

KCNA_A Contig6970.3 (complement 7274-5841)

ATGGACGACGCGCGTTGCTTGAAGATGGCCCCGAGACGGCAGAGCCGCTGACACACGAGTACTGCGAGAGGATC
GTCATCAACGTGTGCGGACTGCGCTTCGAGACGCAGCTCAAGTCGCTCGACCAATTTCCCGGACACCCCTCCTGGGC
AACCCAGCAAGAGGTGCGCTACTTCGACCCACTGCGCAACGAGTACTTCTTCGACAGAAACCGGCCAAGCTTC
GACGCCATCCTCTACTACTACAGTCCGGCGGGCGGCTAAGGCGCCCGGTCAACGTCTCCATCGACGTGTTTCAGC
GAGGAGATCAAGTTCTACGAGCTCGGCAACGAGGCCATGGCCAAGTTCCAGGAAGACGAGGGCTTCATCAAGGAG
GAGGAGAAGCCGCTGCCGTCGGACGAGTTCAGCGGCAGGTGTGGCTGCTGTTTCAATACCCGAGAGCTCCAAC
CCGGCCAGGGGAATTGCCATCGTTTCCGTACTGGTCATTTCTCATCTCCATCATCATATTTCTGCCCTCGAGACTCTG
CCTGAATTCAGGGACGAGAAGGAACAGAAATTTCTCCCAGCAAAGGACATCAATGGCACACAGGTAAAAAATTATG
CATGGCAGCTCTTTCACTGATCCATTTTTTTATTGTGGAAACCATTTGCATCATTTGGTTTTCTTTGAACTGCTG
GTGAGGTTTTTTTGGCTGCCCCAGCAAACCAGGATTTTTTCAAAGCATCATGAACATCATTTGACATCGTGGCCATT
CTGCCCTACTTTCATTACCCTTGGCACCGAGATGGCCAAGCACCAAGGGAGTGGCCAGCAGGCCATGTCACTGGCG
ATTTTGAGGGTGATCCGGCTGGTGCGAGTGTTCCGGATATTCAAGCTGTCCAGGCACTCCAAGGGCTTGCAGATT
CTGGGCCAGACTTTGAAGGCGAGCATGAGAGAGCTGGGCCTTCTCATATTTTTCTCTTCATCGGCGTCATCCTC
TTCTCCAGCGCCGTATACTTTGCCGAGGCCGACCACAAAACCTCGGAGTTCCGCAGCATCCCCGACGCCCTTCTGG
TGGGCCGTGTAACCATGACGACGGTGGGCTACGGCGACATGCGTCCCGTGACGGTGGGTGGCAAGATCGTGGGC
TCGCTGTGCGCCATCGCCGGCGTGCTCACCATCGCCCTCCCCGTGCGCGTCATCGTCTCCAATTCAACTACTTT
TACCACGCGAGACGGACAACGAAGAGCACGCAACTACCTGCACGTCTCAAGCTGCTCGCACCAGGAGGAGAGC
AGAAAGAGCAGGAGCCCGTCCATGAGCAGGTCCGAATACATGGAGATGGACGACGGTCTGAGCAACGACGTTGAC
TTCAAGGTGAAGATGCCCCCTCAAGCCCAACAACTGCGCGCCGCTCAACCACAACATGCATCAACAGAAACGTCGAG
ACCGATGTCtga

KCNA_B Join Contig12452.3 (2948-3415) Contig12452.4 (4-1006)

