTCTGTGTCGCGGCCGACGGAGAAGAACAATTTTCATGGTTTTCATGCTGGTCACTCGCCGGG
 GTCTCTTTGTTCTCCTCAACCTCCTGGAGATCTTCCACCTGGGGGTGAAGAAGATCAAACAG
 AGCCTGTACGGATACAAATACGGGGACGACGACAGCGTGTGACGGTCAAGAAGAAGTCC
 ACGGTGCAGCAGGCGTGCCTGCTCAACAACCTCCTCGCCGAGAGGCTGATGCAGCTCAGC
 CACATGCTCTGCCCCCGGTGTGCGACGCTCACAGGAAGCCTTCGGACCCCGAGTGCAAG
 GAGGGCCCCGGCCACCGGGCGCCCTCGTGCAGCAGCGACGAGTCCACCGGAGGCCGAGGA
 GCCCGGGGCCGCGCAGTACGCGGGGCCCGGGCCACCCTGAGTGCCGGCCACATGGAG
 ATCCCGCTGCCCCGACCGGAGAACCGCAGAGGAAGCAGCAGCAAGGTGAGCGCTGCAAGGAG
 CTGAGCGACATGAGCGATTGCGCCGAGAGCGACTACCACCCACGGGCAGGAAGTGCAGC
 TTCATGTCCCGCGGGATGTGCGAGAGCAAGCTGGCCTCCTCGTCCGACAGCGCCGACTCC
 CGCAGCTTAGGGGACGTGCGAGGCCAGCACTTCAACCAGGGGAGAGTCCGGCGGTGACA
 CCGCCACCTCCGTGAGCGGGAGGAGGATGTCCATGGTGAGGGCAAAAAAACAAAAACA
 AATGTCTTCCAGTCATGTTTTGTCTGGTGGCCCCCTGATCAAGGATACTAAATGGGCCTCG
 CAAAGGGGGCTGAGTTATGGGCCTTTTTTCATTTTTTCAAACATTCAAAGGCTTATAA

>Ga-NP-gja10

ATGGGTGACTGGAACCTGCTGGGCAGCATCCTAGAAGAGGTCCACATTCACTTCTACTATC
 GTGGGCAAGATCTGGCTTACCATACTTTTCATCTTCCGCATGCTGATCCTGGGTGCGGCC
 GCTGAGGACGTATGGGATGATGAGCAGTCCGAGTTTGTCTGCAACACTGACCAGCCAGGC
 TGC AAGCGGTCTGCTACGACCGTGCTTCCCCATCTCCCTCATACGTTTCTGGGTCTTG
 CAGGTGATCTTTGTCTCTGCGCCATCGTTAGTCTACATGGGCCATGCCCTCTACTGCATG
 CGAGCACTTGAGAAGGAGCGCCACCGCAGACGGGCCAGCTGAAGGAGGAGCTGGATGAG
 GTGGAGTTGGCGCTGGACGAACATAAGCGCATGGAGAGGGAAGTGGAGGCTAGACGAG
 CAGAGGAGGGTGAAGAAGGCTCCTCTCAGAGGCTCTCTATTGAGAACGTACATCATCCAT
 ATCCTTACACGCTCTCTGGTGGAGGTCTGCTTCATTTTCGGCCAGCATATACTTTATGGT
 GTCCAAC TAGAGCCCCCTCTATAAG TGT GATAGGCTACCT TGC CCAACAGTGTAGAT TGT
 TACATCTCCAGGCCACGAGAGAACAATATTTCATGGTTTTCATGATTGTCTGCTGGT
 GTGTCACTGTTTCTCAACATACCTGGAATATCCCACTTGGGAATCAGGAAAAATCAAACAG
 AACTGTATGGAGAGAGGTACACGGAAGATGACAGTTTGATTTACAAGGCTAAGAAGAAG
 TCGTTACCACACCTTTGTGTAATGAGTAATGTATCACCTCACAACGGGCCTTTGACTCAG
 ACCTTCAAAGTGATTCCAGAGGCAGATATGAAGCCTCCATATTACAATACTGTGCTCAAA
 GCCAACCAGGAGGCACCAAGACACAACAGCTTGGCCTATATGGGACACAGTCAGACCAGC
 TATATCTGTCCCGAACCTAGGATGCCGCCCGGGTCTGGCAGGAACCTTGCAATTCAAGCC
 CCCAAAACCCATGAAGGTCCAGAAATCCGACAGCTATGGTGGACCATCATCTGGCCTGG
 GCTGCTGTATCAACTGTGGAGGGAACGCAACAAACCATCATCCAGATCCCCATGAGGGA
 GAGTGCCCTCACTCTACCATTTGGAAGCTCTGCTGTCCACTAGCACCTTAAGGCCAGC
 GCTATCAGAGACCTGGATGAGAATCATGAAGGGAGTCAAATGAGAGTGAAGTCTGTGCTA
 TCCAACCCAGGAAGACCAGCTTCATGATTAGGCCACCATCTGACAGCTTGTCTTCTATC

AGTGA^TCTCCACCAGCCCTTCCTTGCATACCTCAGAGGAGTCAGATGAACTGGGCTCCCTG
CAGGGAGACATGCCAATGATGCCGCCCTGCTGGAGGCCGAAGAATGTCAATGGCAAGTAAA
GAGTGGAGATCTTCTAATGTGCTGGAATTTGCTTTTACCTGCCTTTGGTGTCTAGAGCCT
AATAGTCTATATATGTTATATGTATGA

>Ga-cx28.9-G06833 Our modification. Underlined: Exon extended until stop codon.
Splice site.

ATGGGAGAGTGGGGTTTCTGTCTCTCTACTGGACAAGGTCCAGTCCCACTCCACCGTC
ATCGGGAAGGTCTGGGTCATTGTTCTTTTCATCTTCAGGATCATGATCCTCGGAGCTGGA
GCAGAGAA^{GG}TGTGGGGTGATGAGCAGTCAAATATGGTT^{TGC}AACACCAAACAGCCTGGT
^{TGC}AAGAACGCT^{TGC}TATGACCAAGCCTTCCCAATCTCACACATTTCGATTCTGGGTCCCTC
CAGATTATCTTTGTGTCAACTCCAACGCTGATCTACCTCGGCCACGTCTCCACATTATC
CACAAAGAAAATAAGATGAGAGAACAGACGCTGACCTACTCCAAGACCGGAATTGTCAAA
GTTCCAAAGTACTCCGACGACAAAGGCCACGTCAAATTAAGGC^{GACCTGCTGGGAAAC}
TACATGACCTCTATTTTCTTCAGAATCCTCCTGGAGGTAGCGTTTATTGTTGGGCAGTAT
TATCTCTATGGGTTTCATCATGGACCCAAGAGTGGTC^{TGC}ACCCGAGCCCT^{TGT}CCATTT
ACCGTGGAG^{TGC}TACATGTCTCGGCCAACAGAGAAGACCATCTTCATTATCTTCATGCTG
GTGGTGTCCATCATCTCTCGTACTGAACGTAGCGGAGATCTTCTACCTGGGGTGTACT
CGCTCAATCAGGCAAAGGTCTAAAACACATAAAGCATCAATTGCCATTACACTCGTTTA
AACGGGGACACTCTTAT^{GTA}

>Ga-cx32.3-G06829 Our modification. Underlined: Intron predicted by Ensembl is
included as part of exon.

ATGGGAGACTGGGGTTTCTGTCCGGCCTACTGGACAAGGTCCAGTCCCACTCTACGGTC
ATCGGCAAGATCTGGATGAGCGTGCTCTTCTCTTCAGAATCATGGTCTTGGGTGCGGGC
GCGGAGAGCGTCTGGGGCGACGAGCAGTCGGGTTTCGTC^{TGC}AACACCCAGCAGCCTGGT
^{TGT}GAGAACGCT^{TGC}TACGATTGGACCTTCCCCATCTCGCACATGCGTTTCTGGGTCCCTT
CAGATCATCTTCGTCTCAACTCCGACGCTGGTGTACCTGGGCCACGCCGTGCACGTCATC
CACCAGGAGAAACAAGATGAGGGAGCAGCTGTTGAGCGCAGCTGGGTCCCGGCTGTGCAAA
CAGCCCAAGTACACCAACGAAAGGGGAAAGGTGATGATCAAGGGGAACCTGCTGGGGAGC
TACATGACCCCAACTCGTGTTCGAAGATCTTCATCGAGGCCGGCTTCATCGTGGGCCAGTAC
TACCTTTACGGCTTCGTCATGGTGCCCATGTTCCCC^{TGC}TCTCAGACACCC^{TGT}CCCTTC
ACCGTGGAG^{TGC}TACATGTCCCAGCCACAGAGAAGACCATCTTCATCATTTTCATGCTG
GTGGTGGCCTGTGTCTCCCTGTTCCCTCAACTTCTCGAGATGTTCTACCTGATTTGTACC
AGGGTCCGGTGTGGGTCCAGGGCTCGCTCTCGCAAGATCACTACGGCGGATAACCCTGCG
AGCCTGTGCACTCCCCGATGGCCGACGGCAGACGACGCGCTCAGGCACAACAAGGTGAAC
ATTGAGCTGGAGGGCAGCCAGACGCTCGGTGGGAGCCTGGATGGAGCCAAAGAGGAGAAA
CGACTACTGAGTGGT^{CATTAA}

>Ga-cx31.7-G18314 As predicted by Ensembl (transcript ENSGACT0000024257) and in
GenBank AAY27079.1.1 (Q50D51 GASAC.1)

ATGAACTGGGGGAGCTTTTACGCCGTGATCAGCGGCGTAAACAGGCATTCCACCGGCATC
GGGCGCGTCTGGCTCTCCGTCATCTTCATCTTCCGCATCCTGGTCTGGTGGTTCGCTGCC
GAGAGCGTCTGGGGAGACGAGAAGTCCGGCTTCGTC^{TGC}AACACCCAGCAGCCCGGC^{TGC}
AACAGCGTC^{TGC}TACGACCACTTCTTCCCATCTCGCACATCCGCCTGTGGGCGCTGCAG
CTCATCTGGTCTCCACCCCGCCCTGCTGGTGGCCATGCACGTGGCCAC^{CGACGCCAC}
GTTGAC^{AAGAAGGTCTGAAGAAGACGGGCCGCGCGGCCCAAGGAGCTGGAGCTCATC}
AAGAACCAGAAGTTCCAGATCACCGGAGCGCTGTGGTGGACGTACATGATCAGCATCGTC
TTCAGGATCGTCTTGGAGGTGGCTTTTCTCTACATTTTCTACTTGATCTATCCGGGCTTC
AAGATGGTGGCTTGGTGAAG^{TGT}TCGTCGTACCCG^{TGC}CCCAACACGGTGGAC^{TGCTTC}
GTCTCCAGACCCGACAGAAAAGACCATAATCACTGTGTTTCATGCTGGCGGTGTCCGGGCTG
^{TGTGTGCTGCTCAACCTGGCCGAGGTGGCCTACCTCATATTCAGGGCCTGCAAGCGGTGC}
CTCCGAGGCTCCGAGGAAGAGTCCAAAGTCGCTTGGATAAGTGGAAGATTCTCCACTTAT
AAGCAAATGAAATCAATCAGCTGATAGCGGAGCAGGCGCTCAAGTCTAAGTTCGCTGTG
AGCAAAAAGAGCCCGACCGAGAAGGGAGAAAGGTGTTCCGCATTCTGA

>Ga-cx27.5-G20330 As predicted by Ensembl

ATGAACTGGGCGTCGTTTTACGCTGTCTATCAGCGGTGTGAACAGACACTCGACAGGCATC
GGTTCGATCTGGCTCTCTGTCTGTTCATTTTCCGTATCCTGGTCTGGTGGTTGCAGCG
GAGAGTGTGTGGGGGACGAGAAGTCCGGCTTCACC^{TGC}AACACCCAGCAGCCCGGC^{TGC}
AACAGCGTC^{TGC}TACGACCACTTCTTCCCATCTCCACATCCGCCTGTGGGCGCTTCAA
CTCATCTGGTGTCCACCCCGCCCTGCTGGTGCCTATGCACGTGGCCAC^{CGGCGCCAC}
GTCGACAAGAGGCTCTACAGACTTTCCGGGAGGACCAATCCCAAAGACCTGGAGCAGATA
AAGACCAGAAAGATGAAAATCTCTGGG^{GCTCTGTGGTGGACGTACGTCAATCAGCCTGTTG}
TTCCGCATCGTCTTTGAGGTGACCTTCATGTATCTGTTTATATGATCTACCTGGTTAC
AAGATGATCCGGCTGGTGAAG^{TGC}GACTCGTACCCG^{TGT}CCCAACACGGTGGAC^{TGCTTC}
GTGTCGAGGCCACGGAAGACTGTCTTACCGTGTTCATGCTGGCTGTATCGGGGGTT
TGTATTCTGCTCAACATTGCGGAGGTGATCTTCTTGGTGGGG^{AAGGCCTGCAGTAAGCAT}

CTGCACGCTGCTGGAGACTCGACTGTCTGGGGCTTGGATCCAACAAAAGCTCTGCTCATAC
TAA

>Ga-cx30.3-G01368 Our modification. Underlined: Intron predicted by Ensembl is included as exon.

ATGTCTTGGGGGGTGTCTACGCCCAGCTGGGCGGAGTCAACAAACACTCCACCAGCCTG
GGGAAGATCTGGCTCTCCGTCCTCTTCATCTTCCGCATCACCATCCTGGTCCTGGCCGCC
GAGAGCGTCTGGGGGCGACGAGCAGTCCGACTTCACCTGCAACACGCAGCAGCCCGGCTGC
AAGAACGTCTGCTACGACCACCTTCTTCCCGTGTCTCACATCCGCCTGTGGTGCCTGCAG
CTGATCTTCGTGTCCACGCCGCGCTGCTGGTGGCCATGCACGTGGCCTACAGGAAGCGC
GGGGACAAGAGGACCATGCTGGCCTCCAACGGCGCCGAGCGGACGACGGACAACGAGCTG
GAGACGCTGAAGAGGAGGCGCCTGCCCATCGCGGGCCCGCTGTGGTGGACCTACACCTGC
AGCCTCTTCTTCCGCCTCGTCTTCGAGGGCGGCTTCATGTACGCGCTGTACTTCGTGTAC
GGCGGCTTCCAGATGCCGCGGCTGGTGAAGTGCGAGCAGTGGCCCTGCCCCAACAAGGTG
GACTGCTTCATCTCCAGCCCCACGGAGAAGACCGTCTTCACCATCTTCATGGTGTCTCTCG
TCCACCATCTGCATGGTGTGAACGTGGCCGAGCTGGGCTACCTCATCGCGAAGGCGGCG
CTGAGGTGCTCGGCCCGGTCCAACCGGAGGAACCGCCGTACGGCCACGCGGACGGCGTG
CCGACGAGACAACAGCCACCTTCAGAACGTGAAGAACGAGCTGCTGTCTGCCGACTCGCG
GCCAGCAGGACGTGCTGA

>Ga-NN-cx30.3-G14074(1) There are two connexins (wrongly) fused into one Ensembl prediction. For the present connexin, Ensembl only predicts (correctly) the first exon. Underlined: Exons predicted by us. Splice sites. The second sequence is Ga-NN-gja3-G14074(2)

ATGTCTTGGCCGGCTCTGTACTCTCAGTTGGTTCGGGGGGAACCGACACTCCACCAGCTTG
GGTAAATCTGGCTCTCCGTCCTCTTCATTTTCCGGGTCATGGTGTGGTTGTCTGCTGCT
GAGAGCGTCTGGGGGGACGAACAGTCTGACTTCACTTGCAACACACTACACCCTGGCTGT
GAAAACGTCTGCTACGACCAGTTCTTCCCTGTCTCCACATCCGTCTATGGTGTCTCCAG
CTTGTCTTTGTCTCCACGCCAACACTCCTGGTTGCAATGCATGTGGCCTATCGGAACCAC
AGTGACAAAAAGAGGCTCCTACAGGTTTCAGGTAGAGCGGGTTTCCTCACCAGCAAAGGC
CAGGAGGAAGACCTGGAGACTCTGAGGAGAAGGAGACTCCCAATAGCTGGCGCCCTCTGG
TGGACGTACGCCTGCAGCCTGGTGTGCAGGTTACTGTTGAAGGAGGCTTCATGTATGCC
CTGTACGTGGTGTACGACGGGTTCAGATGCCTCGCTTGGTGCAGTGTGACCAGTGGCCG
TGTCCAAACCTGGTGGACTGCTTTCATCTCTCGCCCCACCGAGAAAACCATCTTCACCGTC
TTCATGGCCACCGCCTCCTCTATCTGCATGGTCTTAAACATGGCGGAACCTGCATATCTT
GTTGCCAAGGCTGTCACTAGGTAG

>Ga-cx34.5-G06828 Our suggested modification Our modification. Underlined: Intron predicted by Ensembl is included as part of exon. Splice sites. At first splice site, a part of the exon predicted by Ensembl is now considered as a part of the intron.

ATGGGCGAATGGGACGTGCTGGGCGCCTTCTGGATAAAGTGCAGAGTCACTCCACCGTG
ATCGGCAAGGTCTGGCTCACCGTGTCTGTTGTCTTCCGCATCCTGGTCCTGCGCACCGGC
GCCGACAAGGTGTGGGGCGATGAGCAGTCCGACTTTGTCTGCAACACCTGCAGCCCGGC
TGTGAGAACGTCTTGCTACGACATGGCCTTCCCCATCTCTCACGTGCGCTTCTGGGTCTCT
CAGATCATCGCTGTGGCCACTCCAAAGTTGCTGTACCTCGGTACGTCTCTCCATGTGATC
CACCTTGAGAAGAGATGAAGGAGAGGATGAAGAGGCATGCTGACTTGGACAACAGATC
AGTCTGCTCCTTAGAAGGCGCTACAAAGTTCCCAAGTACACCAAGAGCACCGGCAAGATC
AGCATCCGCGGACTCTGCTTCGCAGTTATGTCTCTCCACCTCGTGGCCAAGATTGTCTCTG
GAAGTCTCTGTTATCTGTTGGTTCAGTACTATCTGTACGGCTTACCCTCAAGGAGCGCTAC
GTCTGCGCCCGCTCTCCGTGCCCCCACAGGTGGACTGCTTCTGTGCGAGGCCGACGGAG
AAGTCGGTCATCATCTGGTTCTATGCTGGTGTGCGCGGTTGTCTCTCTCTCTCTCCTCAGCCTG
ATTGAGCTGCTCTACCTGTGTGTGAAGCTGTGAGGGAGTGTATGACCAGGAGGCAGGAC
TACACCGTGACCCCGGTACCCCTCCGCCTTTGGAGAGGAAAGCTTTTAAAGCCGCGAC
GAGATGCTCCAGAATGGTGTCAACCTGGAGCTGGAGCTCCGTGGAGGAAAGCCAGGGGCG
AACGGGGCCGAGGCGGGTCCACCGAGGCTGCTGTGGATGTGTGCTGGAGAGCAACAAC
ACGGGAGGGGAGGTGCACATCTGA

>Ga-NN-cx35.4-G09240 Our modification. Underlined: Exon extended until stop codon.

ATGGATTGGAAATTCCTCGAGGGGCTCCTCAGCGGAGTCAACAAGTACTCCACTGCCTTC
GGACGCATCTGGCTCTCGGTGGTCTTTGTCTTCCGCGTCTGGTCTTCGTGGTGGCCGCC
GAGCGGGTCTGGAGCGACGACCAGGGACACTTCGACTGCAACACCCGCCAGCCGGGTTGC
ACCAACCTCTGCTTCGACTACTTCTTCCCATCTCCACATTCGCTCTGGGCTCTGCAG
CTCATCTTCGTCACCTGCCCTCCTTTCATGGTGGTGTGACAGTGTCTTACCGGAAGAAG
CGGGACCGCGAGTACCAGCCAAGCACGGCGAGGACACCGGGCTGTACGACAACCCGGGC
CAAAAGCACGGCGGCCTGTGGTGGACGTACCTGATGAGCCTCTTCATCAAGACCTTCTTC
GAGATCACTTTCTCTACCTGTGCTACGTGTACGAAAGCTTCCGGTGGCCAGGAAG
GTGCAGTGCGACGTCAAGCCCTGTCCCAACCTGGTGGACTGCTTACATATCCCGGCCACC

GAAAAGACCGTCTTCACCTACTTTCATGGTGGGGGCGTCCGTCGTGTGCGTGGTGTCTCAAC
 GTTTTGCAGATCTTCTATCTGGTTGCTTTCCGGATGGTGACCTTGAAGAGGACAGGCAGC
 GTCCACACCTCGTCCAGGAAGGTGCACCCGAACGCGAACGACTGCAAGTCTCTCTCGCC
 TCTTAA

>Ga-cx35.4-G07158 Our modification. Underlined: Exon extended until stop codon.

ATGGACTGGAAGACCTTCCAGGCCCTCCTCAGCGGGGTGAACAAATACTCCACGGCGTTC
 GGCCGGGTATGGCTGTCCGTGGTGTTCGTGTTTCCAGGGTATGGTGTACGTGGTGGCGGCG
 GAGCGGGTGTGGGGCGACGAGCAGAAGGACTTTGACATGCAACACCAAGCAGCCCGGCATG
 GCCAACGTCTGCTACGACCACTTCTTTCCCATCTCCACATCCGCCTGTGGGCCCTGCAG
 CTCATCTTCGTACCTGCCCGTCTTCATGGTGGTATGCACGTGGCGTACCGCGACGAC
 CGCGAGCGCAAGTACAAGGCGAAGCACGGAACACCAACCCAGCTGTACCAGAACACGGGC
 AAGAAGCACGGCGGCTTGTGGTGGACATATCTGATCAGCCTCTTCGTGAAGACGGGCATC
 GAGGTCTCCTTCTTACATCTCCACCATCTACGACAGTTTCTACCTGCCGAGGTG
 GTCAAGATGGTGTGTGCGCCATGCGCAACCTGGTGGACATGACATCGCCACCCACC
 GAGAAGAAGGTCTTACCTACTTTCATGGTCCGAGCTTCGGGCCTCTGCATCGTCTGAAC
 ATCTCGGAGGTCAATTTATCTCATCTCAACGCGTGTTCGGATAGCGAGGAAGGCCAGG
 ACTCACCGCCGACCCCTGCCCTGCGCTGCGACGTGCTGACGTGTACAAGGACCAC
 TTTGACAACGCCGACAAGATCATGTGAGGAGGTACCTGAAAGATCAGCCTCCGTCTTT
 AAGACGGCAACCAATCTCCGCCAGGATATCTGGGCTCAAAATGGAAGACAGGTTTCGG
 GCCTCTGCTCCTAATCTGTCCATTTCTTAG

>Ga-cx30.9-G07404 Our modification: Underlined: Sequence is extended in 3'-
 direction to reach a stop codon.

ATGAAGTGGTCTGCTTTGGAGTCCCTCATCAGTGGGGTCAACAAGTACTCCACCGTGTTC
 GGGCGCATCTGGCTCTCCATGGTCTTCATCTTCCGGGTGTGGTGTTCGTGGTGGCGGCC
 CAGCGGGTGTGGGGCGACGATAACAAGGACTTTGTCTGCAACACCATCCAGCCGGGCATG
 ACCAACGTCTGCTACGACCACTTCTCCCATCTCCACATCCGCCTGTGGGCCCTGCAG
 CTCATCTTCGTACCTGCCCGTCCCTGATGGTGGTGGGCCACGTCAAGCTTCGCGAGAAG
 AAGGACATGCAGTACACCGCTCGCACATGGGCGCCATCTGTACGCGACCCCGGAAG
 AAACGAGGGGGCCTGTGGTGGACGTACCTGGCGAGTCTGATTTTCAAGGCAGGCTTTGAT
 GCTGGCTTCTCTACATCCTGTACTACGTCTACGAAGGCTACGACATGCCCCGCCTGTCC
 AAGATGCTCCCTGCAGCCATGCCCAACATGGTGGACATGATATCGCGTCCCACTGAG
 AAGAGGATCTTACCATCTTCATGGTGGTCTCCTCTGCGCTGTGCATCCTAATGTGCATC
 TGCGAGATAGTTTACCTCATCGGCATAACAAATCCAGAAACGCATCAAGAAGAAGTACAAC
 GCAGACAGGATATGTCACAGATCGATCCTACGGCCTCCACTCAAAATCTCAGTAACGCC
 AAGAAAGAGAAGGCGCCTATTAGGGAGAAAATTATGCACGATAGAGCAATGAAGCTTTTT
 GAAAAAGAAATGTGGAAGCAATTCATCAGAGCCAATGA

>Ga-cx28.6-G07635 Our modification. Underlined: Intron predicted by Ensembl is
 included as part of exon. Splice site. At first splice site, parts of exons
 predicted by Ensembl are now considered as introns.

ATGAAGTGGTCAAGGACTTGAGAGCTTGTGAGCGGAGTCAACAAATACTCCACTGCGTTC
 GGGAGGATTTGGCTTTCCATGGTGTGTTGTTCGGTGTATGGTGTGTTGTGGTGGCAGCG
 CAGAAGGTTTGGGGCGACGAAAACAAAGACTTTGTGATGAACACGCGGCAACCGGCATG
 ACCAACATCTGCTATGACCACTTCTCCCATCTCCACATCCGCCTGTGGGCGCTGCAG
 CTGATCTTTGTACAGTGGCGTCCCTGATGGTGTATGGCTCATGTCAAATTCGCGAAGGA
 AAGGACAAAGAAATACGAGGAGCAGCACCGGCTCCCACTGTACGCCAACCCCGGAAG
 AAGAGAGGGGGCCTGTGGTGGACCTACCTGCTGAGCTTGGTCTTGAAGGCTGGATTTCGAC
 ATGTCCTTTCTGTACATCTGTACCGGATATACCACGGATATGACTTGCCCAATGCTATCC
 AAGTGTGCTGGAACCGTGCCTCCCAACACCGTGGACATGCTATCAGCCGCCCCACGGAG
 AAGAAGATCTTCATGTTGTTTCATGGTCTGTTCCAGCGCGGTGTGCATCTTGATGTGCTTC
 TGCGAGATGATTTACCTCATCGGCATGCGCGTGTCAAAGAGATGAGGCTCCGCAAGAAC
 AACGAGATGCTCCGGTTTGTGAGGAGCAGGAGCTACCAACATGGCCCCACCCAGGTGCG
 CAGTATCGCAGGGTGCATCAACGCTGACAGACAGCCAGCTGAGTTTAAACAAGGACAGC
 CAGCTGAGTTTAAACAAGGCGGACAGGGTCAGAAACAGTGCTATGAGTACGAACTTGTAG

>Ga-cx34.4-G07159 Our modification. Underlined: Intron predicted by Ensemble is
 included as part of exon.

ATGAAGTGGGATTTCTCCAGGGCCTCCTCAGTGGGGTGAACAAGTACTCCACGGCCTTC
 GGCCGCGTTTGGCTCTCCATCGTTTTCTCTTCCAGGGTATGGTATTCTGTGGTTCGCGGCG
 GAGAAGGTGTGGGGAGACGAGCAGAAAGACTTTCTGATGAACACGGCTCAGCCCGGCATG
 CACAACGTCTGCTACGACCACTTCTTCCCGTGTCCACGTCCGGCTGTGGGCCCTGCAG
 CTCATCTTCGTACCTGCGCGTCTCTCTGTTGGTGTATGCACGTGGCCTACAGGGACGAC
 CGGGAAACGAAAGAACCAGGCTCAAGTACGGCGAGAAGTCCCGCAGCCTCTACAAGAACACG
 GGAAGAAGCGCGGCGGCTGTGGTGGACCTACGTGCTCACTCTGGTCTTCAAAATAGCC
 GTGGACGCCACCTTCTGTACCTCCTGTACCACATCTACGAGGGCTACGACTTCCCTCG
 CTCATCAAGTCCGAAGAGAAGCCCATGCGCAACGTGGTGGACATGCTTTCATCGCTCGGCC

ACCGAGAAACGGATCTTCACCATCTTCATGGTGGTCACCAGCCTGGCCTGCATCCTCCTC
TCCATCTTTGAAATCCTCTACCTGGTGGGGAAACGCTGCTGCGAATGCGCCACCGCGGGA
AGAAGCTCTCGCCACGTGACACACGACGCTGTCCAGCGGCGGACCCGTATGGATTTCG
AACACCCTTAAGGTGGCGGGCAAATCCCCCCCCGGGACGCCGGCTCCTTCGTACAGCGCG
GCCGTGCTTTGA

>Ga-NN-cx34.4-G09234 Our modification. Underlined: Intron predicted by Ensembl is included as part of exon. Splice site.

ATGAACCTGGGCCTTCCTCGAGGGCCTCCTCAGCGGGGTGAACAAATACTCCACAGCGTTC
GGCCGCATCTGGCTCGCCATCGTCTTCATTTCCGGCTCCTGGTCTTCCTGGTGGCCTGC
GAGAAGGTCTGGGGCGACGACGAGAAGGACTTCGACTGCAACACCCGGCAGCCCGGCTGT
CACAACGTGTGCTACGACCACTACTACCCCGTCGCCTACACGCGCCTCTGGGCCCTGCAG
CTGATCTTCGTACCTGCCCGTCCCTCCTCGTGACGCTGCACGTCTCCTACCGGGAGGAA
CGGGAGCGCAAACACCGGCTGAAGCACGGGGAGGACTGCCCCCCTGTACGACCACACG
GGGAAGAAGCGGGGGGGCTGTGGTGGACCTACTTCTTCAGTCTGCTGTTAAGATACTG
GTGGACGGCGTGTTCGTCTTCCTGCTGTTCTACATCTACGAAGCCACGTTCCTTCCCGCCG
CTGGTGAAGTGCAACGAGGAGCCGTGTCCCAACGTGGTGGACTGCTACATCGCCAGCCCG
ACGGAAGAAGATCTTCACCATCTTCATGGTGGTGACAGCTTTGTGTGCATCCTCCTC
ACTCTCATCGAGGTCTTCACCTGTGCGGTAAAGAGGCTCCGGGAGTGCTGCCGAGGAGGA
GGTCGCCCGGCGAGAGGGAACCTCCTTCAAGATGGTCCGAACCTCCTCTGAGCGGGAAGGAG
AACTCGGCCTACAAGGAGCCGTTTCGCGCAGAAGGATAAGCGGTGGACAAGGAGAGTTTCG
GCGCCAGCGTACAGCGTCGCCATCTCCTGA

>Ga-cx28.8-G12273 Our modification Underlined: Extended until stop codon

ATGAACCTGGGGCTTCTTGAGAAACATCCTCAGCGGGGTGAACAAGTACTCCACGGTGATC
GGCCGCATCTGGCTCTCCGTGGTCTTCCTCTTCGGATCCTGGTGTACGTGGCGGCGGCC
GAGCAGGTGTGGAAGGACGATCAGAAGGACTTTGTGTGCAACACCCGGCAGCCCGGCTGC
GAGAACGCCTGCTACGACCACTTCTTCCCATCTCGCAGGCGCGCCTGTGGGCCCTGCAG
CTCATCGCGGTGTCCACGCCGTCCCTGCTGGTGGCCCTGCACGTGGCCTACCGGGAGCAC
CGCGAGGAGAAGCACCCCGCGGCTGTACCGGGACAAAGGCAGCCTGGACGGGGGGCTG
TTCGCCACCTACGTGCTCAGCCTGGTCTTCAAGGTGAGCTTCGAGGGCCGGCTCCCTGCTG
GCCTTCTACTACGTGTACGGCGGCTTCGCGGTGCCACGCGCCTGCGCTGCAGCCAGAGC
CCGTGTCCCAACACGGAGGACTGCTTTCATCGCCAGGGCCACGGAGAAGAAGGTCTTCCTC
TACATCATGGGCGCCACCTCCCTGCTGTGCATCGTCTCAACCTGGCGGAGCTGGCCTAC
ATCGTGTGGAAAGCACCTGTGGAAGTGCTTCACGCGGCGGTACGTGCCCGCGGGGGGCCG
GCCGCGCGCGCGTCTCCAGAGGCGACGGGTTCGCGTCCGCGGAGCCCGCATGGGCCCG
CAGGTGGAGGACAGGATGACCCGCAGGTGGAGGAGAGGGTGGACCCGAGGTGGAGGAG
GGGAGGGGCGCGCAGGCCCCCCCGCCCACTGA

>Ga-NN-gjcl-G09243 Our modification. Underlined: Introns predicted by Ensembl are included as part of exon.

