

Supplement Fig. 2. Sequences of IGF-II genes for *Homo sapiens*, *Pan troglodytes*, *Pongo pygmaeus*, *Macaca mulatta*, *Callithrix jacchus*, *Microcebus murinus*, *Otolemur garnettii*, and *Canis familiaris*

Just the three coding exons (exons 8,9 and 10) are shown, with flanking sequences. The full very long utr of exon 10 is not shown. Coding sequences are shown in blue (mature protein) or red (signal peptide and E-domain) uppercase, non-coding sequences in orange (transcribed) or black lowercase. Below each sequence is shown the Chromosomal location (ensembl release 47), or traces from which the sequence was assembled, the position of the ATG start codon and other information

Homo sapiens (man)

atgaccgtggagatgggtcaccctcgtgtaaaattactagtgcttcttgcaaaggaag 60
aactgggccttttctgtgtgcttctggacgcttcattctgcacatggccctgcgccctca 120
cctcggcattatgacctgtgtgttacttttgaataaaaaataatgtttataggaaagccg 180
tgctttcaattttcaactgaattttaggttgcaaatttggtttgggaggggacacctct 240
ggcctggggcttggcctggctgccccgctcacgccacttctctcccggccccagacacca 300 exon 8
ATGGGAATCCCAATGGGGAAGTCGATGCTGGTGCCTTCTCACCTTCTTGGCCTTCGCCTCG 360
TGCTGCATTGCTGCTTACCGCCCCAGTGAGACCCCTGTGCGGCGGGGAGCTGGTGGACACC 420
CTCCAGTTCGCTCTGTGGGGACCGCGGCTTCTACTTCAgtaagtagctgggaggggcttcc 480
tcagacctggtcaggccccctagagtgaccggtgaggacgcccacacctcaagccaggggag 540
cacactcctaggtcagcagcccagccgcttgcctctgagactttgaccttcccgcgcgtt 600
tctgagcacgtgcgggtgtcccagggcatccacaccagctgcctttcccacacagcctc 660
cttcgaaggggtgggcccagaggtgccccctagacgtcaggggactcacaggggtctccct 720
gggcatcagaatttctgttgggggcccgtgaggctcctgctcctgaggcaccgcacgccta 780
gtgcagggcttcaggctctggaggaagagcctgcctttcttccctgcaccttttggacatt 840
ctgacaagggacgtgcttccggtgaatgatcagaattaaaatcaataaagtgatttataat 900
aattaaaatcaataagacaagtgacgttgggtgggtggcaggggtgagcgggtgcatgccc 960
tccttgggcccccaaggctgcccgtgggggggtgccacctgctgacctcaaggacgcttcag 1020
cctttcctcatgtttctctcttgggttctccagcctgggggctggcaggtgggtgcatggc 1080
ccattgctcttgagaccccaccccagataggggggctgggtggatgcagagggcagggcat 1140
ggtagctgggtgacctgatggggcaggggaggggcccgctccttactggcagagggcccga 1200
cggcttattccacctgacactcaccacgtgacatctttaccaccactgcttactcacgct 1260
gtgaaatgggctcacaggatgcaaatgacttcaagcttctctctgaaaagtccctgct 1320
gcttgactctggaagccccctgcccgccttggcctctcctgtgccctctctcttgcctgcc 1380
ccatttgggggtaggaagtggcactgcagggcctgggtgccagccagtccttggccagggga 1440
gaagcttccctgcaccaggctttcctgagaggaggggagggccaagccccacttggggg 1500
acccccgtgatggggctcctgctccctcctccggctgatggcacctgccctttggcacc 1560
caaggtggagccccagcgaccttcccccttccagctgagcattgctgtgggggagagggg 1620
gaagacgggaggaagaagggagtggttccatcacgcctcctcactcctcctcccgtc 1680
ttctcctcctcctgccccttgtctccctgtctcagcagctccaggggtgggtgtgggcccc 1740
cagcctcctaggtgggtgccagggcagagtccaagctcagggacagcagtcctcctctgtg 1800
gggccccgaactgggctcacatcccacacattttccaaaccactcccattgtgagcctt 1860
tggctcctgggtggtctccctctgggtgtgggaccaagagcttgtgccatttttcatctga 1920
ggaagggcagcagagggccagggctggctggtcctccactcacctcccctctcacctc 1980
tcttctcctgaggcgcctctgctgccagctctcacttcccctcccctgaccgcaggggt 2040
ggctgctccttccagggcctggcctgagggcaggggtgggttctccccttccagcctc 2100
cgggggctggggctcagtgccgtgtaaacagggctctctctgtgctgtgggacttccagGC 2160 exon 9
AGGCCCGCAAGCCGTGTGAGCCGTGCGAGCCGTGGCATTGAGGAGTGCTGTTTCCGC 2220
AGCTGTGACCTGGCCCTCCTGGAGACGTACTGTGCTACCCCGCCAAGTCCGAGAGGGAC 2280
GTGTCGACCCCTCCGACCGTGCTTCCGgtgagggctcctgggcccccttcccactctctag 2340
agacagagaaatagggcttccggcgcccagcgtttcctgtggcctctgggacctcttggc 2400
cagggacaaggaccctgacttcccttgccttgcctgtgtggcccgggagcagctcagacgct 2460
ggctccttctgtccctctgcccgtggacattagctcaagtcactgatcagtcacaggggt 2520
ggcctgtcaggtcagggcgggctcaggcgaagagcgtggagagcagggcacctgctga 2580
ccagccccctcccctcccagGACAAC'TCCCCAGATACCCCGTGGGCAAGT'TTCCAAT 2640 exon 10
ATGACACC'TGGAAGCAGTCCACCCAGCGCCTGCGCAGGGGCC'TGCC'TGCCCTCCTGCGTG 2700
CCCGCCGGGGTACGTCGTCGCCAAGGAGCTCGAGGCGTTCAGGGAGGCCAAACGTCACC 2760
GTCCCTTGATTGCTCTACCCACCCAAGACCCCGCCCACGGGGGCGCCCCCCCAGAGATGG 2820
CCAGCAATCGGAAGtgagcaaaactgccgcaagtctgcagcccggcgccaccatcctgca 2880
gcctcctcctgaccacggacgtttccatcaggttccatcccgaataatctctcggttccac 2940
gtccccctggggcttctcctgaccagtcctccgtgccccgcctccccgaaacaggctact 3000
ctcctcggccccctccatcgggctgaggaagcacagcagcatcttcaaacatgtacaaaa 3060
tcgattggctttaaacccttccataccctcccccaaaattatcccccaattatccccca 3120
cacataaaaaatcaaacattaaactaacccttccccccccccccacaacaaccctctt 3180

From human genome sequence, chromosome 11: 2113629–2110450. Complement.
ATG start codon at 301–303.

