

Int. J. Aquat. Biol. (2018) 6(6): 296-302

ISSN: 2322-5270; P-ISSN: 2383-0956

Journal homepage: www.ij-aquaticbiology.com

© 2018 Iranian Society of Ichthyology

Supplementary files

Sequencing results for *Cmlc2/pSS536*

Clone no.2 and was sequenced using T7 forward and SSB_P1195 reverse primer. The sequencing results showed that the 278 bp *cmlc-2* promoter region was cloned in the pSS536 vector.

The sequencing results of clone 2 and 4 were as follows:

Clone 2, I.D.: LM_304 sequencing results with T7

>LM304_T7-1.ab1

GAGCAATAGCGAGTGTAGTACTTGAGTAATTTTACTTGATTACTGTACTTAAGTATTATTTTTGGGGATTTTTACTTTACT
 TGAGTACAATTAATAAATCAATACTTTTACTTTTACTTTAATTACATTTTTTTAGAAAAAAAAGTACTTTTTACTCCTTACAA
 TTTTATTTACAGTCAAAAAGTACTTATTTTTGGAGATCACTTCATTCTATTTTCCCTTGCTATTACCAAACCAATTGAAT
 TGCGCTGATGCCAGTTAATTTAAATAGATCTGCAGGTTTAAACGAATTCGCCCTTCATCCCTCAAATCTCTCATTAC
 GTCCCCCTCCCCATCTGCACACTTTATCTCATTTTTCCACCCTGCTGGAATCTGAGCACTTGTGCAGTTATCAGGGCTCCTG
 TATTTAGGAGGCTCTGGGTGTCCATGTAGGGGACGAACAGAAACACTGCAGACCTTTATAGAAGAACAATGATAAGA
 GTCCTCATACATAAAGACTCCATTAGAAACGTCAGTGACCCAGGAGCCCAGACCAACAGCAAAGCAGACAGTGAACAT
 GGTGAGTAGACAAAGCAAGGGCGAATTCGGCCGCTAAATAGATCTGGCCATCTAGAGCGGGCCGCGCGCACTAGTGAA
 TTCCATGGCCAGCTCCGAGGATGTCATCAAAGAGTTTATGAGATTTAAGGTCAAGATGGAGGGAAGCGTCAACGGACA
 CGAGTTCGAGATTGAGGGAGAAGGAGAAGGCCGGCCTTACGAGGGCACACAAACCGCTAAGCTCAAGGTCACAAAAG
 GAGGACCCCTCCCCCTCTCCTGGGATATTCTGAGCCCTCAGTTCCAGTACGGAAGCAAAGCCTATGTTAAACACCCCTGCC
 GACATCCCTGACTATCTGAAGCTCTCCTTCCCTGAAGGCTTCAAGTGGGAGAGATTCATGAACTTCGAGGACGGAGGCG
 TGGTGACAGTCACACAAGATAGCACCCCTCCAGGACGGAGAGTTTATTTATAAGTGAAACTCAGAGGACCAACTTCCCCT
 CCGATGGCCCTGTCATGCAAAAAACATGGGATGGCAGCTCCACCGAAAGATGTATCCTGAAGATGCGCTCTGAAGGC
 GAATTAATGAGACTGAAACTCAAGACGGAGGACTACCGATGCGAGTCAAACA