ATGACCATCGCCAGCGCCAACAACAGCATCACGGCCATGGCAGCACGGGCAGCCTCTACAATCCGACGAACGAG
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ATCAACGTGGCCGGCATGAAGTTTCGAGACGTGCGCGCGGACGCTCGCCAGTTCCCCGACACGCTGCTGGGCGAC
CCCGCGCGACGCGCCAGCACTTCGACCCCCCTGCGCAACGAGTACTTCTTCGACCGCAACCGGCCAGCTTCGAC
GCCATCCTCTACTACTACAGTCCGGCGGGCGGCTGCGCAGGCCCCGCCAACATCCCCCTTCGACCTGTTCTCCGAG
GAGATCCGCTTCTTCGAGCTGGGCGAGGAGACGATCCAGCGCTTCCGCGAGGATGAGGGCTACATCCGCGAGGAG
GAGAGACCGCTGCCCCAGTCCGAGCTCAAGCGCCAGGTCTGGCTGCTCTTCGAGTACCCCGAGAGCTCGAGTGCG
GCCCACCTCGTTGCGATTCTCTCCGTTGTGTCATCTTGGTGCAATTTTCATCTTCTGCATGGAAACGCTGCCG
CAGTTCGAGACCATGCTGATCAAGAAGAGCAGTTCAATGCCACCGAAATTCCTCAACCGCCAGTTTGTGCCACG
GATCCATTTTTTTCTGGTGAAACCTTTGTCATCGTGTGGTTTTCTTCGAGCTTGTGGCAGGATTCCTCTCGTG
CCTAGCAAAACTGCGTTCTTCCAAAACATCATGAACAGCATCGACGTGGTGGCCATCATGCCGTACTTTCATCACG
CTCGGAATGGAGCTGGCCGAGCAGCAGGGCAACGGTCAGCAGACCATGTGCTCGCTCGCCATCCTGCGCGTCATCCGC
CTGGTGCGCTTCTCCGATCTTCAAGCTGTGCGCCACTCCAAGGGCCTCCAGATCCTGGGCCAGACGCTCAAG
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TTCGCGGAGGTGGACGAGCCCAAGACGTACTTCACGAGCATCCCGCACGCGTCTGGTGGGCCGTGGTCAACATG
ACGACGGTTGGCTACGGCGACAAGGTGCCCCGTGACGGTGGGCGGCAAGGCGGTGGGGTTCGCTGTGCGCCATCGCG
GGCGTGCTCACCATCGCGCTGCCCCGTGCCCCGTAATCGTGTCCAACCTTCAACTACTTCTACCACCGCGAGACCGAC
GTCGACGACTCGCACTCTGGCAGGGCCCACTCTCCGAGCACTCTGCTGCCAGGATGTCAATCGTCCAGTCGCTG
AGGAGGAGCGCGCGAGCACACCGGTCCACGCACAGGCTCCATGAGCAAGAGCGACAACACGCGCACACACACA
TATGTGGCCAACAGCTTTGAGCATCAGTGCAAGCCCCACCGATGTGtga

KCNA_C Contig6469.4 (complement 5992-4469)

ATGACGGTGGTGGGTGTCAAGGCCGGCTCGGATGATGCGGCCGTGGCGGTGCAGGGAGGCTACCCGCAGGAGCGG
TACGAGCTGGCACGGCCCGGGCGGGCACGAATTCGCGAGCGCGTGGTCATCAACGTGTCCGGCCTGCGCTTCGAG
ACGCAGCTGCGCACGCTGGCCAGTTCCCCGACACGCTGCTGGGAGACCCCAAGAGCGGATGCGCTACTTCGAC
CCGCTGCGCAACGAGTACTTCTTCGACCGCAACCGGCCGAGCTTCGACGCCATCCTCTACTACTACCAGTCAGGC
GGCAGGCTGCGCAGGCCCCGTGAGCGTGCCCTACGACATCTTTACGGAAGAGGTGCGCTTCTACGACCTGGGCGAG
GAGACGATGCTGCGCTATCGCGAGGACGAGGGCTACGTGAAGGAGCCCCGAGAAGCCGTGCCAGAAAATGAGTTC
CAGCGCCAGGTGTGGCTCCTCTTCGAGTACCCGGAGAGCTCCAGTCCAGCGCGTGCCATCGCCATCGTGTCCGTG
CTCGTCATCCTCATCTCCATCATCATCTTCTGTCTGGAGACGCTGCCCCGAGTTCCGCGACGATGCAGACCTCTAC
AAGGTGTGCTACTACACGAACGGAACGCACTACTTCTACCACAACGTCTTTGCCGACCCCTTCTTCATCATGGAG
ACCATCTGCATCATTATGGTTTTCTTTGAGCTCATGGTCCGCTTCTGCGCGTGCCCCAGCAAGGTTGAGTTCGGC
AAGAACCTAATGAACATCATGCACATTGTGGCCATCTGTCCTACTTCATCACGCTCGGCACGGAGATGGCCGAG
CAGACTGGCAGTGCACACGGGCAGCAGAGCATGTCGCTCGCCATCCTCAGGGTCACTCCGGCTGGTGCGCGTCTTC
AGGATCTTCAAGCTATCACGCCACTCCAAGGGGTGCGATCCTGGGCCATACGCTGCATGCGTCGATGCGCGAG
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AGCAAGAAGACGGAATTCCAAAGCATCCCCGACGCGTCTGGTGGTCATTGGTGACGATGACCACGGTGGGCTAC
GGCGACATGTGCCCCAAGACGGTGGGAGGCAAGATCGTGGCTCGCTCTGCGCCATCGCCGGCGTGCTCACGGTC
TCGCTGCCCCGTGCGGTCATCGTGTCCAACCTTCAACTACTTCTACCAGCGCGAGACGGAAGGCGAGGACCAGACG
GTCTATTTCGCACGTGCACAGCACGCCCTTCCACGAAGCGACGCACGCCGACAATGCCGAGGCCAACTCGGAGCTG