Pan troglodytes (Chimpanzee)

gtgcttcttgcaaatggaaggaactgggccttttctgtgtgcttccggacgcttcattct 60
gcacatggccctgcgccctcacctcggcattatgacctgtgtgttacttttgtaataaaa 120
ataatgtttataggaagccgtgctttcaattttcaactgaatttgaaggttgcaaatt 180
tggtttgggaggggacacctctggcctggggcttggcctggctgccccgctcacgccatt 240
ctctcccgcctccagacaccaATGGGAATCCCAATGGGGAAGTCGATGCTGGTGCCTTCTC 300 exon 8
ACCTTCTTGGCCTTCGCCCTCGTGCATTCGCTGCTTACCGCCCCAGTGAGACCCCTGTGC 360
GGCGGGGAGCTGGTGGACACCCTCCAGTTCGTCTGTGGGGACCGCGGCTTCTACTTCAgt 420
aagtagctgggaggggcttcctcagacctggcagggccctagagtgaccagtgaggacg 480
cccaacctcaagccaggggagcacactgctaggtcagcggcccagccccctgctctgaga 540
ctttgaccttcccgcgcgctttctgagcacctgcggtgtcccagggcatccacaccagct 600
gcctttcccatcacacgcccccttcgaaggggtgggccagaggtgccccctagacgtcagg 660
ggcactcacaggggtctccctgggcatcagaatttctgctgggggcccgtgaggctcctgc 720
tgctgaggcaccgcacgcctagggcagggcttcaggctctggaggaagagcctgcctttc 780
ttcctgcaccttttgacattttgacaagggacgtgcgttcggatgatcagaattaa 840
aatcaataaagtgatttataataataaatacaataagacaagtgcagttgggtgggtggca 900
ggggtagcgggtgatgagcctccttgggcccccaaggctgccgtggaggggtgccacctg 960
ctgacctcagggacgcttcagcctttcctcgtgtttctctcttgggtctccagcctgggg 1020
gctggcaggtgggtgacattggccattgtccttgagacccccccccagatgggggcccgtg 1080
ggtagtgagagggcaggtgctgctgggcatgacctgatggggcaggggaggggcccgc 1140
tcctcactggcagagggcgcagggcttattccacctgacactcaccagtgacacctta 1200
ccaccactgcttactcacgctgtgaaatgggctcacaggatgcaaatgcacttcaaagct 1260
tctctctgaaaagttcctgctgcttactctggaagccccctgccgccccctggcctctct 1320
gtgccctctctcttgcctgccccatttgggggtaggaagtggcactgcagggcctggtgc 1380
cagccagtccttggccagggagaagcttccctgcaccaggctttcctgagaggaggggag 1440
ggccaagccccacttgggggacccccgtgatggggctcctgctccctcctccggctgat 1500
ggcactctgccctttggcaccccaaggtggtggacccccagcagcttcccccttccagct 1560
gagcattnn 1620
nn 1680
nn 1740
cagggacagcagctccctcctgtggggcccccggaacggggctcacatcccacacattttc 1800
caaaccagggcgggtgtgagcctttggctccttgggtgtctgtctgcccgtgggaccaag 1860
agcttgtgccatttttcatctgaggaaggaggcagcagaggccacgggctggtctgggt 1920
cccactcacctccccctctcacctctcttcttctcctgggacgcctctgcctgccagctctca 1980
cttccccccccggaccgcaggggtggtgctgctccttccagggcctggcctgagggcaggg 2040
gtggtttgttctcctccagcctccgggggctgggggacgtgcgggtgctaacacggctct 2100
ctctgtgctgtgggacttccagGCAGGCCCGCAAGCCGTGTGAGCCGTCGCAGCCGTGGC 2160 exon 9
ATCGTTGAGGAGTGTGTTTTCCGCAGCTGTGACCTGGCCCTCCTGGAGACGTACTGTGCT 2220
ACCCCGCCAAGTCCGAGAGGGACGTGTGACCCCTCCGACCCGTGCTTCCGgtgagggtc 2280
ctgggccccctttcccgtctcttagagacagagaaatagggcttcgggcccagcgtttc 2340
ctgtggcctctgagacctcttggccagggacaaggaccctgacttcccttgcctgctgtg 2400
tggccccgggagcagctcagacgtggctcctttctgtcctctgccccctggacattag 2460
ctcaagtcactgatcagtcaccgggggtggcctgtcaggtcagggcgggctcagggcga 2520
aaagcgtggagagcagggacctgctgaccagccccttcccctcccagGACAACCTCCCCA 2580 exon 10
GATACCCCGTGGGCAAGTTCCTCCAATATGACACCTGGAAGCAGTCCACCCAGCGCCTGC 2640
GCAGGGGCTGCCTGCCCTCCTGCGTGCCCGCCGGGGTACATGCTCGCCAAGGAGCTCG 2700
AGGCGTTCAGGGAGGCCAAACGTCACCGTCCCCTGATTGCTCTACCCACCCAAGACCCCG 2760
CCCACGGGGGGCGCCCCCAGAGATGGCCAGCAATCGGAAGtgagcaaaactgccgcaag 2820
tctgcagccccggcggccaccacctgcagcctcctcctgaccacagacgtttccatcaggt 2880
tccatcccgaatactctcgggttccacgtccccctggggcttctcctgaccagctccccg 2940
tgccccgcctccccgaaacaggctactctcctcggccccctccatcgggctgaggaagca 3000
cagcaacatcttcaaacatgtacaaaatcgattggctttaaacacccttcacacaccttc 3060
cccccaattatcccccaattatccccacacataaaaaatcaaaacattaaactaaccctc 3120

From chimpanzee genome sequence, chromosome 11: 2184276–2179057. Complement.

Completed (except gap as indicated) using Traces:

S217P60466RE9.T0 G591P624921FG12.T0 G591P606559FC5.T0
sqj09e09.b1

ATG start codon at 262-264.