Clone 2, I.D.:LM_304 sequencing results with SSB-P1195

>LM304_p1195.ab1

GGGATTGTCGTTGAGCTTCCCTCCATCTTGACCTTAAATCTCATAAACTCTTTGATGACATCCTCGGAGCTGGCCATGGAA
 TTCACTAGTGCAGCGCGCCGCTCTAGATGGCCAGATCTATTTAGCGGCCGGAATTCGCCCTTGCTTTGTCTACTCACCAT
 GTTCACTGTCTGCTTTGCTGTTGGTCTGGGCTCCTGGGTCAGTACGTTTCTAATGGAGTCTTTATGTATGAGGACTCTTA
 TCATTTGTTCTTCTATAAAGGTCTGCAGTGTTCGTTCCCTACATGGACACCCAGAGCCTCCTAAATACAGGAGC
 CCTGATAACTGCACAAGTGCTCAGATTCCAGCAGGGTGGAAAATGAGATAAAGTGTGCAGATGGGGAGGGGGACGTGA
 ATGAGAGATTTGAGGGATGAAGGGCGAATTCGTTTAAACCTGCAGATCTATTTAAATTAAGTGGGCATCAGCGCAATT
 CAATTGGTTTGGTAATAGCAAGGAAAATAGAATGAAGTATCTCCAAAAATAAGTACTTTTTGACTGTAAATAAAAT
 TGTAAGGAGTAAAAAGTACTTTTTTTTTCTAAAAAATGTAATTAAGTAAAAGTAAAAGTATTGATTTTAAATTGACTCA
 AGTAAAGTAAAAATCCCCAAAATAACTTAAAGTACAGTAATCAAGTAAAATTACTCAAGTACTTTACACCTCTGGGC
 CCAATTCGCCCTATAGTGAGTCGTATTACAATCACTGGCCGTCGTTTTACAACGTCGTGACTGGGAAAACCCTGGCGTT
 ACCCAACTTAATCGCCTTGAGCAGTACATCCCCCTTCGCCAGCTGGCGTAATAGCGAAGAAGGCCCGCACCGATCGCCCT
 TCCCAACAGTTGCGCAGCCTTGAATGGCGAATGGACGCGCCCTGTAGCGGGCGCATTAAAGCGCGCGGGTGTGGTGGTTT
 ACGCGCAGCGTGAACGCTACACTTTGCAGCGCCCTAGCGCCCGCTCATTGCTTTCCCTTCCCTCTTTCTCGCCACGTG
 CAGGCTTCCCGGTCAGCTCTAATCGGGGCTCCCTTAGTCGATTATGCTACCGACCTTGACAAAACCTGAATAAGGTTA
 ATGGTCAGCAGGTGAGATG

ClustalW analysis for Cmlc2

```

CLUSTAL 2.0.11 multiple sequence alignment

1          TGCAGGTTTAAACGAATTCGCCCTTCATCCCTCAAATCTCTCATTACAGTCCCCCTCCCC 60
2          -----ATGCATTCATCCATCCTTTTCATCCCTCAAATCTCTCATTACAGTCCCCCTCCCC 55
           * * * * *

1          ATCTGCACACTTTATCTCATTTCACCCCTGCTGGAATCTGAGCACTTGTGCAGTTATCA 120
2          ATCTGCACACTTTATCTCATTTCACCCCTGCTGGAATCTGAGCACTTGTGCAGTTATCA 115
           *****

1          GGGCTCCTGTATTTAGGAGGCTCTGGGTGTCCATGTAGGGGACGAAACAGAAACACTGCAG 180
2          GGGCTCCTGTATTTAGGAGGCTCTGGGTGTCCATGTAGGGGACGAAACAGAAACACTGCAG 175
           *****

1          ACCTTTATAGAAGAACAATGATAAGAGTCCCTCATACATAAAAGACTCCATTAGAAACGTC 240
2          ACCTTTATAGAAGAACAATGATAAGAGTCCCTCATACATAAAAGACTCCATTAGAAACGTC 235
           *****

1          AGTGACCCAGGAGCCCAGACCAACAGCAAAGCAGACAGTGAAACATGGTGAGTAGACAAAAG 300
2          AGTGACCCAGGAGCCCAGACCAACAGCAAAGCAGACAGTGAAACATGGTGAGTAGACAAAAG 295
           *****

1          CAAGGGCG----AATTCGGCCGCTAAATAGATCTGG----- 333
2          CTATACTTTTTGGTTTTGAATATAAATATTAATGTGAAAATAAAAAGC 343
           * * * * *
    
```

1 is the *cmlc2* gene sequence from Ensembl
 2 is the query sequence (cloned product)

Figure S1. Screen shot of ClustalW analysis.