TGCCGCCGCGAGCATTTCGAGCTTCTCGTCTCGTTCGAGAAGATCGACTGCAAGGAGGCGGACGAGCACGCGGACGAG
GACTCATGCGTCGAGGGCGAGCTCAAGCTCAGCAACTGCAACGTGGCGACGGCGCAGCAGACAAGCACGTCGGC
GGCAGTCGGATCGAGACGGACGTGtga

KCNA_D (assembly after identity with a *Lampetra* EST (NY0AAB158YC06RM1) that spans the underlined section). Join Contig39975.1 (complement 504-71), Contig4036.1 (471-1243: a "C" deleted at pos 1238), Contig4036.2 (1368-1808)

ATGGAACACAGCTCGCCGGTAGCAGGCGCAGCACGAGGTCGCCTGAGCCTCGTGCGCGCCGAGGGCGACGGCGCG
TGGATGACCGCGGGACTCAAGTGCGACGCGGCTCTCAAGCAGAGCTGCTTCGAGACGCTGGCGTTGGACAGCAGC
GTCAGCGGTGGCGGCAGTGGCGCGGAGGCGCGGATGGGCGACCGCGTGTGCATCAACGTGTCGGGCGCGCGCTTC
GAGACGCGGCGGGCCACGCTGGCCCGGTTCCCGGCCACGCTCCTCGGGAATGCGCACCGTCTTGCGCGCCACTAC
GACGCGCAGCAAAACGAGTACTTCTTCGAGCGACACCGCGACAGCTTCGCCGCCATCCTGCATTTCTACCAGTCG
AGCGGCAGGCTCCAGCGTCCACGATGGTGCCCATCGACATCTTCTGGGATGAAATCAGGTACTTTGACCTGGGA
GACAAGGTGTTGTACAGTTGCGTGAAGAAGAAGGCATGGATCCACAGAGGACCTGGTGAACCCAAACGCCATG
CCGGTCCACACACGTGGTTTTCCACAGCCACCTTTGGCTTCTCTTCGAGTCGCCCCGAGAGCTCCAATGCCGCGCGG
GTCATCGCCATCGTCTCCGTGTTCTGTCATCGTCTCGATCGTCATCTTCTGCTTGGAGACGTTGCCCGAATTC
CGCGAGGAAGAAACCCATTTCAAGCAAGGGCTTGCCGGCAACACCACCGACACGACAAATGTCGTAGATCCATTC
TTCTTGGTGGAGACCACGTGCATGGTGTGGTTCTCGTTCGAGTTCATCGTCAGGCTCATTGCCGTGTCCGTGCAAA
CCCACGTTTCATCCGTGACCTCATGAACGTCATCGACCTATCGCTATCCTGCGGTACTTCATACCCCTCATCACC
GACTTGACGGGGTCCATGGTGCCGGAGTACGTCTCGGAGGCGGCGACCAACCAAAACGCGTACAGCTCAGTGGCC
ACCTCCTTGGCGACCGCGAGCCAGGCACGGGGGACAGCATCAGCGAGATCGTTCCAGCCGGTGGCCTTCCCAGC
GTCACCGGGAACAACGGCCGTGGTGGCACAGTGACGGCCGGGACCGGGAGCAGTGGCAGTGGGGGGCAGACCATG
TCCCTCGCCATCATTTCGCGTGGTGCCTCTCGTGCGCGTCTTCCGCATATTCAAGCTGTCGCGCCACTCCAAGGGC
CTCCAGATCCTGGGTCAAACACTGAAGGCCAGCATGCGGGAGCTGGGACTCCTCATCTTTTTTCTCTTCATCGGA
GTCATCCTCTTCTCCAGTGTCTGCCTACTTTGTGGAGGCCGATGACCCCCGACTCGCACTTCACGAGCATCCCAGAT
GCCTTCTGGTGGGCCGTTGTGACGATGACCACGGTGGGCTACGGTGACATGCGGCCCCATCACACTGGGAGGAAAG
ATTGTTGGCTCTCTGTGTGCCATCGCGGGCGTGTCTACGGTGGCACTGCCCCGTTCTGTTATTGTGTCCAAC TTC
AACTTCTTCTACCAGCGAGAGCGCGATAGGCCTGAAGCCAAGGAGTCATTTTTGCTGGAGTTGGATGACACTCAC
ATGGACGCATCAGATCAAGAAGATGGAGACAGTGAATACGGGGTGTACGAGAATCACGTGGAGACAGATTTTtga