Pongo pygmaeus (orangutan)

ccaccctcgtgtaaaataactagtgcttcttgcaaatggaaggaactgggccctttctg 60
tgtgcttccggacacttcattctgcacgcggccctgcgccctcaccttggcattgtgacc 120
tgtgtgttacttttgaataaaaaataatgtttataggaaagccgtgctttaaattttcaa 180
ttgaattttaggttggcaaatttggtttgggaggggacactctggcctggggcttggcc 240
tggctgccccgctcacgccacttctctcccggccccagataccaATGGGAATCCCAATGG 300 exon 8
GGAAGTCGATGCTGGTGCCTTCTCACCTTCTTGGCCTTCGCCTCGTGCTGCATTGCTGCTT 360
ACCGCCCCAGTGAGACCCCTGTGCGGGGGGAGCTGGTGGACACCCCTCCAGTTCGTCTGTG 420
GGGACCGCGGCTTCTACTTCAgtaagtagctgggaggggcttcctcagacctggtcaggc 480
ccctagagtgaccggtgaggactcccaacctcaagtcaggggagcacactcctaggtcag 540
cggcccagcccccttgcctctgagactttgaccttccagccgcatcttctgagcacctgcggt 600
gtcccagggcatctacaccagctgcctttctgtcacacgcctccttcaaggggtgggcc 660
agaggtgccccctagatgtcaggggactcacgggggtctccctgggcatcagaatttct 720
gttgggggcccgtgaggctccttctgctgaggcgtcacaccctaggccagggtttcaggc 780
tctggaggaagagcctgcctttcttctgcaccttttgacattttgacaagggatagc 840
gttcagtgaatgatcagaattaaaatcaataaagtgatttatagaattaaaatcaatcag 900
acaagtgcagttggtgggtggcagggctgagcagatgcagcctccttgggcccccaagg 960
ccgcccgtggaggggtgccacctgctgacctcagggagccttcagcctttcctcatgtttc 1020
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cctgccccagatggggggctgggtggatgcagagggcaggtggtgcctgggcatgcct 1140
gatggggcaggggaggggcccgcctccttgcctggcaggggcccgcagggcttattccacctga 1200
cactcaccagctgacatctttaccaccactactgactcacgctgtgaaatgggctcacag 1260
gatgcaaatgcacttcaaagcttctctctgaaaagttcctgctgcttgactctggaagcc 1320
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gtggcactgcagggcctggtgccagccggtccttggccagggagaagcttccctgcacca 1440
ggctttcctgagaggaggggagggccaagccccacttgggggacccccgtgatggggct 1500
cctgctccctcctccggctgatggcacctgcccttggcaccccaaggtggagccccag 1560
cgaccttccccctccagctgagcattgctgtgggggagagggggaagacgggaggaaaga 1620
agggagtggttccgtcacgcctcctcactcctcctcccgtcttctcctcctcctgcct 1680
tgtctccctgtctcagcagctccaggggtggtgtgggccccctccagccttctaggtggtg 1740
ccagggcagagtcgaagctcagggacagcagctccctcctgtgggggccccctgaactgggc 1800
tcacatcccacatattttccaaaccactcccattgtgggcttgggtcctggtggtgtcc 1860
gtctggccatgggaccaagagcttgtgccatttctcatcggaggaaggaggcagcagag 1920
gccacgggctggtcctggctcccactcacctcccctcactcctccttcttctcctgggacgc 1980
ctctgcctgccagctctcacctcccctcccctgaccgcaggggtggctgcaccttccagg 2040
gcctggcctgagggcctcctggggcagggggcagtgcggtgctaacgaggctgtctctgt 2100
gctgtgggacttccagGCAGGCCCGCAAGCCGTGTGAGCCGTGCGAGCCGTGGCATCGTT 2160 exon 9
GAGGAGTGCTGTTTCCGCAGCTGTGACCTGGCCCTCCTGGAGACGTACTGTGCTACCCCC 2220
GCCAAGTCCGAGAGGGACGTGTGACCCCTCCGACCGTGCCTCCGgtgagggctcctgggc 2280
ccccttcccgctctctagagacagagaaatagggcttcgggcgccagcgtttcctgtgg 2340
cctctgggacctccttggccagggacaaggaccctgacttcccttgccttgttgtgtggctg 2400
gggagcagctcagatgctggtccttctgtccctctacctatggacattagctcaagtca 2460
ctgatcagtcagagggggcggcctgtcgggtcagggcgggctcaggggaagagcgcgg 2520
agagcaggcactctgtgaccagccccctcccctcccagGACAAC'TCCCCAGATAACCCG 2580 exon 10
TGGGCAAGTTC'TCCAATATGACACCTGGAAGCAGTCCACCCAGCGCTGCGCAGGGGCC 2640
TGCC'TGCCCTCC'TGCGTGCCCGCCGGGTACAGTGTCTGCCAAGGAGCTCGAGGCGTTCA 2700
GGGAGGCCAAGCGTACCGTCCCTGATTGCTCTACCCACCCAAGACCCACCCACGGGG 2760
GCACCCCCAGAGATGGCCAGCAATCGGAAGtgagcaaaactgccgcgagctctgcagcc 2820
cggcgccaccacctccagcctcctcctgaccacggatgtttccatcaggttccatcgcg 2880
aaaatctctcgggttccacgtccccctggggcttctcctgaccagctccccgtccccgcc 2940
tccccgaaacaggctactctcctcggccccctccatcgggctgaggaagcatcatagcaa 3000
catcttcaaacatgtacaaaatcgattggctttaaacaccctccacacaccctccccca 3060
aattatcccccaattatccccacacataaaaaatcaaaacattaaactaacccttcccc 3120
caccacacaacaaccctctt

Assembled using traces:

PPAE-abn64d08.b1	PPAE-abn55c05.g1	PPAE-abn41f05.g1
PPAE-abn38b03.b1	PPAE-abn42h04.g1	PPAE-abn41b07.g1
PPAE-abn45f04.b1	PPAE-abn55g04.b1	PPAE-abn22g05.b1
PPAE-abn40h05.g1	PPAE-abn50g06.g1	PPAE-abu27d11.g1
PPAE-abn60h06.g1	PPAE-abu28d05.b1	PPAE-abn64e03.b1
PPAE-abn41d10.g1	PPAE-abn43f02.b1	PPAE-abn05g09.g1
PPAE-abu35f11.b1	PPAE-abn32a02.g1	PPAE-abn42d10.b1
PPAE-abn40a06.b1	PPAE-abn38c04.b1	PPAE-abn32f03.b1
PPAC-amm88a05.g1	PPAE-abn09c11.b1	PPAE-abn43e09.b1
PPAE-abn05d08.b1	PPAE-abn16f10.b1	PPAE-abn42e03.b1
PPAE-abn40d01.g1	PPAE-abn43c06.g1	PPAE-abn05a08.g1
PPAE-abn45e11.g1	PPAE-abn05d07.b1	PPAE-abn60e07.g1
PPAE-abn06h07.g1	PPAE-abn38c07.b1	PPAE-abn38f01.g1
PPAE-abn64g03.g1	PPAE-abn16b08.b1	PPAE-abn50d11.b1
PPAE-abn41b05.g1	PPAE-abn27g04.g1	PPAE-abu27d09.g1
PPAE-abn45b08.g1	PPAE-abn11g07.g1	PPAC-aja59d11.g1
PPAE-abn08b04.b1		

ATG start codon at 285-287.