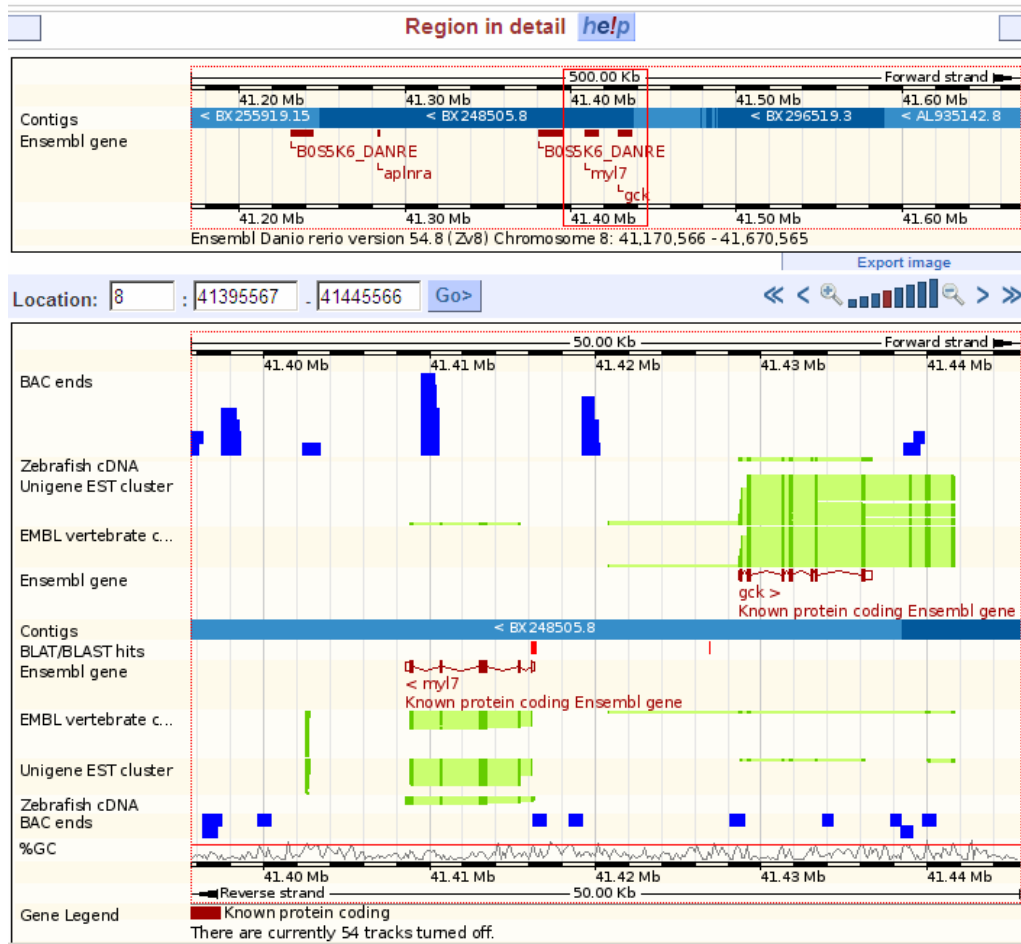


Figure S2. Screen shot for BLAST results of *Cmlc2*.

Sequencing results for Pak2a/pSS536

>LM314_T7.ab1

ACCAGAGTGTAGTACTTGAGTATTTTTACTTGATTACTGTACTTAAGTATTATTTTTGGGGATTTTTACTTTACTTGAGTACA
ATTAATAATCAATACTTTTACTTTTACTTAATTACATTTTTTTAGAAAAAAAAGTACTTTTTACTCCTTACAATTTTATTTAC
AGTCAAAAAGTACTTATTTTTTGGAGATCACTTCATTCTATTTTCCCTTGCTATTACCAAACCAATTGAATTGCGCTGATGC
CCAGTTTAATTTAAATAGATCTAGTACCTCGAGGCTGTGAGATTCATGAAAGCAGTAGACTAACTATTTCTGATGCAGAAA
CCCCAAACTCAGGCTCTCAAGAAAAAAAATCTTCTGAAATGGACCATGTAGAAGTGCGTTTAAGCCTATAAAACACTG
TGTGCTTGAAGAGAGCCACTCCCATCTCAAATCACTGTCATTACGGGGAAAACAAGTTGAGACTTGATTATTCCAAATAAC
ATTCCTTAAGGAAAAATGGAAAACCTTTGACTGAAATCAGTAAATATCTGGCAGTCAGTGTAGCGTTATTCAGTACAGAA
AGAAGATATAAAAATTAGTTATACCTACAATTCTTGAGAAATTGTGATGTTAAAAGGCTCTAATCAAGCTCTTAAAACACC
TCCTATAATCCTGCTACATTCCTAGTAGTGTGATTGTTATGTGATGGTGGTGATTGGTTATTTTTGAGCAAGAGGCAGTGGT
GTGTAAGGTATTTTTGGTCTGTGTTCCCGCTGTAGGGCCTTACATCAAGCCCGAGGGGTGGTAC