KCNA_E Contig8849.3 (complement 3020-1695)

ATGCGCGTAGATGAGGGGGATGCCCTCGCTTCGCGAGGTGGCGAGGGAACGGGGGCCGTGCCTGCGACCTTCGGC
CGCTGCAAGCCAAAGGTGAAGCACAAAGCGGCATCGCGTGCCAATGGGGCCAGTCCGCTCGCCCCGTCTGCGGAAT
GAGGGTGGCGTACACCTCCGCGTGGTGATTTGCAGCGAGTGGAATAAATGTGTCCGGAGAACGGTTTGAGACG
CAGTTGAAGACGCTGGACCAGTTCCCAGACTCGCTCCTGGGCCACCCGGACAAGCGAGCGGATATTTTGACCCA
CTCCAAAACGAGTACTTTTTTTGACAGAAGCCACGTCAATTTTTGATGCCATCCTCTTCTACTACCAGTCTGGGGGA
AGGCTTTGCAAGCCTGTTGACGTGCCTTCGGATGTCTTCAGAGAGGAGGTAGAATTCTACGAACCTCGGAGAAGAA
GCCGTTGCAAAGTACGGAGAGAATACACTCGACACCCCTGAAGAGGAAAACGTGCACGGAAAAGACTTTTCAGCAG
CACGTATGGCGCTTGTTTTGAATCGCGAGACGGTTCCATCGCTGCAAAGATGTTATCCCTCATGTCTGTTGTGACG
ACTATACTGTGATTACGGTCATGTGTTTGAGACACTGCCACAATTTTCGCAAAGATAATCAAGTCCATGCCAAT
CGTACCGAGTTTACGATTCGAACAAGTATCTACAATCTCGATCCTTTCTTCATGTTGGAAACGGCGTGTGTTGTT
TGTTTCAATATTTGAGCTTGCCGTTTCGCTTTTACGCCTGTCCAAGCAAGACGTCCTTTATGAAGGATTTTCATGAAT
CGCATCGATCCTTGGCAATAATGCCATATTTCTCATACGCTTGTCTTGGAGATCATGCAACGCAAGATCAGACC
CGGCAACCTTTTGCTGAAGATCATACGCCTCGTAAGGGTCTTTCGAATAATTCAAACGTCTCTGTCCTACTGCCAAGAT
CTGCAAATCCTTGGGCTGACGCTGAAGGCCAGCCTGCGGGAGTTGGCCATGCTAAGCTTTTTTCTCTTCGTCGCT
GTGGTAATATTCTCCGGTGCATCTACTACGTGGAAGCTGACGACCCGAGAAAACCTTCAGCAGCATCCCAGAC
GCCTTCTGGTGGGCGGTGGTCACAATGACGTTGGTTGGCTACGGAGATATGTGGCCCATGACGGTGGGAGGCAAG
ATCGTGGGTGCGCTATGTGCTATCACTGGAGTGCTCACCATCTCTTACCAGTACCCGTCATTGTTTCGAACTTC
AAATACTTCTATAATCTAAAAACAAGGACATTAAGAGATGTCTGCTGCTGttaa

KCNA_F Contig109.11 (3418-5049)

ATGCCCGCCGTTTCGAGGAGAACTGTTCTCGCTCGACGAGAAGGACCTACTGCTGCCCACGAATTGGCCAGCTTTG
GCCGACCCGACGGACGACACGCCGCCAACAAAGGAGTCCGGTGTCTTGCCGGCGACCGCCGCCGAGAGGATC
GTCGTCAACGTGTCTGGGCTTCGCTTCGAGACGGAGCGGCTACCCCTCGAGCGCTACCCCGGCACCCCTGCTGGGC
GACGCGTACGTCGCGCCCCGTTCTACAGGCCCGACCTCGCGAGTTCTTCTTCGATCGCCACCGTTCAAGCTTC
GAGTCGGTGTCTCCACTTCTACCAGTCGGGCGGAGAGCTGAGACGGCCGTCGCGCCGTGCGCCGTCACCTTCGTC
GGCGAGGTGCTCTTCTTCGACCTGGGCGACGAGGCCGTGGAGAGGCTCAGGGAGGAGGAGGGCTTAGCGGACGAC
GACGAGGTGGAGGAGGCGACGCTGAAGGCTGAGAGGAAGATGGCGAAAAAGGAGGCTCAGCAGCGGCTGCCTTCG
GGGAAGGTGCGCCGCTACCTGTGGAATCTATTTCGAGACCCCGACACGTCCACGTCCGCCAAGGCCACGGCCGTC
TTCTCCTTGGTCATGGTGTCTGTGTCGTTCTGCGCGGAGACCCGCCCACGTTTCAGGAACAGGCAC
CACCGGCGGCACCAGCACGGCCGAACGACTCCGCGGACTCGCAGCCGAGCTCCGAGTGGATGGACCCCTTCTCG
GACCCGCTTTTTCTGTTGGAGACCGTGTGCATCGCCTGGTTTCGGCCTGGAACCTCTCATCCGCGCCTTCGCGTGC