ATGAGCTGGAGCTTCCTCACGCGGCTGCTGGAGGAGATCCACAACCACTCCACCTTCGTG
GGGAAGCTGTGGCTCACCCTGCTCATCGTCTTCGCATCGTGCTCACCCTGTTGGGGGA
GAGTCGATCTACTACGACGACGAGCAAGTTTGTGTGCAATCGGGCCAGCCGGGCTGC
GAGAATGTGTGCTACGACGGCTTCGCACCTCTGTCTCACGTTCGCTTTTGGGTCTTCCAG
ATCATCTTAGTGGCGATGCCTTCTCTCATGTACATGGGCTACGCTGTCAATAAGATCGCA
CGAATAATGAGGGCCAAAGGGGGCGGTGGATCTGCTGCAGTTAGAACAGGAGGAGGAGGC
TATACGCACAGGAAGCCAGGAAAATCTGCTTTGGAGCGCGGCAGCACCGGGGCATTGAG
GAGACCGAGGACGACCAAGAGGATGATCCTATGATCTATGAAGTGCCAGAAATCGAGCCC
CCAAAAAGACCGCGGGATCCATTGCAACCCGCACCCAGACCCAAAAATCAGGCATGATGGG
CGCAAGCGCATCAGAGACGAGGGGCTGATGCGGGTCACGTTTTGCAACTGGTGACTCGT
ACGCTGCTTGAAGCAGGCTTCCTTGACAGGCCAGTATTTGCTGTACGGGTTTCGTGTGACG
CCCGTGTGTGTGTGCTCGAGGAATCCTTGTCCCCACAGCGTTGACTGCTTTGTGTGCGGT
CCCACGGAAGACCATCTTCTGCGCATCATGTATGGTGTACACGTCCTTTGCCTCACG
CTCAACGTTTGGGAGATGCTCCATCTGGGTATCGGCACCATTTGTGACATTCTGCGCCGC
CGGCGCCACCAACCTCAGGAAGATGAGTACCAGTTGGGATTGCTGGGCAACAGTGGAGGT
GTGGAGGGCTCAGTAGGCGCTGCAGGGCCGAGGCAGGCTCCGAGGGAGGGTGGGTGGA
GATGGGGCTGCAGCTATGTGCGTTACCCCTTCTCGTGAACACCCCGTCTGCTCCACCT
GGCTACAACATTGTGGTAAAGCCAGAGCAGATGCCGTACACAGACCTTAGCAACGCAAAG
ATGGCGTGCAAGCAGAACCGGGAAAACATTGCCCAAGAGGAGCAGCAGCAATTTGGTAGC
AATGAGGATAACTTTCCACCGCGGGGAGGCCCCGCGTAGCTTTGAACAAAGACATGATC
CAGCAAGCTCATGAGCAGCTGGAGGCGGCCATCCAGGCCTACAGTCAGCAACACCGAGCC
GAGGAACAGCTCGGGGACAACCGGGACGACAAGCCCCAAAGCAACATCATCCTGGCCCAA
CCTCAGCCTCAGCCTCAGCCTCAGAAAAGAGCGCAAGCATAGATTCAAACACGGGAAAGGA
GGCAGCAGTGGAGGAGGCAGCAGCAGCAACAGCAGCAGCAGTAAGTCAGGAGAGGGTAAG
CCCTCCGTGTGGATTTAA

>Ga-NN-gjcl-G06369 Our modification. Underlined: Introns predicted by Ensembl are included as part of exon.

ATGAGTTGGAGTTTCTCTGACTCGCCTGCTGGAGGAAATCCACAACCACTCCACGTTTCGTG
GGCAAGATCTGGCTCACCCTCCTCATCGTGTTCGCGATCGTGTGACGGCCGTGGGAGGC
GAGTCCATCTACTCTGATGAGCAGAGCAAGTTTCGTCTGCAACACGGGCCAGCCGGGCCTG
GAGAACGTCCTGCTACGACGCCTTCGCGCCGCTCTCGCACGTCCGCTTCTGGGTTTTCCAA
ATCATTTCTGTTGACCACCCCTCGCTCTTGTACCTGGGCTACGCCGTCAACAGATCGCT
CGGGCAGATGAGCGGACCGGCTGCGGGGAGAGGAGGCCGGGAAGCCGTATCTGGCGGGC
AGAAGGCAGCACCGCGCGCTCGAGGAGCGGAGGATGACCAAGAAGAAGACCCGATGATT
TCCGAAACGGGAGGGGGAGGGCGATGGCGACGGACCGGTGAAAGGACGCAGCGATCCG
ACAAAGTCTCCGCTGCGGAATGACCGGCCAGCGCATCCAGGAGGACGGACTGATGCGC
ATATATGTCTCTTACGCTCTTGATCCGCGCCGCGCTGGAGGTGGCTTTCTGTTCGGACAG
TATGCCCTGTACGGCTTCGCTGTGCCCCACACCTACGTGTGCTCGGCCAGCCCCTGCC
CACAGCGTGGACTGCTTTGTGTGAGGCCCCACTGAGAAAACCATCTTCTCATCATCATG
TACACGCTCTCCCTGCTCTGCTGGCGCTCAACATATGGGAGGTGCTTCACTCGGCATC
GGCACCATCTGCGAGATTGTGCGCTCGCGCCAGGTGCAGCACCCCGACGACGAGCAGCGT
GGGCTGATGGGGGCACAGGTAGCTCCTCATGAGGAAAGGCTGGGGGCAGATGATTACAGG
CACTACTCTTTTTTCTCGGAATGCCCATCGGCCACCCGGGTACAACGCCGCATCGAGC
CTCTTCTGGTTACGACAAAGCACCGCGACAAGCCGCTACCCAACTCTGACATCAGCGACA
CCAAGACAGCGTCCCGCGAGAACCACGTGA

>Ga-cx47.1-G17416 Our modification. Underlined: Intron predicted by Ensembl is included as part of exon.

ATGAGCTGGAGCTTCTCTACTCGTCTCCTGGAAGAGATCCACAACCACTCCACCTTTGTG
GGGAAAGTGTGGCTGACGGTGCTCATCTTCCGCATCGTGTCTACGGCCGTTCGGAGGC
GAGTCCATCTACTCGGACGAGCAGACCAAGTTCACCCTGCAACACCAAGCAGCCGGGCCTG
GACAACGTCCTGCTACGATGCGTTTCGCCCCCTCTCTCGCACGTCCGCTTCTGGGTCTTCCAG
ATCATCATGATCTCCACTCCCTCCATCATGTACATGGGCTACGCTATCCACAGATAGCC
CGAACACAGAGGAGGATCGCAGGAAGCGCCAGAGGCTCCGCAAGAAGCACACTCCTCAC
TCCAGATGGAGGGAGGGCCACCATCTGGAAGATGTCTTGGAGGAGGAGGAAGATGACGAT
GCTGAGCCCATGATCTACGAGGATCCGCTGGGGGAGCAAGAGGCCAAGCCGAACCGATG
ACCAGCTTAGGCAAAGATCCGCCGAAACACGACGGCCGCGGAAGGATAATGCAGGAAGGC
CTGATGAGAATCTATGTGCTGCAGCTCATGTCCAGAGCTATTTTTGAAATCGCTTTTCTC
GCCGGACAGTATCTCCTCTACGGCTTTTCGAGTTAGTCCATCGTATGTAAGCAAGGATC
CCCCTGCTCCACACAGGGTGGACTGCTTTCATCTCCAGGCCACAGAGAAAACAATCTTCTC
CTCATCATGTATGTGGTGAGCTGCCTTTGTCTGGTGTGAATGTGTGCGAGATGCTCCAC
ATCGGAATCGGCACCTTTCGGGACACCTTGCATGAAGAGGAACCGGGGCATGAGGACG
TCCTACGGCTACCCGTTTTCTCTGAAACATCCAGCCTCTCTCCGGGGTACAACCTTGTG
ATGAAGACAGACAAACCCGGCAGGATCCCCAACAGCCTCATCACCCACGAGCAGAACATG
GCCAACGTGGCCCAGGAGCAGCAGTGCGCCAGCCCGGACGAGAACATCCCGTCTGATTTG
GCGAGCCTGCACCGGCACCTACGGGTGGCCAGGAACAGCTCGATATGGCTTTCAAACA
TATCAAACAAAACCAACCAGCAAACATCGCGGACCAGTAGTCTGTATCTGCGGGCACC
GTGGCAGAACAAAATCGGGTCAATACAGTCCAAGAGAAACAAGGAGCGAGGCCAAATCT
GCCACAGAGAAGGCTGCCACCATCGTCAAGAATGGAAGACCTCTGTTTGGATCTAG

>Ga-NN-cx43.4-G14294 Our modification. Underlined: Introns predicted by Ensembl are included as part of exon. Splice sites. At the first splice site, parts of the exons predicted by Ensembl have been removed

ATGAGTTGGAGCTTCTCTACTCGTCTGCTGGATGAGATCTCCAACCACTCCACCTTTGTG
GGGAAAGATCTGGCTGACTATGCTCATCGTCTTCCGCATCGTGTGACTGCCGTTCGGCGGG
GAATCCATCTACTACGACGAGCAGAGTAAATTTGTCTGCAACACGCAGCAGCCCGGCCTG
GAGAACGTCCTGCTACGACGCCTTTCGCGCCGCTCTCGCATGTTTCGATTCTGGATCTTTCA
GTGATTCTGATCACCAACCCCAACATTATGTACCTGGGCTTTGCCATGCACAGATCGCC
CGCACGGAGGACAGCGAGTACTGCCCCCCCCGACCCAGAAGAAGAGGATACCCATCGTG
AGCCGGGGGGCAGTTTCGGGACTACGAGGAGGCCGAAAACAACGGCGAGGAGGACCCCATG
ATCGTGAAGAGGTGGAACATAGAGAACTCAACAAGGCAGAAAAAGCTCTGGGAAGAAG
CACACGCGCGTTCGGGACTCATGCGGACGGCTGATGAAAGTCTATGTGTGCCAGCTG
CTTTGGCGCACCTCCTTCGAGGTGGCCTTCTCTTTTGGCCAGTATGCTCTTACGGCTTT
GAGGTGATGGCCTCCTACGTCCTGACTCGCTCGCCCTGCGCACACTGTGGACTGCTTT
GTGTCGCGCCCCACCGAGAAGACCATCTTCTGCTGGTGTGTACGTTGTGTCTTTCTC
TGCCTGCTCCTCACAGTCTTTGAAATCATCCACTTGGGGGTCGGAGGCATCCAGGACACC
TTCCGACGGCGGGCCACGCTCTGCTCTCGCACCCCCCTCCGTGCTCTCTCGCCCCGGG
CACGCTGCTCCGCCGGGATACCACGCCACCATGAAGAAGGAGAACTGAAGGGAGAGCCG
AGGAATCCCCAATGGGGGACTCTGGGCGGGAGAGTTTCAGGGACGAGTTGCCCTCATCC
AGGGAGCTGGAGCGGTTGAGGGGTACCTGAAGCTGGCGCAGCAGCACCTGGACCTGGCC
TACCAGGCCGATGAGGGAAGCCCTTCCCGGAGCAGCAGCCCGAGGGCAACCGGGCTGCG
CAGATGGCCCGGAGCAGAACCGCCTCAACTTCGCCAGGAAAAGCAGGGGGAAGCGAGC
GAGAAAGGTAACAAGCTTTTCGAGGGATTTCAACTTAG

>Ga-cx43.4-G02384 Our modification. Underlined: Introns predicted by Ensembl are included as part of exon. cc (2 locations in the sequence): Both places, a third C has been removed to keep the reading frame. The number of Ns has been adjusted to fit reading frame and pattern expected in the second conserved domain.

ATGAGCTGGAGCTTCCTCACGCGTCTGCTGGACGAGATCTCCAACCACTCCACCTTCGTG
GGCAAAATCTGGCTCACCTCCTCATCGTCTTCCGCATCGTGCTGACGGCCGTCGGGGGC
GAGTCCATCTACTACGATGAGCAGAGCAAGTTTCGCGTGC AACACGCAGCAGCCCGGC TGC
GAGAACGTG TGC TACGACGCGTTTTCGCGCGCTGTGCGACATCCGCTTCTGGGTGTTCCAG
GTGATCATGATCACCATCCCCACCATCATGTACCTCGGCTTCGCCATGCAC AAGATCGCC
CGCATGACGACGAGCTACCGCCCCGCAAGCGGATGCCGATAGTGAGCCGCGGCGCC
AACC CGC ACTACGAGGAGCGGAGGACAACGGCGAGGAGGAGCCCATGATCCTGGAGGAG
ATTGAGCCGGAGAAGAAGGAGAAGGAGGCGCGGAGAAGAAGCCGAGCAACAAGCACGAC
GGACGGCGGCGCATCAAGCGCGACGGCTGATGAAGGTC TACGTGTTCCAGCTGCTGTGCG
CGCGCCATCTGCGAGGCTCGTCTCCTC NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
NNNNNNNNNNNNNNNNNNNNNTTCGCCC TGC ccGCACACGGTGAAC TGC TTCGTGTGCG
CGCCCCACAGAGAAGAccATCTTCTGCGCATCATGTACGGCGTGAGCGCCCTGTGTCTG
CTCTCACCCTGCTGGAGATCCTGCACCTCGGCATC AGCGGCATCCGGGACTGTGTTGCG
AGGCCGCGGACGCCGACCCCCCGGCGCACGGCCCCGCCAGCCAGCGTCTCCATCAGC
CGGCAGCCGTCGGCGCCCGGGCTACCACACGGCGCTGAAGAAGTACCCGTCGGGGAAG
ATGGCCTTCCGGGACAACCTGGTGGACTCGGGGCGCGAGTCGCTGGGGGACGAGGCTTCG
TCGCGGGAGCTGGAGAGGCTGCGCAGGCACCTGAAGCTGGCCAGCAGCATCTGGACCTG
GCCTACCAGAACGGGGAGAGCAGCCCGTCGCGCAGCAGCAGCCCCGAGTCCAACGGCACC
GCGGTGGAGCAGAACCGACTCAACTTTGCCCAGGAGAAGCAGAGTGCTACCTGCGAGAAA
GGTGAGGCTTCTTGA

>Ga-NN-gjd2*1-G05651 No modifications. Splice site.

ATGGGGGAGTGGAACATATTGGAGCGCTCTTGGAGGCGGCTGTCCAACAACATTCTACA
ATGATCGGAAGGATCCTGCTGACCGTGGTTCGTGATCTTCCGTATCTTGATCGTGGCCATC
GTGGGAGAGACCGGTGTACAACGACGAGCAGTCCATGTTTGTCTGT AACACCTTACAGCCA
GGC TGC AACAGGCA TGC TACGACAAGGCGTTCCCAATCTCCACATCAGGTACTGGGTG
TTCCAGACCATCATGGTGTGCTGCCCCATCCTCTGCTTTCATCACTTACTCAGTGCAC CAG
TCTACCAAGCAGAAGGACCGGCGCTACTCCACAGTTTTCTCTCCTTGGACAAAGGCATG
GATTTTATGAGGAGAGACAACAGACGGCTCAAGAATACCATTGTGAACGGGATGCTACAG
AACACAGAAAACCTCTAACAAGGAAGTAGAGCCGACTACACTGAGGTAAAGGAAATTCAC
AACTCAGCCATGCAAACTACTAAGTCAAAGATGAGAAGGCAGGAGGGCATCTCCAGGTTT
TACATCATCCAGGTCGTGTTCAAAAACGCACTAGAGATAGGGTTTCTGGTGGGTCAATAC
GTCTGTACGGATTCTATGTCCCTGGGTGTATGAA TGT GATCGATACCCT TGC ATGAAA
GATGTAGAG TGC TATGTTTACGGCCAACAGAGAAAACAGTGTTCCTCGTCTTCATGTTT
GCGGTCAGTGGTATTTGTGTACTGCTGAACCTGGCAGAGCTCAATCATCTTGGCTGGACA
AAGATAAAAACCTGCTGTGAGGAGTGCAGGCTAGGAGGAAGTCCACTTATGAGATCCGG
AACAAAGACTGCCCAAGGATGAGTATGCCAATCTTGGGCACACCCATTACAGGTGACTCT
GCATATGTGTAA

>Ga-gjd1a-G20357 Our modification. Underlined: Intron predicted by Ensembl is included as part of exon. Splice site.

ATGGGGGAATGGACATTTTGGAGAGGCTGCTGGAGGCGGCTGTCCAGCAGCACTCGACC
ATGATCGGAAGGATCCTGCTGACAGTGGTGGTGATTTTCCGTATTCTAATAGTAGGCATA
GTGGGGGAGAAGGTGTACGAGGACGAGCAAAATCATGTTTCATCTGT AACACCATGCAGCCC
GGC TGC AACAGGCT TGT TACGACAAGGCTTCCCCATCTCGCACATCCGCTACTGGGTC
TTTCAGATAATCCTGGTGTGCACGCCGAGCCTGTGCTTCATCACATATTCTGTTTACCAG
TCTGCCAAAAGCGCGTGACCGAAGCTACTCTCTCCTGCATCCTTACATGGACAGCCACGGC
CACGGTGGCCACCACGGGCGCCATCACGACCACCACGCCCCGAAGCTTCACTCTCGCAAC
ATCAACGCGATTCTGGTGCACCCCGACAGCAGCAAGGAGGATCACGACTGCCTGGAGGTC
AAGGAGATCCCCAACGGACCCCGGGGACTCCCGCAAACACACAAGAATGCTAAAGTGCGC
CGGCAGGAAGGCATCTCCCGTTT TACGTCATCCAGGTGGTGTTCGCAACGCACTGGAG
ATCGGCTTCTGGCCGGCCAGTACTTCTGTACGGCTTCAACGTGCCAGGGATGTTTGAG
TGT GATCGCTACCCG TGC GTGAAGGAGTGGAG TGT TACGTGTCTCGACCCACGGAAG
ACCGTGTTCCTGGTCTTCATGTTTGCCGTGAGCGGCGTTTGTGTGCTGCTCAACCTGGCT
GAGCTCAACCACCTCGGCTGG AGGAAGATAAAGACGCCATCCGAGGGGTGCAGGCCAGA
AGGAAGTCAATCTGTGAGGTCCGCAAGAGGATGTTTTCACACCTGTCCAGACCCCAAAC
CTGGGCAGGACGCAGTCTAGTGAGTCAGCCTACGTCTGA

>Ga-gjd2b-G10416 Our modification. Underlined: Intron predicted by Ensembl is included as part of exon. Splice site.

ATGGGGGAATGGACTATACTAGAGAGGCTCCTGGAGGCTGCTGTCCAGCAGCACTCTACT
ATGATAGGAAGGATCCTACTAACAGTGGTGGTCATCTTCCGATTCTAATCGTAGCAATA
GTTGGAGAGACTGTCTATGATGACGAGCAGACCATGTTTGT TGT AACACCTTACAACCG

GGC TGC AACCAGGCCA TGC TACGACAAGGCATTCCCCATTTCACACATTAGATATTGGGTT
 TTTCAAATCATCATGGTGTGCACCCCCAGCCCTTTGTTTTATCACGTACTCGGTGCATCAA
 TCGGCCAAGCAGAAGGAGCGGCGGTACTCAACAGTCTATCTGACGCTAGATAAGGATCAA
 GATTCTACTGAAGCGAGACGAGAGCAAAAAGATAAAGAACACCATTGTTAACGGAGTACTT
 CAGAAACACAGAGAATCCACCAAAGAAGCCGAGCCGGACTGTTTAGAAGTCAAGGAAATC
 CCAAATTCGGCAATGAGAACTACAAAGTCCAAAATGAGGCGACAAGAGGGCATCTCCCGC
 TTTTACATCATCCAGGTGGTTTTTACAGAAACGCGCTGGAGATCGGCTTCTTGGTGGGTGAG
 TACTTCTGTACGGATTCAACGTCCCCTCGGTGTATGAA TGT GATCGCTACCCC TGC ATT
 AAAGATGTGAG TGC TACGTCTCCAGACCTACGGAGAAGACCGTGTTCCTGGTCTTCATG
 TTCGCGGTACGCGGCTTTTGGTGGTGTGAACCTGGCGGAACCAATCATTTGGGCTGG
 AGGAAAAATCAAAACCCCGGTGCGCGGTGTGCAGGCTCGGCGGAAGTCCATTTATGAGATC
 AGAAATAAGGACTTGCCGAGGATGAGTGTGCCTAATTTTCGGCCGCACTCAGTCCAGTGAC
 TCTGCTTATGTGTA

>Ga-NN-gjd2*2-G05764 Our modification. Underlined: Intron predicted by Ensembl is included as part of exon. Splice site.

ATGGGAGAATGGACCATCTGGAGCGCCTCCTGGAGGCCCGCTGCAGCAGCACTCGACT
 ATGATCGGAAGGATCCTGTGACTGTAGTGGTCATCTTCGCGATCCTGATCGTGGCCATC
 GTCGGCGAGACCGTCTATGAGGACGAGCAGACCATGTTCTGTC TGC AACACCCTGCAGCCA
 GGC TGC AACCAGGCC TGC TACGACAAGGCCTTCCCCATCTCCACATCCGCTACTGGGTC
 TTCCAGATCATCTGGTGTGCACGCCAGCCCTCTGCTTCATCACCTACTCGTCCACCAG
 TCGGCCAAGCAGAAAGACCGCCGCTACTCCTTCCTCTACCCCATCATGGAGAGGGACTAC
 GGGGGAAGGGAAGGACGCGGAAGATCCGCAACATCAACGGGATTCTGGTGCAGCACGGC
 GCGCGCGGACGCGCGCGCGGGGGAGGAGGAAGCCGACTGCCTGGAGGTGAAGGAG
 ATCCCCAACGCGCGCGCGGGCCTCACCCACGGGAAGAGCTCCAAGGTTCCGCGGCAGGAA
 GGGATCTCCCGCTTTTACATCATCCAGGTGGTGTTCAGAAACGCGCTGGAGATCGGCTTC
 CTGGCGGGCCAGTACTTCTGTACGGCTTCAGCGTGCCGGGGATTTTCGAG TGC GACCGC
 TACCC TGT CTGAAGGAGGTGGAG TGC TACGTGTCCCGTCCCACGGAGAAAACGGTTTTTC
 CTGGTCTTCATGTTTCGCGGTGAGCGGCATCTGCGTGGTGTCAACCTGGCGGAGCTCAAC
 CACCTGGGCTGGCGCAAGATCAAGGCCGCCATCAGGGGCGTGCAGGCCCGCAGGAAGTCC
 ATCTGCGAGATCCGGAAGAAGACATGGCGCATCTGTCCAGCCGCCAACCTGGGCGCG
 ACGCAGTCCAGCGAGTCCGCCTACGTCTGA

>Ga-GJD3-G08497 Our modification. Underlined: Exon extended until stop codon.

ATGGGGGAATGGAGCTTCCTCAGCGAGCTCTTCGACAGCCTCCGGGCCCTACTCCACCATG
 CTCGGCCGTTTCTGGCTCCTGGTCACCGTCATCTTCGGATGCTGATCCTGGGAACCGTG
 GCAGCGACCTGTTTGAAGACGAGCAGGAGGAGTTACCC TGC AACACCCTGCAGCCGGGC
TGC AAGCAGGTG TGC TACGACATGGCCTTCCCCATCTCCCAGTACAGGTTCTGGGTGTTT
 AACATCGTCCTCATCGCCACGCCAGCCCTGGTCTTCCTCGTGTACGCCGTGCAT CACCAC
 AACAAGAGGGCCGACGCGGCCAAAGCAGCGGCCGGGACGACCTGGCAGATCTC CACTTG
 AGGAAGTTC TACGTCTCAACGTGGTCTTTCGCATACTGGCGGAGGTGGGCTTCCTCGTG
TTCCAGTGGACGCTGTACGGCTTCACGGTGGAGGCCCACTTCCCC TGC AGCCGCTTCCCC
TGC CCCCACGTGGTGGAC TGC TTACCTTCCGCCCCCTCGGAGAAAACCGTGTCTCTCCGC
 TTCTACTTCGGGGTGGGCTGGTGTGCGCGGCCTCCAGCTGCGCCGAGCTTTTCTACAGC
TCCGTGAAGTGGTTCTGCTGCTCGAGGAGGCCGCTCTTCGCCCCGACCGCCGCCACCAC
 GACGACGACGACGAGGAGGCGGGGGCGCGCGCGGGTTCGAGGAGAAAACCGCGA
 GGGGGCGCGGAAGGGCGGTGGCGCGAGCCACAAGGGAGGAGCGCGAGCGGAAGGTCT
 CCGTCCCGCAGCAGAGTGAGGAAGGGCGGAAGTACGCGCGCGCGGGCGCTCGTGGCGT
 GAGGCCGCCCTGCTTTCGAAGCAGGCAGCGGGCGCTCAGGGTCAATGAGTGA

>Ga-cx36.7-G14369 Our modification. Underlined: Introns predicted by Ensembl are included as part of exon.

ATGACGGAGTGGACACTGCTCAAGAGACTCCTGGACGCTGTGCACCAACACTCCACCATG
 ATCGGTGCGCTGTGGCTACCGTCATGGTCATTTTCCGGCTGCTCATCGTTGCTGTGGCC
 ACTGAGGACGTGTACACCGACGAACAGGAGATGTTTGTG TGC AACACGCTGCAGCCGGGA
TGC TCCACCGCT TGC TACGACGCCTTTGCGCCAATCTCGCAACCTCGCTTCTGGGTCTTC
 CACATCATCAGCTCTCCACGCCATCCCTCTGCTTCATCATCTACAGTGGCAC AACCTG
TCCAAGCTG CCCCACAAATGGCACCCGAGGCAACGGCTGGGACAAGGAGGTATCCCAAGG
 CCGGGAGGCCCGGATGTGCGGCAAGGCAGTGGACGCGAGGTGTACGATCGGAGCTGTGAC
TCAGACAGCTGCTCAATTCGCTCCCATAGCACTTGGGTACAGTTTGGCGGATGTGCTA
 GAGGGCGTTACAGCTCACAACCTCCGGAGGGGAGACCACAACAAAGCGATGTCCTTGAGT
 CCTGCTCGAGGTTACGCCGTCTAGAGGCGACTCAAGAGGCCCTCTGGAGCGTTCTGTCT
 AAATGTTACATCTTCCATGTGTTTTGCGGGCTGTTCTGGAGGTGAGTTTTGTGGTGGCC
 CAGTGAAGCTGTTTGGCTTCCAGGTACCTGTCCATTTCTTT TGT ACGTCTGTCCCC TGC
 AGCCAGCCGGTGGAC TGC TACGTCTCCAGGCCACGGAGAAGACCATTTCTTGTCTCTTC
 ATGTTTTGTGTGGGATTTTCTGCATCCTGCTCAACCTGCTGGAGCTCAACCACTTGGGC
TGGAAGAAGATCAGACAGTCTGTGAGGCTGAAGGAGAGGGCGTCTGGGAGGCTGTCCA
GGTATGAAAGGGGGTATGAAACCTTCCCCCAGACAGCCCTGTCTCACAACCTCGTTA

GGCTACAGGGACGTGACCAGCACCCTTCCCTGCCCACCTTGGACCTGGTGGTGGGGCAC
CAGCCTGACTGGACCTGCGCTGTGAACGTGGCAGGATGAGGGAGCATGAGGAGGTCAGA
GAGACGAGACCAGATCAAAACAAAGTCACAGGACTCCCATAAAGGAGAGAGGCAGCCTCTG
AAGAGTAAGACGGCGATCAGAGAGTACAAACAGAGGAGTGCTGAGGTCTGGATATAG

>Ga-NP-cx39.2 Not predicted by Ensembl

ATGGGAGACTGGTCCATTCTTGGCCGCTTCCTAACGGAAGTCCAGAACCATTCCACGGTC
ATCGGCAAGATATGGCTGACTATGCTGCTAATCTTCCGCATCTTGCTTGTGGCTCTGGTG
GGGGATGCTGTCTACAGCGACGAGCAGTCCAAGTTTACC **TGC**AACACCCCTGCAGCCCGGC
TGCAACAACGCT**TGC**TACGACACCTTCGCCCCCGTCTCACACCTGCGCTTTTGGGTCTTT
CAAATTGTGCTGCTCCACACCCTCTATCTTCTACATCGTCTACGTCTTGCAAACATT
ACCAAACATGAAAACTGGAGGACAGGAAGCTTCAAGTGTGCCCGGGCCTCACTTTCA
CTTGAACGGGACAAACACACTGTTAGAGAACAAGAGAGCACACTGGAGGCCCGCAGTCCT
CGTGAAGGGGAATGTGATGGTAAGAGCCAACCTGGAGGAGGATGCGAGAGAGGTAGAAAAG
GACCCGACCCAGCTCTCCAGC **CAAGT**GCTACTTATC **TACAT**CATCCACGTTTTTCTGCGC
TCCATCATGGAGATAATCTTTCTCGTTGGACAGTACTGCTCTTCGGATTGTGAGGTCCCA
AACCTTTTCCGCT**TGT**GAGACCTACCCA**TGC**CAAACAGGACCGAC**TGC**TTTGTGTCCCGA
GCAACAGAGAAGACCATCTTTCTCAACTTCATGTTTCAGCGTCAGTCTAGGCTGCTTTGTC
TTGAACATTGTGGAGCTGCATTATGTGGGCTGGATTTACATTTTCAGGGTGTGTGTTCTCT
GCATGCTGTCCGTGCTGTGAAACAGGTAGAAACCCTGGGCAGCAGGGGGACTTGTACTCT
GACAACAGGCAGGGTTGCCCTGCAGACCACCTTGTTGACCCGTGTTGA

>Ga-NN-cx39.2-G00420 Our modification. Underlined: Extension of exon to reach initiation codon. **N**: One nucleotide added to keep reading frame.