>LM314_p1195.ab1

AAGGACTGTCGTTGAGCTTCCTCCATCTTGACCTTAAATCTCATAAACTCTTTGATGACATCCTCGGAGCTGGCCATGGA
ATTCAGTAGTGC GCGCGGCCGCTCTAGAAATGATGCAATCAGCGCCCAACGACATCACTTTAACCATCTCACCCCTGAGG
AACCCCTGATGGAAAGCTCCAGCTCACAGCCCTGGCTCTGGTCTGGCACACTACTGAAACATTGAGGGTCTTCACTATCG
TGTGTCCACAGTCTCTTCTTCCCTGTGCTTCCACTGAACTGCACCGAGATAGAGGCATGTTGATGCAGGCATGCTTCATT
CCACAGTAGGATGAACTGCTGCGAGTGCAGTCATGCCTTTGCGCTGCGAATTGCTATAGATGTACCACCCCTCGGGCTT
GATGTAAGGCCCTACAGCGGAGACACAGGACTGAAAATACCTTTACACACCACTGCCTCTTGCTCAAAAAATAACCAATC
ACCACCATCACATAACAATCACACTACTAGGAATGTAGCAGGATTATAGGAGGTGTTTTAAGAGCTTGATTAGAGCCTT
TTAACATCACAATTTCTCAAGAATTGTAGGTATAACTAATTTTTATATCTTCTTCTGTACTGAATAACGCTACACTGACT
GCCAGATATTTACTGATTTTCAGTCAAAGGTTTTCCATTTTTCTTAAGGAATGTTATTTGGAATAATCAAGTCTCAACTG
TTTTCCCCGTAATGACAGTGATTTGAGATGGGAGTGGCTCTCTTCAAGCACACAGTGTATTTATAGGCTTAAACGCACTTC
TACATGGTCCATTTTCAAGAAGATTTTTTTTTTCTTGAGAGCCTGAGTTTCGGGTTTCTGCATCAGAAATAGTTAGTCTACTG
CTTTCATGAATCTCACAGCCTCGAAGTACTAGATCTATTTAAATTTAACTGGGCATCAGCGCATTCAATTGGTTTGGTAA
TAGCAAGGGAAAATAAAAATGAAGTGATCTCAAAAAATAAGTACTTTTTGACTGTAAATAAAAATTGTAAGGAGTAAAAG
GTACTTTTTTTTCTTAAAAAATTGTATTAAGTAAAGGTAAGTATTGGATTTTATTGTAATCAGGTAAGTAAAATCCCC
AAATAATACTTAGTTACAGTAATCCAGTTAATTTACCAGGTACCTTTAACCCCTTCGGGCCAATTCGCCCTTAAGTGGGAT
CGATATACATTACGTGGGGCGGCGTTCAAGGCTTGGACTGAAAACGTGGTATACCATAATCGCTGGGAGCCA