CCGAACAAGCTGGCGTTTCGCACGCGACCCCATGAACATCGTCGACTTCATCTCCATCCTGCCCTACGGCATCACC
CTGGCCATGGACCAGCTCGGCTCGTCGGCCACCGGCGAGAAGAGCAAGGCGAGCAACCTGGCCGTGCTCAGGACC
ATGCGGCTGCTGCGCGTGTGCCGATTCTCAAGCTGTGCGGCCACAGCCAGGCCCTGCAGGTGCTGGCGAAGACG
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ATCTACTTCGCGGAGGTGGGCGCGGACGAGGCGCACTTCAACAGCGTGCCGACGCCTTCTGGTGGGCCGTGGTG
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AAGAAGAAGATGATGATGATGAAGAAGAAGAAGAAGAAGACGATGATGACGACTAAGAAGGGGACGTTGAAT
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CAGCAGAGGTGCTCGCCGTGTGGGGTCTTTGCTGCGTGCATGGGCCGCGCCGGTGGTGCGACACGGAGGAGAAG
CTGGGACCTCGAGAGCGGCAGCAGAATGAGCTTCGATACCCACATGAGACCAAAGTGtga

**KCNA_G Join Contig16470.1 (complement 379-1) trace [GenBank ti|1427225648]
(complement 498-1)**

ATGTCCAGCGTCAGTGTGCGGGAGCTCACCATGAGACGCGACTGCGCTTCCGCCACAACCCGCCACGGACAGCAGC
TACACCACCTCTTACCACGGAGGACCTGCCGAACAATCACCACCACCACAGTGTCCCCAACAACAACAGCAT
CAGCAGCAGCATCAGCAGCATCAGCAGGGCCAGGAGCTGCCGGTTCGCGGCTTGGAGCGAGCGAGTGCCATCAAC
GTGTCGGGCCCTCAGGTTTCGAGACGCGGCGCAGCACACTGGAGCGTTCCTCCCCGCACGCTCCTGGGCGACGGCGCT
CGCTTCGCTGCGCTTCTTTCGACCCGCTGCGCGCAGGAGTACTTCTTCGACCGCAACCGCGACAGCTTTGGCGCGATC
CTCTTCTACTTCCAGTCGGGCGGCGAGCCTCCACGGCCCTCCGCGGTGCCCCACGGCCCTTTCGTGCGAGGAGTG
CGCTTCTACGACCTGGGCGCCGAGGCGCGCGCCGCTCTGCGAGGAGGAGCGCTGTTCCCGCGAGGACCCCGAG
AGGCCGCCCCCTGCCGCGCAACCGCCTGCAGCGGCGCGCTGGCTACTCTTCGAGCACCCCGAGAGCTCCGTGTGG
GCGCGCGCGGTGCGCCTGGTCTCGGTGCTCGCGACGCTCGCGTCCGTGGTGGTCTTCTGCCTCGAGACGGTGCCG
TACGGCGAGCGGAAGAGCGGCGGCGAGGAAGGGCAGCGGCGAGGGGGAGGAGGGGGAGGAGGGTGGTGGTGGTGGT
GGTGGTGGCGGCGGCGCGCTTCGCCGTGAGGTGGCGTGCATCGCCTGGTCTGCCTCGAATTCACCACATTC
GGAGCTTCAGCTGCTCGAGATGGTCATAGCTGTTCTGCGTATGTGTATTAC???