ATGGGTGACTGGTCCATACTTGGTCGCTTCCTGTCAGAAGTCCAAAACCACTCTACAGTG
ATAGGCAAGATCTGGCTCACCATGCGGCTGATTTTCCGTATTCTGCTCGTGGCCTTAGTG
GGTGACGCTGTCTACAGTGATGAGCAGTC**N**ACTCATGTTACATTACAT**TGT**AACACCCAG
CAGCCTGGAT**TGT**AACAACGCT**TGT**TATGACACTTTTGCCTGTTTTGCATCTTCGGTTT
TGGGTCTTCCAAATTGTGCTGGTCTCCACTCCATCCATCTTCTACATAGTTTTTATTCTA
CATAAGATTGCCAAAGATGAAAAGCTGAATGGCCAAAGGGCACAGATGGTAGCCCAGAGG
TATCCCAATCGAGATGTGGGCGCATTGGGAAGGATGGCATGGAGGTCTTAAAGGTTGAC
ATGCCACCTACTGTCTATTACAGGGAAGATTGGGATGCAAAAGAGAGAGAAGGAGTAGAG
CAAAGCTCTCTGGAGGAGGATGGTGGCAAAGTAGGAGAGGACCCTACGCAGCAGTCCAAT
CGGGTTCTGCTCATC **TACATT**CTTCATGTGTTACTACGATCAGTCATGGAGATTACCTTT
CTGGTGGGCCAATTCTTCTTGTTCGGGTTACCGGTGCCCAACTGTACCGCT**TGT**GAGACC
TACCTT**TGT**CCCACACGTACAGAC**TGC**TTTGTGTGCGGTGCCACTGAGAAAACCATCTTC
TTGAACCTTCATGTTTCAGTATAGGTTTTAGCTGCTTTCTACTCAACATAGCAGAGCTCCAC
TACCTTGGCTGGGTCTACATTTTCCGCATCCTCTGCTCGCGCTGTTTCACCTGCTGCAGT
CATGAGAGGGACACTATCAGACTCTACTCAAACCACAACGCCCTCCTGCTGCAGCTAAGG
CATTTCTCTTAGGAGCCAGTTGGCTCTGTAG

>Ga-NP-gjd4(1) Not predicted by Ensembl. **Splice site**

ATGACGGGAATGAGTGGCTCTGAGGTCATCTTCATCTCTGTCAATCACAAACATCACTTTG
AT**GGG**CAAGGTTTGGCTCGTCGTGATCTTCTCCGTATCCTGATCCTCCTCCTGGCT
GGTTATCCTCTCTACACAGGACGAGCAGGAGCGATTCTGT**TGT**AACACCATTTCAGCCCGGC
TGTGCCAACGCT**TGC**TATGATCTGTTTTCTCCCATCTCACTCTTCCGCTTCTGGCTGGTG
CAGCTCGTCACCTTGTGTCTCCCTACTTCATCTTCATTATCTACGTGGTCCACAAGGTC
TCGAAGGGCCTCACAGTGGACCCGTACCCCTCGGGCCGCACCAAAGCCCCACCTTTGCTC
GAGAACCACCAGGAGCCGTTACCAAGACATCTGTAAACAAGACGGCTGAGCACAGGGGG
GCTCGG**TGCTT**CACGGGAGCC**TACAT**CCTCCATCTGTTGTTTCAGAACGTTGCTGGAGGCA
GGGTTTGGGGCAGCTCACTACTATCTGTTGGTTTTCCACATCCCAGGAGGTTCTCT**TGC**
CAGCATCCGCGC**TGC**ACCACCCAGGTGGAC**TGCT**TACATCTCTAGGCCCACTGAAAAGACC
GTGATGCTCAACTTCATGCTCGGCGCGGCTGCTTTGTCCCTTTTCTCAACGTGCTGGAT
TTCTTCTGTGCCATCAAGCGGTGGTGAACAGAAAAGCAAGAGCAGGATGACGGTAGTG
GAGAAGATATATGAGGAAGAGCAATGTTTCCTTTCCGGTAAGCAGGAGAAAAGAGGGGCT
GGTCTCCCGGGGAGCTTCCGAAAAGGCGAGGCAGCAAGGGCTCTAGTGCAGGGCTTGCT
TTAGGTCAGGAACACCCGGCATGGAGCGCTCTTCTCTTCCACTCTCCAGGACATCCT
GGCTGCAACACCAACGGAACAAACGGCTACTCTGTTTCCAGGAGGAAGCTCTGGAAGG
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>Ga-NP-gjd4(2) Not predicted by Ensembl. Exon 1 not found; **Splice site**

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>Ga-GJE1-G13559 No modifications. Splice sites.

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Suppl. Fig. 9. Atlantic herring (*Clupea harengus*) connexins.

Yellow: Conserved domains as defined by Cruciani and Mikalsen (2007)

Green: Conserved cysteine codons (cysteine signature)

Grey: 15 nt added at the ends of the conserved domains

Other colors are explained where necessary.

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>Ch-gjd2like-XM_012817227 Underlined: previously predicted intron is now included as part of exon.

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GGGTTCCGCGTGGAGGCCGCTTCCCCTGCAGCACGTTCCCCTGCCCTACACGGTGGAC
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CTCCTCTCTGCACTCTTACGCCTGGCGGAGCTCATCCACGTCTTCACCAGTGGAGGCGC
CGGAAGAGGGCGGCCATGACGGGGGACCCCCGGACGAGGAGACGTCTGGACGGAACCAG
AAGGAACTCCAGAAACTGACCCAGGTGGCGGTGGGTGACGAGGGTGGCTTGGGGGTTTCAG
AGGGGCAGGAGTGGGAGTGGAGGTGGGAAGAGGGGGCATGGGGGCACTAGTGGCAGCAGC
AGCGGTGGGGGAAGGGAGGGTGTGCTGGGCAGGAGCAACTCCAGCGTCGGACACAAG
ACCTCCAGACACAGCAGCCAGAAGAGCCGCACAGGGTTGTTGTTGTGA

>Ch-gjd4-cx40.1-XM_012823059 Splice site

ATGGGGGGCCAATCTGCGTCTGAAGCCATTTTATTGCTGTCAACCACAACATCACTCTA
GTAGGAAACTGTGGCTGCTCATTATGGTGTTCCTGCGCATTTTCATCCTCATCTTCGCT
GGATACCCACTCTATCAGGATGAGCAGGAGCGATTTGTGTGCAACACCATTTCAGCCAGGC
TGTTCAAATGTGTGTACGACCTATTGCTCCCCCTTTCCCTCTTCCGCTTCTGGTTGCTT
CAGCTCACCATCCTCTGCCTGCCATATTGACGTTTCGTACCTACATCATTCACAAAGTG
CTGTGAGATATCGCTGTTTTCTCTGACGCGTCACACAAGATGAAAGCCAGGTCTCTCATT
GGAATCCAGCAGGGATCTCTCCAGAAAGGAGCCCTAAGCAAGGCACGTCACATCCAGGCA
GAGCTCAGCACGTTGAGGACCTTCACTGGAGCTTACATCACCCAGCTGCTCCTCCGGATT
CTTTTCGAGGCTGGCTTTGGGGCGGCTAACTACTATCTATTTGGCTTCTACATCCCCAAG
CGCTTCCTGTGCCAGCAATCACCTGTACAACCTACAGTAGACTGCTATGTCTCCAGACCC
ACAGAGAAAACCTGTTATGCTGAACCTTCATGTTAGGGACGCGCCGGCCTTTCCCTTCTTCTC
AACGGGTTGGACATGATCTGTGCCATCAAGCGCTCCGTGAGGCAGAAGTCCAAGAGGAAG
ATGCTGGTGCGGAATATGTACGAGGAGGAACAGTTCTACCTCTCCCCTGAGGGGAGCCAG
GGAGCCATCGATGCCAACGTTTCCACAGTGGAGGAGATGGTGGCCTCAGTAGCAAGCGGA
AGTTTCCGGAAGAGAGGGATGAGTAAGTCCAGCAGGGCCGATCTGGAGGACGCTCCGTGT
GGTCGAGGGACACCTCTGTCCCGGGATGCTGGGTCTACAAACGCTCACAGTGAGAAT
AATGTCTATCCAATCCCGGCTCTGGAGGAATGCCCGGACCGAGAGGGCAGTGAGGTGGCA
CTGTGTCCACAGAGCAAATGGGCACGCCAGACCCATACGGGTGAGTAAACGGAGCCGC
CTGAAACCAACCCCGCCGCCAGACGGGACAACCCCTTGGGGCGGGTTCTGTGGACGTG
GTTCCAGGAGCGACGGCACTGTGCACCAGAAGAGTCGGACACTACACACTGGTGGAGATG
AGTGGCGTTGGCCTGCCCTCGTGCAGTGGGGACAACCAGGAGAAAAGGTCAGAGTGGGTC
TGA

>Ch-gjellike-XM_012822376 Splice sites

ATGTCTTTAAACTACATCAAGAAGCTTTTATGAAGGATGCTGCGGCCTCCCACTGTGATT
GGCCAGTTCCACACTTTGTTCTTTGGCTCTGTGCGCATGTTCTTCTGGGGGTTCTGGGA
TTTGCAGTTTACGGAAATGAAGCCCTTCACTTTAGCTGTGATCCAGACAGCAGGGAACCTC
AACCTCTTCTGTTATAACCAAGTTTCGACCGATAAATCCGCAAGTTTTCTGGGCCTTGCAA
CTGGTGACTGTTCTCGTACCTGGGGCTGTTTTCCACCTCTATGCTGCTTGCAGAACATT
GACCAGGAGGACATCTTAGAGCGGCCCATCTACACTGTCTTCTACATCATATCTGTGCTC
CTGCGGATCATTCTAGAAGTGGTGGCTTCTGGCTTCAAAGCCACCTGTTTGGCTTCCAA
GTGCACCCCTGTACATGTGACGCCAGCGCTGGAGAAGGCCTACAACCTTCACCAAG
TGCATGGTGCCTGAGCACTTTGAGAAGACCATCTTCTCAGCGCTATGTACATTTTACC
ATCATCACCGTTGTGTTGTGTGCTGAGATCTTTGAAATACTTTGCAGGAGACTTGGC
TATTTAAGCAGTCCATGA

Suppl. Fig. 10. Atlantic cod (*Gadus morhua*) connexins.

Atlantic cod, *Gadus morhua* (Gm).

Assembly: gadMor1, Jan 2010.

Genebuild: Aug 2011.

Database version: 98.1.

Yellow: Conserved domains as defined by Cruciani and Mikalsen (2007)

Green: Conserved cysteine codons (cysteine signature)

Grey: 15 nt added at the ends of the conserved domains

Other colors are explained where necessary.

The Ensembl gene abbreviation is as follows: ENSGMOG00000009844 = G09844.

>Gm-NN-gja1-G09844 Our modification. Underlined: Predicted as intron by Ensembl; here included as part of cds. Lower case letters: Located on an unplaced contig (in the scaffold, there is just a row of Ns). The chromosomal cod assembly in GenBank (GCF_902167405) and the subsequent gene prediction XM_030362165 confirmed that the lower case letter sequence indeed is a likely part of the cds. In fact, XM_030362165 predicts that the lower case sequence should be extended approx 90 nt in 5'-direction. **Splice site.**

ATGGGAGACTGGAGCGCTCTGGGGAACTGCTGGACAAAGTCCAGGCCTACTCCACAGCC
GGAGGCAAG**GT**ATGGCTCTCCGTCCTCTTCATCTTCCGTATCCTGGTCATCGGTACTGCG
GTGGAGTCTGCGTGGGGCGACGAGCAGTCGGCCTTCAAG**TGC**AACACCGCCAGCCGGGC
TGTGAGAACGT**TGC**TACGACAGCTCCTTCCCCATCAGCCACGCACGCTTCTGGGTCTG
CAGATCATCTTCGTCTCCACGCCAACGCTGCTCTACCTCTGCCACATCTTCTAC**CTCATC**
CACAAGGAGGAAAA**Ga**tgaagtacggcatcgagaagaacggaaggtgaagatgaaagga
gctctgctcaggacc**tacatcttcagcatcctgctcaagtccttctttga****gGT**GGGCTTC
CTACTGCTGCAGTGGCACATCTACGGCTTCAGCCTGGCGCTCGCGCTACGAG**TGC**GAGGCG
TACCC**TGC**CCCCACCGCACCGAG**TGC**TTCCTGTGCGGGCCACCGAGAAGACCATCTTC
ATCGTCTTCATGCTGGTGGTCTCCCTGGTGTCCCTGCTGCTCAACCTCATCGAGCTCTTC
TACGTCACTACAAGTGGGTCAAGGACACCATGAGGGCGTCCGAGGGCCAGCAGCTCCAC
CCCCGCCTCCGCTGTGCGGGGGCCGGAGGAGGAGTGGGAGGAGGAGTGGGAGGA
GAAGAAGGAGGAGCGCGTACCCTACTGCAACGGCTGCCCCCCCCCTCCGCCCTGTC
TACAACCTGGATGCCACGGCGACGGTGGCAAGGGGCGACTCGGTGAACCACTACAACAAG
ACGGCGAGCGAACAGAAGTGGACCAACTTCAGCACGGAGCAGAACAGCTGGGCCGCTCC
CCGCCCCGTGCGCCACGGCAGCCAGCGCAGTACCGGCAAGAACAACAACAACAATAAC
CACAACAACAAGGCCGGCGCCAACGCGAGTGACTGCAACCGCGACAGCCCTGCCTTCCTG
GGCCCCGCTTCGTAGCCCCCGCCACGGCCAGCCACCGCCGTGGGACAAGGTGGAGACC
AAGGAGCTTACCTCTCCGGGGGCTGGAGCCGCGGCCCGGCGAGCCGCGCTCCAGCCGC
GCCCCGACTGACGACCTGGACATCTGA

>Gm-cx43-G20304 Our modification. Extended in 3'-direction. No reasonable stop codon in frame, but in other reading frames, there are translated sequences that become reasonable similar with other GJA1 orthologs. Hence, potential small intron or sequencing error towards 3'-end.

ATGGGTGACTGGAGTCTCTGGGCCGCTGCTGGACAAAGTCCAGGCCTACTCCACCGCT
GGGGGGAAGGTGTGGCTCTCCGTCCTCTTCATCTTCCAGGATCCTGGTCCTGGGACGGCC
GTGGAGTCCGCCTGGGGCGACGAGCAGTCGGCCTTCAAC**TGC**AACACTCAGCAGCCCGGC
TGCGAGAACGT**TGC**TATGACAAATCCTTCCCCATCTCCCATGTGCGCTTCTGGGTGCTG
CAGATCATCTTCGTGTCCACGCCACGCTGCTGTACCTGGCCACAGTCTTCTAC**CTGATG**
AGGAAGGAGCAGAAGCTGAACAGGAAGGAGGAAATGCTGAAGGCCGTGCAGAACGATGGC
GGCGACGTTGACATCCGCTGAGGAAGATCGAGATGAAGAAGCTGAAGCACGGCTGGAG
GAGCACGGCAAGGTGAAGATGAAGGGC**GCCCTGCTGAGAACC**TACATCGTCAGCATCTTC
TTCAAGTCCATGTTTCGAGGTGGGCTTCTGGTCATCCAGTGGTACATATACGGCTTCAGT
CTGGCAGCGGTGTACACC**TGC**GAGAGAGAACCC**TGT**CCCCACAGGTGGAC**TGT**TTCTTG
TCTCGGCCACAGAGAAGACGGTGTTCATCATCTTCATGCTGGTGGTGTGCTGGTGTCC
CTGCTGCTCAACGTCTACGAGCTCTTCTACGTGTTCTTC**AAGAGGATCAAGGAC**CGTGTG
AAGGGCCGCCAGCCGCCACCCCTTACCCACGCGTGGCACCCCTGAGCCATACCCCAA
GATCTTCCACAGCCAAGTACGCTACTACAATGGCTGCTCTCCCCACCGCCCCGCTC
TCGCCCATGTCCCCGCCGGGCTACAAGCTGGCCACGGGCGAGCGCGGTACCGGCTCATGT

CGCAACTACAACAAGCAAGCCACCGAGCAGAACTGGACCAACTATTCCACGGAGCAGAAC
 CAGCTGGGCCAGCAGCGCGCGGGCAGCACTATCTCAAACCTCCACGCGCAGGCTTTTGAT
 TTCCCGACGATACGCACGAGCATAAGAACTGACGTTCATCCGAGCTGCACACGAGATG

>Gm-NN-gja3-G09100-2 Our modification. **Splice sites**. This Ensembl prediction contains two separate and unique connexins sequences, the present and a cx30.3 sequence.

atgggtgactggagctttctgggacgccttctggagaatgctcaggaacactcaactgtg
 atcggcaaaggtgtgtgtgacgcgtctcttcatcttccgcattctgtgtgtggcgcgcc
 gcagaggaggtgtgggagacgagcagtcggacttcaccTgcgaacacgcagcagcccggt
 TgcgagaacgtctTgctacgaccagccttccccatctcccaactgctgcttctgggtgctg
 cagatcatcttctgtgtccacgcccacgctcatctacctggggccacgtgctgcacatcgtg
 cgcattggaggagaagcggtgagaaggaggaggagctgcgaaggcggtgtggcgacg
 gaggagctcctcgggcaNNNNGGAGGCGGGAAGAAGGAGAGGCCGCCGATCCGCGACGAG
 CACGGGAAGATCCGCATCCGCGGGGCGCTGCTCCGGACC**TACGTCTTCAACATCATCTTC**
AAGACCTTCTGGAGGTGGGCTTCATCCTGGGCCAGTACTCCCTCTACGGCTTCCGCCTC
AAGCCGCTGTACAAGTGCGGCCGCTGGCCT**TGCC**CCCAACACGGTGGAC**TGC**TTTCATCTCC
AGGCCCACTGAGAAAACCATCTTCATCATCTTCATGCTGGTGGTGGCCTGCATCTCCCTG
CTGCTCAACCTGCTAGAGATGTACCACCTGGGCTGGAAGAAGGTCAAACACAGCGTCACC
 CACAAGTTTCGCGGCTGACTGCGGGTCCCTGCGGCTGGGCCCCGGCGACGACGCCGGCGAC
 CCCCCGGCGGTCCCCGAGTGCGCCACCCTGGTTTCGGACCACTGCCTGCAAGGCTACACC
 GGCAGGAGCACCATGGAGCGGGTCCGCTACCTGCCCCGTCCAGAACTCCTC

>Gm-gja3-G04087 Our modification. Ensembl-predicted introns are included (underlined). There is probably an intron or something wrong in the 3'-end (after the conserved domain), but we have not tried to solve the problem here. In the first conserved domain at the position indicated by lower case "ga", the Ensembl sequence indicates a row of approx. 100 Ns. "ga" has been found by Blast against GenBank cod wgs.

ATGGGCGACTGGAGCTTTCTGGGCCGGCTTCTTGAGAACGCGCAGGAGCACTCGACGGTG
 ATCGGCAAGGTCTGGCTCACCGTCTCTTCATCTTCCGCATCCTAGTGTGGGTGCCGCA
 GCAGAGGAGGTGTGGGGCgaCGAGCAGTCGGACTTCACC**TGCA**ACACGCAGCAGCCCGGT
TGCGAGAACGTCT**TGC**TATGACCAGGCCTTCCCCATCTCCACATCCGCTTCTGGGTGCTG
 CAGATCATCTTTGTGTCCACTCCCACGCTCATCTACCTGGGCCACGTGCTGCACATCGTG
 CGCATGGAGGAGAAGCGCAAGGAGAAGGAGGAGGAGCACCGCAAGGTGACGGGGTTCCCC
 GATGACAAGGAGCTGCCGTACCGGAACGGGGCGGCGGTAAAAAGGTGAAGCCGCCGATC
 AGAGACGAGCAGCGCAAAATCCGCATCCGCGGGGCTTGTGCGTACC**TACGTGTTCAAC**
ATCATCTTCAAGACTCTGTTTGAGGTGGGCTTCATCCTGGGCCAGTACTTCCTGTACGGC
TTCTCGCTGCGGCCGCTCTACAAGTGCTCCCGTTGGCCG**TGC**CCCAACACGGTGGAC**TGC**
TTTATCTCCAGGCCACGAGAGAAGACTATCTTCATCATATTTCATGCTTGTGTGGCTTGT
GTGTCGCTTTTACTCAACCTGCTGGAGATCTACCACCTGGGCTGGAAGAAGCTGAAGCAG
 GGCCTGTACCAACCCGACCACTGCTGCGGGCGCCGCGCCAGCTGGCCACGCGCGAGGGC
 GTGGCCTGCTAGGGGCCCGGCTCTCTCAACTACCCCCCACTACAGCCACATAGCG
 GCCGGCATGGGGTCCCCACCGACGCCGAGTTCAAGATGGAGGAGCTCCAGCGGGAGGAG
 GGGGCGCGGACGCCTCCCCGACTCCCCCGGCCGCCCCACTACTACATCAGCAGCAACAAC
 AACCACCGTCTGGCCGACAGCAGAACTGGGCCAACCTGGCCACCGAGCAGCACACCCGC
 CAGATGAAGGCCACCTCCCCACCCCCACGTCCTTCTCCTCCTCAAGCAGTGAAGCGGCC
 CCGCCCTGCTCAACTAGCCCCACCCCTTAATGGCAACCCCGGGCAACGCTGCAGCCCCC
 GGTGATGTGGCGACAGCGCGACGGAGCCGGCTGACCCCCGAGCCGGCCAGCGGGAG
 GAAGAGGATGTACCATGGCGACGGTGGAGATGCACCTGGAGGGGGTGTTCOCGGAACCC
 CGGCGCTTAGCAGAGCCAGTAGAAGCAGCATCCGCGCCCGGCACGATGACCTCGCCATC
 TGA

>Gm-NN-cx39.9-G20599 Ensembl prediction. No modifications

ATGGCCGACTGGAACCTGCTAGGGAAGCTGCTGGAGGCCGCTCAGACACACTCCACCGTG
 GTGGCGAAGGTGTGGCTACCGTGCTCTTCATCTTCCGCATCCTGGTTTTGGGCACGGCC
 GCCGGAAGGTTTGGGGCGCAGAGTCGTCGGGCTTCACC**TGC**GACACCAAGCAGCCTGGC
TGTCAGAACGTCT**TGC**TACGACCGTACCTTCCCCATCTCCACATCCGCTTCTGGGTGCTG
 CAGATCATCTTCGTGTCCACGCCCACGCTCATCTACCTGGGCCACATCTGCACCTGGTG
 CGCATGGAGGAGAAACAGACGCAGAAGGAGAAGGACCGCGAGGAGGAGGCCGCCGCGCG
 GCCGAAGGTGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGCAAGGCCAAGAAGGGGCCG
 GTGAAGGACGGCCAGGGCCGGGTGCGTCTACAGGGGAGCTGCTGCGGACG**TACGTCTTC**
AACATCATCTTCAAGACGCTGTTTCGAGGTGGGCTTCCTCGTGGCCAGTACATGCTGTAC
GGCTTCCAGCTGAAGGACATGTACACC**TGC**GACCACTGGCCC**TGC**CCCAACATGGTGAAC
TGCTACATCTCGCGGGCCACCGAGAAGACCATCTTCATCCTGTTTCATGCTGGTGGTGGCC
TGCGTGTGCTGCTGCTCAACCTGGTGGAGATCTGCCATCTGGGCTTCACCAAGTTCCAA
 AAGGGCCTCTGCTTCCTCTGCCAACGCCGAAGAACGCGGAGCCAGCGAGACACCCAAC

TACAACGACTACACGGAT

>Gm-cx39.9-G14144 Our modification. Ensembl-predicted introns are included (underlined). Has been extended by Blast into GenBank cod wgs (lower case).

ATGGCCGACTGGAACCTGCTGGGGAAGCTGCTGGAGAGCGCCAGACGCACTCCACCGTG
GTGGGCAAGGTGTGGCTCACCCTGCTCTTCATCTTCCGCATCCTGGTTTGGGCGCAGCC
GCCGAGAAGGTTTGGGGCGACGAGTCGTCGGGCTTCACC TGC GACACCAAGCAGCCTGGC
TGT GAGAACGTCT TGC TACGACCGCACCTTCCCCATCTCCACATCCGCTTCTGGGTGCTG
CAGATCATCTTCGTGTCCACGCCACGCTCATCTACCTGGGCCACATCCTGCAC CTGGTT
CGCATGGAG GAGAAGCAGCAGCAGAAGGAGAAGGACCGGAGGAGGAGCAGCACTGCAC
AGCGAGGAGCGCCGGCTGCTGGCGGCCGAAGGAGGAGGTGGAGGCAAG GCC AAGAAGGCG
CCGGTGAAGGACGGCCAGGGCCGGGTGCGTCTGCACGGGTGCTGCTGCGGACGTACGTC
TTCAACGTCATCTTCAAGACGCTGTTCAAGTGGGCTTCATCGTGGCGCAGTACCTGCTG
TACGGCTTCCAGCTGAAGGCCATGTACACCT TGC GACCGTTGGCCC TGC CCAACACGGTC
AAC TGC TATATCTCGCGGCCACCGAGAAGACCATCTTCATCCTGTTTCATGCTGGTGGTG
GCCTTCTGTGCTGCTGCTCAACCTGGTGGAGATCTACCACCTGGGCTTCACC AAGTGC
CACCAG GGCCTCCGCTTCCGGCGCTCGCGCCAGAGGAAGGCCGAGCTGACCCGGATGCC
AGCGAGGCGCCGGCTGATGCTGTCCTTGTCCCAACTACAATACTACACCGCGCACGCG
CAGCGCGCGCGGggggggcgggcgggcggtggcgggaggcctttcagggcgactcc
agctacggcctggccgagcccgggcgccgacctacagcaaccctacagcagcaagcc
gtgtccaagcagaaccgcgacaacctggcggtggagcgcgggcgagagcgacgacgcc
ggcgcgggcgggcgggcgggcggttcctcgagagaccggcgagaaacagcgacgcaac
agccagacgagcaaacacagcaacactaagacgcgcgcgacgatctgaagatctag

>Gm-NN-cx39.9-G20196 Ensembl prediction. No modification.

ATGGGGGACTGGAACCTGCTCGGCAAGCTCCTGGAGAACGCCAGGAGCACTCCACCGTG
GTGGGCAAGGTGTGGCTCACCCTGCTCTTCATCTTCCGCATCCTCATCCTCAGTGCAGCC
ACTGAGAAGGTGTGGGGCGACGAGCAGTCGGGCTTCACC TGC GACACCAAGCAGCCCGGC
TGC GAGAACGTG TGC TACGACGTCACCTTCCCCATATCCCATGTGCGCTTCTGGGTCTTG
CAGATCATCTTCGTCTCCACGCCACGCTCATCTACCTGGGACACATCCTCCAC CTGGTG
CGCATGGAG GAGAAGCAGCAGCAGAGGAGGACAAGCTGAAGGAGCAGCCCGGGGAGAAGCAG
GGCCTGATGGAGGTGGCCAAGCCCAAAAAGCTGGTGCGGGACGACCGGGGTGCGTGCAGC
CTGCAGGGGGAGCTGCTGCGCACCT TACGTGTTCAACATCATCTTCAAGACCCTGTTTCGAG
GTGGCCTTCATCGTGGCGCAGTACCTCCTGTACGGCTTCGAGCTGAGGCCCATGTACACG
TGC GACAAACACCCC TGC CCAACACGGTCAACT TGC TACATCTCCCGGCCACCGAGAAA
ACCATCTTCATCATCTTCATGCTGGGCGTGGCCAGCGGTGTCGCTGCTCCTCAACCTGGTG
GAGACTACACCTGGGCTTC ACCAAGTGTGCGCCAGGGCATCAGTACCGGAGGGGGCGG
CTGCTGGCCGCGCAGCCGCGGAGGCTAAGTCCAAGGAGCTCAGCGACGCGGTGGCG
CCCTTCGCGCCACCTACGACGACTACTTCCACGGGCACCAAGGTGTCGCGCGGTAC
CCGCGGTGCCCCGGCTACAACGTCTCCCCCTGTGCGAGGAGACAGACTCTCCCTTCCAG
CCGTACCACAGCAAGGCCGCTACAAACAGAACAGGACAACCTGGCGGTGGAGAGGAGC
GGCAGCAGCAGGCCGAGGAATGCGACCCGAGAGGTAAGAGTACGGGCGCGGGGTGCGCG
CCGGGTACCGGGCTGGCGAGGTCCAGCGGCTGGTGGTCTGTCATGGCAAGCACAGCAAC
AACAAGACTAGAAATAGACGATCTGAAGTCTGA

>Gm-cx39.4-G20255 Our modification. Extended in both 5' and 3'-directions (underlined).

ATGTCCCGGGCCGACTGGTCCTTCTGAGCACCTGCTGGAGGAGGGCCAGGAGCACTCG
ACGCGCGTGGGCGCGGTGTGGCTCACCCTGCTCCTCCTGTTCCGCATGCTGGTGTGGGC
GTGGCCGCCGAGTCGGCTGGGACGACGAGCAGTGCAACTTTGTG TGC AACACGGAGCAG
CCCGGC TGC GAGTCGGTG TGC TACGACCGCGCCTTCCCCATCTCCCACTTCCGCTACTTC
GTGCTG CAGGT CATCTTC TGC TCGCCACGCCACCATCTTCTACTTCGGCTACCTGGCGGTG
CGCACGGCCAAGGAC CAGTCCGAGGAGGAGGAGGCGGAGGAGGAGGACGGGGTGGCGGAG
GGGGAGAGGGCGGCGCAACAAGAGGGGCGGGGCCGAAGCGCGCGGTGGCGTCTCCGGG
GCGAGGGCGGCTAGGAAGGGCAAGGGACTGGAGGTATCCAGGAAGAGGGGGGCGAGGAA
GAGGGCTTGCAGAGAACGCCGGAAGGCCGCAAGGAGGCGTGGAGTCTCCGAAGCTG
AAGGGGAGGCTGCTGGGGGTG TACACCGTCACCATCTCCGTACCGTGCTCCTGGAGGCG
GGCTTCATTTGCCGGCCTGTGGGTGCTGTACGACGGCTTCGTGATCGCCGCGCGCTACGAG
TGC GTGGGGCTGCCC TGC CCAACACGGTGGACT TGC TCGTGTGCGGGCCACCGAGAAG
ACCATCTTCACCATCTACACGACAGGCCATCGCCGGCCTCTCCCTGCTGTGAACCTGCTG
GAGCTCCTCCACCTGCTCCAG CTGGCCGTCTCCAG CGACTGGAGAAGCGCTACCGCCGC
GGCGCCACCTCGCTGCGGTGCGCGCGGTGGCGGCGGGCGCAACCGGGGGGAGACCACAC
CCCCATCCAACCTCCGGCGCAAGAAGCCCTTCGTACTGCCCCGCGTCCCCGGAGAGGG
CTACCCGAGCCCCCGGAGCTACGTGGTGGTGGACACCTGAGGTCCGAGGTGAACCTG
GGGGGCGGCGGGGAGCGGGGAACGGCGAGGGCGACATCCCGCCAGCTACCTGAACCTG
CTTGGGCGGGATGCGCAGCACACATTTCCCCAGGGCCACGTGAAGAAGCAGCTCCACGG
CAACGGGAACACAGAAAAGACAACCATAA

>Gm-GJA5-G04028 Our modification. Ensembl-predicted introns are included (underlined). Runs into row of Ns.

ATGGGGGATTGGAGCCTGCTGGGTAACCTTCTTGGAGGAGGTGCAGGAGCACTCCACGTCA
GTGGGCAAGGTGTGGCTACCGTGCTCTTCATCTTCCGCATCCTGGTGTGGGCACGGCC
GCCGAGTTCGTCTGGGGCGACGAGCAGATCGACTTCCTGTGCACACGCTGCAGCCCGGT
TGACCAACGTGTGTACGACAACGCCTTCCCCATCGCCACATCCGCTACTGGGTGCTG
CAGATCGTGTTCGTGTCCACGCCGTGCTCATCTACATGGGCCACGCCATGCACATTGTG
AGGCGCGAGGAGAAGCGCCGGCGCCGGCAACAGGAGGGCCAGGAGGAGGAGGAGGAGGAG
GACGACGACGAGGACGGAGGAGGAGGGGAGGAGGCGGGGGAAGAGGCACGACGCGGAG
CGCGAGAAGGAGTACCTCCAGCAGAAGGAGAGCGGGAAGGGCGAGGGCATGGGCCGCGTG
CGCTTGAAGGGGGCGCTGCTGCAGACCACGTCCTCAGCATCCTGATCCGCACGGTGATG
GAGGTGACCTTCATCACCGTGACGTACCTGATCTACGGCGTGTTCCTGAAGGCGCTGTAC
CTCTGCAGGCGCTGGCCCGCCCAACCCCGTCAACGTGTACATGTCGCGGCCACCGAG
AAGAACGTGTTTCATGCTGTTTCATGCTGGTGGTGGCGGGCGTGTCCCTGCTGCTGTCGCTG
GTGGAGTCTACCACCTCGGCTGGAGGCGCTCCGGAAGTGCCACCGC

>Gm-gja8a-G19707 Ensembl prediction. No modifications.