ClustalW analysis of Pak2a/pSS536

```

CLUSTAL 2.0.11 multiple sequence alignment

1          -----AGTACTTCGAGGCTGTGAGATTCATGAAAGCAGTAGACTAACTATTT 48
2          AGTTGTGGAAATCAGTACTCTCGAGGCTGTGAGATTCATGAAAGCAGTAGACTAACTATTT 60
          *****

1          TGATGCAGAAACCCGAAACTCAGGCTCTCAAGAAAAAATACTCTGAAAATGGACCAT 108
2          TGATGCAGAAACCCGAAACTCAGGCTCTCAAGAAAAAATACTCTGAAAATGGACCAT 120
          *****

1          GTAGAAGTCCGTTTAAGCCTATAAAACACTCTGTGCTGAAAGAGAGCCACTCCATCTCA 168
2          GTAGAAGTCCGTTTAAGCCTATAAAACACTCTGTGCTGAAAGAGAGCCACTCCATCTCA 180
          *****

1          AATCACTGTCATTACGGGAAAACAAGTTGAGACTTGATTATCCAAATAACATTCCTTA 228
2          AATCACTGTCATTACGGGAAAACAAGTTGAGACTTGATTATCCAAATAACATTCCTTG 240
          *****

1          AGGAAAAATGAAAACCTTTGACTGAAATCAGTAAATATCTGGCACTCAGTGTAGCGTTA 288
2          AGGAAAAATGAAAACCTTTGACTGAAATCAGTAAATATCTGGCACTCAGTGTAGCGTTA 300
          *****

1          TTCAGTACAGAAAGAAGATA-----AAAATTACTATACCTACAATCTTGAGAAATTC 344
2          TTCAGTACAGAAAGAAGATACTCCAAAACACTAGTATATACCTACAATCTCGAGAAATTC 360
          *****

1          TGATGTTAAAAGGCTCTAATCAAGCTCTTAAAACACCCTCCATAATCTGCTACATTCC 404
2          TGATGTTAAAAGGCTCTAATCAAGCTCTTAAAACACCCTCCATAATCTGCTACATTCC 420
          *****

1          AGTAGCTGATTGTTATCTGATGGTGGTATTGGTTATTTTTCAGCAAGAGCCAGTGGTG 464
2          AGTAGCTGATTGTTATCTGATGGTGGTATTGGTTATTTTTCAGCAAGAGCCAGTGGTG 479
          *****

1          TGTAAGGTATTTCAGTCCCTGCTCTCCGCTGTAGGCCCTTACATCAAGCCCGAGGGGT 524
2          TGTAAGGTATTTCAGTCCCTGCTCTCCGCTGTAGGCCCTTACATCAAGCCCGAGGGGT 539
          *****

1          GGTACATC--TATAGCAATTCCGAGCGCAAAGGCACTGACTGCACTCCGAGCACTTCATCC 582
2          GGTACATCACATAGCAATTCCGAGCGCAAAGGCACTGACTGCACTCCGAGCACTTCATCC 599
          *****

1          TACTGTGGAATGAAGCATGCTCCATCAACATGCCCTATCTCGGTGCAGTTTTCAGTGGAA 642
2          TACTGTGGAATGAAGCATGCTCCATCAACATGCCCTATCTCGGTGCAGTTTTCAGTGGAA 659
          *****

1          CCACAGCAAGAAAGAGACTGTGACACACGATACTGAAGACCCTCAATGTTTTCAGTAGTG 702
2          CCACAGCAAGAAAGAGACTGTGACACACGATACTGAAGACCCTCAATGTTTTCAGTAGTG 719
          *****

1          TGCCAGCCAGAGCCAGGCCCTGAGCTGGAGCTTTCATCAGGGTTTCTCAGGGTGAGA 762
2          TGCCAGCCAGAGCCAGGCCCTGAGCTGGAGCTTTCATCAGGGTTTCTCAGGGTGAGA 779
          *****

1          TGGTTAAAGTGTGTTGGGGCCCTGATTGCATCATTT----- 800
2          TGGTTAAAGTGTGTTGGGGCCCTGATTGCATCATTTTCCTTTACTTTTCAGGTTTC 839
          *****

1          -----
2          GATGTTGATTGTGACTGTTTCTTACATGCTCAAATGTATGCTGGCTATTATACAGCTAAA 899

1          -
2          C 900

```

1 is the gene sequence of *Pak2a* from ensembl
2 is the query sequence (cloned product)

Figure S3. Screen shot for ClustalW analysis.