KCNA_H Contig22917.3 (18-1490)

???GAGCGCGTGGTGGTGAACGTCTCCGGCCTGCGCTTCGAGACGCAGCTGCGCACGCTCGCGCACTTCCCCGAC
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CGACCGAGCTTCGACAGCCATCTCTACTACTACCAATCGCGCGGCAAACTGCGCAGGCCACCAACGTGCCCTAC
GACATCTTTTCCGAGGAGGTGCGCTTCTACGAGCTCGGCGAGGAGACGATGGCGCGCTACCCGAGGACGAGGGC
TACGTGAAGGAGGAGGAGAAGCCGCTGCCCGAGAACGCGCTCCAGCGCCAGGTGTGGCTCCTCTTCGAGTACCCG
GAGAGCTCGAACCCCGCGCGCTCATCGCCATCGTGTCCGTGCTCGTCATCGTCATCTCCATCGTGATCTTCGTG
GCCGAGACCCTGCCGAGTTCGCGACGACAAGGACCTCCACTCGGGCACGCGCCACGACGTCGGTGCCGGCGGAC
GCCGCTGTTGCCGCTGCTGGCAACAGCAGCGGCGGCGAGCAGCGGCGGCGGCGAGCGGCCACGCGCACGGAGGTCAC
GCGCACCCGGGCGGCGGCGGCGGTGGCGGCGGCGGCTCGGCCACGGTTACGGCCACGTGCCGGGCGTGACGCTG
GCTGTGCCGCACGGCCGCGGAGGCCACCCCCGAGTTCGGCAAAGACCCGTTCTTCATCGTGAGACCGTGTGC
ATCGTGTGGTTTCAGCTTCGAGCTGCTCGTGCGCTTCTGCGCGTGCCCCAGCAAGCCGGGCTTCTTCAAGAACATC
ATGAACACCATCGACATCGTGGCCATCATGCCCTACTTTCATCACGCTGGGCACGGAGCTCGCGGCGCAAGACACG
GGCGCCAACAACGGGCGAGCAGACGATGTGCTCGCCATCCTCAGGGTCATCCGGCTGGTGCGCGTCTTCAGGATC
TTCAAGCTGTGCGGCCACTCCAAGGGGCTGCAGATCCTGGGCCAGACGCTGCGCGCGTCGATGCGCGAGCTGGGC
CTCCTCATCTTCTTCTCTTCATCGGCGTCATCTTCTCTCGAGCGCGATTACTTCGCCGAGGTGGACGACCCC
AACACGCACTTCCACAGCATCCCCGAGGCCCTTCTGGTGGTTCGCTCGTACCATGACCACGGTGGGGTACGGAGAC
ATGTTCCCCGCTGACGCTGGGCGGCAAGATCGTGGGCTCGCTGTGCGCCATCGCGGGCGTGCTCACCATCGCTGTG
CCCGTGCCCGTTCATCGTGTCCAACCTTCAACTACTTCTACCACCGCGGCTCGGAGGCCGAAGAGCAGACGCTGTCT
GTGCAGGAGGACAGCGGCGGCGAGCTGCGAGGCCGGAACCAGATCAAGAGGAGTAACAGCGTCTCGTCCGTCAGC
AAGTCCGAGTACATGGACGACATGGCCTTCCTCGGACCCAACTACATCGAGtga

KCNA_I Contig25309.7 (2nd exon: complement 1912-1295)

agACCATGTGCTCGCCATCCTGCGCGTCATCCGCTGGTGCGCGTCTTCCGGATCTTCAAGCTGTGCGGCCACT
CCAAGGGCCTCCAGATCCTGGGCGAGACGCTCAAGGCGAGCATGCGCGAGCTGGGGCTGCTCATCTTCTTCTCT
TCATCGGCGTCATCCTCTTCTCGAGCGCCGCTACTTCGCCGAGGTGGACGAGCCCACGACTACTTCACGAGCA
TCCCGCACGCGTTCGTTGGTGGGCGGTGGTACCATGACGACGGTTGGCTACGGCGACACGGTGCCCGTGACGGTGG
GCGGCAAGGTGGTGGGGTTCGCTGTGCGCCATCGCGGGCGTGCTACCATCGCGCTGCCCGTGCCCGTCATCGTGT
CCAACCTCAACTACTTCTACCACCGGAGACCGAGCTCGACGACTCGCACTCCAACGTAGCGCAGTCGCCGAAAA
ACTCCGCAAGTTAATTACCCCTCGAATGAGTCGCTGAAGAAGAGCGCGCCCAAGCACACCCGTTGACACGCGGCT
CCGTGAGCTGCCACTCCGTGAGCAAAGGCGACAACACGCACACACACGTCAGTGCCCAACAGCTATGAACATA
AGTGCCAGCCACCGACGTGtga

KCNA_J Contig78404.1 (complement 1594-980)