ATGGGGGACTGGAGCTTCTTGGGGAAACATTTTAGAGGAAGTGAACGAGCACTCGACGGTG
ATCGGCCGGGTGTGGCTACCGGTGCTCTTCATCTTCCGCATCCTGATCCTGGGGACGGCG
GCCGAGTTTGTGTGGGGCGACGAGCAGTCCGACTACGTGTGAACACCAACCAGCCCGGT
TGCGAGAACGTGTGTACGACGAGGCCTTCCCCATCTCCACATCCGCTGTGGGTGCTG
CAGATCATCTTCGTGTCCACGCCGTGCTGGTCTACGTGGGCCACGCCGTGCACCATGTG
CACATGGAGGAGAAGCGCAAGGAGCGCGAGGAGGCGGAGCTCAGCCGCCAGCAGGAGCTG
AGCGAGGAGCGGCTGCCGCTGGCGCCGACAGGGCAGCGTGCGCACCAACGAAGGAGACC
AGCACCAAGGGCAGCAAGAAGTTACGGCTGGAGGGCACCTGCTGCGGACGTACATCTGC
CACATCATCTTCAAGACGCTGTTTCGAGGTGGGCTTTGTGGTGGGCCAGTACTTCTGTAC
GGCTTCCACATCCTGCCGCTGTACAAGTGAGCCGCTGGCCCGCCCAACATCGTGGAC
TGCTTCGTGTCGCGCCCCACCGAGAAGACCGTCTTCATCATCTTCATGCTGGCCGTGGCG
TGCGTCTCGCTCTTCTCAACTTCGTGGAGATCAGCCACCTGGGCCTGAAGAAGATCCCG
TTCGTGTTCGCAAGCCGGCGCCGGCCCCGGCGCCCGGGGAG

>Gm-NN-gja9-G09903 Our modification. Underlined: Extension of sequence into Ensembl-predicted intron. Splice site. Lower case letter: Found by Blast in GenBank cod wgs.

ATGGGGGACTGGAACCTCCTGGGGGGGATCTTGGAGGAGGTCCACATCCACTCCACCACG
GTGGGCAAGATCTGGCTGACCATCCTGTTTCATCTTCCGCATGCTGGTCTGGGCGTGGCG
GCCGAGGACGTGTGGAACGACGAGCAGAGCGCCTTCGTCGAACACGGAGCAGCCGGGC
TGCGAGGCGCTGTGTACGACCGCGCCTTCCCCATCTCCCTGATCCGCTACTGGGTGCTG
CAGgtgatcttcgtgtcgccccctcgctggtctacatggggccacgcctgtacgcctg
cgggcgctggagaaggtccgccagcgccgcaaggcctcctccgcccagctggagctgc
tggaacgcggcgggcgctcgggcgcgcgcgggcgcgcgaggcggaagcagGCAG
GTGGAGCAGGGCCGGCTCAACAAGGCGCGCTGCGGGGGCGCTGCTGCGCACCTACGTG
GCGCACGTGTTACGCGCTCGGCCGTGGAGGTGGGCTTCATGGCGGGCCAGTACCTGCTG
TACGGCGCGCGGCTGCGGCCGCTGTACCGCTTGCGAGCGCGCCCCCGCCCAACGCCGTG
GACGTGTACGTGTCGCGGCCACCGAGAAGAGCGTGTTCATGGCGTTTCATGCAGGCCATC
GCGGGGGTCTCCCTGCTGCTCAACCTGCTGGAGATCCTGCACCTCGGCTACAAGAAGCTC
CGCAAGTCTTCAGTACGG

>Gm-cx52.9-G20571 Ensembl prediction. Ensembl sequence runs into a row of Ns, and this part has been extended by Blast into GenBank cod wgs (lower case).

ATGGGGGACTGGAACCTCCTGGGGGGGATCTTGGAGGAGGTCCACATCCACTCCACCATG
GTGGGCAAGATCTGGCTACCATCCTTTCATCTTCCGCATGCTGGTCTGGGCGTGGCG
GCGGAGGACGTGTGGAACGACGAGCAGTCCGACTTCATCGAACACGGACCAGCCGGGC
TGCCGCAACGTGTGTACGACCGCGCCTTCCCCATCTCCCTGATCCGCTACTGGGTGCTG
CAGGTTCATCTTCGTGTCTTCCCGTCCCTCGTCTACATGGGCCACGCCATCTACAGCTG
CGTGCCCTGGAGAAGGAGCGCCACTGCAAGAAGTCGGCGCTGCGGCGGAGCTGGAGGCG
GTGGAGGCGAGCATCGGAGGTGCGGCGCCGGATCGAGCGGGAGATGCGGCAGCTGGAG
CAGGGCAAGTGAACAAGCGCCGCTGCGGGGCTCGCTGCTGCGCACCTACGTGGCCAC
ATCGTGACGCGCGCCCTGGTGGAGGTGGGCTTCATGTCGGGCCAGTACCTGCTCTACGGC
CACCGCTTGGACCCGCTGTTCAAGTGAGCGGGAGCCCGCCCAACCTGGTGGACGTG
TTCGTGTCGCGGCCACCGAGAAGACGTTTCATGATGTTTCATGCAGGCCATCGCCTGC
ATCTCGCTGTTCTCAGCGTGTGGAGATCCTGCACCTGGGCTACAGGAGGCTGAAGAAG
GGCCTGCTGGACTACTACCCCCACCTCAAGGACGACCTGGACGAGTACTACGGCAGCAAG
TCCAAGGAGAACTCGACGGCGCACAGGTGTGCACGGGGCGCCTCGGCGGGCGCGCAAGCCC
ACCTCCCCACCGCGCCAGCGGTACACGCTGCTGCTGGAGAAGCAGGGCAACGGGCCG
ACCTACCCCTCTCAACACCTcccccgcttcgtcccccgctcccccgagctcggc
ggggggcgagacggccccgggagccgaacgaggcgctggcgcgcggtgttgcc
ccggtccacggagcagaacagcaactccaacaacacggcgctcgagccgctccccgc

cgcggaacaagcaggccccggccccgaggggcttctggccccggggcgccctccccgggga
cacggaagtgcgggggctccgagtagccccaccttccccgtcagagacacctcctcgtgcc
ctccctggcggggaaccccgtaggaagatccgcccgcgccagcccgccctggaactgctc
cacggtgcaggagggcaacgtgtccgacagcggggactcgtaccggggaacgtccacgg
gaaagtccggggctcctcctcgtcgggccccgcacccggaccgtcgccaagtgcgaggccaa
gagccgagcggtccagagccccgactctgtgggagagctgagctcgcggtcgcgga
cagccgggagagcaacagcccccccgctcgctcctcccccaaccgcgcacctcgggggc
tag

>Gm-NN-gja10-G02098 Our modification. Sequence extended in 3'-direction (underlined). The very 3' end (lower case letters) is taken from XM_03035622, which otherwise differs only one nucleotide from the present sequence.

ATGGGTGACTGGAACCTGCTGGGCAGCATCCTAGAGGAGGTCCATGTCCATTCCACCATC
GTGGGCAAGATCTGGCTTACCATCCTCTTCATCTTCCGCATGTTGGTGTGGGGGTGGCT
GCCGAAGATGTGTGGGAGGACGAGCAGACAGAGTTTGTGTGTAACACTGACCAGCCGGGC
TGCAAGGCTGTGTGTGTACGACCGTGCCTTCCCCATCTCCCTCGTTTCGCTTCTGGGTGCTG
CAGGTTCATCTTCGTGTGCGCACCCCTCTCTGGTCTACATGGGCCATGCCCTCTACCGCATC
CGCTTCCTGGACAAGGAGCGCCACCGGCGACGTGCCAGCTGCGCGACGAGCTTGGCGAG
CCGGAGGTGGCCCTGGAAGAGCACCGGCGCCTGGAGAGGGCGCTGCGTGGCTGGAGGAG
CAGCGCCGGGTGAAGAAGGTGCCCCCTCAGAGGCTCCTTGTGAGGACCTACATCATCCAT
ATCCTCACACGCTCCGTGGTGGAGGTGTCTTCATCCTGGGCCAGTATGCTCTCTATGGC
CTGCGCCTGGAGCCTCTCTACAAGTGGAGCGGCTGCCGTGCCCAACAGCGTGGACGTGT
TACATCTCCCGGCCACCGAGAAGACCATCTTCATGGCCTTCATGTTCTGTCATCGCCGCC
GTCTCGCTTTTCTCAACCTTCTGGAAATATCCACCTGGGAGTGAGGAAAATCAGGCAG
ACGATATACGGAGATAAGTACTCCGAAGAGGACAGCTTGATTACAAAGCCCAAGAAGAAG
CGCACCTTGACGACCTTTGTCTTATGCGCCACTTGTGCGCTCATAACGGACCGTCAACT
CAAACCTTATTTAAGGGGATTCTTGAGGGAGGGACGAACGAGTGCATCAGAACATAGGG
CTCAGAGCTAACAGCAGACAACGACAACAACAACAGACATAACAGCCTGGCTCCT
CTTGAGCACTATCAGACAACTGCATCGCACCTGGATCAATGGTACCACAGAACCAATAC
CAGACCGGGCAGGAGGGGGCCACTCAAGGCCTCCAAACCATGAAGGCCAGAGACAAAC
TCCAGGGCCTTGATGGACCAACACCCCTCTGGTCTGGCCTGCGGTTCTTTGTAATGTAGAA
GGCTGGCCAAAGGAGCAGACTCAATACCTGAGGAGCTCCTTCGACCCATGGAGCCTCCT
CGAGTGTCCAGACTCAGGGGTACACAATGGCCACAGGCCAGCCTCGCAGCCAGGGAC
ATGGAGGAGGATGTGGAGAGAAAGTACTCGATAGGCAGTGACCTCTTTCATCTGAACCAC
AGGAAGACCAGCTTCATGGTAAAGCCTCCGTCCGAGAGCATGTCCACCATCAGCGGCTCA
AGCAGCCCTCGATCCATTCGTCTGAGGAATCTGATGAGCTGGGCTCTCTGCAGGGGGAC
ATGCCATGATGCCCCCTGCTGGAGGGCGCAGGATGtccatgagtgtgttcctggatatc
tcctcaatcatga

>Gm-cx52.6-G05425 Our modification. Ensembl-predicted intron included in sequence (underlined)

ATGGGGGACTGGAACCTACTGGGTAGCATCTTGGAGGAGGTCCACGTCCACTCCACCATC
GTGGGGAAGATCTGGCTGACCATCCTCTTCATCTTCCGCATGCTGGTCTGGGCGTGGCC
ACGGAGGAGCTGTGGGACGACGAGCAGAGCGAGTTTCGTCTGCAACACCGAGCAGCCGGC
TGCAAGAACGTGTGTGTACGACCGTGCCTTCCCCATCTCCCTGATCCGCTACTGGGTGCTG
CAGATCATCTTCGTGTCTCGCCCTCGCTGGTGTACATGGGCCACGCCCTCTACCGCCTC
CGGGCGCTGGACAAGGAGCGCCACCGCAAGAAGGCGTGGCTGAAGGCGGAGCTGGACGGC
GGCGAGCCCTCCAGGAGGACAGCACCGCAGGATGGAGCGCGAGCTGCGGCGGCTGGAC
GAGCACCGCAAGGTGAGGAAGGCCCCCTGCGGGGGCGCTGCTGCGCACCTACGTCTTC
CACATCTTGACGCGCTCGGTGGTGGAGGTGGGCTTCATCGTGGGCCAGTGCGCGCTCTAC
GGCATCGGCCTGGCGCCGCTCTACAAGTGTGAGCGCGACCCGTGTCCTCAACAGCGTGGAC
TGCTTCGTGTGCGGGGCCACCGAGAAGAATCTTCTGGTGTTCATGCTGGTGTATCGCC
GGGGTCTCCCTGATCTCAACCTGCTGGAGATCTTCCACCTCGGCCTGAAGAAGATCAAG
GACAGCCTGTACGGCTCCAAGTACGGCGACGAGGACAGCGTCTGCCGCTCCAAGAAGAAC
TCCCTGGCGCACCCCGCTGCCACCTGTCCAACCTCTCCCCCGCGGACGCTGCACCTC
GCCACACCGCCTCCGGCTGCCTGGCCACGACGGCCAGCCGGGCGGTGCGCCTTCCACC
CGGGGCGCGGCGGGCCCCAGCACACCGGACGGGGCCCCCTTCGACACCAACGCC
CGGGAGGCGCCTCCGACCGGGGCCGACCGCTCCCCGTCTGCCTGCACAGCTGGGGG
CGGTGGGGCGCGCTACACCTGGATGACCCCGGAAGCCCTCGTGCAGCAGCGAGGAGT
CGGCCGGGGCCAGGGCGCGGGGCCAGAGGTACGCCGGGGCCAGCCGAGGGCCACCC
TCACCGAGCTCCCGGCCGCCCTGCGGAGCGCCAGCGCAAGCAGAGCCGCTGA

>Gm-cx28.9-G18912 Our modification. Sequence extended in 3'-direction (underlined).
Splice site.

ATGGGTGAGTGGAGTTTCTAGCGTCTCTCCTTGACAAGGTCCAGTCCCACTCCACGGTC
ATCGGGAAGGTCTGGCTCACAGTGTCTTCAATTTTCCGGATCATGGTCTCGGGGCCGGA
GCAGAAAAGGTGTGGGGTGATGAGCAATCCCAAATGATCTGTAAACCAAGCAGCCAGGC

TGCAAGAACGTGTGCTACGACCACGCCTTCCCCATCTCCACATCCGCTTCTGGGTGCTG
CAGATCATCTTCGTGTCGAGCCCCACGCTGGTGTACCTCGCTCACGTCTCCACGTTATC
CACAAGGAGAAAAAGCTGAGGGAGCGTATGCAGACCAGCAGCGAGCCGACCAAGAACCCA
AAATACTCGGACGACAAAGGTCAAGTCAAGATCAAAGGGGACCTTCTGGGCAGCTACCTG
GCCACCATCTTCTTCCGGATCCTTCTGGAGGTGGCGTTTCATCGTAGGGCAGTACTATCTG
TACGGCTTCGTTCATGGACCCAGAGTGGTGTCCTCCAGAGCACCCGTCCCTTCACTGTG
GAGTGCATATGTCCCGGCCGACCGAGAAGACCATCTTCATCATCTTCATGCTGGGGGTG
TCCTGCGTGGCCCTGCTGCTCAACGTTCTGGAGGTCTTACCTGCTGTGCAGAGGCAGG
TGCTCCAAAGAGACGGCAGCTGGCCCCCTTTACCATGCCAGCCACTCGGCTGTCTGGAG
ATGAAGCAGGTGCCCCGACACCTAA

>Gm-cx32.3-G18903 Our suggested modification. Ensembl-predicted intron included in sequence (underlined)

ATGGGTGATTGGGGCTTTCTATCTCCCTGCTGGACAAGGTCCAGTCCCACTCCACGGTT
ATCGGGAAGATCTGGATGAGCGTGCTGTCTCTGTTCCGGATCATGGTGTGGGGGCAGGG
GCGGAGAGCGTCTGGGGCGATGAGCAGTCGGGCTTCTCTGCAACACTCAGCAGCCCGGC
TGCAGAACGTGTGCTACGACTGGACCTTCCCCATCTCACACATCCGCTTCTGGGTGCTG
CAGATCATCTTCGTGTCGACACCAACGCTCATCTACCTGGGCCATGTCATGCATGTCACC
CACAAGGAGAAACAAGATGAGGGAGAATCTGGCCAGCCCCGGGTGCGCCAGCACGAGAGAAG
CAGCCCAAGTACACCAACGAGAAGGGCAAGGTGAAGATCAAGGGCAACCTCTGGGGAGC
TACCTAGCCAGCTGGGGCCCAAGATCATCATCGAGGCCGCTTCATCGTGGGCCAGTAC
TATCTGTACGGCTTCATCATGGTCCCCATGTTCCCCGTCCAAGAAACCCGTCCCTTC
ACCGTGGAGTGCATATGTCCCGGCCACCGAGAAGACCATCTTCATCATCTTCATGCTG
GTGGTGGCCTGCGTGTCTCTGCTCAACGTTCTGGAGGTCTTCTACCTGCTGGTGAGC
AGGAGCAGATGTTCCCCCAGGAAGCGCTCGCACATGATCAGCTCCGCTCGGCACCCGGCA
CAGCTCTCAGGCCCCATGTGGCCAACGGCAGAACGCCCCGAGGCCAACAGATGAAC
ATGGACTTTGAGAGCGGCCAGAGTACTGCTGGGAGCCTCAACGGGGCCAAGGAGGAGAAG
AAGCTTCTGAGTGGTCACTAG

>Gm-NN-gjb1-G14169 Our modification. Ensembl-predicted intron included in sequence (underlined)

ATGAAGTGGGCGTCTTCTACGCGGTGGTGAGCGGCGTGAACCGTCACTCCACTGGCATC
GGCCGCATCTGGCTGTGCGGTGCTCTTTATCTTCCGAATCCTAGTGTGGTGGTGGCGGCC
GAGAGCGTGTGGGGCGACGAGAAGTCGGGCTTCACTGCAACACGCAGCAGCCCGGC
AACAGCGTCGCTACGACCACTTCTTCCCCGTGTCCACATCCGCTGTGGGCGCTGCAG
CTCATCTGGTGTCCACGCCGCGCTGCTGGTGGCCATGCACGTGGCCACCGCCGCCAC
GTGCAACAAGAATCCACAAGCTGGCGGGCCGCTTGGGCCCAAGGAGCTGGAGCAGATC
AAGAGCCAGAAAGATGAAGATCGTGGGCGCGCTGTGGTGGACCTACGTCACTAGCCTGTTT
TTCCGCATCATGCTGGAGGTTCATCTTCATGTTCTCTTCTACATGATCTACCCCGGTAC
AAGATGATCCGCTGGTCAAGTGCAGCTGTACCCCTGCCCCAACACGGTGGACTGCTTC
GTGTCGGGCCCCACCGAGAAGACGGTGTTCACCGTGTTCATGCTGGCCGTGTGGGCGTC
TGCATCTCTGCTGAACATCGCCGAGGTCTCTTCTGTTGGCGAAGGCCTGCGGGGAGGCAG
CTTAGCAACACCAAGGACGGGGCGGCCTCTGGGGCTGGCTGGCCACAAAGATCTCTTAC
TAG

>Gm-GJB1-G20195 Ensembl prediction. No modifications.

ATGAAGTGGGGTCTTTTATGCCGTGATCAGCGGCGTAAACAGGCATTGACGGGCATC
GGGCGAATATGGCTCTCGGTCAATTCATCTTCCGCATCTGGTGTGGTGGTGGCGGCC
GAGAGTGTGTGGGGCGACGAGAAGTCGGGCTTCACTGCAACACGCAGCAGCCCGGC
AACAGCGTGTGCTACGACCACTTCTTCCCCATCTCCACATCCGCTGTGGGCCCTGCAG
CTCATCTGGTGTCCACGCCGCTCTGCTGGTGGCCATGCACGTGGCCACCGCGGCCAC
ATCGACAAGAAGATCTGAAGCGGTGCGGCGCGGCAGCCCCAAGGAGCTGGAGCACGTC
AAGAGCCAGAAAGTCCAGATCGTGGGCGGGCTGTGGTGGACGTACATGGTCAGCATCGTG
TTCCGCATCGCCCTGGAGGTGGTCTTCTCTACATCTTCTGGCGATCTACCCCGACTTC
AAGATGGTGGCGCTGGTCAAGTGCAGCTCCTTCCCGTCCCAACACGGTGGACTGCTTC
GTGTCGGGCCCCACCGAGAAGACCATCTTACCGTGTTCATGCTGACCGTGTGGGCGTC
TGCTGTGCTGCTCAACCTGGCCGAGGTGGTCTACCTGGTGGGGAGGCGTGCCAGCGATGC
GCCCCGACCCGAGGAGACAAAGGTGGCGTGGATGGGCCAGAAAGATGTCCACGTAC
AGGCAGAACGAGATCAATCAGCTCATAGCCGGCCAATCGATCAAGCCCAAGTCCCCGTG
ACTAGAAAGGGTTCGCGCGATAAAGGCGACCGGTGCTCCGCTTTCTGA

>Gm-NN-cx30.3-G09100-1 Ensembl-predicted intron included in sequence (underlined). Further modified according to XM_030354646 (lower case letters). Suggested Splice sites. This Ensembl prediction contains two separate and unique connexins sequences, the present one and a gja3 sequence.

ATGCCGTCGTGGGGGGCCCTGCTGGCCAGCTGAGCGGGGTCAACCGCTACTCCACCAGC
TTGGGGAAGGTGTGGCTGTGGTGTCTTCATCTTACGGGTGATGGTGTGATCGTGGCG
GCCGAGAGCGTGTGGGGAGACGAGCAGACAGACTTCACCTGTAAACACCTGCAGCCGGGC

TGTGAGAACGTCTGCTACGACCACTTCTTCCCCGTCTCCACATCAGACTCTGGTGTCTC
 CAGCTGTCTTTCGTCTCCACGCCTACCCTCCTCGTCGCCATGCACGTGGCCTACCGTAAC
 CACGGCGACAAAAAGagactcctacaggccgaggaggcagagctagagaacctgaagagg
 cggagactccagctgactggcgcctctggtggacgtacgctgcagccttgtggtccgg
 ctgctgtttgaagcgggcttcatgtacgtcctgtacgcctctaccgcggttccagatg
 ccgcggtggtgacagTggtgagtgccctTgcaccaacgtggtggacTggttcgtgtcg
 cggccccaccgagaagacggtgttcaccgtgttcattggtccgcctccagcgtctgcatg
 ctctcaacgtggccgagctggcctacctggtcgctcaaggccgtcactaggaagtcttga

>Gm-cx30.3-G15795 Our modification. Ensembl-predicted introns are included (underlined).

ATGACTTGGGGCGCGCTGTACGCCCCAGTTGGGCGGAGTCAACAAGCACTCCACCAGCCTG
 GGAAGATCTGGCTGTCTGCTCTTTCATCTTCCGCATCACCATCCTCGTCCTGGCGGCC
 GAGAGCGTGTGGGGCGACGAGCAGTCCGACTTCACGTGCAACACGCAGCAGCCGGGC
 AAGAACGTCTGCTACGACCACTTCTTCCCCGTGTCCACATCCGCCTGTGGTGCCTGCAG
 CTGATCTTCGTGTCCACGCCGGCGCTGCTTGTGGCCATGCACGTGGCCTACCGTAACCGG
 GCGGACAAGCGCACCATGCTGCGGTCCAACGGCGGGGAGAAGACCGACCTGGAGCTC
 GAGGGGCTGAAGCGCCGGAGGCTGCCATCACGGGGTCCCTGTGGTGGACCTACACCTGC
 AGCCTGTTCTTCCGGCTGATCTTCGAGGGCGGGTTCATGTACGCCCTGTACTTCTGTAC
 GCGGCTTCCAGATGCCGCGGCTGGTCAAGTGCAGCAGTGGCCGTGCCCAACAAGGTG
 GACTGCTTCATCTCGCGGCCACGGAGAAGACGGTGTTCACCATCTTCATGGTGTCTGTCG
 TCCACCATCTGCATGGTGCTGAACGTGGCGGAGCTGGCCTACCTGGTGGCCAAAGGCGCTG
 TTGCGCTGCTCCAACCGTGGCGCCCGCAGGAAGATGCCCTACGTCCACCACGACGGCGGG
 CGCGGAGAGACCTGGCCCTGA

>Gm-cx28.6-G18713 Our suggested modification. Splice sites. Underlined: Predicted by Ensembl as intron, here included as part of exon.

ATGAACCTGGTCCGGCCTGGAGAGCTTGATCAGCGGGGTCAACAAGTACTCCACCGTGTT
 GGCCGCTTGTGGCTGTCCATGGTCTTTGTGTTTCGGGTTCATGGTCTTTGTGGTTGCAGCT
 CAAAGAGTTTGGGGTGACGAAACAAAGATTTTGTCTGTAAATACGAAACAACCGGGCTGT
 ACCAACCTGTGCTATGACAGCATCTTCCCATCTCCACATCCGTCTGTGGGCCCTGCAA
 CTGATCTTCGTACCTGCCCGTCCCTCATGGTGGTGGCCACGTGAAGCTGCGTGAAGAA
 AAGGACCTTAAGTACACCGTACTGCACGAGGGCTCCACCTGTACAGCAACCCGGGCAAG
 AAGAGGGGGGGGCTGTGGTGGACCTACCTGCTGAGTCTGGTCTTCAAGGCAGGCTTCGAC
 GCCTCGTTTCTCTACGTTTGTATCGGATATACCACGGATATGACATGCCCAAGTTGTCC
 AAGTGCCTCCCTGGATCCCCTGCCTAACACCGTGGACGTGCTTCATCAGCCGTCCACAGAG
 AAGAAGATCTTACCCCTGTTCATGGTGGTCAACAGCGCCATCTGCATCTTGATGTGCTTG
 TTTGAGATGTTGATACCTCATTTGGCAACCGGATTTCAGAAAACCCCTCAGGGTTCAGAACTCC
 ATTAACAGGCTCCTATTTCGCGGAGCGGCACGAGATCAAAAACCTGGTCCCGCCAGATCA
 CAAACCCGCCGCACTATTCCCCTCAGAGCAAAAGTTTAAGCAAGATGGACAAAGCCAAG
 GAGACCACGACAACCTGTAG

>Gm-cx30.9-G07064 Our modification. Splice site. Ensembl-predicted introns included (underlined)

ATGAACCTGGTCTACCTGGAGGGGCTCATCAGCGGGGTCAACAAGTACTCCACGGGCTTC
 GGCCGCATCTGGCTCTCCATGGTCTCATCTTCCGCGTGATGGTGTTCGTGGTGGCCGCG
 CAGCGCGTGTGGGGCGACGAGAGCAAGGACTTTGTGTGCAACACCGTCCAGCCGGGC
 AACACCGTGCTACGACAGCATCTTCCCATCTCCACATCCGCCTGTGGGCCATGCAG
 CTCATCTTCGTACCTGCCCGTCCGTGATGGTGGTGGCCACGTGAAGTACCGCAAGAAG
 AAAGACCTGCAGTACACACCTCTCATGAGGGCCATCACCTCTACGCCAACCCGGGGAAG
 AAGCGCGGGGGGCTTTGGTGGACGTATCTGCTCAGTCTGATCTTCAAGGCAGGATTTCGAC
 GCCGCTTCTCTACATCTCTACTACATCTACGAGGGCTACGACATGCCCCGCTCTCG
 AAGTGCACCTGGCGCCCCTGCCCAACGTGGTGCAGTGTACATCTCCCGGCCACCGAG
 AAGAAGATCTTACCCCTGTTCATGGTGTCTCTCCAGCTTGTGCGTGTCTATGTGCATC
 TGTGAGATGGTGTACCTCATCTTCAGCGCATCCAAAAGCTACTGGTGAAGAAGAGGGAG
 GCGGACAGTAGGTTGTTGCGCGAACGCCACGAGATGAAGCCGCTGGCCCGGCCGCGGTG
 GACTTCAGGTGGAAGATGTCCATCCGGGTGGACCCACGAACACGGCGTCCATACAGAAC
 CTGAGCAACACAAAACGAGAGGAGCGCCCATACAGAACCTGAGCGAGGATTTGTTGAAA
 AAGAAGAGAGTAACTGCAAAATAGATGGATAG

>Gm-cx34.5-G18894 Exon 1 suggested by Ensembl is here shortened by 12 nt. Underlined: Sequence not included in Ensembl transcript prediction, but we consider likely as a part of cds.

ATGGGTGAATGGGACCTGTTAAGTCGCTGCTGGACCAGGTCCAGACCACTCCACCGTC
 ATCGGCAAGGTGTGGCTCACCTGCTGTTCTGTTCCGCATCCTGGTGTGAGCACCGCC
 ACAGAGAAAGTGTGGGGTGATGAGCAGTCCGACTTTGTGTGCAACACCAACCGCGGGG
 TGTAAAGACGTGTGCTACGACACGCCTTCCCATATCACACGTCCGCTTCTGGGTGCTG
 CAGATCATCTCGGTGGCCACGCCAACCTGGTGTACCTGGGCCACGTCTCCAAGTCATC

CACGCTGAGCGCAAGGTGAGACTGAAGATCCAGAGGCAGGCGGAGCTGGACGAGGACGCC
CACCTGTTCTCTGAAGAAGGGCTACAAGGTCCCCAAGTACAGCCACAGCAACGGCAAGATC
AACCTGCGGGGGAGCATCCTGCGCAGCTACCTGCTCAACCTGGTGGCCAGGATCCTGTTG
GAGCTGGGCTTCATCCTGGGCCAGTACTTCTGTACGGCTTCACACTGCAGGCCGCTAC
GTCTGCAGCATGTGCGCCTGCCCGCACAAGGTGGACTGCTTCTCTCCAGACCCACGGAG
AAGTCCATGTTTCATATGGTTTCATGCTGGTGGTGGCCTGCGTGTCTCTCCTCCTCAGCATC
GTGGAGCTGCTTCATCTGTGTGTAAGTGGCGGGCGAGTGCATAGCTCGGAGGCAAGAC
TACACCGTCACCCCGCTACCCCGCCGCTCTTGGAGAGGAAGGCCTTCAAGAACCGAGAG
CAGAGGATCCAGGACCATTACAACCTGGAG

>Gm-NN-cx35.4-G04675 Our modification. Sequence extended in 3'-direction
(underlined) until a stop codon.

ATGGATTGGAAGAGCCTTGAGGGTCTGCTCAGTGGGGCCAACAAGTACTCCACCATCTTC
GGGCGCATCTGGCTGTGATCGTCTTCTGTTCCGGGTGATGGTGTTCGTGGTGGCGGCA
GAGCGCGTGTGGAGCGACGACCAGGCCAACTTTGACTGCGACACCCGGCAGCCCGGCTGC
AAAAATGTCTGCTACAACCACTTCTTCCCGGTCTCCACATCCGCCTTTGGTCCCTTCAG
CTCATCTTCGTACAGTGCCCGTCTTCTTGGTGGTTCTGCACGTGGCGTACCGCGAGGAG
CGCGAGCGTAAGTACCGCATCAAGCACGGCGAGCAGGCGCGTCTCTATGACAACACGGGA
CAAAAGCACGGGGGGTGTGGTGGACCTACCTGTTGAGCCTCTTCTTCAAGACGGCCATC
GAGCTGGGGTTCCTCTACCTCCTCCACCTCATGTACGACAGCTTCAAGCTCCCCAGGCGC
GTCAAGTGCGGCGTCAGCCCCTGTCCCAACGTGGTGGACTGCTACGTGGCCAGACCCACC
GAGAAGACAGTTTTACCTACTTTCATGGTGGCTGCGTCCATGGTGTGCGTGGTCTCTGAAC
CTGTGCGAGATATTCTATTTGATCACCGTGCGCCTGTTGACGATGAAGCGCCAGGGTAGG
CCTACAGTCCGCACGGCTTCGAAGAGGATCATCTCTGAAAATAAGGATTGATGTAA

>Gm-cx34.4-G19007 Our modification. Underlined sequences are added from the
Ensembl-predicted introns, giving the indicated stop codon.