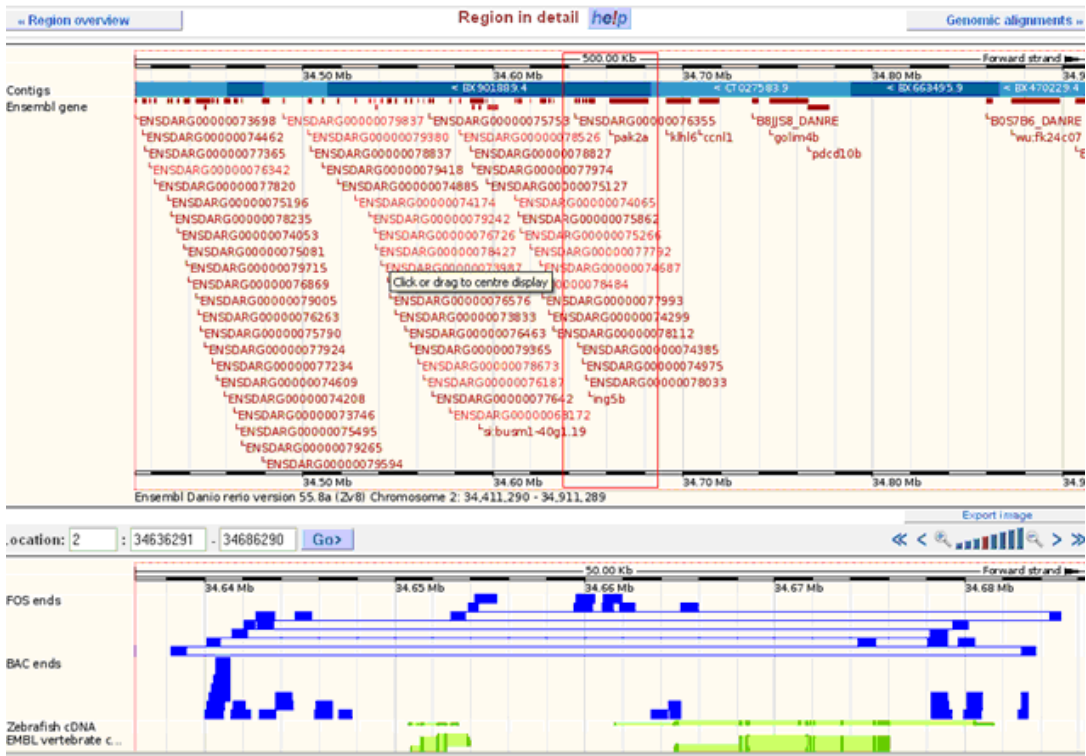


Figure S4. Screen shot for BLAST results of *Pak2a*.

Sequencing results of Rac1/pSS536

>LM334_T7.ab1

GCCATAGCTGTAGTACTTGAGTATTTTACTTGATTACTGTACTTAAGTATTATTTTTGGGGATTTTACTTTACTTGAGTACAATTAATAAATCAATACTTTTACTTTTACTTAATTACATTTTTTTAGAAAAAAAAGTACTTTTACTCCTTACAATTTTATTTACAGTCAAAAAGTACTTATTTTTTTGGAGATCACTTCATTCTATTTCCCTTGCTATTACCAAACCAATTGAATTGCGCTGATGCCCAGTTTAATTTAAATAGATCTGAGCAACAGTTGAAGCGGTCTAAACACAAACTCATTTTTTTAAAGCTTGTAGTATTATCAAACCTTTAAAAAGACATGAAAGTTTTGGATTGTGTTCTCATTTTAAGTGTATAATAAATATATTTATTGCATTTTAATATAATTACGTTATGATTTAAAATACTTATAATGAGACAAAATTTATATGGATTACATGATATTCATTAACACACACTGGATATGCAAGTATGTCACACACTTCTACTTTTTTCTGTGTTTTGTTAAAAATGTAGTTTACATAATAAAAAATAACTCAAAAATAATCTGTTGGGCAGAAAATATTAGTTTAGTAAGTTATCTAGCCAGCACTGTTTACCTGCTGACCTAGAAATGCCCTGTTTTTTTTAGGATGAACGCAGCTCTTCTCCAGTCCATCAGGAGGCAGCAGAGAGTCTGTTTATTGTTCCGGGACGGGACGGGATATATATGTGTGTGCGTGCGGACCGGGATCTGAGATTTTTTTGGGTGGTGGCTGTTTGTTTAACTGGAAGCAGCGGCCGTAATGCGCCGAGAATGCAGGATTCAGCT

>LM334_p1195.ab1

AGGGAAATGTCGATGAGCTTCCTCCATCTTGACCTTAAATCTCATAAACTCTTTGATGACATCCTCGGAGCTGGCCATGGAATTCAGTAGTGCGCGCGCCGCTCTAGACCGCTAGCTGTATCTGTGAATGAATCAATAAAAGCTGCTGTGCCAGAGACACCCGCCCTCACAATTCAACACGCAAAAACAAGAGCGGAGTGCATAGAAGTCGACAGAAAATGAGGAATTTTCGCTCAAACTCGACGGAGAAAAGTTAGCTGGAATCCTGCATTCCGGCGCATTACTGCCGCTGCTTCCAGTTAAACAAACAGCCACCACCCAAAAAATCTCAGATCCCGGTCCGCACGCACACACATATATATCCCGTCCCGTCCCGAACAATAAACAGACTCTCTGCTGCCTCCTGATGGACTGGAGAAGAGCTGCGTTCATCCTAAAAAAACAGGGGCATTTCTAGGTCAGCAGGTAAACAGTGCTGGCTAGATAACTTACTAACTAATATTTTCTGCCAACAGATTATTTTTGAGTTATTTTTATTATGTAAACTACATTTTAACAAAACACAGAAAAAAGTAGAAGTGTGTGACATACTTGCATATCCAGTGTGTGTTAATGAATATCATGTAATCCATATAAATTTTGTCTCATTATAAGTATTTTAAATCATAACGTAATTATATTAATAAATGCAATAAATATATTTATTATAACACTTAAAAATGAGAACACAATCCAAAACTTTCATGTCTTTTTAAAGTTTGATAATACTACAAGCTTTAAAAAAAATGAGTTGTGTTTAGACGCTTCAACTGTTGCTCAGATCTATTTAAATTAACCTGGGCATCAGCGCAATTCAATTGGTTTGTATAGCAGGAAAATAGAATGAAGTATCTCAAAAAATAACGTAATTTTTGACTGTCAATGAAATTGTAGAGTAAAAGTACTTTTTTTTCTAAAAATGTATAGTAAGTAAGTATGATTTTGATTGAACTCAAGTAGGTAAAATCCCAGAAATAATACTAAGTTACGTATCAAGTTAAATACTCAACTACTTTACCCTTGCATCGACTATTGAGTCGAATACAATTACTTGGCCTCGTTACCGCTGACGGACCTGCTCCCTTATTGCTGGAAAAAT