Probable polymorphisms at 742 (t/g), 836 (t/c).

Macaca mulatta (rhesus macacque)

cacggagatgggtcacttgtcgtgtaaaattactagtgttcttgcaaatcgaaggaactg 60
ggccctttctgctgtctccagacacttcattctccaggtggccctgcgccctcaactcg 120
gcattgtgacctatgtgttacttttgaatgaaaataatgtttataggaaagccatgctt 180
taaatttttaattgaattttaggttggccaacggcctctggtttgggaggggaccttt 240
ggcctggggcttggcctggctgccacgctcacaccacttctctcccggccccagatacca 300
ATGGGAATCCCAATGGGGAAGTCGATGCTGGTGTCTTCACCTTCTTGGCCTTCGCCTCG 360 exon 8
TGCTGCATTTGCTGCTTACCGCCCCAGTGAGACCCTGTGCGGGGGGAGCTCGTGGACACC 420
CTCCAGTTCGTCTGTGGGGACCGCGGCTTCTACTTCAgtaagtagttgggaggggcttcc 480
tcagatccggtcaggccccctaaagtgataggtgaggacgcctaacctcaagccaggggag 540
cacactcctaggtcagcggcccagcccctgctcggagactccgaccttccagctgcgtt 600
ctgagaacctgcagggctccagggcatccacaccagctgactttcccttcacaagcctcc 660
ttcgaaggggtggccagaggtgtcccctagacgtcgggagcacttacgggggtctccctt 720
ggggtcagaatttctgttgggggctgtgagctcccgtgcggaggcgccgcacccctagg 780
gcagggcttcaggctctggaggaagagcttgcctttcttccctgcaccttttggacat 840
gacaagggatgtgcttccagtgaatgatcagaattaaaatcagtaaagtgatttatagaa 900
ttaaatacaataaaacaagtgcagttgggtgggtggcaggggtgaacggtgcatgcgcctc 960
cttgggcccccaaggccaccatggaggggtgccacctgctgacctcaaggacgattcagcc 1020
tttctcctccttctctcttgggttttccggcctgggggttggcgggtgggtgcacagctc 1080
attgtgcttgagaccgcccccagatggggggctgggtggatgcaaaggcaggcagctggt 1140
gcctaggtgcctgatggggcaggggagggccacttctcgtggccgggaccacacgg 1200
cttattccacctgacactcaccagctctcactttaccacttactacttactcacgctgt 1260
gcaatggactcacaggatgcaaatgcacttcaagcttctctctttaaagttcctgctgc 1320
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cctgtgatggggctgctgctcccctcctccggctgatggcacctgccctttggcacc 1560
gggtggagccccagtgaccttccccttccagctgagcattgctgtgggggagaggggaa 1620
gacgggaggaaagaaggaggtggttccatcgcgcctcctcactcctcctcccgtcttc 1680
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ccctgaaccggactcatatcccacaggttttccaaatcaccacagtggtgggctttgggtc 1860
ctgggtggtgtctgtctggccatgggaccaagagcttgtgccatttttcatctgaggaag 1920
gagcagcagagggccagggctggctgggtcccactctctcccctctcacttctcttc 1980
ttcctgggggtgctctgctgcccagctctcacttcccctcccctgaccgcaggggtggcct 2040
catctttccagagcctggcctgagggcaggggtggtttgctcctccttcggcctcctggg 2100
gcagggggcagcaggtgctaacaatggctctctctgtgctgtgggacttccag**GCAGGCC** 2160 exon 9
CGCAAGCCGTGTGAGCCGTGCGAGCCGTGGCATCGTTGAGGAGTGTGTTTCCGCAGCTG 2220
TGACCTGGCCCTCCTGGAGACGTACTGTGCTACCCCCGCAAGTCCGAGAGGGACGTGTC 2280
GACCCCTCCGACCGTGTTCGGgtgaggatcctgggccccttcccactctctagagata 2340
gagaaatagggtttcggggcggccagcattgcctgtggcctctgggaccccttggccaggg 2400
acaaggaccctgacttcccttgccttgttgtgtggctggggagcagttcagacgctggctc 2460
cttctgtccccctgctgtggagcttagctcgagttgctgatcagtcacaggggtgacct 2520
gtcaggtcaggggggtggctcgggggaaagcgtggagagcagggcactgctgaccagc 2580
ccctcccctctcag**GACAACCTCCCCAGATACCCCGTGGGCAAGTTCTTCCGATATGAC** 2640 exon 10
ACCTGGAAGCAGTCCACCCAGCGTCTGCGCAGGGGCCCTGCCTGCCCTCCTGCGTGCCCCG 2700
CGGGGTGCGATGCTCGCCAAGGAGCTCGAGGCATTCAGGGAGGCCAAGCGTCACCGTCCC 2760
CTGATTGCTCTGCCACCCAAGACCCACCCACGGGGGCGCCTCCCCAGAGATGTCCAGC 2820
AATCGGAAGtgagcaaaactgcccgaagtctgcagccagcaccaccacctccagcctcc 2880
tcctgaccagcgacgtttccatcaggttccatctccaaaatctctcgggttccacttcccc 2940
cccggggcttctcctgaccccagccccctgccccgcctccccgaaacaggtactctcc 3000
tcggccccctccatcgggctgaggtccacagcaacatcttcaaacatgtacaaaatcgat 3060
tggctttaaaccacctcccctccaaattatcccccaattatccccacacataaaaaatcaa 3120
actttaaactaacccttccccccaccacaacaaccctctttaaataattggctttt 3180

From Macaca genome sequence: chromosome 14, location not defined.

Completed and corrected using traces:

147123091	147123086	147194067	147193984	147204525	147134589	147128249
147206362	147206310	147217619	147216143	147216131	147123146	147123132
147199988	147198275	147183256	147183250	RHLII29TR	RHCNP88TR	MQAA-adv70g11.b
99284994	147143736	147137661	147164085	147152786	147187957	147187164
147226256	147223242	147116138	147116060	147221922	wsx45a09.g1	RHPXH89TF
147110524	147110523	147211868	147210365	147210358	147223221	147223207
147221937	99189006	98493898	71866468	147152780	147143756	

Probable polymorphism at 2860 (a/g)

ATG start codon at 301-303.