ATGAAGTGGGCATTTCCTTCAGGGCCTCCTCAGCGGGGTCAACAAATACTCCACGGCGTTT
GGCCGCGTGTGGCTCTCCATCGTCTTCTCTTCCGCGTCATGGTGTTCGTGGTGGCCGCC
GAGAAGTGTGGGGCGACGAGCAGAAGGACTTCAAGTGCAACACGGCGCAGCCCGGCTGC
CACAACGTGTGCTACGACCACTTCTTCCCGTGTCCACGTGCGCCTGTGGGCCCTGCAG
CTCATCTTCGTACCTGCCCTCGCTGCTGGTGGTTCATGCACGTGACCTACCGCGAGGAG
CGGGAGAAGAAGAACAAGGCGAAGCACGGCGAGAAGTGCAGCCCGCTGTACGCCAACCCG
GGCAAGAAGCGCGGCGGCCTGTGGTGGACCTACGTCTGACGCTGGTGTTCAGATCGGC
GTGGACACGGTGTTCGTGTACCTCATCTACTACATGTACGAGGGCTACGACTTCCCCTCG
CTCGTCAAGTGCGTGGAGGCGCGCTGCCCCAACACGGTGGACTGCTACATCGCGCGGCC
ACCGAGAAGCGCATCTTACCCTGTTTCATGGTGGTACCAGCATGGTGTGCATCCTGCTC
TCCATCTTTGAGATCTGTACCTGGTGGCAAGAAGTGCCGAGGGCGTGGTGAAGCTG
CACTACCAGCACCGCTCGCACCAAGAACAGCAGGCGAGGACTTGGGCCCTCGCTGGCG
GGGGGCAAGAGCGGGAACCTGGTGGAGGCCAACACTCTGAGGCTGGTGGAGAAGGTTCTC
CCCGGCACGCTGCGCGCTCGTACAGCGTGGCCGTGCTTCGGACGAGGTACCCCCAGA
TGA

>Gm-NN-cx34.4-G04662 Our modification. Ensembl-predicted introns included
(underlined). Splice site. Essentially identical to ENSGMOG0000004650, which ends
at the splicing site.

ATGAATTGGGCCTTTCTCCAAGGCCTCCTGAACGGAGTCAACAAGTACTCCACCGTCTTC
GGCCGCATATGGCTCTCGTGGTGTTCATCTTCAGGCTCATGGTTTTCTGTGTGGCTGCT
GAGAAGTGTGGGGCGACGACCAGAAGGATTTGACTGCAACACGAGGCAGCCCGGCTGC
CACAACGTGTGCTACGACCACTTCTTCCCATCTCCACACCCGCTCTGGGCTCTGCAG
CTCATCTTCGTACATGCCATCATTTGCTGGTGTGCTGCATGTGGCCTACCGGGAGGAG
CGCGAGCGCAAAACACCGGCTGAAGTACGGCGAGGACTGCAAGCCGCTCTACGACAACACG
GGAAAGAAGCGCGGAGGTCTGTGGTGGACCTACTTCTCAGCTTGCTGTTCAGATGCTG
GTGGAGGCGGTGTTTGTCTTCTGCTCTTCTACATTTACGAAGCCCCCTTCTTCCCGCG
CTTGTCAAATGTGATGAATCCCCGTGTCCCAACGTGGTGGACTGCTACATCGCCAGACCT
ACAGAGAAGAAGGTCTTACCCTGTTTCATGGTGGTACCAGCTTTGTGTGCATTCTGCTC
ACTATTTGCGAGGTATTTTATCTCTGTGGTAAGAGGTTCTGGGAGTGTGTGCTGAACAA
CAGCACCCGCTCGACACAACGGCAACTCCTTCGTTCATGGCCAAAATCCCCAGACCAGA
AGTGTAACTCCGTCTACAAAGAGCCTCTCACATCAGAGAAGATGACGATGGTGGATGGT
AAAGGCCAACGACTCCGGAGAGTTCTGCACCGCGTACAGTCTGGCCATCTCTTGA

>Gm-cx35.4-G20298 Underlined: Extended in 3'-direction to reach stop codon.

ATGGACTGGAAGACCTTCCAATCCCTGCTGAGCGGTGTGAACAAGTACTCCACGGCGTTT
GGGCGGATATGGCTGTCCATCGTGTTCGTGTTCCGCGTCATGGTGTACGTGCTGGCGGCC
GAGCGGTGTGGGGCGACGAGCAGAAGGACTTTGACTGCAACACCAAGCAGCCCGGCTGC
GCCAACGTGTGCTACGACTACTACTTCCCATCTCCACATCCGCCTGTGGGCCCTGCAG
CTCATCTTCGTACCTGCCCTCCTTCATGGTGGTTCATGCACGTGGCGTACCGCGACGAG

CGCGAGCGCAAGTACCGCATCAAGTTCGGCGAGGAGAAAAAGCTGTACAACAACACGGGC
AAGAAGCACGGCGGCTTGTGGTGGACCTACCTGATCAGCCTCTTCGTCAAGACGGCCATC
GAGGTGGCCTTCTCTACATCCTGCACTACATCTACGACAGCTTCTACCTGCCGCGCCTG
GTCAAGTGCGAGGTGTCCCTTTGCCCGAACAAGGTGGACTGCTACATCGGCCATCCACG
GAGAAGAAGGTGTTACCTTACTTTCATGGTGGGCGCCTCGGCCCTGTGCATCGTGCTCAAC
ATCTGCGAGATCATTTACCTCATCTCCAAGCGTGTGGCGCGCTGCGCCAACAAGCTCAAG
AAGCGGACCCGAGGCATGCCGAGGAGACGCACGCCGGCTACGACGACAACCACGCCCC
AACAGTACCCCATGGAGATGATGTCCAAGCGAGACGTACCAGGGACTTGCTCCGTCC
TTCAGGACAGCTGCAAGCCTCCGTACCAGCCGCCATGCATTTGCTGAGGGCGGAGAAG
AGGGCGGAGATGA

>Gm-cx28.8-G20475 Our modification. Extended in 3'-direction until reasonable stop codon (underlined)

ATGAAGTGGGGCTTCTTGAGAACGTGCTGAGCGGCGTGAACAAGTACTCCACCGTCATC
GGTCGCATCTGGCTCTCCATCTCTTCATCTTCCGCATCCTGGTGTACGTGGCGGCCGCC
GAGCAGGTGTGGAAGGACGAGCAGAAGGACTTCACCTGCAACACCCGGCAGCCGGGCTGC
GAGAACGTCTTGCTACGACACCTGTTCCTCATCTCCAGACGCGCCTTTGGGCCCTGCAG
CTCATTATGGTGTCTACCCCGTCCCTCCTGGTGGCCCTGCACGTGCGATACCGGGAGCAC
AAGGAGTCCAAGTGCGCCACACGCTCTACGAGGACCGGGGCAGGATCGACGGGGGGCTG
CTTGGCACCTACATCGCGAGCATCATCATCAAGACCTTCTTCGAGGTGGCTCGCTGCTC
GCCTTCTACTTCTGTACAGCGGGTTTGAAGTGCCCTGTTGTACCGCTGCGAGGAGAGC
CCCTGCCCCAACATAGTGATTGTTACATCGCCAGGGCCACGGAGAAAAGATCTTCCTG
TACATCATGGGATGTACGTCCGTCTTTGCATTGTGCTGAATGTGGTCGAGCTTTTCTAT
ATTCTATGGAAGCAGTGTCCAAGTACTTTAACAAGCGTTATGTCTCCGTGGAAGAGAGG
CAACGCAGACGCCACAGTTTATGGTTCTAATTACAATCTGCCTGTTTCTAACGTCAGC
AAGCCCGCATCCCCGAGGCTCCACCCGGGCCGAACAAGGGCCTCAGGCGATCAGAGCCG
TCCTGTACACAAAGCCTCCACATCTGATGAGACATTGA

>Gm-cx36.7-G16800 Our modification. Ensembl-predicted introns included (underlined). Splice site.

ATGACGGAGTGACGCTGCTGAAGCGCTGCTGGACGCGCTCCACCAGCACTCCACCATG
ATCGGCCGGCTCTGGCTCACCGTCATGGTGATCTTCCGGCTGCTGGTGGTGGCGGTGGCC
ACGGAGGACGTGTACGCAGACGAGCAGGAGATGTTCTGTTGCAACACCCCTGCAGCCGGGC
TGCGCCACCGTGTTGCTACGACGCTTCGCCCCCATCTCGCAGCCCCGCTTCTGGGTCTTC
CACATCATCAGCGTGTCCACGCCCTCGCTCTGCTTCATCATCTACACCTGGCACAACTC
TCCAAGCTGCCCCACCGCACGGGACACAGGCCAGGGCCAGGCCAGGCCGGGGCCCCGAC
CACCCCCCGAGGTTCCCCGAAGGGTCTCTCCAAGTGTACGTCTTCCACGTGTGCGTG
CGGGCGCTGCTGGAGTGGGCTTCTGTGACGGCCAGTGATGCTGTTTCGGCTTCCGGGTG
CCCGTGCACCTTCTGTGCCGTCCGGCGCCTGCACCCAGCCGGTGGACTGCTACGTGTCC
CGGCCACGGAGAAGACCATCTTCTGCTCTTCATGTTCTGCGTGGGGGTGTTCTGCATC
CTGCTCAACCTGCTGGAGCTCAACCACCTGGGCTGGAAGAAGATCCGCACGCTGGCCAAG
CTCCGGGAGACGGGTCTTGGGAGGCTCGCCCCGCGAGGAGGGCGGGCTACGTGGCCTTA
CCCCCGGGATGCCCTCGCTCGCGTCCACGCTGGGCTTCAGGGACGTGACCAGCACCACG
TCCCTCCCCACCTGGACCTGGTGGTGGGACACGACCCGACTGGACGTGCGCAGGGAAC
TGCACCTGTTTCGGGGCCACCGGGCCGGGCACGAAGGCCGAGCCGCGGGCCCGGGAGG
CCAGAGGGTGTGAGGAAGGAGGGACAGCCGCTGAGGATTAAGAGAGAGAACCAGGGGACCC
AAGCAGCACAGTGCTGAAGTGTGGATATGA

>Gm-GJCl-G14340 Our modification. Ensembl-predicted introns included (underlined).

ATGAGCTGGAGCTTCTCAGCGGGCTGCTGGAGGAGATCCACAACCACTCCACCTTCGTG
GGGAAGCTGTGGCTCACCGTGCTCATCGTCTTCCGCATTGTGCTCACGGCCGTGCGAGGC
GAGTCCATCTACTACGACGAGCAGAGCAAGTTTCATCTGCAACCTCGGGCCAGCCGGGCTGC
GAGAACGTCTTGCTACGACGCTTTCCTCCGCTCTCTCATGTGCGCTTCTGGGTCTTCCAG
ATCATCTTGGTGGCCATGCCCTCCCTCATGTACATGGGCTACGCCGTCAACAAGATCGCC
CGCGCGGACGAGGCCAAGGGAGGCACCGCGCCGCGGCTGTACGACCCCGCTCGGGGCG
TCCGGGGGCTACACCCACCGGAAGCCCCGAAGATCTGTTTCGGGGACGGCAGCACCCG
GGCATCGAAGAGGACAGGAGGACACGAGGACGACCCATGATCTACGAGTTCCCGAA
ATTGAGCCGCCACATCCGGCACGGGACCCTTTGCAGCCCACTCCAGGCCCAAGATCCGC
CACGACGGCCGCACACGCATCCGGGACGAGGGGCTGATGCGTATCTATGTGTTGCAGCTG
GTGACCCGTACCGTCTTGAGGCGGGCTTCTTGGCGGGGAGTACCTGCTGTACGGGTTT
CGCGTGGCGCCCGTGTGTTGTGTGCTCGGCGAGCCCTGCCCCCATAGCGTGACTGCTTT
GTGTCGCGTCCACCGAGAAAACCATCTTCTGCGCATCATGTACGGGCTACCCGTGCTC
TGCCTACGCTCAACATCTGGGAAATGCTGCACCTCGGCGTCGGATCCATCTGCGACATC
CTGCGACGCCCGCGCTGCCCGCCCGGAGGACGAGTACCAGCTGGGTCTGCTCGGCACC
ATTGGAGCCAGCGAGGGGTCTGTGGGCGTCTCGGGTCCCGAGGCCGGCGAGGGCGAAGGA
CCGGTTCGGGGAGGGCGGTGCGGACTACATCGGATACCCATTCTCTTGAACCCATACCCCG
TCGGCACCCCCGGGATACAACATCGTAGTGAAGCCGGAGCAGATCCCGTACACGATCTC
AGCAACGCTAAGATGGCGTGCAAGCAGAACCGGGAGAACATCGCCCAGGAGGAGCAGCAG

CAGTTCGGCAGCAACGAGGACAACCTTCCCCACCGAGGGGAGGCTCGCGTGGCGCTGAAC
AAGGACATGATCCAGCAGGCTCACGATCAGCTGGAGGCCGCCATCCAGGCCCTACAGTCAG
CAGCACTGTGTGGAGGATCTGGGAGAACACAGGGACGATAAGCCTCGCAGTAACATTATT
CAGACCCAGCCCCGCCCGCATGCAGCCGAGAGGAGCGCAAACAACGGTCCAAACAC
GGCAAGGAGGACGACCGCGGATGTAGCAGCAGCAACAGTAGCAGCAGTAAGTCAGCA
GAGGGGAAGCCCTCTGTGTGATTAA

>Gm-NN-gjc1-G06421 Our modifications. Underlined: Extended into intron predicted by Ensembl. The extended sequence runs into a row of Ns (in Ensembl) Lower case: Sequence extended by Blast into GenBank wgs.

ATGAGCTGGAGCTTCTGACCCGCTGCTGGAGGAGATCCACAACCACTCCACCTTCGTG
GGGAAGATCTGGCTGACGGTGCTCATCGTGTTCGCATCGTGCTGACGGCGGTGGGCGGC
GAGTCCATCTACTACGACGAGCAGAGCAAGTTTCATCTGC AACTCGGGCCAGCCGGC TGC
GAGAACGTC TGC TACGACGCCTTCGCCCGCTCTCCACGTCCGCTTCTGGGTCTTCCAG
ATCATCTGGTGGCCACGCCCTCCCTCATGTACCTGGGCTACGCCGTCAAC AAGATCGCC
CGCGCCGACGACCGGGCGGGcgctcgccgcgccgctcgccgccccagcgc
cgccgcccaggaagtctgtaccggcgcccgaggcagcaccgcccgtggaggaggc
ggaggacgaccagagaggaccccatgatctacgaggtggccgagccggagagcgacgg
cggagggcgccggggagcgccggggcgccgacggggcgccgcccggggcgccgacggg
ggaggggtcaaggccaaggcgccgccaCGACGGGCGCCAGCGCATCAAGGAGGACGGGCTG
ATGCGTATCTACGTGCTGACGTGCTGGCGCGCTCCCTGCTGGAGGTGGGCTTCTGCTC
GGGCAGTACGCGCTGTACGGCATGGCGGTGCCCTCCACGTACGCC TGC TCGGGCCCGCC
TGC CCGCACACGGTGGAC TGC TTTGTGTGCGGGCCACCGAGAAGACCATCTTCTGCTC
ATCATGTACGCGGTGTCCCTGCTCTGCTGGCCCTCAACTTCTGGGAGATGCTGCACCTG
GGCGTG GGCACCATATGTGACATCCTGGGCTCCAGCGCTCCCCAGCGCCCTCCAACGAC
GAGGCCTGA

>Gm-NN-cx43.4-G08258 Our modification. Ensembl-predicted introns are included (underlined).

ATGAGCTGGAGTTTCTGACGCGTCTGCTCGACGAGATCTCCAACCACTCGACGTTCTGTC
GGCAAGATCTGGCTCACGCTGCTGATCGTGTTCGCATCGTGCTGACGGCGGTGGGCGGC
GAGTCCATCTACTACGACGAGCAGAGCAAGTTTGTG TGC AACACGCAGCAGCCCGGC TGC
GAGAACGTC TGC TATGACGCCTTCGCCCGCTCTCCACATTCGCTTCTGGGTGTTCCAG
GTGATCATGATCACCACGCCACCATCCTGTACCTGGGTTTCGCCATGCAC AAGATCGCC
CGCATG GACGACTCGGAGTACCAGCCGCGCCGCGCAAGCGCATGCCGTTGGTGAGCCGG
GGCGCCAACCGGACTACGAGGAGCGGAGGACAACGGCGAGGAGACCCCATGATCCTG
GAGGAGATCGAGCTGGAGAAGGACGCCGCGCGACAAGGCACCGGAGAAGCCGTGCCGC
AAGCACGCGGGCGCCGCGCATCAAGCGCGACGGGCTCATGAAGGTG TACGTCTTCCAG
CTGATGGCGCGCGCCACCTTCGAGGCGGCCTTCTGTTTCGGCCAGTACGTCCTGTACGGC
CTGGAGGTGGCGCCGTCGTACGTG TGC ACGCGCTCGCCC TGC CCGCACACGGTGGAC TGC
TTCGTGTGCGGGCCACCGAGAAGACCATCTTCTGCTGATCATGTACGGCGTCAGCGCC
CTGTGCTTCTTACACGCGCTGGAGATCCTGCACCTGGGCTTT AGCGGCATGCGCGAC
TGCCTGTGCGGGCGCCGCTCGCCGCCG

>Gm-cx44.2-G14499 Modified according to XM 030353496. Ensembl-predicted introns are included (underlined). Suggested splice site.

ATGAGCTGGAGCTTCTCACGCGGCTGCTGGACGAGATCTCCAGCACTCTACCTTTGTG
GGCAAGGTGTGGCTGTGCGTGCTCATCTTCCGCATCGTGCTGACGGCGGTGGGTGGA
GAGACCATCTACCAGATGAGCAGAGCAACTTTGTG TGC AACACGCAGCAGCCCGGC TGT
GAGAACGTC TGC TACGACGCCTTCGCCCGCTCTCGCAGTCCGCTTCTGGGTCTTCCAG
GTGCTGATGATCACCACGCCACCATCATGTACCTGGGCTTCGCCACGCAC AAGGTGGCC
CGCATG GGTGACCCCCAGTACCAGCCACCCGCGCGCCGCAAGCGCATGCCTATTGTG
ACCTCCGGGGCGCGCGCAACTATGAGGAGGCAATGGAGGACGGGAGGAGGACCCATG
ATGGAGGAGGAGATCGAGCCCGAGAAGGCGAAGGCGGACAAT GGCCCGGAGAAGAAGCAC
GACGGCGGCGTCAGATCCAGGCGGACGGCCTGATGAAGGTG TATGCCCTGCCAGCTGCTG
ACCCGCGCGCCTTCGAGATGGCCTTCTCTACGGCCAGTTCTCTGTACGGCTTCCGC
GTTGCGCGGACTACGTG TGC ACGCGTCTGCCCTGC CCGCACACGGTTGACT TGC TATGTG
TCACGCGCCACCGAGAAGACCATCTTCTGCTGATTATGTACGTGGTGTCTTTCTCTGC
CTGCTCCTCACGCTCTGGAGATGGTGCACCTCGGCGTT GGCGGCTCCGCGACACCTTC
CGCCGACAGGGCCACCTGGTCTCCCGAACAGGCCAGCCGGAGGAGGAGGAGGAGGA
GCCTCGCGCGCCCCAGGCTACCACGCCACGGTGAAGCATGA

>Gm-cx43.4-G17444 Our modification. Ensembl-predicted introns are included (underlined).

ATGAGCTGGGACTTCTGACGAGTCTGCTCGACGAAATCTCCAACCACTCGACGTTCTGTC
GGCAAGACCTGGCTCACGCTGCTCATCGTGTTCGCATCGTGCTGACGGCGGTGGGCGGC
GAGTCCATCTACGAAGACGAGCAGAGCAGCTTCGTC TGC AACACGCTGCAGCCCGGC TGC
GAGAACGTC TGC TACGACGCCTTCGCACCCCTCTCGCACATTCGCTTCTGGGTGTTCCAG

GTGATCGTGATCACCACGCCACCGTCTCTACCTGGGCTTCGCCATGCACAAGATCGCC
CGCATGGACGACTCGGAGTACCGGCCGCTCCGCGGCAACGCCTGCCGTCAGTGAGCCGT
GGCGCCGGCCGCGACCACCAGGAGGCGGAGGCCAACTGCGAGGAGGACCACGTGATCCTG
GAGGAGAACGAGCCGAGAAAGGACACCGCGCACAAGGCGCCGAAAAGCTGCGCCGCAAG
CACGACGGGCGCCGGCGCATCGAGCGCGACGGGCTCATGAAGCGTACGTCTTCCAGCTG
ACGGCGCGCGCCACCTTCGAGGGGGCCTTCTGTACGGCCAATACCTCCTGTACGGCCTG
GAGGTGGCGCCGTCTGACGTGTGCACGCGCCCGCCCTGCCCGCGCACGGTGGTCTGCTTC
GTGTGCGGGCCACCGAGAAGACCATCTTCTGCGGGTCATGTACGGCGTCAGCGCCCTG
TGCCTGCTCTTACGGCGCTGGAGATCCTGCACCTGGGCGTCAGCGCGCTTCGGGACTGC
CTTTGCGGCCGCGGCCCTCGGCCCGCCCCCGGCTACCACTTGA

>Gm-cx47.1-G19771 Our suggested modification. Underlined: Predicted by Ensembl as intron, here included as part of exon.

ATGAGCTGGAGCTTCTCACACGGCTGCTGGAGGAGATCCACAACCACTCCACCTTTGTG
GGCAAGTGTGGCTGACGGTGCTCATCATCTTCCGCATCGTGCTGACGGCGGTGGGCGGC
GAGTCCATCTACTCGGACGAGCAGACCAAGTTACCCTGCAACACCAAGCAGCCCGGCTGT
GACAACTGTTGCTACGACGCCTTCGCGCACTCTCCACGTGCGCTTCTGGGTCTTCCAG
ATCATCATGATCTCCACGCGTCCGTTCATGTACCTGGGCTACGCCATCCACAAGATCGCC
CGCAGTTCCGAGGACGAGCGCAAGAGGAGCGGCCACCGCCGCTCCGCAGGAAACCC
CCGCCGCACACCCGGTGGCGGGAGAGCCGGCGGCTGGACGAGGCGCTGGAGGAGGAGCTG
GACGTCGACGACGGCGAGCCAATGCTGTACGACGACGCTCTGGACGCCAGGCCAGAGCCG
GCGGTGGCCGGCGGCGGAGGTCCGCGAAGCAGACGGCGCCCGGAGGATCGTGCAGGAG
GGCCTCATGAGGATCTACGTCTTGCAGCTCATGTCCCGGGCCATCTTCGAGATCAGCTTC
CTGGCGGGGCAGTACCTGCTGTACGGGTTCCGCGTCAGCCCGTCGTACGAGTGCGACCGC
CTGCCCTGCCCGACCCGCTGGACTGCTTTCATCTCCAGGCCACGGAGAAGACCATCTTC
CTGCTCATCATGTACGTGGTGAGCTGCCTGTGTCTGCTGCTCAACGTGTGCGAGATGTT
CACCTGGGCATCGGAACGTTCCGGGACACCCTCCGCCAGAAGAGGGACCGCGCCGGCGG
ACGTCTACGGCTACCCTTCTCCCGAACATCCCGTCGTCCCGCCCGGGTACAACCTG
GTGGTGAAGTCGGACAAACCGCTCCACCGGATCCCCAACAGCCTGATCACACACGAGCAG
AACATGGCCAACCTGGCCAGGACGAGCAGTGCACAGCCCGGATGAGAACATCCCTCC
GATCTGGCCACCTCCACGCCACCTCCGGGTGGCCAGGACGAGCTGGACATGGCCTTC
CAGACGTACAGCTCCAAGAACGACAACCAACCCCCCTCCAGGACGAGCAGCCCCATGTCA
GGGGGCACCATGGCCGAGCAGAACCGGGTGAACACGGTTCAGGAGAAGCAGGGAGCCCGG
CCGAAGTCGGCCACGGAGAGACCGGGACCCTTTTAAAAACGGGAAGACTTCTGTGTGG
ATTTAA

>Gm-NN-gjd2-G14288 Underlined: Sequence predicted as introns by Ensembl are here included as exon. Italics: Ensembl has a long row of Ns in this area, which we have partially replaced by sequences found by Blast in GenBank cod wgs.

ATGGGAGAATGGACCATCCTGGAGCGCTCCTGGAGGCGCTGTGCAGCAGCACTCTACC
ATGATTGGGAGGATCTCTGCTGACAGTGGTGGTGATCTTCCGCATCCTGATCGTTGCCATC
GTGGGCGAGACGGTGTACGAGGACGAGCAGACCATGTTTCATCTGCAACACCTCCAGCCG
GGATGCAACAGGCCTGCTACGACAAGGCCTTCCCCATCTCCACATCCGCTACTGGGTG
TTCCAGATCATCTAGTGTGCACGCCCAGCCTCTGTTCATCACCTACTCTGTGCACCAG
TCGGCCAAGCAGCGGACCGCGCTACTCCTTCTGTACCCCATCCTGGAGCGGGACTAC
GGCGGCTTGGGGGGCGGCTTGGGGGGCGGCTGGGGGGCGGCTGGGGGGCGGAGCGCGGC
GGAGGCGGGGGCGGCTGGGACGCAAGCTGCGCAACATCAACGGCATCCTGGTGCAGCAC
GGCGACAGCGTGGGCGCAAGGAGGAGCGGACTGCCTGGAGGTGAAGGAGATCCCCAAT
GCGCCGCGCGGCTCACGCACAGCAAGAACTCCAAGGTGCGGCGGCAGGAGGGCATCTCA
CGCTTCTACATCATCCAGGTGGTGTTCGCAACGCTCTGGAGATCGGCTTCCTGGCGGGC
CAGTACTTCTGTACGGCTTCAGCGTGCCGGGCATCTTCGAGTGTGACCGCTACCCGTGT
CTGAAGGAGGTGGAGTGCTACGTGTACGCGCCACCGAGAAGACGGTGTCTGTGGTGTTC
ATGTTTGGCGTGAGCGGCTGTGCGTGGTGCTCAACCTGGCCGAGCTCAACCACCTGGGC
TGGAGGAAGATCAAGCGGCCATCCGGGGCGTGAGGCCCGCAGGAAGTCCATCTGCGAG
ATCCGGAAGAAGGACATGGCGCACCTGTCCAGCCACCAACCTGGGCCGCACGAGTCC
AGCGAGTCCGCCTACGTCTGA

>Gm-NN-gjd2-G03494 Underlined: Sequences predicted as introns by Ensembl are here included as exon. Lower case: Sequence extended in 5' direction by Blast in GenBank cod wgs. Exon 1 found from XM_030360300.

atgggagagtggaccatcctggagcgacttctggaggetgcggtccagcagcactccact
atgatcgccggatctctactgactgtagtggtatcttcggatcctgatcgtaggaaTC
GTCGGTGAGAAGGTGTACGAGGATGAGCAGATCATGTTTCATCTGCAACACCATGCAGCCG
GGCTGCAACAGGCCTGCTACGACAAGGCCTTCCCCATCTCCACATCCGCTACTGGGTG
TTCCAGATCATCTGGTGTGCACGCCAGCCTGTGCTTCATCACCTACTCGGTGCACCAG
TCGGCCAAGCAGCGCGAGCGCAGCTACGCCTTCTGTACCCGTACATGGACGGGGCCACC
GTGGCCACACGAGCGCACGGCCAGACCGGCCACGGCGGGGGCCACGGCCGCCACGACCAC
CACGCGGCCCGCAAGTGTGCAACATCAACGGCATCCTGGTGCAGAACGACAGCAGCAAG

GAGGACCACGACATGGAGACCAAGGAGATCCCCAACATGGCGCGCAGCCTGCCGCACGGC
AAGAGCGCCAAGGTGCCGCGGCAGGAGGGCATCTCGCGCTTCTACGTCATCCAGGTGGTG
TTCCGCAACGTCTCTGAGATCGGCTTCCTCGCGGGCCAGTACTTCTGTATGGCTTCAAT
GTGCCGGGGATGTTTGAGTGCAGCCGTACCCCTTGTGTGAAGGAGGTTGAGTGCATCGTA
TCGCGGGCGACAGAGAAGACCGTCTTTCTGGTCTTCATGTTTCGCCGTTAGCGGCATCTGT
GTGCTGCTCAACCTAGCAGAACTCAACCACCTCGGCTGGCGGAAGATTAAAACGGCCGTC
AGAGGGGTGCAGGCGGTAGGAAGTCCATCTGTGAGGTGCGTAAGAAGGACGTGTCCAC
CTCTCCAGGCCCAACCTTGGCAGGACCCAGTCTAGCGAGTCGGCTACGTCTGA

>Gm-GJD2-G09811

ATGGGGGAATGGACTATACTAGAGAGGCTCCTGGAGGCTGCTGTCCAGCAGCACTCGACT
ATGATAGGAAGGATCCTACTCACTGTGGTGGTCATCTTCCGGATCTTAATCGTAGCGATA
GTCGGAGAGACTGTCTATGATGACGAGCAAACCATGTTTGTGTGTAAACACCTTACAACCG
GGCTGCAAACAGGCAATGTACGACAAGGCATTTCCCATTTACACATCCGATACTGGGTG
TTTCAAATTATCATGGTGTGCACGCCGAGCCTGTGCTTCATCACCTACTCGGTGCACCAG
TCGGCCAAGCAGAAGGAGCGGCGCTTCTCAACGGTGTACCTGACGCTGGACAAGGACCAA
GACTCCATGAAGAGGGAAGAGAGCAAAAAGATCACCAGAGCACCATCGTGAACGGAGTA
CTGCAGAACACGGAGAACACCACCAAGAGGCGGAGCCGACTGCTTGGAGGTCAAGGAG
ATCCAGAACTCGGCCATGAGAACTAAGTCGAAATTAAGGCGCCAGGAGGAATCTCGAGG
TTCATCATCATCAAGTGGTGTTCAGAAACGCGTTGGAGATCGGTTTTCTGGTGGGGCAA
TATTTCTGTACGGATTCAACGTGCCGTCCGTGTACGAGTGCATCGATACCCGTGCATC
AAAGACGTCGAGTGCATCGTCTCCAGGCCACGGAGAAGACCGTGTTCCTGGTGTTCATG
TTCGCCGTGACGCGGTTTTGTGTGATTCTGAATCTGGCGGAACCTCAATCATCTGGGCTGG
CGAAAGATCAAGACGCCGTGCGGGGCGTGCAGGCGGACGAAAGTCCATCTATGAGATC
CGAAACAAAGACTTGCCGAGAATGAGTGTGCCCAATTTCCGGGCGTACTCAATCCAGTGAC
TCCGCTTATGTGTAA

>Gm-NN-gjd2-G01582 Modified according to XM 030345236 Splice site

ATGGGGGAATGGACCATCCTCGAGCGTCTACTGGAGGCGGCCGTTCAACAGCACTCTACT
ATGATAGGAAGGATCTCTGCTCACGGTGGTGGTGATCTTCCGGATCCTGATCGTGGCCATC
GTCGGGAGACCGTCTACGATGACGAACAGGAGATGTTTGTGTGTGAACACCCCTGCAGCCG
GGCTGCAAACAGGCGTGCATCGACAGGCCTTCCCCATCTCCACATCCGGTACTGGGTT
TTCCAGATCATCATGGTGTGCTGCCCCAGCCTCTGCTTCATCACCTACTCCGTCCACCAG
TCGTCCAAGCAGAAGGAGCGCGGCTTCTCCGGCGTGTACCTGTGCGTGGACCGGACGGGC
CGGCCAGACGACAACCTGCTGAAGAACACTCTGGTGAACGGCCTGCTGCAGAACTCGGAG
AACTCGTACAAGGAGGCGGACCCGGACGCTCACATCTTCCCCCGGCAGTGTGTGAGGACG
CAGTCCAAGATGAGGAGGAGGAGGCGATCTCCCGCTTCTACATCATCCAGGTGGTCTTC
CGGAACATGCTGGAGGTGGGCTTCTTGGTGGGCCAGTACTTCTGTACGGGTTCAACGTG
CCCCCGTGTACGAGTGCAGCCGTACCCGTGCATCAAGGACGTCGAGTGCATCGTCTCA
CGGCCACCGGAGAAGACCGTGTTCCTGGTCTTCATGTTGCCCATCAGCGGCGTCTGCGTG
GTCTTCAACCTGGCGGAGCTCAACCACCTGGGCTGGGAAGATCAAGGAGGCCGTGAGG
GGCGTGCAGGCCCGGAGGAAGTCCGTCTACGAGATCCGCAAGAAGGACCCGGCCAAGATG
AGCGGATTTGGACACATCCAGTCCAGTGACTCCGCCTACGTTTGA

>Gm-NP-cx39.2

ATGGGGGACTGGTCAATACTGGGACGTTTTCTGTCCGAAGTGCAAAACCATTCCACAGTG
ATAGGAAGATTTGGTGACCATGCTGCTCATCTTCCGCATCCTGCTGGTGACCCTGGTG
GGAGACGCCGTCTACAGTGACGAGCAGTCCAAGTTCACCTGTAAACCCAGCAGCCCGGA
TGAACAACGTCTGTGTACGACACCTTTGCACCTGTGTACATCTGCGTTTTCTGGGTTTTT
CAGATTGTGCTGGTATCCACTCCATCTATCTTCTACATCGTTTTTGTCTCCATAAAATT
GCCAAGGATGAGAAGCTGGATGTCCAGAAAGGAAAGTTCAATCCAAGCCCCCTCCAAA
AATAACTATGTTGAGCTTGGTAGCAGTTGTATGGAGGGCACCAGGTGGAGCCCATCTAC
AGTCCCAAGTACATGGAGGAATGGGGCAGAAAGACCAAGAAGGAATGGAGCAAAGTCTC
CTTGACGAGGATTATGCTGAACCTGGTGAAGATCCAACCAGCTATCGAGCCAAGTCTTA
CTCATTTACATTCTTCACGTGTTGTTACGTTCTGTTATGGAGATAACCTTTTTGGTGGGC
CAGTATTACTTGTTTGGTTTTGAAGTGCCGCACCTGTATCGCTGCAGACCTATCCCTGC
CCAACACGCACTGACTGCATTTGTTTCTCGTGCCACAGAGAAGACAATTTTCTGAATTTT
ATGTTTACAGCTAGCCGTGGGCTGCTTTGTTCTCAACATCGCCGAGCTTCACTATCTTGGC
TGGGTGTACATATTCCGCATCTTGTGCTCAGCTTGTCTACGTGCTGTACTCATGAGAGG
GATGCTAAGGGGCGGTACTCCCACCAGAACCCCTTGCTGCTGCAGCTGAAGCACTCCCTC
AGGGGGAGGCTGGTCTTACAGACGCCGTGCCCCAGGAGCCAGGAGAAGGCTCGAGGTCTG
CTCAGTCACGCCCCGCCATCTCCTTTGAGACGGATTCCACCGTGAATGCACCTCCAAG
AGGACTTTAGAGGAGAGGGACAAAGTGAAGCTCAAATTAGCCAACATGGCAAAACTAGGA
AGAACTAAGAAGTCTGTTTATAA

>Gm-GJD3-G20235 Ensembl prediction. The sequence has been extended in 3'-direction (underlined) until stop codon.