ClustalW analysis of Rac1/pSS536

```

CLUSTAL 2.0.11 multiple sequence alignment

1          CTATCACACTGTTGAGACAGATTCTCAGCAAAGTTACATAACAGGAAAAATTTAATTTGTTT 60
2          -----

1          TGTAAAAATATCAACAACAAAACCAGTTTGGATCGTAATATTTTTATGATGTACAATCT 120
2          -----

1          CAAACCAGACCCTGAAATCTAGTATATTTGAGCAAACAGTTGAAAGCGGTCTAAACACAAA 180
2          -----AGATCTGAGCAA-CAGTTGAAAGCG-TCTAAACACAAA 35
          * * * * *

1          CTCATTTTTT-AAAGCTTGTAAATATTATCAAACCTTTAAAAATAAAAGACATGAAAGTTTTG 239
2          CTCATTTTTTAAAGCTTGTAGTATTATCAAACCTTTAA---AAAGACATGAAAGTTTTG 91
          * * * * *

1          GATAGTGTCTCATTTTAAGTGTATAATAAATATATTTATTGCATTTTTAATAATAATTA 299
2          GATTGTGTTCTCATTTTAAGTGTATAATAAATATATTTATTGCATTTTTAATAATAATTA 151
          * * * * *

1          CGTTACGATTTAAAAATACCTTATAATGAGACAAAAATTTATATGGATTACATGATATTTATT 359
2          CGTTATGATTTAAAAATACCTTATAATGAGACAAAAATTTATATGGATTACATGATATTTATT 211
          * * * * *

1          AAAA---ACTGGATATGCAAGTATGTCACACACTTCTACTTTTTCTGTGTTTTGTTAAA 416
2          AACACACACTGGATATGCAAGTATGTCACACACTTCTACTTTTTCTGTGTTTTGTTAAA 271
          * * * * *

1          AATGTAGTCTACATAAATAAAAAATAACTCAAAAAATAATCCGTTGGGCAGAAATATATTAGTT 476
2          AATGTAGTTTACATAAATAAAAAATAACTCAAAAAATAATCTGTTGGGCAGAAATATATTAGTT 331
          * * * * *

1          TAGTAAAGTTATCTAGCCAGCACTGTTTACCTGCTGACCTAGAAATGCCCCCTGTTTTTTTA 536
2          TAGTAAAGTTATCTAGCCAGCACTGTTTACCTGCTGACCTAGAAATGCCCCCTGTTTTTTTA 391
          * * * * *

1          GGCTGAACGCAGCTCTTCTCCAGTCCATCAGGAGGCAGCAGAGAGTCTGTTTATTGTTCC 596
2          GGATGAACGCAGCTCTTCTCCAGTCCATCAGGAGGCAGCAGAGAGTCTGTTTATTGTTCC 451
          * * * * *

1          GGACGGGACGGGATATATATGTGTGTGCGTGCGGACCGGGATCTGAGATTTTTTGGGTGG 656
2          GGACGGGACGGGATATATATGTGTGTGCGTGCGGACCGGGATCTGAGATTTTTTGGGTGG 511
          * * * * *

1          TGGCTGTTTGTTTAACTGGAAGCAGCGGCAGTAAATGCGCCGGAATGCAGGATTCCAGCT 716
2          TGGCTGTTTGTTTAACTGGAAGCAGCGGCAGTAAATGCGCCGGAATGCAGGATTCCAGCT 571
          * * * * *

1          AACTTTTCTCCGTCGAGTTTGAGCGAAATTCCTCATTTTCTGTGCGACTTCTATCGACTCC 776
2          AACTTTTCTCCGTCGAGTTTGAGCGAAATTCCTCATTTTCTGTGCGACTTCTATCGACTCC 631
          * * * * *

1          GCTCTGTTTTGCGTGTGAAATTGTGAGGGCGGGTGTCTCTGGCACAGCAGCTTTTATTG 836
2          GCTCTGTTTTGCGTGTGAAATTGTGAGGGCGGGTGTCTCTGGCACAGCAGCTTTTATTG 691
          * * * * *

1          ATTCATTCACAGATACAGCTAGCGGGATAGCGTGCTAAAACGAACACAGATGCAGGCCATA 896
2          ATTCATTCACAGATACAGCTAGCGGGATAGCGTGCTAAAACGAACACAGATGCAGGCCATA 722
          * * * * *
    
```