???CAGCACGCCATGTGCTCGCCATCCTCAGGGTCATCCGCTCGTGCGAGTCTTCAGGATCTTCAAGCTGTGCG
CGCCACTCCAAGGTCTGCGATCCTGGGCCAGACTCTGCGCGCCTCCATGCGCGAGCTGGGCTGCTCATCTTC

TTCTCCTCATCGGCGTCATCCTCTTCTCGAGCGCCGTCTTCTTCGCCGAGGCGGACAGCGACGAGTCGCACTTC
ACGAGCATCCCCGACGCCTTCTGGTGGGCGGTGGTCACCATGACCACGGTGGGTACGGCGACATGAGGCCCCGT
ACAATCGGCGGGAAGATCGTGGGCTCGCTGTGCGCCATCGCGGGCGTGCTCACCATCGCGCTGCCCCGTGCCCCGT
ATCGTCTCCAACTTTAACCTTCTACCACCGCGAGACGGACAATGACGACTCGGCGGTCAAAGTCCAGGGCGGC
GGTGGTGGCGGTGGTGGCGCCGGTAGCGGTGGCGGCTCCTCTGGTGCCGTAGGGCCGCGTTCTGTCGAGGGGAGT
GGAACGCCGAGGAAGCGCCGCCCCAGCAGCGCCCAGGGCCTCGACGCCGAGACGGACTCGAGCACGGAGTCGGA
GATCCAAACTCCTCGGA???

KCNA_K Contig46381.2 (1-519)

???GGCCTCTTCATCTTCTTCTGTCATCGGGGTCATCCTCTTTGGAGCGCCGATCTACTTCACCGAGTCCGAC
GATTCCGACACGGAATTCACGAGCATCCCGACGCCTTCTGGTGGGCGGTGCTCAGCATGACCACGGTGGGCTAC
GGCGACATGTGGCCCAAGACCGTGGGCGGGAAGATCGTGGGCTCGCTGTGCGCCATCGCGGGCGTGCTCAGCATC
GCGCTGCCCCGTGCCCCGTGATCGTCTCCAACCTCAACTACTTCTACCACCGCGAGATGGACAGCGAGGACCAGGGT
GAGTACTCGCACGTGTCCAGCCTCAACACCAGTGACGACGGAGGAGGTGGAGGAGGGGGAGGAGGTGGAGGCGAT
GAAGAAGTCTTCAAGCAAATGTCCATGGAGGTCAACCCGAGAGCGGCAGGGGCGATGGGGCTGACGTGGTGTCC
ATCCTCAAGGAGGTGGACTCCGGACAAGTGCCCAATAGCCTGAGTGAGCAGACGGGGCTAAGACCCATTGCCtag

KCNA_L [GenBank:ti|1291002197] (complement 813-1) (No hit in contigs)

???TGCGCTTCGAGACGACGTGGGCGACGCTCGCCAGTTCCCCGACACGCTGCTGGGCGACGCGGAGAGCGGT
CGTGTACTTTCGACCCCTGCGCAACGAGTACTTCTTCGACCGCAACCGACCCAGCTTCGACGCCATCCTCTACT
ACTACCAGTCGGGCGGCGAGGCTGCGCAGGCGGCGAGCGTCCCCCTTCGACATCTTCGCCGAGGAGATCAAGTTCT
ACGAGCTGGGCGACGAGGCGATGGTGCCTTCCGCGAGGACGAGGGCTACGCCAGGGAGGAGGAGAGGGCCATGC
CGGCGAGCGAGTTCCAGCGCCGCGTGTGGTGTCTTTCGAGTACCCGAGAGCTCGGGGGCGGCGCGGCATCG
CCATCGTGTGCTGCTCATCATCGTCTCCATCATCATCTTCTGCGTCGAGACGCTGCCATGTTCCGGGAGG
AGAGGGAGAACACCTCGCTCGCCGTGCCATTTCGTAACGGCACTGAGGTGGAGGGCGCGGCTCCGGCAGCTCGT
TCATGGACCCGTTTCTTCATCATCGAGACCATCTGCATCGTGTGGTTTTCAGTTTCGAGTTCACGGTGCCTTCTCG
CAAGTCCCAGCAAGCCGGCCTTCTTCAAGGACATCATGAACATCATCGACATCGTGGCCATCGTGCTTACTTCA
TCACCCTGGGCACTGAGCTGGCGGAGCAGCAGGGCAACGGGCAGCAGACGATGTGCTCGCGATCTTCAGGGGAA
TTCCACCACATTGGAGCTTCAGCTGCTCGAGATGGTCATAGCTGTTCTGCGTATGTGTAGAAAAG???