ATGGGGGAATGGAGCTTCCTGGGTGATCTGTTTGAACACCTCCAGGCACACTCGCCCCATG

CTGGGTCGCTTCTGGCTCTTCATCATGCTCGTGTTCGCGATTCTGATCCTGGGCACCGTG
 GCGTCTGACCTGTTTTGACGACGAGCAGGAAGAGTTCTCCTGCAACACCCCTGCAGCCGGGC
TGCAAAGCAGGTGTGCTACGACCATGCCCTTCCCCATCTCCCTGTACCGGTTCTGGGTCTTC
 CACATCATCTCATCTCCACCCCGGAATGCTCTACCTGATGTACGCCATGCACCACGTC
TCCAAGAAAAAAGCCCTCCTCGTCCGCCGACGGCACCGCCTCCACCTGCAGCCAGGATAAC
 CAAGAGGAGAGGCGCCTGAGGCAGCTCTACCTGGTGAACGTGGCCTTCCGCCTGATGGCG
GAGGTGGGCGTGCTGGTGGGCCAGTGGTGGCTGTACGGCTTCAAGCTGGAGGCCAGTTC
 CCCTGCAGCCGCTACCCCTTGCCCGTACACGGTGGACTGCTTACCTCCAGGCCCGCCGAG
 AAGACCGCTCTTCTTGGTGTCTACTTTGGGGTGGGCGTGGTGTGCGCCGCTCCAGCCTG
GTGGAGCTCCTCTACGCCGCTGTCAAGTGGTTCTGCCCCAGGAAACAGGGGCGGCGCGGC
 ATGCCGATAGGTCTACGAGTCTCATAGCCTCAGCAACCTGCGGAAACAGGAGGAGGAG
 GCGAACCCTGCGGTTTTGTGGGAGGGGGGAAGGCGCTGTCCGACAGCGCGCTGAGCAGCGCG
 AGGATGAAGACAGGCCCGCTGAGGAGCAGCGGTGCGAGGAAGACCTCCAGCGTCCGACAC
AAGACCTCCAGGCTCCCCAGCAGCCGGTCCTTCATGGCGTGA

>Gm-NN-gjd4-G11373

ATGGGCATGCTGGATGCAGTCCCTTGTCGCCATAAGCCACAACATCTCCTTTGTGGGTAAA
 ACCTGGTGGCTACTCATGGTAGGCCTACGTCTTATTGTGGTCTGCTGGCCGGCTTCACC
 CTCTTCAGTGATGAGCAGGAGCGCTTCGTCTGCAAACACCATCCAGCCGGGTTGCTCCAAC
 GTCTGCTTCAACCTGTTGGCGCCCGTTCCCTGTTCCGCTCTGGCTGCTCCACATCGTC
 CTCCTGTCTCTGCCGTACCTCATGTTCTGCTACACACATCGCACACAGGCTCCTGTGGGAT
 CCCAAGTCTGGAGCGGGCTACGTGGCGATAAACCGCCATGGGAGTCAGGGAAGCCCTTGC
 TCCACGCCAGAGATTTCCAGTTCCCTCCTTCTTCATCATCATCATCTTCTGGGCAGGAC
 CCCTCCAGTGCCTGCGGCCCGTGCAGCTTCCACTATGCCTACCTATTGGTCGTGACC
GTGCACATCCTGATGGAGGCGGCCCTTCGTGGCGGGTCACGTCTCTTCTCGGGTTCTTC
ATCCCAAGAAGCTTCCTGTGCTACGAGGCCCGTGCACGTGCGGCGTGCAGTGCCTACGTC
TCCCGGCCACAGAGAAGACGCTGATGCTCGACCTCATGCTGGGCCTGGCCTGTCTGTCA
GTGGTGTGAGCCTGGTGGACCTTGTGGCCGGCGCACGCCGGGCTCTGAGCGCGCGGAGG
 AGAGCGACGTCTGTGTCGGAGGAGATGGGCAAAGGAGAGCAGAGCAGCGTGTCTCCAAC
 GTGAGTGGTGCAGGAGACCTCAACCTCCTCTTGAACAAGAGGATGGCCAACGGGTTTGAG
 AGCGACATCCAAGCCACGCTAGCTCCTCTACAGACAGTGTGCCTAATGTGCGCCCGCGC
 CTGAAGGGCGAGGCAGAGGGTAAGGCTGGCAAGCTGACCGACGAGAAGGGCTTGCCGTGG
 CAACACAGTGCCAACGGAAAGATCGGGTTCTCGACGAATCCAAAAGCCATGCCGCTGCCC
 TTCGTCTGCCACAACCAGCAGAAACCTCCAGAGTTGGCTTCCCTGGACGGCAGCCTAGCA
 CCGAGGCTGGAGAACTTCAACCCCGCTGACACTAGGAAACAGGGCCAGCTAGCCTCAATG
 GAGTCCACCTCTACCTCCAGGCAGAACTCTACCCCCAGTGAGGGTCCTGACAAGAGGGCT
TGGGTTTAG

>Gm-NN-gjd4-G17736 Splice site. Underlined: sequence extended in 3-direction, and was further extended (lower case) by Blast against GenBank cod wgs

ATGAGTGGAGCCAGTGCTGTGAAGTCATCTTCATCTCGTTCAGCCATAGCACCACACTG
 ATGGGGAAGGTGTGGCTGGTCATCATGGTGTTCCTCCGGGTCCTCGTCTGCTGCTGGCC
 GGCTACCCGCTCTACAGGACGAGCAGGAGCGCTTCGTGTGCAACACCATCCAGCCGGGC
TGCGCCCAACGTCTGCTACGACCTCTTCGCCCCGCTCTCCCTCTTCCGCTTCTGGCTGGTG
 CAGCTGGTGTCCGTCTCCCTGCCCTACCTCGTCTTCGTAGTCTACGTGGTCCACCGGGTC
CTGTGCGGGCTGACTGCCGGCTCTGCCCTTCCTCCTCCTCCTCTGCACCTCCTCTTCCT
CTGGCACAGGACGTGCGGAGGGCTGGGAAGGACCCGCGGGACGGCgcgcgcgcgcgcg
 gcggcctcgctgcccagctcgccccggcgcggtgcttcgcgggggcctacactcctg
 cagctggtcttcgcacatcctggttagaggtgggcttcgcgcgcgccactactacctgttt
 ggcttcacatccccagcgcttcctgTgccagcaggcgccgTgcaccaccaggtggac
Tgctacatctcgcgccccaccgagaagagcgtgatgctgtgcctcatgctgggcgccggc
gcgctctccctggggctcaacgcgctggacgtggtgtgcgccgtcaagcgctcggtgagg
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 gtgcaccacgaggcgcgctgcacgggaggagcgtcccgcggcggaagcttcgggaagcgg
 gggcgagcaaggcctcgagcgtctgcgccccgtccccgaccactgctcggtacggggc
 tccctgtgcccctcagccccggggcccccgcgccctgaacaccaacaacggcaacaac
 ggctacgggcaggccccagcgggaggagcgcgccccacggcagcgacgtggccacgga
 cctccgagcccccgccacgccccgtccatccgcgtcaacaagcaggcgccctcaag
 cccctcccccgccgcggggaccccccgcgccgctgggggtcgttcggggtcgtc
 tccaaggcgacagcgagcgggcgagcagaagggcggtcagtaactcaggtggaactt
 ggcggttgccaggacgagcgccaggcggaaggtcggaatgggtgtga

>Gm-GJE1-G16314 Ensembl prediction. No modifications. Splice sites.

ATGTCTTTAACTACATTAATAAACTTTTATGAAGGATGCCTCAGGCCTCCTACGGTGATA
 GGCCAGTTCCACACCCCTTTCTTCGGCTCCGTGCGGATGTCTTCTTAGGGGTGCTGGGC
 TTTGCTGTGTACGGTAACGAGGCGCTCCACTTCAGCTGTGACCCCGACCGCAGAGAGCTC

AACCTCTACTGCTACAACCAGTTCCGACCAATCAGCCGCAAGTTTCTGGGCACTACAG
 CTGGTGACGGTGCTGTTTCCCGGGCCGTGTTCCACCTCTACGCCGCTGCAGACCATC
 GACCAGGAGGAGATTCTCCAGAGACCCGTCTACACCGTGTTCTACATCATCTCAGTGCTG
 CTGCGCATCATCTTGGAGGTCATCGCCTTCTGGCTGCAGAGCCACCTCTTCGGCTTCCAG
 GTCCACCTCTCTTCATGTGTGACGCCATTGCGCTGGAGCGCTCCTTCAACGTGACCAAG
 TGCATGGTCCCGGAGCACTTTGAGAAGACCATCTTCTCAGCGCCATGTACACCTTCACC
 GTCATCACCATCTGCTCTGTGTGGCCGAGATCTTCGAGATCCTCTGCAGGAGCTGGGG
 TACCTCAGCAACAAGTGA

Suppl. Fig. 11. Japanese eel (*Anguilla japonica*) connexins.

Yellow: Conserved domains as defined by Cruciani and Mikalsen (2007)

Green: Conserved cysteine codons (cysteine signature)

Grey: 15 nt added at the ends of the conserved domains

Other colors are explained where necessary.

We here use the Japanese eel linkage groups (essentially equals a chromosome level assembly) as identification in addition to the naming of each sequence.

>Aj-NN-cx43-BEWY01000019 **C**, added to keep reading frame; nucleotide chosen according to BDQN01000172, AVPY01141929 (both *A. japonica*), AZBK01844958 (*A. anguilla*) and LTYT01001410 (*A. rostrata*).

ATGGGTGACTGGAGCGCTTTAGGGAGACTTCTGGACAAGGTCCAGGCCTACTCCACCGCT
 GGAGGAAAGGTCTGGCTCTCTGTCTCTTCATCTTCCGTATCCTGGTCTTGGGGACGGCC
 GTGGAGTCCGCTTGGGGCAGCAGCAGTCGGCCTTCAAGTGCACACCCAGCAGCCCGGT
 TGCAGAGAACGTCTGTGTACGACAAGTCTTCCCTATCTCGCACGTCCGCTTCTGGGTCTCTC
 CAGATCATCTTCGTCTCCACGCCAACGCTGTCTACCTCGCCACGCTCTTCTACCTGATG
 CGCAAGGAGCAGAAGCTGAACAAGAAGGAGGAGGAGCTGAAGGCGGTGCAGAACGACGGC
 GGCGACGTGGACATACCGCTGAGGAAGATCGAGCTGAAGAAGGTCAAGCACGGGCTGGAG
 GAGCATGGGAAGGTCAAGATGAAGGGCGCCCTCTTGCGCACCTACATCGTCAGCATCTTG
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>Aj-gja3-BEWY01000008 Likely assembly error. The indicated sequence is repeated on either side of a row of Ns.

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>Aj-NN-cx28.6-BEWY01000007 (3'-term; underlined)+ BEWY01000024 (5'-term) The latter is unplaced, but that these two parts belong together is indicated by AVPY01364480 and BDQN01002772 from *A. japonica*, AZBK01632506 from *A. anguilla*, and LTYT01005556 from *A. rostrata*

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>Aj-NN-cx28.6-BEWY01000004 1:25112498-25113309 **C**, inserted to keep reading frame, nucleotide chosen according to AVPY01029196 and BDQN01000086 (both *A. japonica*), and supported by LTYT01001691 (*A. rostrata*) and AZBK01815961 (*A. anguilla*).

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>Aj-gjd2-BEWY01000019 Splice site

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Suppl. Fig. 12. *Connexin39.2* ("gjd2like") from mammals.

Note that some entries present in GenBank have wrong subfamily designation. In humans and koala the sequence is said to belong to the alpha subfamily, in Egyptian rousette it is said to belong to the gamma subfamily, while in black flying fox it is said to belong to the delta subfamily (which is correct). The corresponding opossum sequence (Md-*GJD2like-39.2*-XM_001376506), which was the first *cx39.2* sequence found in mammals (Cruciani and Mikalsen, 2005), is depicted in Suppl. Fig. 3. Several of these sequences are (supposed) pseudogenes (indicated by *GJA4P*, *cx39.2P*). To show the exact alignments of these sequences used in the phylogenetic analyses, which showed that they belonged to a single orthologous group, we have indicated the gaps (-). The gaps have been adjusted to fit the codon borders as much as possible. Be aware that most alignment tools remove gaps before performing alignment.

The previously non-predicted sequences (indicated by "NP") were found by blasting other *cx39.2* sequences into Ensembl genomes or GenBank wgs (using Placentalia, marsupials, bats, or Afrotheria as species groups).

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>Pv-NP-cx39.2 *Pteropus vampyrus* Latge flying fox

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>Pa-GJD2like-XM_006925175 *Pteropus alecto* Black flying fox

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>Tm-NP-cx39.2P *Trichechus manatus* Manatee

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 ---CAGAAGG---TGCTGGTGGCCACACCTCCATCTTCTATGTCGTCTGTGTCCTGCAC
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 TTCCTAGAGGGACAGCTCCTGGTACGAGAGGGCGATTCTCCCCAAATGCCTTGGGGCTGC
 AGCCAGGACCCAGCCTTTGGTCTCACAGCGTCTTGGTCATC~~TACATTGCCCATGCT~~

GCTGCTGGCCTTTATGGAGCTGGCCTTCCTGGTGGGGCCATACTATCTGTTTGGGTTTGA
TGTCCCATACTTATTTTCACTTGTCACTCCTACCCC-GTCTTACC---AGTATTAACTGCTT
TGTTTCCAACGCCACAGAG---ATGATCTTCCTGAACCTTCATGTTTGG-AGTGGGGCAGG
CTGCTTCCCTTTGAACCTGGTGGAGCTGCACTAGCTGGGCTGA-GTCTTCACCTGACAGAC
CCTCTTTGTGGCCTGTGCCAGCTGCTGCCA

>La-NP-cx39.2P African elephant *Loxodonta africana*

ATGAGCGACTGGTCATTTGTGGGCCAGCTCCTGACCCAAATG-AGAACCATCCCACCATG
GTCAGCAAGGTGTGGCTCACCGTCCTCCTGATCTTCCACATCCTGCTGGTCACTCTGGTG
AGAGACACTGTCCATAGGGACGAGCAGTCTAACTTCACC-TGCAACACCCTGCAGCCTGGC
TGCACCAACATCTGCTGTGACCGCTTCTGCCCCGTCTCCCACTTCTGCTTCTGGGTCTTT
---CAGATC--CCTGCTGTTGGCCATGCCCTCCATCTTCTGTGCATCTGTGTCTGCAC
CAGATCACAAGGGAGGAGAGAGTCAGTGTGGAGAAAGGGTACCTGCTGGAGACCTTGCAG
AAGCTGGTGGCAGGGGAGCCCTGCAGGGACCAGGCCAGTGTTCCTGGGTCTCTCATTT
CCTAGAGGGACAGCTCCTAGTGGGAGAGGGAGATTCTCCCCAAATGCCTTGGGGCTGCAC
CTCAGGACCCACAGCCTTTGGTCTTGCAGGGTCTTGGTCATCTACATTGCCCATGTGGTGC
GGCAGGCCTCTATGGAGCTAGCCTCCCTGTTGGGGCAATACTATCTGTTTGGGTTTGAATG
TCCCATAGTTATTTTCACTTGTGCTCCTACCCC-TGGGCCACC---AGTATTGACTGCTTTT
TGTCCAGGGCCACAGAG---ATGACCTTCCTGAACCTTCACATTTGG-GGTGAGGTAGGCT
GATTCCTCCTGAACCTGGTAAAGCTGCGCTACCTGGGCCGA-GCCTTCACCTGCCAGGCC
TCTTTGCAGCCTGTACCAGCTGCTGCCA

>Afer-NP-cx39.2P Aardvark *Orycteropus afer*. Note that the first Cys codon in the first conserved dokmain is mutated.

-----GTCATTCTGGGTTGGCTCCTGACCCAACTGCAGAACCATTCCACCATG
GTCAGCAAGGTGTGGCTCACTATCCTCCTGGTCTTCTGCGTCCTTCTGGTCACTCTGGTG
GGAGACTCTGTCTATGGAGACAAGCCATCCGAGTTCACT-TGCAACACCCTGCAGCCTGGC
TGCACCATATCTGCTATGATTGCTTCTACCCCTTCTCCCACTTCCATTCTATGTC---
---CAAATC---ATGCTGGTGGTGCACACCCTCCATCTTCTATGTGCATCTCAGTCCT-CAC
CGGATCACAAGGGAGGAGAGAGTCAAAGTGGAGAGAGGTTATCTATTGCAGACCTTGCAA
GAGCTGGCAGCTGGGGATCCCTGCAGGGACCCAGGCCAACAGTTAGTGGGATCCTCTCAC
TTCCTAGAGGGACAACCTCCAGTGGGAAAGGGGATTCTCTCCAAATGCCTTGTGGCTGCA
GCCAAGGACCCCAACCTTCTGTCTTGCAGGATCTTGGTCGTC-TACATTGCCCATGAGGTG
CTACAGGCCTTTATGGAGCTGGCTTTCTTGGTGGGGCAATGCTAT--GGTAGGCTT-GAT
GTCTCATAG-TATTTTCACTGCTCACTCCTACCCC-TGTCCTACA---AGTACTGACTGCTTT
GTGTCCAGGGCCACCAGAGAATATGACCCCTCCTGAACATCATGTTTGG-GGTGGGGTAGGC
TGCTACCTCCTGAACCT-TGAGAGCTATACT-CCTGGGCTGGGTCTTTACCTGCC--

>Dn-NP-cx39.2P *Dasypus novemcinctus* Armadillo. Note that the first Cys codon in the first conserved dokmain is mutated.

ATGAGCCACTGGTGGTTCCTGGGCCAGCTCGTGACCCAAAGTGCCAAATCCGTCCACTGTG
ACGGGCAAGGTATGACTCACCATGCTCCTGGCCTCCTGCATCCTGCTGGTCACTTGCAGG
GGAGAAGCTGCCTATGGGGACGAGCAGTCCAAGTTCACC-TGCAATCCCCTGCAGCCTGGC
TGCACCAATGTCTGCTGTGGCCACTTCTCACCTGTCTCC-ACTTCCACTCCTGGATCTTC
--CCAGATT---GTGTTGGTG-ACCCACTGCCCATCTTCTGTGTGCATCTGTGTCTGGAC
CAGATCAGGAGGAGAGAGTGGAAATGGAGGGGTCTTGTCTGGAGAATTTGCAAATGCTGG
TGGCTCGGGGAGCTCTGCAGGGACTGCGACTGGGACTCTGGGGTCTCTTACTTCCTAGA
TGGACAACTCCTGGTGGGAGAGGGGATTCTCCCCAAGTGCCTTGGGGTCAACAGCCAG
GCCTTGGGCCTGCAGTCACAGAGGGTCTTGGCCGTT-TGTGCGGCCGCAC-GGTGCTGCCA
GCCTTTATGGAGCTGGCCTTGTCTGGTGG-ACAGTGTTCCTGTTTGGGTTTGTATGTTCCA
CACTTATTTTCACTTGCACGCCTATTCCCT-TGTCCAC--GAGGACTGA-TGCTTAGTGTCC
TGGGTCACT-GAA--GATGACCT---TGAGCTTCAGGCTCGGGGAGGGGGTGGGCTGCTTC
CCCTTGAGGCTAGCGGAGCTGCATCACCTGGGCTGGGTCTTCACCTGCCGGGCACGCTTT
GTGGCCTGTGCCAGCTGCTTCCACTTCTGGAGATGACCTGCTGGTC

Suppl. Fig. 13. Comparisons of human “GJA4P” against *connexin39.2* and *GJA4*.

Suppl. Fig. 13A. Alignment of conserved domains in human “GJA4P” (NG_026166) against *connexin39.2* (“*gjd2like*”) in various species at protein level.

The cx39.2 sequences given in Suppl. Fig. 12 were translated to protein and aligned. Among the pseudogenes, only the human sequence is included, as aligning several pseudogenes strongly decreases the total number of identities (*) or similarities (: or .). Also the corresponding sequence from eel (Aj-NN-cx39.2) was included. ?, corresponds to a codon that contains one or more unknown nucleotides or a gap. <, corresponds to a stop codon. n, the first conserved domain is N-terminal to n, and the second conserved domain is C-terminal to n; thus this n corresponds largely to the intracellular loop. The Muscle (<https://www.ebi.ac.uk/Tools/msa/muscle/>) identity matrix is found in Suppl. Table 8.

Hs-GJA4P	MSDWSFLGWLLTRVQNDSTVVGKVWLT??LVLHILLVALLGSAVC?DEHCKFICNTRLRPG
Aj-NN-cx39.2	MGDWSILGRFLTQVQNHSTVIGKIWLTMLLIFRILLVTLVGDVAVSDEQSKFTCNTLQPG
Pv-NP-cx39.2	MSDWSFLGRLLTQVQNHSTVVGKVWLTVLLVFRILLVTLVGDVAVGDEQSKFTCNTLQPG
Pa-XM_006925175	MSDWSFLGRLLTQVQNHSTVVGKVWLTVLLVFRILLVTLVGDVAVGDEQSKFTCNTLQPG
Ra-XM_016138748	MSDWSFLGRLLTQVQNHSTVVGKVWLTVLLVFRILLVTLVGDVAVGDEQSKFTCNTLQPG
Wallaby-NP-cx39.2	MGDWSFLGRLLTQVQNHSTVIGKIWTALLIFRILLVTLVGDVAVRDEQSKFTCNTLQPG
Koala-XM_020963328	MGDWSFLGRLLTQVQNHSTVIGKIWTALLIFRILLVTLVGNVAVGDEQSKFTCNTLQPG
Md-XM_001376506	MGDWSFLGRLLNEVQNHSTVIGKIWTALLIFRILLVTLVGDAIYGDEQSKFTCNTLQPG
	*.***:*.:. * * * * *.***:*** *:.*****:*.:. * * * * *.***:***
Hs-GJA4P	CT???????DHFSHR?GAFQIVLVAVPSIFFVVCVLH<MVNGnRVLAVCTAHVVLRA
Aj-NN-cx39.2	CNNVCYDTFAPVSHLRFWVFQIVLVSTPSIFYIVYVLHAKIADnQVLLIYIVHVLR
Pv-NP-cx39.2	CTNVCYDRFSPVSHFRFWVFQIVLVATPSIFYVIYVLHQAIREnRVLAIIYIAHV
Pa-XM_006925175	CTNVCYDRFSPVSHFRFWVFQIVLVATPSIFYVIYVLHQAIREnRVLAIIYIAHV
Ra-XM_016138748	CTNVCYDRFSPVSHFRFWVFQIVLVATPSIFYVIYVLHQAIREnRVLAIIYIAHV
Wallaby-NP-cx39.2	CTNVCYNSFAPFSLHFRWIFQIVLVATPSIFYIVCLMHQVLEnRVLIIYIAHV
Koala-XM_020963328	CTNVCYNSFAPISHLRFWIFQIVLVATPSIFYIVCMHQVLEnRVLVIYIAHV
Md-XM_001376506	CTNVCYNSFAPISHLRFWIFQIVLVATPSIFYIVCVLHQVLEnRALIIYIAHV
	*. .***: * * * * *.*****:*****: : : * : . . * : .*****: :
Hs-GJA4P	ELAFVLG???LSGCDMPWLLHCHS?PCPSSPDCFVSRAMRKKIFLNFMCF?VGLGCFLLNP
Aj-NN-cx39.2	EIAFLVGQYYLFGFVPHLFRCEYPCPNRTDCFVSRATEKTIFLNFMFSISLGCFILNI
Pv-NP-cx39.2	ELAFVLVGQYYLFGFDVPYLFHCHSYPCPTSTDCFVSRATEKMIFLNFMFGVGVGCFLLNL
Pa-XM_006925175	ELAFVLVGQYYLFGFDVPYLFHCHSYPCPTSTDCFVSRATEKMIFLNFMFGVGVGCFLLNL
Ra-XM_016138748	ELAFVLVGQYYLFGFDVPYLFHCHSYPCPTSTDCFVSRATEKMIFLNFMFGVGVGCFLLNL
Wallaby-NP-cx39.2	ELGFLVGQYYLFGFDVPHLYRCETYPCTKTDCFVSRATEKMIFLNFMFGVGLGCFLLSL
Koala-XM_020963328	ELGFLVGQY<LFGFNVPHLYRCETYPCTKTDCFVSRATEKMIFLNFMFGVGLGCFLLNL
Md-XM_001376506	ELGFLVGQYYLFGFDVPHLYRCETYPCTKTDCFVSRATEKMIFLNFMFGVGLGCFLLNL
	*:.***** * * : * * . * : * * * . .***** * * * * * :.*****:.
Hs-GJA4P	MELCYLGVWFPCQ
Aj-NN-39.2	VELHYLGVVYIFR
Pv-NP-cx39.2	VELHYLGVVFTYR
Pa-XM_006925175	VELHYLGVVFTYR
Ra-XM_016138748	AELHYLGVVFTCR
Wallaby-NP-cx39.2	AELHYLGLWLTFR
Koala-XM_020963328	AELHYLGLWLTFR
Md-XM_001376506	AELHYLGLWLTFR
	* * * * * : .

Suppl. Fig. 13B. Alignment of conserved domains in human “GJA4P” (NG_026166) against GJA4 (connexin37) from human and eel at protein level.