Callithrix jacchus (marmoset)

accgtggagatgttcacccctcgcgtccaattactagtgcctctcacaaatcgaagcggg 60
cggcctttctgtatgttccagacgcaccgccctccacgtggccagtgccctcaccttggc 120
atcatggcctgtgtgttacttttgaataaaaataatgtttctaggaatccatgcttta 180
aatgttcaatggaatcttaggttggctgagcgccttgggttcgggaggggacaccttg 240
ctggggcttggcccagctgccccgctcatgcagcttctctcccggccgaggtaccaAT 300 exon 8
GGGATGCCAATGGGGAAGTCGATGCTGGTGGCTTCTCACCTTCTTGGCCTTCGCTCGTG 360
CTGCATTGCTGCTTACCGCCCCAGGGAGACCTTGTGTGGCGGGGAGCTGGTGGACACCCT 420
CCAGTTCGTCTGTGGGGACCGCGGCTTCTATTTCAgtaagtggtaggggggttccttaa 480
cgtgctcaggccccctagcctcaagccaaggtgagcacactccaatgtcagcggctcggcc 540
ccttgccgtgagactttgacctccagccgaatctccgagcgcggcaccgctgacctt 600
cccatacatgctcctgtgaaggtgggcccagagggggcactcacgggggtcggccttgg 660
catcagaattcctgatgggagccaggaggctccgggtgccgcggggcagggcttcaggctc 720
tggaggaagagcctgcctttcttctacaccttttggatattttgacaagggacgtgtgt 780
tcaatgagtgatcagaattaagataaagtcacttaaagaattaacccaataaagccagt 840
gcagctggcaggtggcagggctgagcatgcatgcgcctcctgaccgtgcatgcagcgtgg 900
ggggtgcccgcctgctgacggcaagacacttcggcctttcttctctctctcctcctc 960
ttccagcctgggggctggcaggtgggtgcacagcttgcctgagaccccaccctca 1020
gagggggggctgggtgtagcagaggcaggtatgggtgcctgggcatgctgacgggggtgg 1080
cgggggacagtgcctcactggctggggtgcacggcttatcctacctgacactcaccgg 1140
agtacatcttcaccaccttacttacgcactctgtgaaatgggctcacaggatacaaat 1200
gtacttcaaaacttttctctgaaaagtgtttctgctgcttgaccctggaagccccgccc 1260
gccctggcctctcctgtgccccctctgtctcctgccccatttggggtaggaagtggcac 1320
tgcagggcctgggtgccagccagtcttggcccaggagaagcttccctgtaccaggctttcc 1380
tgagaggaggggagggccgagccccacttgggggaccccgtgatggggctcctgctccc 1440
tcctctggctgatggcacctgccccttggcaccccaaggtggagccccagcaactcacc 1500
cttccagctagctgagccttgcctgtgggggagagggggaagacgggaggaaagaaggag 1560
tggttccatcgcgcctcctcactcctcctcctcccgtcttctctcctcctgcccgtctcc 1620
ctgtctcagcagccgcagggcggtgtgggccccctccagcctcaaggggtggtgccaaagca 1680
gagtccaagctcaggacagcagctcccctcctgtgtgatgaactactgcnnnnnnnnnnnn 1740
nn 1800
nnnnnnnnnnntgtcccattgttcatctgagggaggaggcagcagaggccaggggctgg 1860
tctggatcccgcctcactcccctcccactctcttcttctgggacacctctgcctgccag 1920
ctctggcttccatcccctgacctgaagagtggcctgggacagggctgttccctcctcct 1980
ccagcctcccgggacactggggcagtgccgggacagtggggtgctaacgccctct 2040
ctctgtgctgtggacttccagGCAGGCCCGCAAGCCGTGTGAGCCGTGCGAGCCGTGGCA 2100 exon 9
TCGTCGAGGAGTGTGCTTCCGCAGCTGCGACCTGGCCCTCCTGGAGACCTACTGTGCCA 2160
CCCCGCCAAGTCCGAGAGGGACGTGTCGACCTCTCCGACCGTGTTCGGgtgagggttc 2220
tgggcccccttctctctcccataagagagagaaacagggctttgggctcccgggtgttcc 2280
tgtggccactgggacctcttagccggggacgaggacctgacttcttggcttgcctgtgt 2340
tgctgggtagttggccccctcccgtccccctgcccctggacaatagccagtgcagtcacag 2400
gggtgaggggtgggctgtcagatcagatgggtggctcaagcgggtggagtggcgagtaggc 2460
acctgctgaccagaccttctctctcccagGACAACTTCCCCAGATACCCCGTGGGCAAGA 2520 exon 10
TCTTCCAATACGACACCTGGAAGCAGTCCACCCAACGCCCTGCGCAGGACTCTGCCTGCC 2580
TCTTGCGAACCCGCGGGTTCGCGTTCTCACCAAGGAGCTCGAGCTGTTTCAGGGAGGCCA 2640
AGCGTCACCGTCCCCTGACTGCTCTGTCCACCCAAGACCCCGCCACGGGGGCACCCCC 2700
CAGAGATGTCCAGCAATGAGAACTgagaaaaactgcctgccacaagtctgcagcccagca 2760
ccaccaccttctcctgaccacggacgttccatcaggttccatcgctaaatctctcggtt 2820
ccacttccccctggggcttctcctgacccccagccccatgccccgtctccccaaaaaacag 2880
gctactctcctctgccccctccatcgggctgaggaaacagcaacatcttcaaaaatgtac 2940
aaaatcgattggctttaaacattctctatgcccccatcaattatccccacacataaaaa 3000
atcacatcaaaactaacccttccccctacacacaacggccctcttaaaactaattggctt 3060

Assembled from sequence traces (note gap):

143231578	143231547	ghi20h01.x1	ghi20c02.x1
ghi15e10.y1	ghi15d11.x1	CXAG-0057B03.g1	CXAF-
ach68c02.g1			
164839911	ghi12e11.x1	ghi10e06.x1	ghi06b09.y1
146556252	146550492	143888026	143460651
163215141	161457244	154221855	

Probable polymorphisms at 471-472 (gt/gct), 531 (c/t).

ATG start codon at 299-301.