KCNA_M 1st exon: join [GenBank:ti|1427218636] (54-741) [GenBank ti|1449626312] (599-817) (No hit in contigs)

ATGTGGTGGAATTCCGGCGGCGGCGGCGGAGGAGGTCCCCGGGGTTCGCGAGGATTTCGGCGGCTGCCGCGCC
CCGCACGGCCACGCGGTGCTGACGCCGACGCGCTCGACGTCCTGCTGCTGGACGCGGCTGCGTGCGAGCCCTAC
TACCAGCACTACAACAACCACCACCACCACCACAACAATCTGCAGCAGCAACAACCGCAGCAGCAGCCGCAA
CAGCAGCACAACAACCATCACAACCACCATCACCAGCAGCATCGCGGCAGCAGCAGCGGCGGAGCAGCAGCAGC
TTCAGCGCCGGCGGCGGCGTTCGACTCGGGCGGGTTCCCCGAGGCGGGCGAGCGGCTCACCATCAACGTGTGCGGG
CTGCGCTTCGAGACGCACGCGCGCACCTGGCGCGCTTCCGCGCACGCTGCTGGGCGACCCGCGCAAGCAGCG
CCCTACTTCGACGCGCTGCGCAACGAGTTCTTCTTCGACCGCAACCGCCAGAGCTTCGACTCCATCCTGCACCTAC
TACCAGTCACGCGGGCGCCTGCGCAGGCCCCGCGGGCGTGCCCGTGGACGTGTTTCGCCGAAGAGCTGCGCTTCTAC
GAGCTGGGCGACGAGGCGATGGCGCGCTACCGCGAGGACGAGGGTTGCGCGCCCCGAGGAGGCCGAGCGAGTCCCTG
CCGCGCGCGCCCCCTGGCCCGCAGCTGTGGTCTCTTTCGAGTACCCCGAGAGCTCGGCGCCCCGCGCGGCCATC
GCCATCGTGTGCGGTGGCGGTTCATCGTCTCTCCATTATCGTCTTCTGCCTCGAGACGCTGCCGAGTTCCGAGAC
GAGAGGCGGACGCGCGCCGCCGCATACAACAACGATAACAACAATAACGACAACCTACAACAACAACCTGTGCA
TCAGCACgt

KCNA_N join [GenBank:ti|1489701441] (complement 502-22) [GenBank ti|1223432487] (247-1) (No hit in contigs)

???GCCTCTCTGACGACCCGTTCTTCGCCGTGGAGTCGCTGTGCGTGGTGTGGTTTCAGCGTCGAGCTGCTGGCAC
GCTTCCTCGCCTGCCCCGGCAAGGCGGCCTTCTTCCGCGACGTCATGAACACCATCGACGTCGTCGCCATCGTGC
CGTACTTCGTCACGCTGGGCACCGAGCTGGCTGAGCGAGGCGGTGGAGGCGGCGGCGGAGGCGGTGGAGGCGGTG
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CGCGCCACTCCAAGGGCTCCAGATCCTGGGCCAGACCCTCAGGGCGTCCATGCGCGAGCTGGGCTGCTCATCT
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TCCTGAGCATCCCGCACGCCTTCTGGTGGGCTCGTACCATGACGACGCTGGGCTACGGCGACGCGGTGCCGG
CGACGACCGGCGGCAAGGTGGTGGGCTCGCTGTGCCCATCGCCGGGTGCTCACCATCGCCCTGCCCGTGCCCCG
TCATCGTCAGCAACTTCAACCACTCTACCACCGAATCCACCACAGTGGCGAAAAC???

KCNA_O join [GenBank:ti|1443482662] (148-794) [GenBank:ti|1383256050] (complement 391-62) (No hit in contigs)

ATGGAGGGCGGAGAGCGTGGCAGGCGAGACGTCCACGGGCGGGCCGCTGCGGCGGCTACGAGCGCGTGGTCATC
AACGTCTCGGGGCTGCGCTTCGAGACGCAGCTCGAGACGCTGGCGCATTTCCCGGACACGCTGCTCGGCGACTCG

GCGCGGAGGATGAACTTCTTCGACTTCCTGCGCAACGAGTACTTCTTCGACAGGAACCGGCCGAGCTTCGACGCG
ATCCTCTACTACTACCAGTCCAAGGGGAAGCTGCGGAGGCCCCGACAGCGTCCCGTACGACATCTTCATCGAGGAG
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TCA???