The human *GJA4P* *cx39.2* sequence given in Suppl. Fig. 12 were translated to protein and aligned with eel *cx39.2*, human *GJA4*, and the two eel-*gja4* (*cx39.4*) sequences. Identities (*) or similarities (: or .) are indicated below the alignment. . ?, corresponds to a codon that contains one or more unknown nucleotides or a gap. <, corresponds to a stop codon. n, the first conserved domain is N-terminal to n, and the second conserved domain is C-terminal to n; thus this n corresponds largely to the intracellular loop. The Muscle (<https://www.ebi.ac.uk/Tools/msa/muscle/>) identity matrix is shown in Suppl. Table. 9.

```

Hs-GJA4P      --MSDWSFLGWLLTRVQNDSTVVGKVWLT??LVLHILLVALLGSAVC?DEHCKFICNTLR
Aj-NN-cx39.2  --MGDWSILGRFLTEVQNHSTVIGKIWLTMLLIFRILLVTLVGDAVYSDEQSKFTCNTLQ
Hs-GJA4-Cx37  --MGDWGFLEKLLDQVQEHSTVVGKIWLTVLFIFRILILGLAGESVWGDEQSDFECSNTAQ
Aj-NN-cx39.4-1 MSKSDWTFLELLLEQQGVHSTGVGKMWLTVLFVFRVLVLTAAESVWGDEQSDFVCNTQQ
Aj-NN-cx39.4-2 MSRADWGFLERFLEEGQEYSTGIGRVWLTVLFVFRMLILGTAAESAWDDEQSDFVCNTQQ
               .** :* :* * ** :*.:*** :...*: :... **:. * *** .

Hs-GJA4P      PGCT??????DHFSHFR?GAFQIVLVAVPSIFFVVCVLH<MVNGnRVLAVCTAHVVLRA
Aj-NN-cx39.2  PGCNNVCYDTFAPVSHLRFVWFQIVLVSTPSIFYIIVYLHAKDnQVLLIYIVHVVLR
Hs-GJA4-Cx37  PGCTNVCYDQAFPISHIRYVWLQFLFVSTPTLVYLGHVYLSRREnALMGTYVASVLCKS
Aj-NN-cx39.4-1 PGCEAVCYDKAFPISHFRFFILQVIVASPAIFYLSYAALHARWQnKLLRVYLCVTVLKL
Aj-NN-cx39.4-2 PGCELACYDRAFPISHFRFFVLQVIFVSTPTIFYFIYVALRMGWEnKLLCAYTSLIVLKV
               *** .**:* :*.:*: *.:... . . : : .

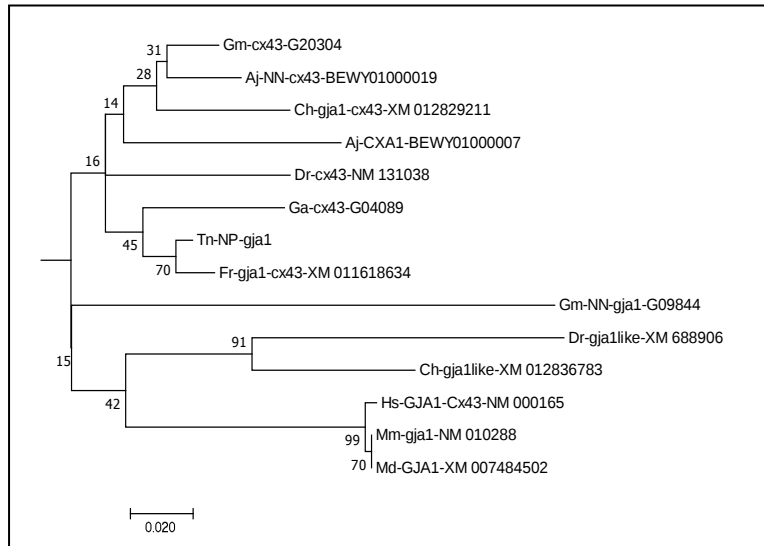
Hs-GJA4P      CMELAFLVG???LSGCDMPWLLHCHS?PCPSSPDCFVSRAMRKKIFLNFM?VGLGCFLL
Aj-NN-cx39.2  IMEIAFLVGQYYLFGFEVPHLFRCEYPCPNRTDCFVSRATEKTIFLNFMFSISLGCFIL
Hs-GJA4-Cx37  VLEAGFLYGQWRLYGWTMEPVFVCQRAPCPYLVDVCFVSRPTEKTIFIIIFMLVVGLISLVL
Aj-NN-cx39.4-1 LLEAAFILVLWHLYGFTVPARYVCQRWPCPHTVDCFVSRPKEKTVFTVYMQAMAGVSLLF
Aj-NN-cx39.4-2 LLEAGFILGLWFLYGFFVHAKYVCQRPPCPHTVDCFVSRPTEKTIFTVYMQAIAGVSMLL
               :* .*: * * : * *** ***** .*.:* :* :. :...

Hs-GJA4P      NPMELCYLGWVFPCQ
Aj-NN-cx39.2  NIVELHYLGWVYIFR
Hs-GJA4-Cx37  NLLELVHLLCRCLSR
Aj-NN-cx39.4-1 NLLEVCVLLRRYCCP
Aj-NN-cx39.4-2 NVVEFLYLAQHTVTH
               * :* . *

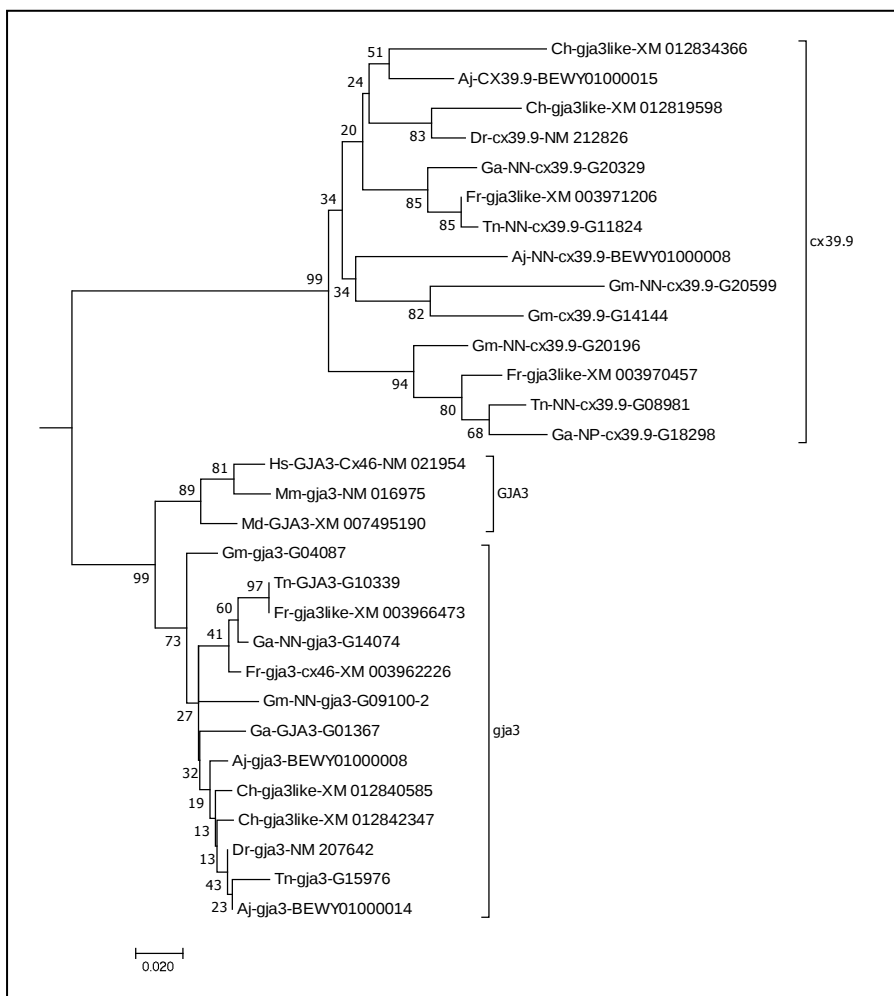
```

Suppl. Fig. 14. Expanded branches from the phylogenetic tree shown in Fig. 1.
For simplicity, we will in the title of the Figures often refer to both the mammalian and teleost sequences using the mammalian annotation.

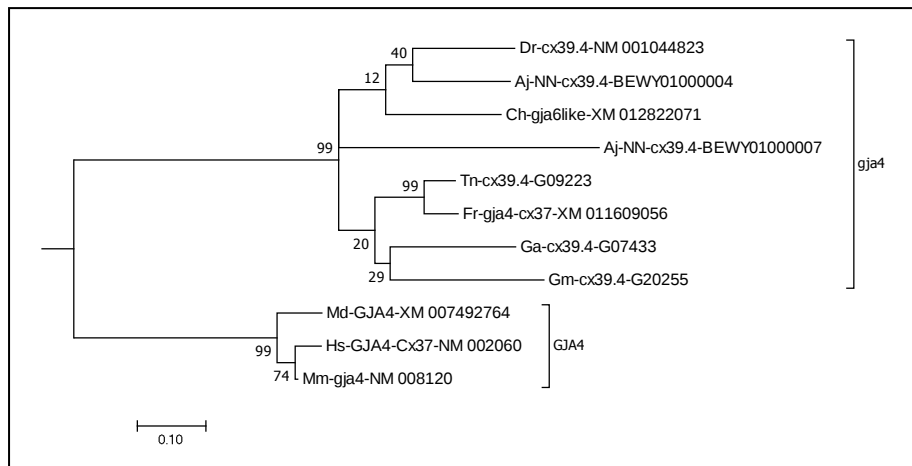
Suppl. Fig. 14A. Expanded view of mammalian and teleost *GJA1* branch.



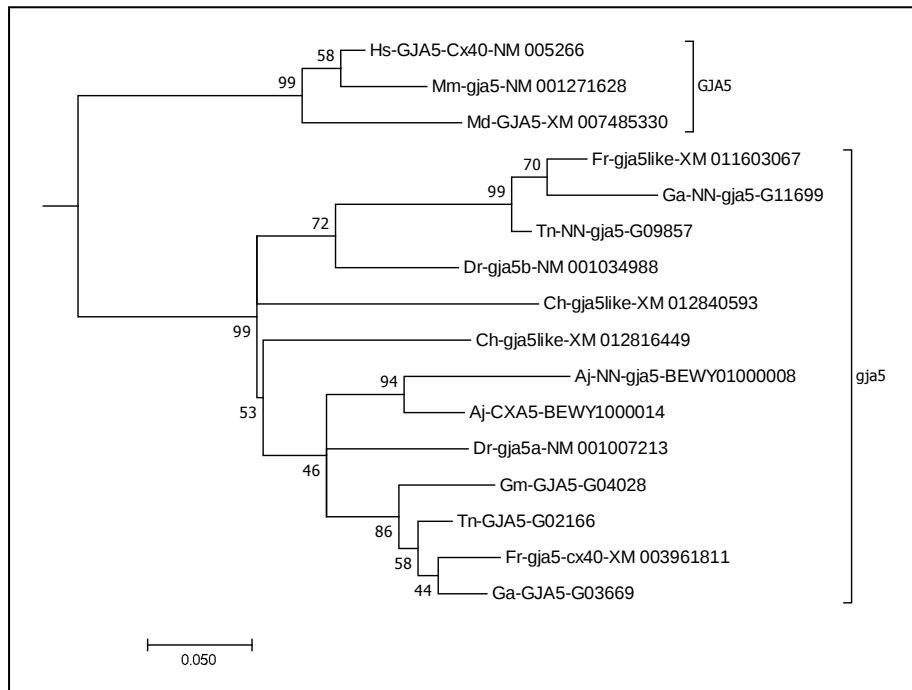
Suppl. Fig. 14B. Expanded view of the mammalian and teleost *GJA3* branch, and the associated teleost *cx39.9*.



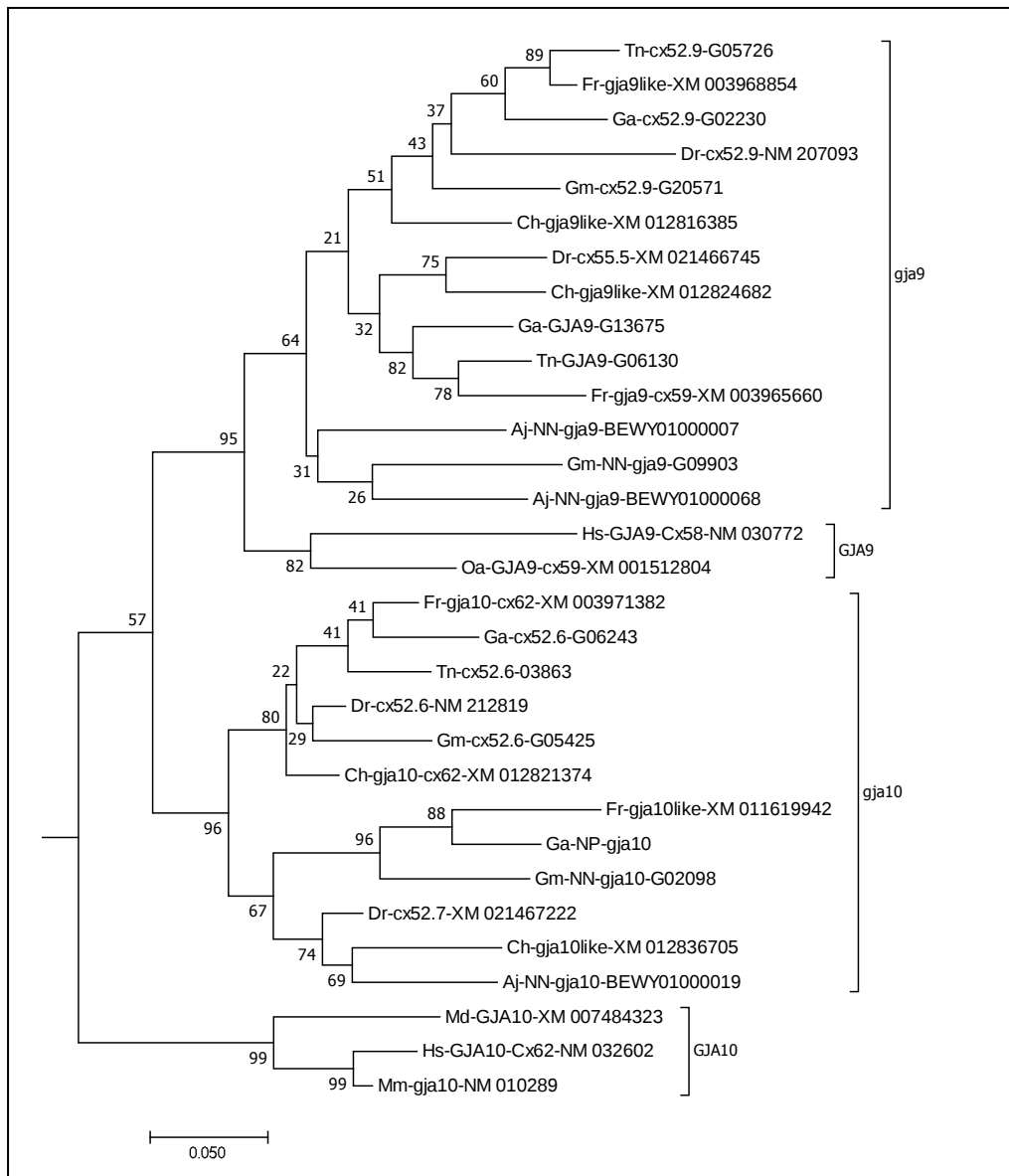
Suppl. Fig. 14C. Expanded view of the mammalian and teleost *GJA4* branch.



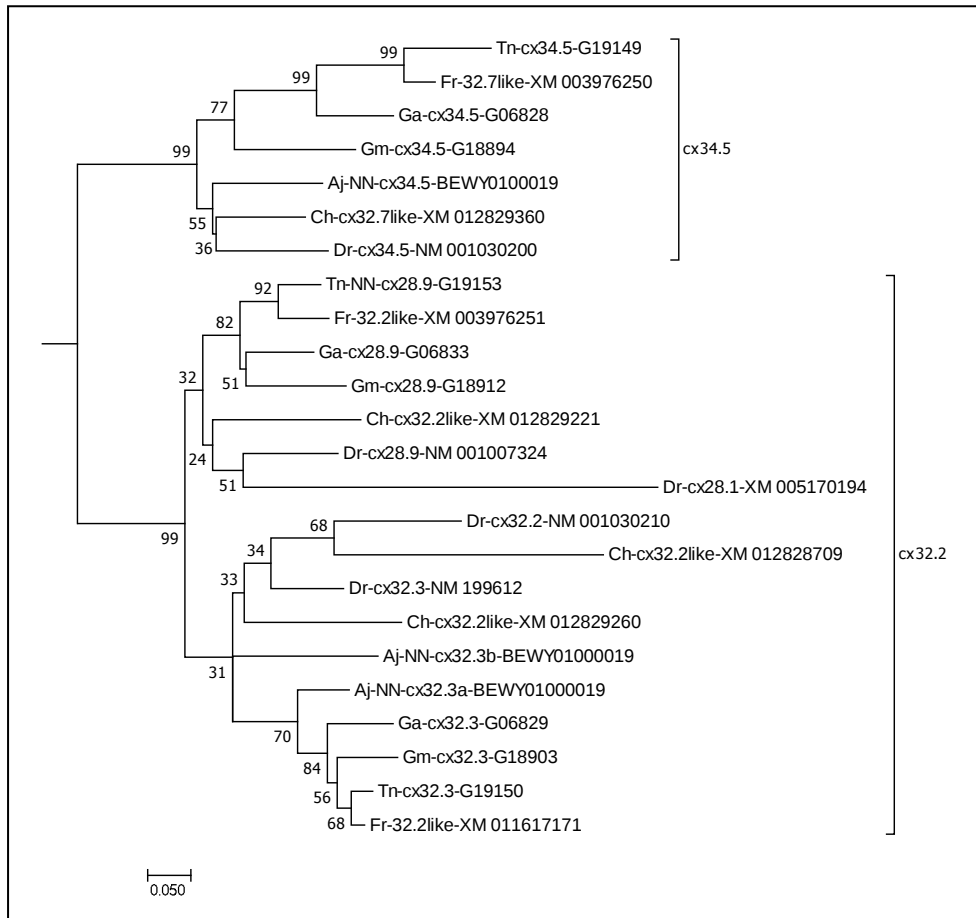
Suppl. Fig. 14D. Expanded view of the mammalian and teleost *GJA5* branch.



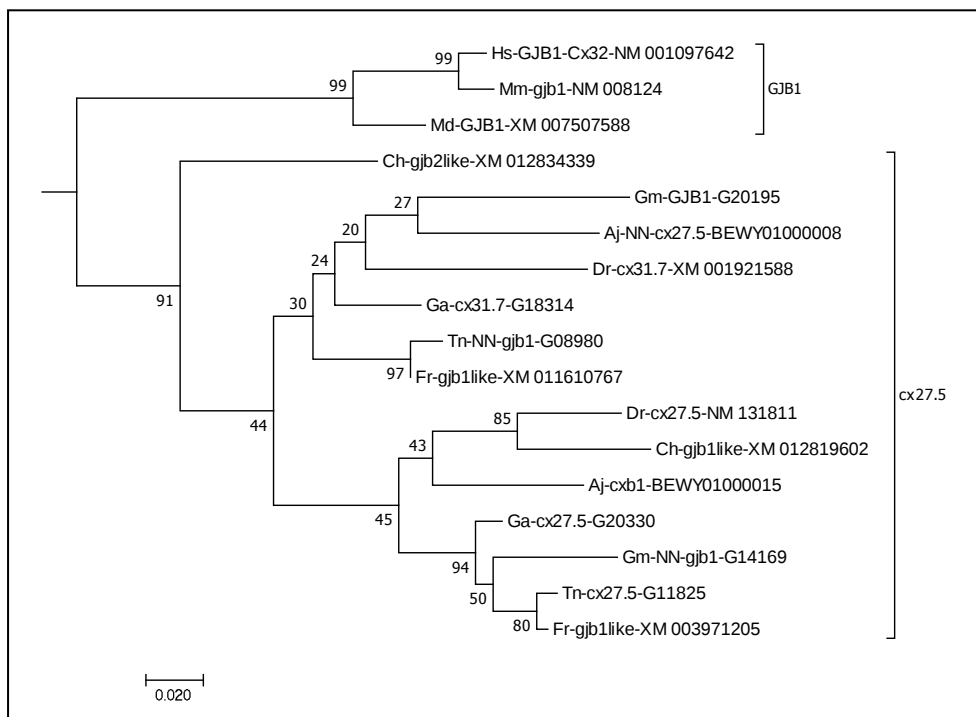
Suppl. Fig. 14E. Expanded view of the mammalian and teleost *GJA9* and *GJA10* branches. In most of the statistical analyses, *GJA10* and *gja10* switched location, i.e., *gja10* was locating outside ((*GJA9* – *gja9*) – *GJA10*).



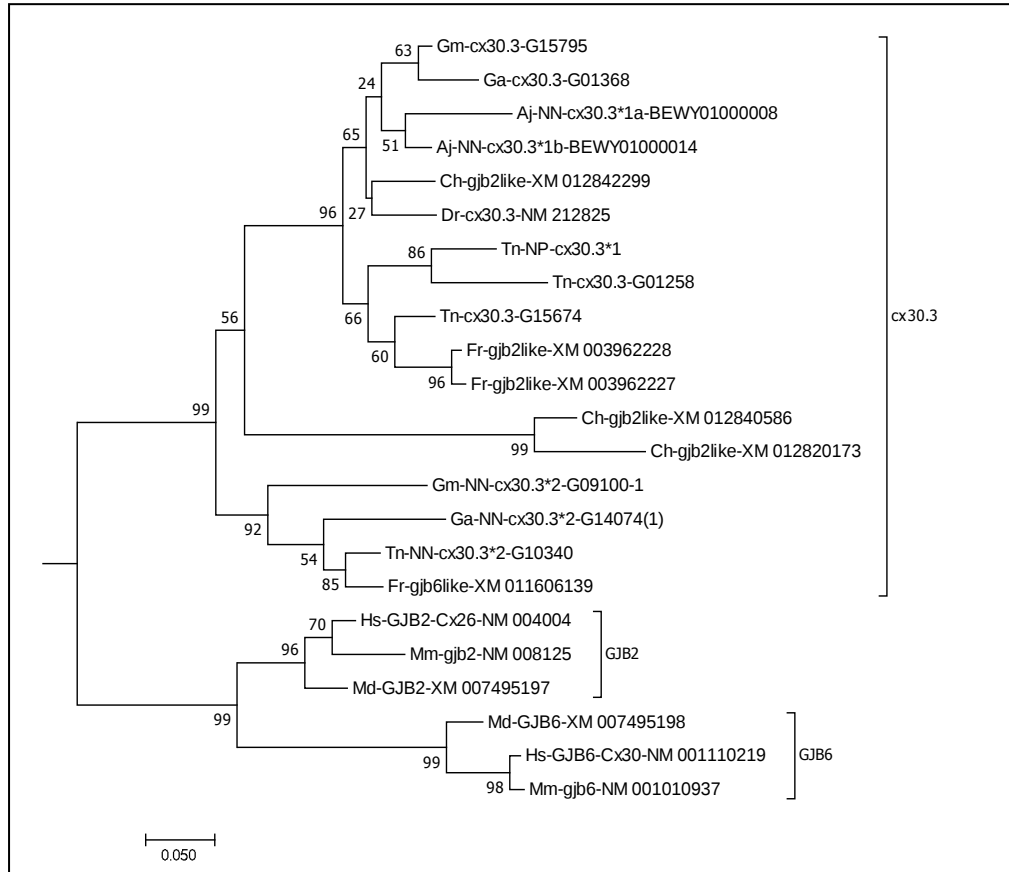
Suppl. Fig. 14F. Expanded view of teleost *cx34.5* and *cx32.2* branches. No mammalian sequence did ever locate together with these two groups.



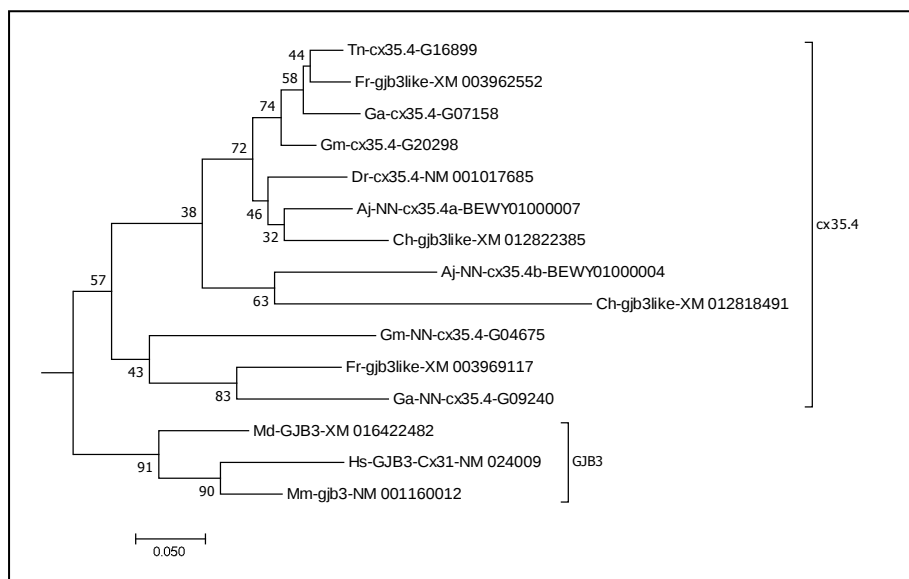
Suppl. Fig. 14G. Expanded view of mammalian and teleost *GJB1*.



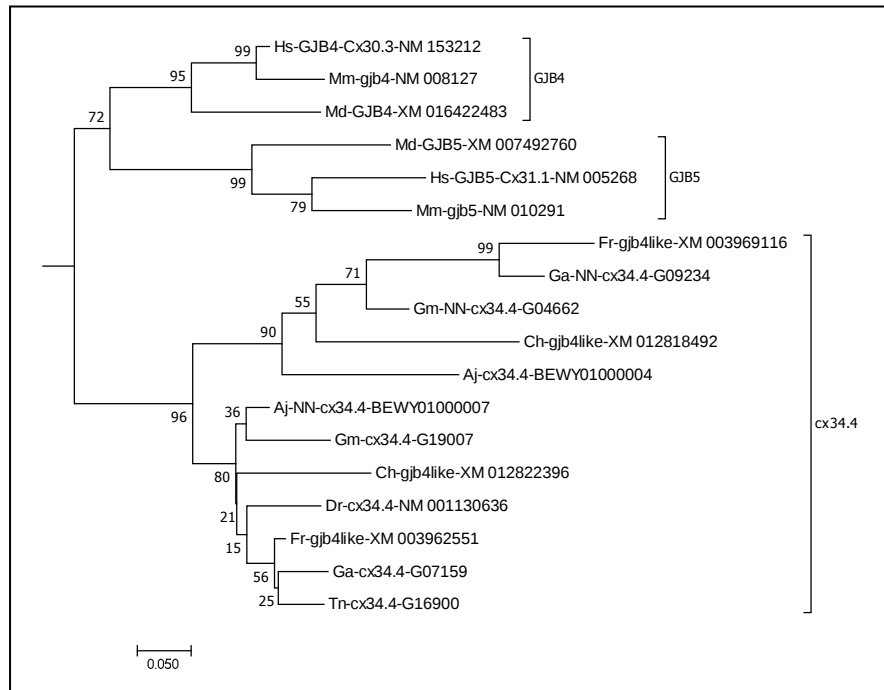
Suppl. Fig. 14H. Expanded view of mammalian *GJB2* and *GJB6*, and teleost *cx30.3*. *GJB2* and *GJB6* always located together in a dichotomous topology, and *cx30.3* did never locate in a dichotomous topology with either *GJB2* or *GJB6*. Thus, there is no reason to claim that *cx30.3* is more closely connected with *GJB2* than with *GJB6*, as the naming of some *cx30.3* sequences could suggest.



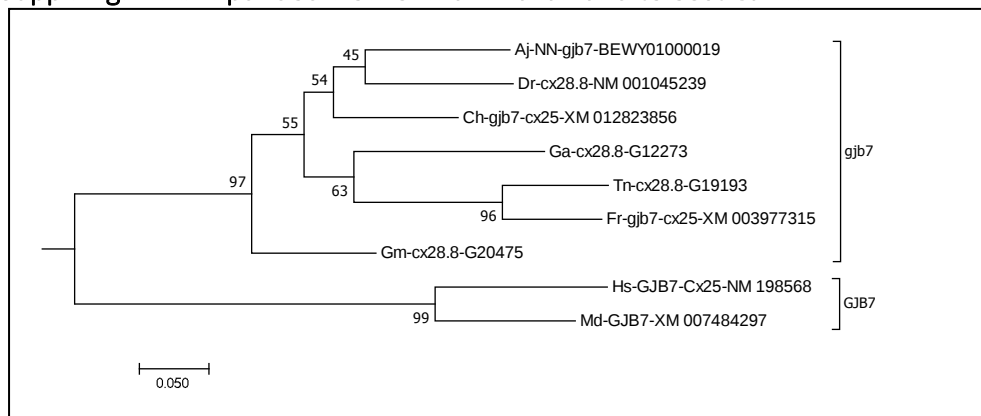
Suppl. Fig. 14I. Expanded view of mammalian *GJB3* and teleost *cx35.4*. These two groups located together in all analyses, and it is reason to suggest that these groups are orthologs, despite that the teleost sequences are lacking the hallmark of mammalian *GJB3* protein sequences, the CX₅CX₅C motif in the second extracellular loop, but rather have the standard CX₄CX₅C motif.



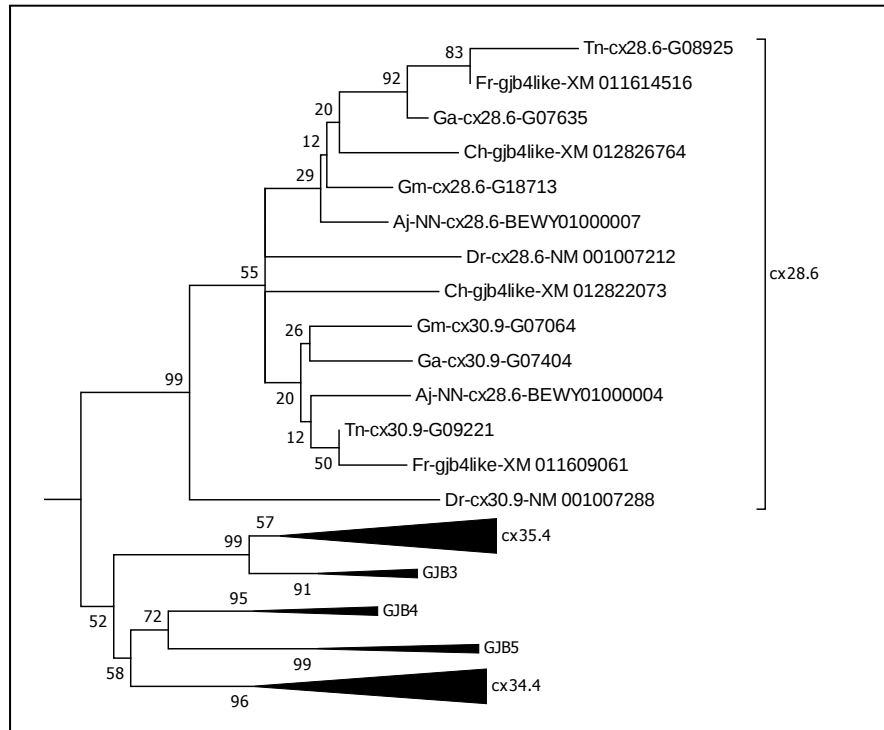
Suppl. Fig. 14J. Expanded view of mammalian *GJB4* and *GJB5*, and teleost *cx34.4*. *GJB4* and *GJB5* always located together in a dichotomous topology, and *cx34.4* did never locate dichotomously with either *GJB3* or *GJB4*. Thus, there is no reason to claim the *cx34.4* is more closely related to *GJB4*, as the naming of some *cx34.4* sequences could suggest.



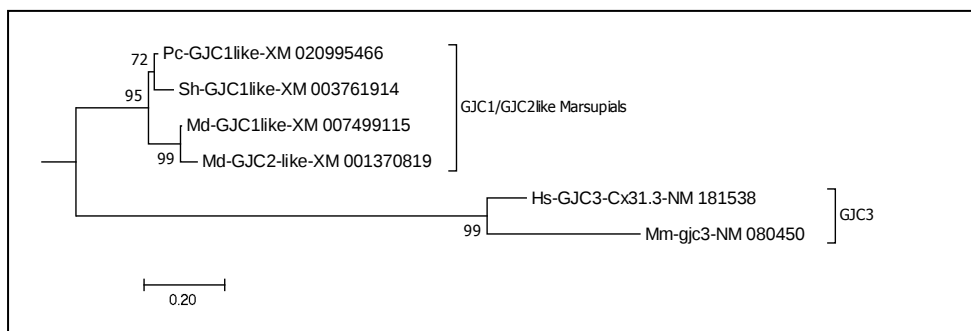
Suppl. Fig. 14K. Expanded view of mammalian and teleost *GJB7*.