Microcebus murinus (gray mouse lemur)

cggagaccaggcccactgtccagcaagggccctggcgcgccgsggggtgtggccagaccctg 60
ccatagtgccggcgggcatggccaccccacgctactagctcgtcctgtggctccaccacc 120
cagccctctccaccccagccgctgaggcgtgtgtgttattttgcgattaaaatgccagcg 180
cctatggggaagccgagcttcagagttgcaattgcgttgcctcccagtcgccggggc 240
accggctcacgggtgtgtgtgtctcctgccccagataccaATGGGGGTCCCAGCGGGG 300 exon 8
AAGTCGATGCTGGTGCCTTCTCACCTTCTTGGCCTTGGCCTCGTGCTGCTTTGCTGCTTAC 360
CGCCCCAGTGAGACCTTGTGCGGCGGGGAGCTGGTGGACACCCCTCCAGTTTGTCTGTGGG 420
GACCGCGGCTTCTACTTCAgtaagtagcccgggctggggctggggggggggctggggc 480
tggggctgggggggtggggcgtacacagcaggcaccagtcgggtgggggtggcttcagca 540
cacctagggcagacctccctgggtgacagctgaggacgcctagcctcattggggcaggac 600
acgccaggtgaccgggcccagcccttgcctctgaggccttgagtcaccagctgggtgttggc 660
caagcagctgcagctcacctgggctcgggtgtcacctgccacacgcactcacagttcctgt 720
tgggggtggccggagggtgccggctcctcatgcactcgcagggggctgccggggggcc 780
ggagctcccgggtgggaatgccagccccaccgtggagcctctggcgggtgaggagcaac 840
ccgcctcttctcctgcactcgggtgggcatttgacagggcctgtgtgcacagatggcagg 900
atttaaaaccggatgaaatcggtttaagatcaataaaagcaaaagcaaacgtggtctgtg 960
gtgccggggctgagtggtgcacacgggcgggcgggcggggtggcaggaggagggcggtg 1020
gggtgccccctgccgcccccccagagtgtcggatactgctcttctgtttctctcctgat 1080
ctccggcctgggggggtggaggggtgggctcactgctcgtccttcagactcacccccct 1140
ggaagggggctgggtgggcacctgggtgggctcggggcaagcttgacagggcgggcgt 1200
gccccgtgcatggggcgccccgtccttgccacctgacacttgccgcgcaaacacctccac 1260
agcctctgcttggccacgctgcctgccacactgagggtgggctcacaggatgcacatgcct 1320
ttcgaagcttctctctgaaaagcacacccactactgacgctttcgaagtctgctgccct 1380
ggcctccctgggcccctccctcccgcagcctcactgggggcaggaagtggaggagggatg 1440
ggcggaggagccccgctgctcctgggaccccactatgggtggggctccctctccccctcc 1500
cctgtgactttcttcttacagctgagccctgccgtgggggagagggggaaggcgggaggg 1560
aagaagcagtggttccatggcctcctcactcctctcctcccgtcttctcctctcctgcc 1620
tgtgcctgcctgcctcggcggtcccggggtgtggcccacgctgggtgtccaccagtggt 1680
cccttgctgggtggtgtccgaactgggctcacaccccacagctcccaaacactgccagc 1740
acgggctctggtcctggtggtgtctgcccggcgggcgtgtggccgggggctttgcccg 1800
atttaaacctgtggaaggaaggagggccccgaggccaggggctaatgcatgcacccccctc 1860
ctctgtcctcgcctctggggcacctctgcctgcagcactcacttcccctcctgccctg 1920
aaggtgcccggcctccccaggggcccggccctgtgcccggcgggtgccagtg 1980
taaagccatccccctgtgtcctgtgggacttccagGCAGGCCCGCAAGCCGTGTGAACCGC 2040 exon 9
CGCAGCCGTGGCATCGTTGAGGAGTGCTGCTTCCGCAGCTGTGACCTGGCCCTCCTGGAG 2100
ACCTACTGCGCCACCCCGCCAAGTCCGAGAGGGACGTGTGACCCCTCCGACCCGTGCTT 2160
CCGGTGAGACCCGTCCCTCCAGCAGCGGGCTCCCAGCCAGGGGCAGGGTGGGCAGCC 2220
AGCGTCCCTGGCTGGCGGGGCCACCACTGGGAGGCCATTCTCGTGGCTGCCACCGTCTCTC 2280
CCCAGCACCGGTTGCTGACCAGTCGCACTGCCACGTGGCGGCTACACGGTGGCGGGCGTG 2340
GCCAAGGTCCCCCGCCGGGTACGGAGAGAGGCCCATGCATGCAGGAGGGCGGGAGGCT 2400
CGGGTAGGGGCACCCGGGAGTGGGCCCTTGGTACCAGCCCTTCCCTCCCCAGGACAAC 2460 exon 10
TTCCCCAGATACCCCGTGGGCAAGTTCTTCCAATATGACAGCTGGAAGCAGTCCACCCAG 2520
CGCCTGCGCAGGGCCCTGCCCTGCCCTCTGCGCGCCCGGGGTACGAGCTCGCCAAG 2580
GAGCTCAAGGCGGTGAGAGAAGCTCAGCACCCCGAGCCCTGCCCCGCCAAGACCCAC 2640
CACGGGGACGCCCTCTTCGGAGATGCCAGCGATCAGAAGtgaaccaaagcgtcgtcctcc 2700
tgagcaccgatccatcgtcctgtgaactcctgaccagggacatttccagcaggttccac 2760
ccctgaaatctctctgtgccacctccccctcgagggctccccccagcccagccccctgc 2820
cccgctccccaggtcaggctgccccccagccccctccatcgggcccacagtaacatct 2880
tcaaaaccatttagaattgattggctttcaacatcctccacaaccccgacttgcccccta 2940
aattacccccaaattacacatgcgcatacaaaaaattggaacataaaaccctaaactaca 3000
cacaccagcccccttaaaactaattggctttctaaaaacaccagaaaaaaaaaactaatta 3060
gcttaaaaaaaaaaaaaaactaaaaaaccaattggctgaaaaaaatactaaaaacaaattg 3120
gcttcgaaacaattggcaaaataaaggaatttggcgcccccccccttcttctcttccat 3180

Assembled from sequence traces:

mmi12e01.x1	mmi12a04.x1	mmi11h10.x1	mmi10h05.x1
mmi10g08.y1	mmi10e11.x1	mmi10d04.y1	mmi09d10.y1
mmi09c03.x1	mmi09a05.x1	mmi08g11.x1	mmi08d11.x1
mmi08a09.y1	mmi06d05.y1	mmi05f02.y1	mmi05d10.y1
mmi04h04.x1	mmi04d09.x1	mmi04b04.x1	mmi02h12.x1
mmi02b08.x1	mmi01b12.y1	mmi01b11.x1	mmi15d03.y1
mmi14e12.x1	mmi14e05.x1	mmi14b06.x1	mmi12h06.x1
mmi12e11.x1	mmi17f06.x1	mmi15h04.x1	mmi20b02.x1
mmi18d02.x1	mmi18b02.x1	G730P66042FH24.T0	
G730P69023FM6.T0	G730P6710FA12.T0	G730P65105RI6.T0	
G730P64286FC14.T0	G730P64062RD12.T0	G730P62697RO8.T0	
G730P62324RH7.T0	G730P61609FP4.T0		

Probable polymorphisms at 1919 (t/c), 1941 (a/g), 1953 (c/t)

ATG start codon at 283-285

Otolemur garnettii

accccaaattattagcacttcttgcaactcggagtcactgagccctttctgtgcaccttg 60
agacattcctttttgaaggacctcgtgccaccacctcagcaattaaagtgtgcgagtta 120
tttttataattagtacattttataagaaagtcatgctttaaaatttccattgcattttta 180
cgtccgagatggctgggcaacctgacagcacctggctcatggcatgtctctcctgcccc 240
agataccaATGGGGAGTCCCAATGGGGAAGTCGATGCTGGTGCTTCTCACCTTCTTGGCCT 300 exon 8
TTGCCCTCGTGCTGCATTTGCTGCTTACCGCCCCAGTGAGACCCCTGTGCGGCGGGGAGCTGG 360
TGGACACCCCTCCAGTTTGTCTGTGGGGACCGCGGCTTCTACTTCAgtaagtagctcgggg 420
gtggggctgggggtggacacagcaggtgctcagtcagtggtggatggtttcagcagacc 480
taggtgagacctccctgggtgacagatgagaacacctagcctggctaaggagcatactcc 540
aaggtgaccagcccaccttggctctgaggcctcggcctccctgtcgggtgtttgctgagcgc 600
ctgctgtgtgccctgctggtggccctgacacatgactcacattcacctgctgcacttt 660
gtgggcactttgacaagggcgatgtttatggatgatcagatttaaaatgtgataatag 720
atttaaaatcaaaacaaataaaagcaaatgtgggtgtgggggtgacagagctttctcccca 780
gcagactcagcccaggggaggggaggtatgggggggattttggggcccagggcccca 840
tgtgtggtgcctgcctgctgtccccaaaagtgcttgactgctcctcacatttctcacct 900
gatttccagcctggggggctgggtgggtgggctcactgctggctgtcattcagactcagcc 960
cccagaagaggggggctgggtgggcacctgggtggggccttgggacaagcttgaccctgg 1020
aagcgtgctccatccatcaggagtggtggctctccttgcctggcatgggctgccctgtct 1080
tttccactcaataccttacctggcactcctgcagcctcacttaccacactatgacatg 1140
ggctcccagacacaaaatgcattttgaagcttctgtctgaaagtgcgcctgccgtgac 1200
accctgaagccccgccaccctggcctctcctgtgccctccccacccttgcctgcctc 1260
attggggccaggaagtggcactgcaggggacctgggtgccatccggctctcctgagagga 1320
ggagtaagcctagccccacttttagggaccccacgatggggctccctctccctcttcccac 1380
cgatggcacggggcctttgcccagtgacttctccttgcagccgggcacactgtgggggag 1440
agggggaaggcgggaggggaagaagagagctgttccatctcggttcctcactcctctcctc 1500
ccgtcttctcctctcctgcccctttctccctgccctggcggctccaggggtacgtgggccc 1560
cctccaggctcaaacatggtggcgggtgagaggccaagttcagaggccacacttgtattc 1620
agtcagtggcctctgaactaggttcatacccgtttccaaagcaccttcattgtgagcctc 1680
tagtccctggcagtatctatccagccctggggccaagagtcctggctccattttaaatctat 1740
ccagccctggggccaagagtcctggtccattttaaatctgaggaaggaggcacctgaggc 1800
cagggcctagtgtcactgcacctcacctctttctcactttccgggcacctctgtctgca 1860
gctctcactttctccccaccctgaagggagggcagccctgctggggggcccaccctc 1920
ccagccctggggccagtggtgctagatgctaataatcagctcctctatcctgtgggact 1980
tccagGCAGGCCCGCGAGCCGTGTGAACCGTCGCAGCCGTGGCATCGTGGAGGAGTGTTG 2040 exon 9
CTTCCGCAGCTGTGACCTGGCCCTTCTGGAGACCTACTGTGCCACCCCCGCCAAGTCCGA 2100
GAGGGACGTGTGACCCCTCCGACCGTGTTCGGGTGAGGGCCCCGGCGACCTTCTCC 2160
TTTCTCTAGCTGTCTTCTACAGAAGTTGGGGGCGGCTCTTAGCCCAGGGTAAGGGTGCAG 2220
CCAGCTTCCCTGGCTGGAAGAGCAACTGTCCCACTCCACCACCATGGACACTATTGACTAG 2280
TCACACTGTGGCCACAAAATGACAGATGTGACCCAGAGTCCCTGTCAAGTCGCCAAGAGA 2340
GGCCCATGCAGGAGGGTGGGCAGCTTGGGTGGAGGACCGAGGAGTGGGCACCTGGTGACT 2400
GGTCCCTTCCCTCCTCAGGACAACCTCCCCAGATACCCCGTGGGCAAGTTCTTCCAACAT 2460 exon 10
GACACCTGGAAGCAGTCCACCCAGCGCTGCGCAGGGGCTGCCTGCCCTCCTGCGCGCC 2520
CGCCGGGGCCGTGTGATCACC AAGGAGCTCAAAGCGGCCAGGGATGCCAAACATCCCAGT 2580
GTCCGTGGCCGCCCCTGCCACCCACGACCCCGCCACGGGGACGCTTCTCCGGAGATGCC 2640
AACAATCAGAAGTgaaccaaagtacgtagtctctgacagcatggatcatcgccctgtgac 2700
ctcctgaccaaggacatttccagcaggttccacctccgacatttctctgtcctacttccct 2760
cctccaggactctcccagcccagcccccttggccccctcccccaagtcaggctgcttccc 2820
tggggccccgtccatcgggctgagggaacaccatttaacagcttcaaaaataacccaaatt 2880
gattggcttttaataaccaccccaaccccccatgacccccctaaattatctccaaattat 2940
acatacatgtcaaaaaattgaaaatataaatctccaaaccacacaagcacatgcattcac 3000
acaccagcccccttaaaactaattagcttttttaaaaacaccaggaagtaattagctta 3060
aaaaacaacaacccaaaaaatcaattggctgaaaaaataactaaaaaatgaattggcatag 3120
aaacaattggcaattaaaggaatttggcacccccccttcccttctcttcccctttggac 3180
ttcaagtcaaattggcctggacttaagtccctgaatcagtaagagaaaggaaggaccca 3240
aaattgcaggtgggcatgccactgcttccgcaccatctcccttcagattgactata