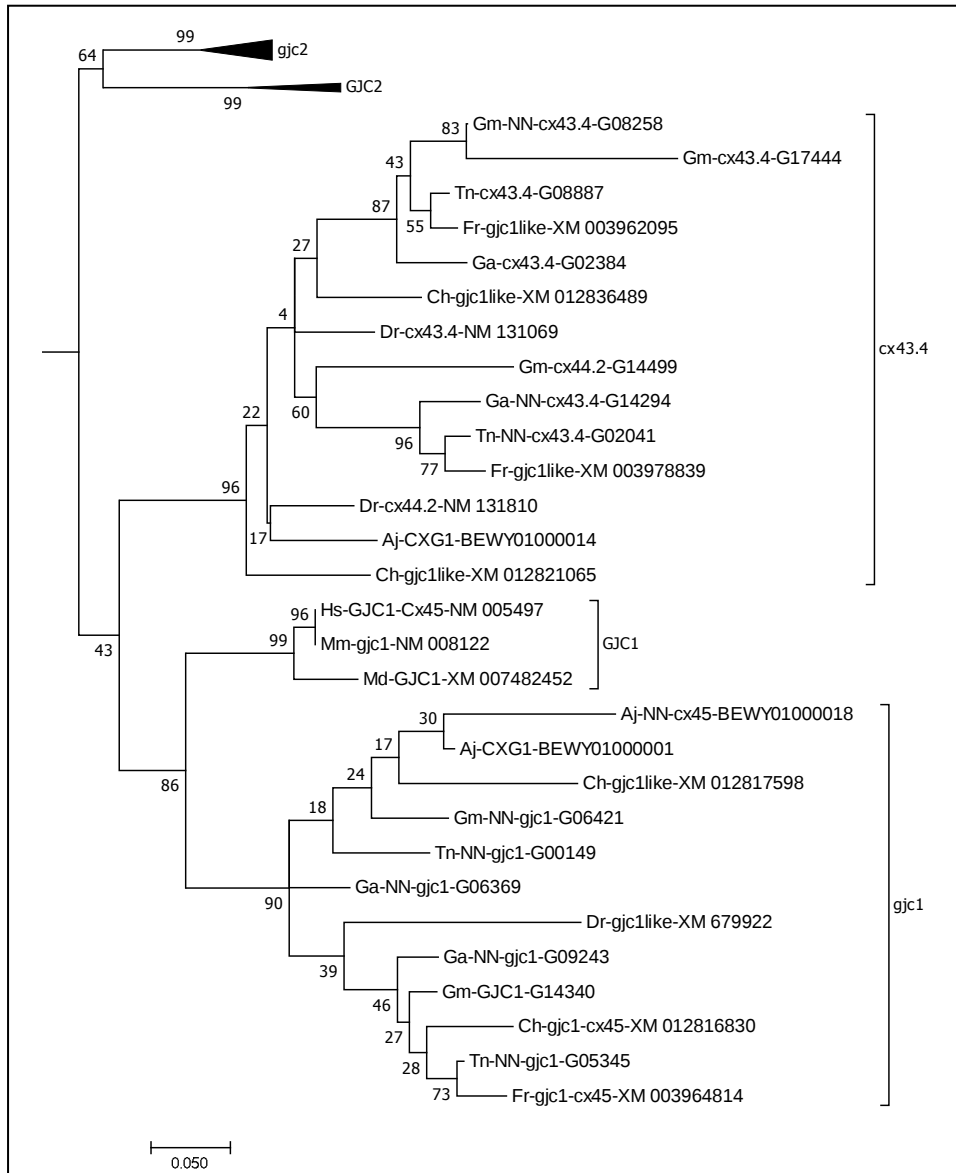
Suppl. Fig. 14L. Expanded view of the teleost *cx28.6* group, and its relationship with *GJB3/GJB4/GJB5*. *Cx28.6* located in most cases outside *GJB3/GJB4/GJB5* as this figure illustrates, but in some cases it was located outside the *GJB3-cx35.4* clade, but generally with poorer statistics. Thus, there is no reason to claim that *cx28.6* is more closely related to *GJB4*, as the naming of some sequences could suggest.



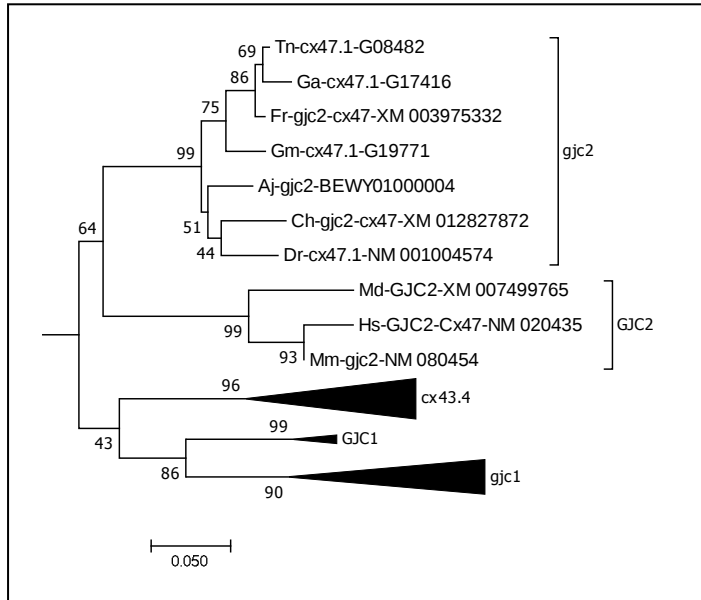
Suppl. Fig. 14M. Expanded view of eutherian *GJC3* and marsupial *GJC1like* and *GJC2like*. In spite of different names, there was only one single statistical analysis (of 21) (Suppl. Table 1) that did not group them together dichotomously. Thus, it is likely that *GJC1like/GJC2like* are orthologs of eutherian *GJC3*.



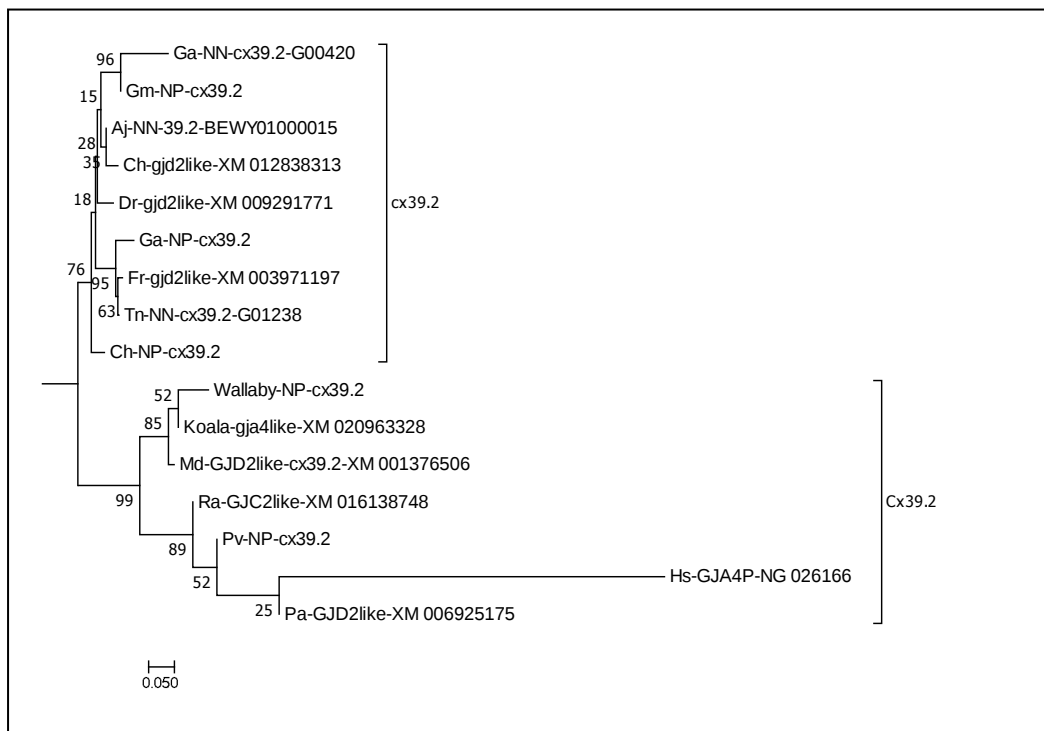
Suppl. Fig. 14N. Expanded view of mammalian and teleost *GJC1* and teleost *cx43.4*. *Cx43.4* had variable locations in the different analyses, and could locate close to *GJC1/gjc1*, or *GJC2/gjc2*, or outside ($(GJC1 - gjc1) - (GJC2 - gjc2)$). Whatever the location of *cx43.4*, the statistics was usually relatively poor (<50).



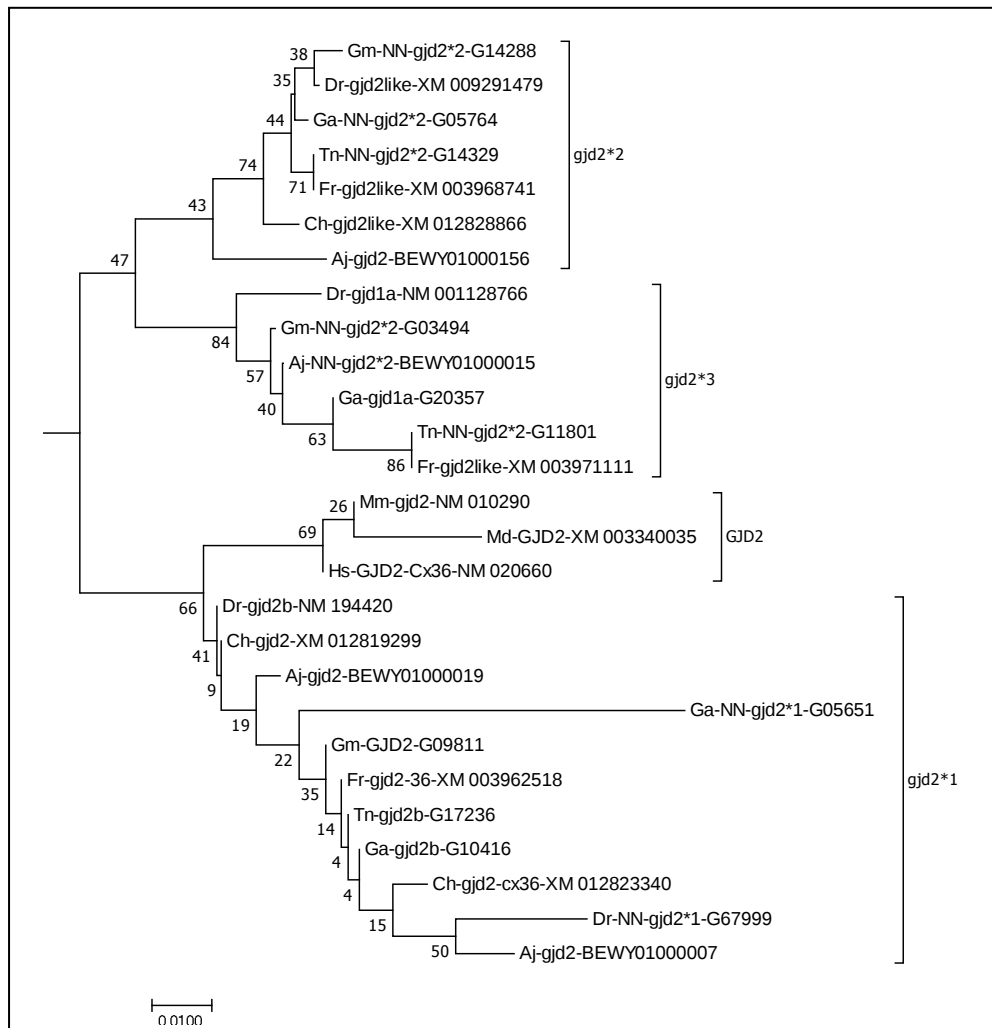
Suppl. Fig. 14O. Expanded view of mammalian and teleost *GJC2*, and its relationship with *GJC1* and *cx43.4*. In phylogenetic analyses using amino acid sequences, the relationship between *GJC2* and *gjc2* was as shown here, while when using nucleotides, the relationship broke, and *GJC2* and *gjc2* located themselves with other relationships to *GJC1/gjc1* and *cx43.3*.



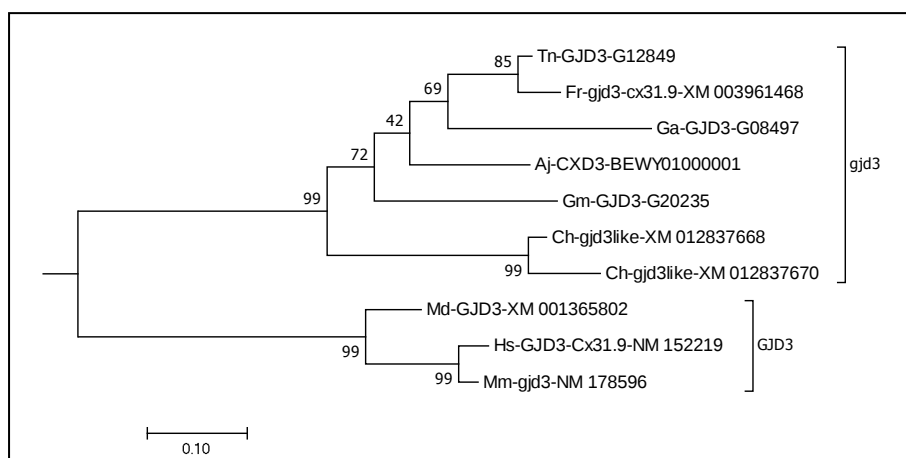
Suppl. Fig. 14P. Expanded view of mammalian and teleost *Cx39.2*. Note the position of human *GJA4P-NG_026166* among the other mammalian sequences. Further note the confusion in naming of these orthologs (*gjd2like*, *gja4like*, *GJC2like*).



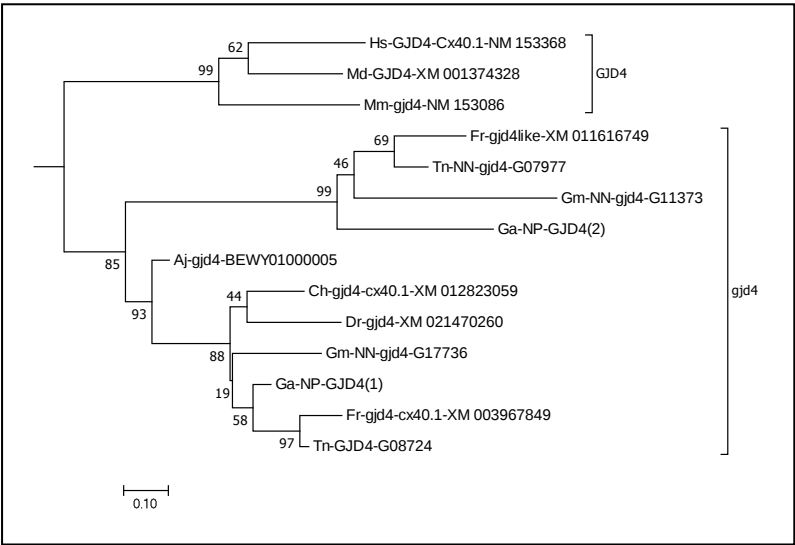
Suppl. Fig. 14Q. Expanded view over the central *GJD2* complex. Mammalian *GJD2* most often located dichotomously together with *gjd2*1*, and with the *gjd2*2* and *gjd2*3* dichotomously located outside, as indicated in this figure. However, in several instances the relative locations of the groups differed, including the non-dichotomous splitting of the *gjd2*2* and *gjd2*3*.



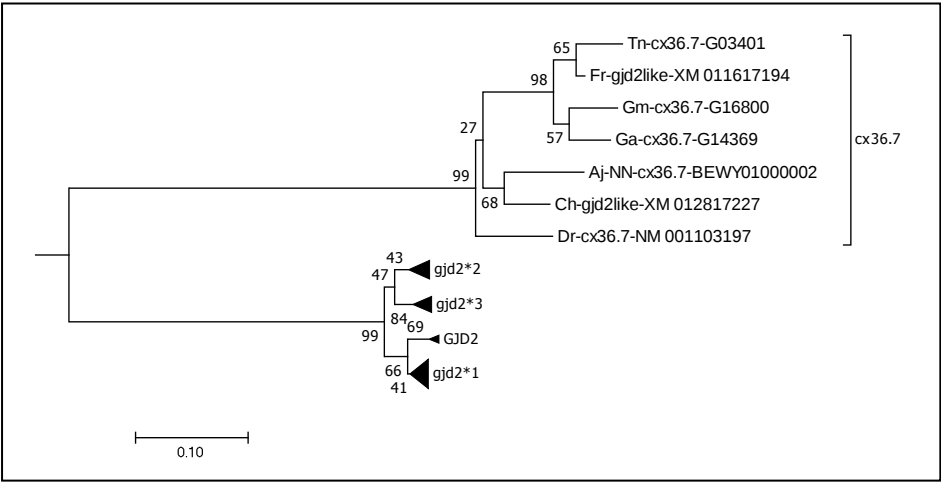
Suppl. Fig. 14R. Expanded view of mammalian and teleost *GJD3*.



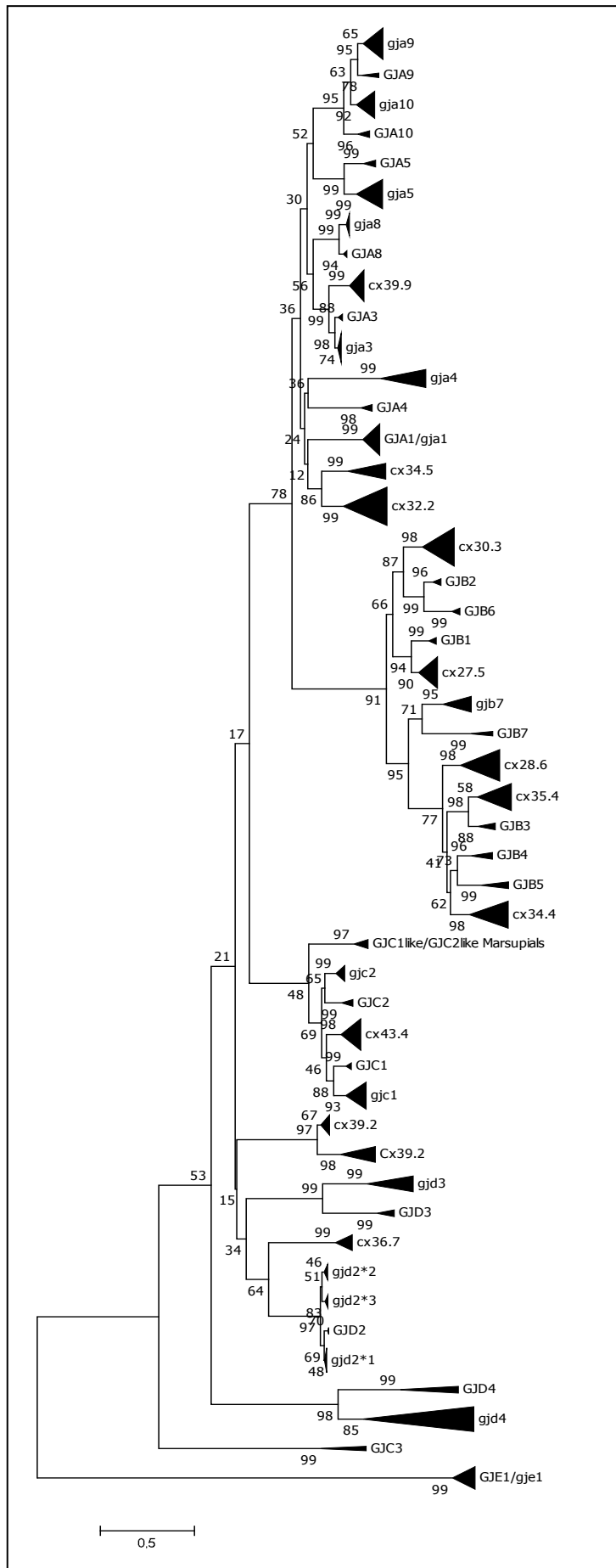
Suppl. Fig. 14S. Expanded view of mammalian and teleost *GJD4*.



Suppl. Fig. 14T. Expanded view of teleost *cx36.7*. This is one of several groups containing sequences called *gjd2like*. *Cx36.7* most often split off from the root of the *GJD2* complex, but did on occasions associate with the *GJD3* or *GJD4* groups.

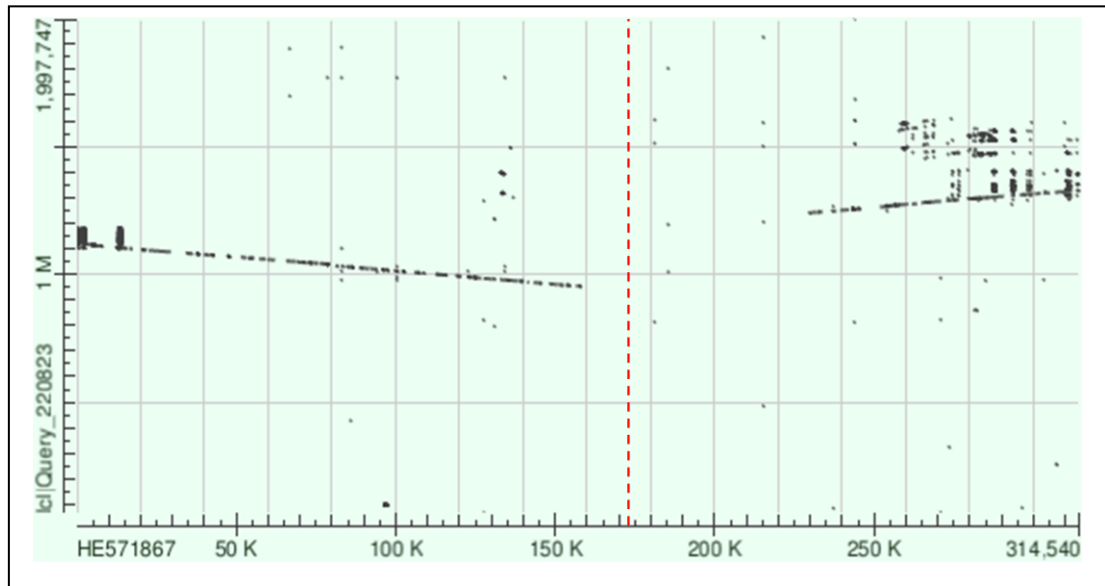


Suppl. Fig. 15. Compressed phylogenetic tree illustrating long-branch attraction between *gjc3*, *gjd4* and *gje1* groups. The tree is made under the same conditions as for Fig. 1 in the manuscript, except that *GJE1/gje1* has been added, and that necessary adjustment of alignment (introduction of aligned gaps in all other sequences) were performed. (Figure on next page.)

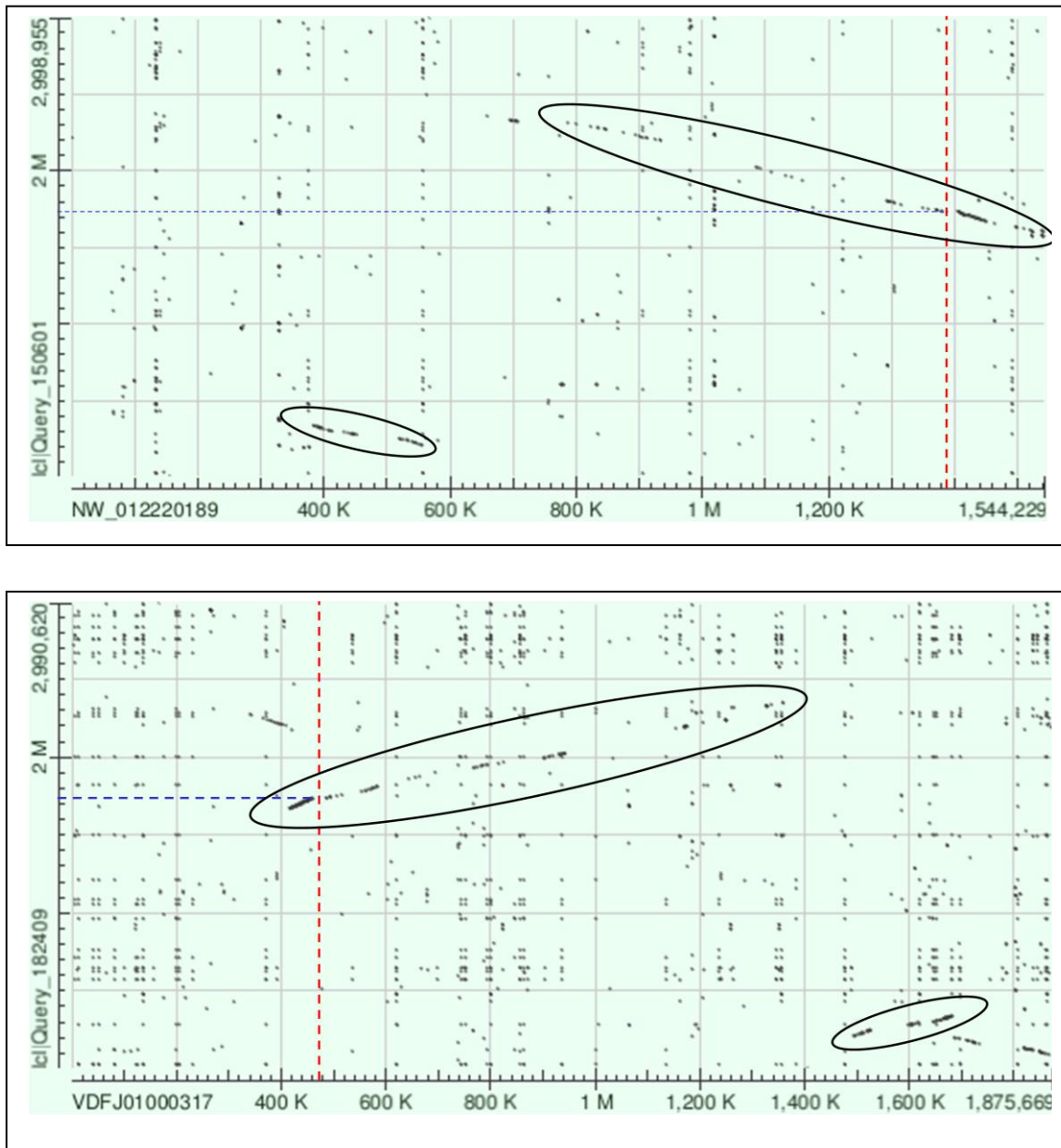


Suppl. Fig. 16. Searching for positions of connexins lacking in chromosomal assemblies.

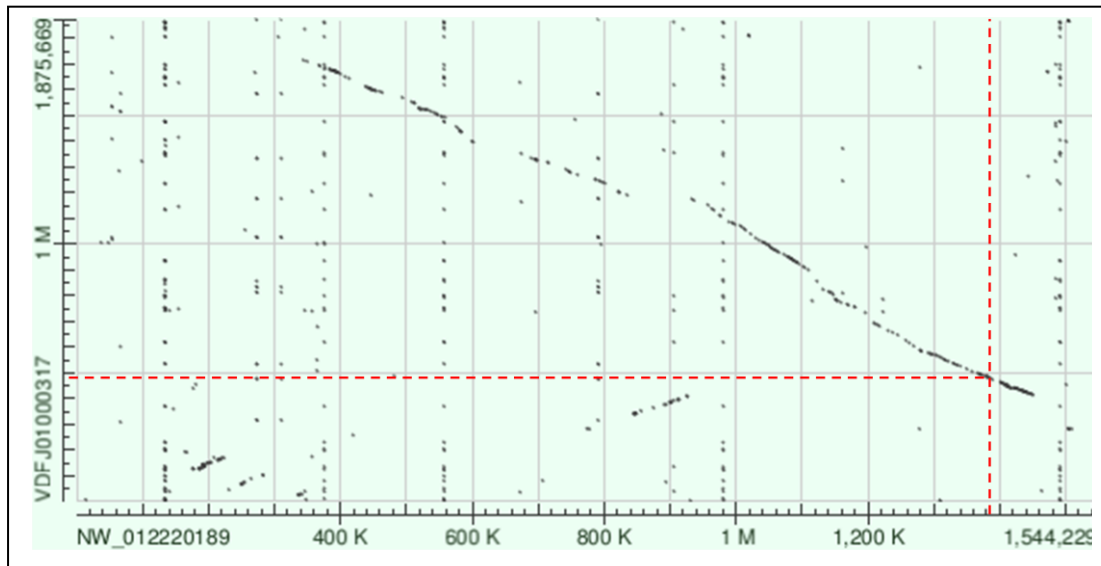
Suppl. Fig. 16A. Problem in cod assembly of chromosome 20 at assumed position of *gja5*. Cod scaffold HE571867 contains *gja5* in position 173000-174000. This scaffold was aligned with cod chromosome 20 assembly LR633962 position 0 to 2,000,000 using the alignment option in Blast and word size 32. Dot plot is one of the options on the results page. The position of *gja5* on HE571867 is indicated by the red dotted line. There is an obvious lack of alignment between the scaffold and the chromosomal assembly in the area where *gja5* was expected, and there is an inversion in the sequence corresponding to the scaffold.



Suppl. Fig. 16B. Alignments with sequences from herring and stickleback point to the same area on cod chromosome 21, indicated expected position of *gja10-cx52.6*. Cod chromosome 21 (LR633963) position 1,000,000 to 4,000,000 was aligned with (upper panel) herring scaffold NW_012220189 (where *cx52.6* is in position 1,390,000) and (lower panel) stickleback scaffold VDFJ01000317 (where *cx52.6* is in position 476,000). Word size 16 was used in both cases. Dot plot is one of the options on the results page. The position of *cx52.6* on the two scaffolds are indicated by the red dotted line, and the blue dotted line indicate the expected position of *cx52.6* on cod chromosome 21. Both herring and stickleback alignments indicate a problem with the cod assembly at position around 2.7 – 2.8 million (as this alignment starts at 1 million). Note the similarities in alignment pattern for the herring and stickleback scaffolds (ovals; see also Suppl. Fig. 16C).



Suppl. Fig. 16C. Alignments of herring and stickleback scaffolds containing *cx52.6*. Herring scaffold NW_012220189 (where *cx52.6* is in position 1,390,000) and stickleback scaffold VDFJ01000317 (where *cx52.6* is in position 476,000), both used in Suppl. Fig. 16C were aligned. Word size 16 was used. Dot plot is one of the options on the results page. The position of *cx52.6* on the two scaffolds are indicated by the red dotted lines. The extensive alignment between these two species, which are evolutionary further apart than either of herring-cod or cod-stickleback that both gave poorer alignments (Suppl. Fig. 16B) supports the possibility of erroneous assembly in the relevant area of cod chromosome 21.



Suppl. Fig. 17. A homogeneous and consistent nomenclature for gap junction protein genes .



Fig. 17. Legend: The following annotation is used for the compressed branches: UPPER CASE, mammals. The classic size nomenclature for humans is also shown in parentheses. Lower case, teleosts. For the teleosts, some of the previous or commonly used names in the group are given first, and after the dash, our suggested Greek nomenclature name. If we find ohnologs in the group, this is indicated by a/b after the suggested name (e.g., *gja1a/b*). Note that ohnologs may only apply to some of the investigated species (i.e., ohnologs may not be found in all species). For example, for *gja4*, ohnology has only been established in eel. In one case only herring support ohnology (*gjd5*), which potentially means that the other member of the pair must have been lost three times (in eel [diverged before herring], zebrafish [diverged together with herring], and in the line leading to later diverging fishes (the remaining species in this investigation). In two cases, we indicate that duplicated genes within the group probably have been generated by tandem gene duplication (*gja12.1/2* and *gja13.1/2*).

The tree was made using the Neighbor-Joining method at amino acid level. The substitution model was JTT, and the rate variation among sites was modelled with a gamma distribution = 1.0. To simplify the tree, all sequences within the *GJE1* group were excluded, together with the pseudogenes within the *Cx39.2 (GJD5)* group, except for the human pseudogene with accession number NG_026166. Additionally, a single sequence that often branched off from the stem of the corresponding group was excluded (Aj-NN-32.3b-BEY01000019). Similarly, sequences that disturbed a clear dichotomy for GJA1/gja1 (Mm-*gja6*-NM_01001496, Dr-*gja1like*-XM_NM_688906, Ch-*gja1like*-XM_012836783, Gm-NN-*gja1*-G09844, Aj-CXA1-BEY01000007) were excluded. This gave a total of 347 sequences in this tree. The root branches of the *gjd* subfamily have been fused using the root function in the MEGA Tree Explorer.

Suppl. Fig. 18. Schematic outline of the major procedures.