Assembled from sequence traces:

gqs05f04.x1	gqs04b12.y1	krr03e10.x1	krr04h07.x1
krr01b02.y1	krr07b05.x1	gqs15a07.y1	qyq02b10.p1
gqs14a04.x1	gqs07h05.y1	gqs13b06.x1	gqs17d02.x1
gqs14a12.x1	krr07f10.y1	gqs06c05.x1	krr06e03.x1
gqs11g09.y1	qyq02f07.r1	gqs06a04.y1	gqs07a03.x1
qyq02g04.p1	krr02d02.x1	krr07d10.y1	qyq02c11.r1
gqs04f11.x1	gqs01f02.x1	qyq02d04.p1	krr07d10.x1
qyq01d05.p1	gqs07a03.y1	krr01e07.x1	gqs01g08.x1
G829P62847RM17.T0			

ATG start codon at 249-251

Canis familiaris (dog)

tcctgctggggatgatgatgggggatgatcatccccacatgagactgctgaccagcaccgg 60
gtgccaatcagagatgtgcttcaggcaccgccctgggcagtgaaagtgcgtgttatttc 120
tgcaattaaagattcgtgttttaggaggacgccgcgctctcaagctgtaatggaacttg 180
aacgaggggacagctgggctggtgtttgggggtgggggtaggtggtggggccaggcccca 240
gcggggcaggcgggtgagctcatggcctcttccctctaccgccagATGCCGATGGGGGT 300 exon 8
CCCGATGGGGAAAGTCGATTCTGGTGCCTGCTGACCTTCTTGGCCTTGGCCTCGTGCCTT 360
TGCTGCTTACCGCCCCAGTGAGACTCTGTGCGGGGGAGCTGGTGGACACCCTCCAGTT 420
TGCTGTGGGGACCGCGGCTTCTACTTCAgtgagtagctcagcgtgcggtgaggccagg 480
gcagggcgcacacagcaggcactcaataaatgctggagggcaccccccccccccgcaa 540
aacatcaccagatgcctgtggacgccctctaggatgcctgttgtggggggccaggcaga 600
gggaaactcctacaaggtgaccgccaggctctcttgcctctgagcctttgtgagcacaac 660
tgagtccacgttttagggggcgcctgcagtgctgctgggtgggctcacactccctgacttg 720
tccacaatacagacttgaagtagaacactctcctcccaggaaggggggatatctgagtgga 780
ggccagcccttggcaggtgggggtgggggcgctggactgggagagggggaggagggggt 840
tgctttccctcactacttcttctggacctgcttgcagacagagctgtgagcactgaagt 900
ccccccacatttgcaccgtgcccaccttctgcacagtgggattacctgaattaaaattaa 960
ataaaataggtcagagaccagtaaaaaccaaagcatctgtcgcagctccacctgggcaca 1020
gtgggggtgagaggcatccctgctatcggacagcactggggggcgggcccaccatgtgggg 1080
gcccactgtggtcctcaagagctctctggtgctcctcatgcttctctatttccatccct 1140
gagacctctgcttctccttgccttgccttgcctatgtggaacccccagggtggaggtgatcc 1200
tcctcgggggtgtggggccttgacctcacctcccagaaagctgggcctccgttctcttac 1260
ctaaggatggggcagaggagcaggcccagggtggaccttgcaggtggagagggaagtatg 1320
cctcctgggttagccctgatgccggagctgggtgggggtgggggacgccctcatggtca 1380
ggcctggcccttgcactccacatgtggcaggccccctctgcagcctctacttaccacaaa 1440
caccagcctcagtatctcacagcttctctctgaaaagcgcctcctgcttctccttgcctt 1500
gaagccctggccaccctggctctcacctgtgccctctctcgcgtgagcacctgcctcgttt 1560
gggggcaggaagtggcatggttagggctggtgcccaggagtggtcccttggcaggagg 1620
gcccggctgagccccctgccccctgaggacatcctccccagggtgctgccccttggccc 1680
cccaaggtgagggccgagaccttctcctcgcagctgaccttggagcctgagcagcggagg 1740
acggggaggagcgggaggaaaggaggacgtggttctcatgcaggtcctcactcctccccct 1800
cgtcttctcttctcttcccaggctgctcagcgtggcgtctcaggggtgggagccac 1860
ccgggctcctgctctcctcagggacggcggcacttgcgtcccacctggccttcaagatg 1920
ggacctgtgccccgcactgtggggctggatccctggtggcggcctcctgagccggcc 1980
tcatgccagcacatttccccacttccctgggcagcgggactgggggtgggggctgtgtcc 2040
actctccatgcgagcagggaggcaccaggaggccaggggctggtcctggcacatgaccc 2100
ccacttccccctcctgtccttcttgggcacccccacctgcccactcttaccaccttctcca 2160
cgaggtggtatccccctgtcctgcccctccccccgcttgccttggggggccaccggcca 2220
aaagcccgttgtggggggaccgtgggggcccgggtgctcaagtgcggctcttcttccccct 2280
gtgggacttccagGCAGGCCGGCGAGCCGCGTGACCCGCCGACGAGCCGTGGCATCGTG 2340 exon 9
GAAGAGTGCCTGTTTCCGTAGCTGCGACCTGGCCCTTCTGGAGACCTACTGTGCCACCCC 2400
GCCAAGTCCGAGAGGGACGTGTGACCCCTCCGACCGTGTCCGgtgagaggggacctg 2460
gtgtcgggggtgggaggtgtcacctctgagctgggggaccagggtgtggccggcgcccagg 2520
gctcagctgtgactgggggtccccacgctgtggtcgtggctggcaccatcggatggcc 2580
ccccagagccagcagccccctgactggcccttccccctcagGACAACCTCCCCAGATAC 2640 exon 10
CCCGTGGGCAAGTCTTCCAATACGACACCTGGAAGCAGTCCGCCAACGCCTGCGCAGA 2700
GGTCTGCC TGCCCTCCTGCGCGCCCGGGGTGCGATGCTCGCCAAGGAGCTCGAGGCG 2760
TTCAGAGAGGCCAAGCGTACCGTCCGCTGATCGCCCTGCCACCCACGACCCCGCCACC 2820
CACGGGGGCGCCTCTCCAGAGGCATCCGGCAATCAGAAGtgagccaaaatgtcgcgtaat 2880
tctgcaagacggcaccgtccacctcgtgccctcctcttaccagggggccattccatcggg 2940
tcccgcctctaacatctctcagaggtcgcgcttccctctgcccggctccccacccccagcc 3000
ccatgccccaacctccccatgtcaggctcttctctccttggccctctccatcaggctgag 3060
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ttaaaaacaattggcatcatgaaagaattaggcccccccttccttctcttccccagggg 3420
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From dog genome sequence, chromosome 18: 49323227-49319568. Complement.

ATG start codon at 287-289.

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