1 is gene sequence of *Rac1* from ensembl
 2 is the query sequence (cloned product)

Figure S5. Screen shot for ClustalW analysis.

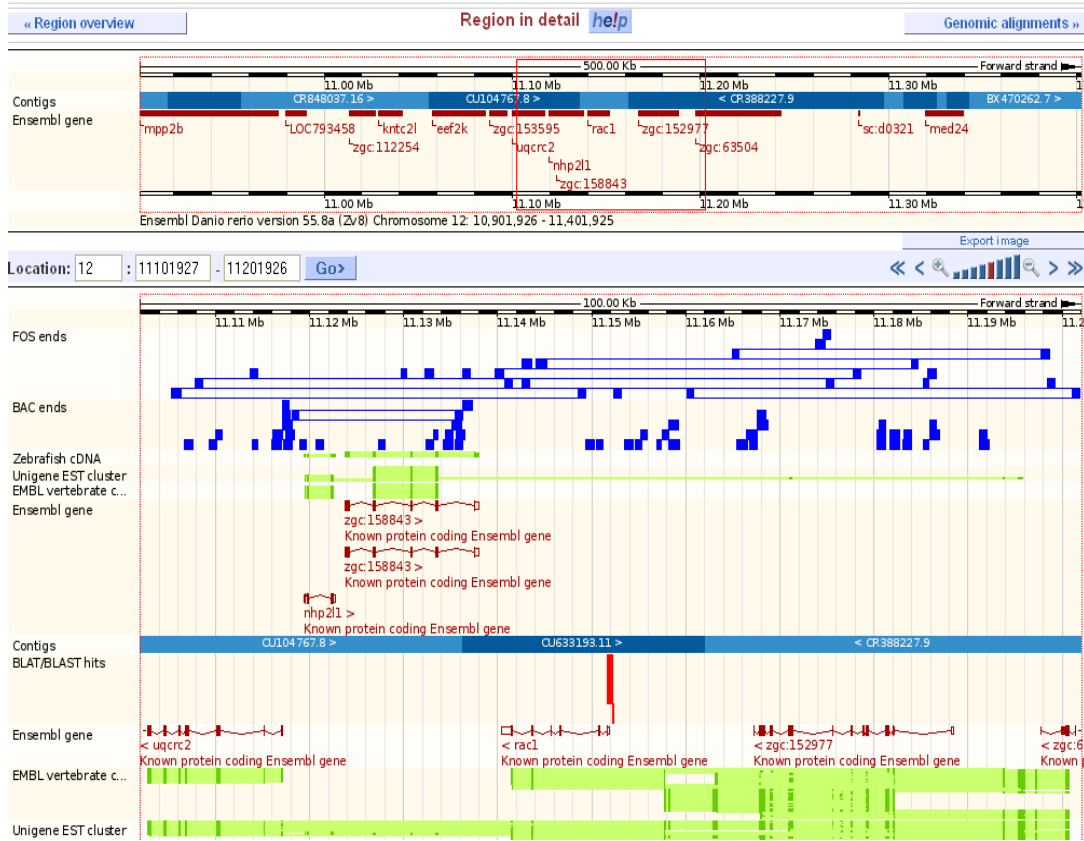


Figure S6. Screen shot for BLAST results of *Rac1*.

Sequencing results of Cdc42/pSS536

>LM335_T7.ab1

CCGGAGTCAGGCAGAGTGTAGTACTTGAGTATTTTACTTGATTACTGTACTTAAGTATTATTTTTGGGGATTTTACTTTA
CTTGAGTACAATTAATAAATCAATACTTTTACTTTTACTTAATTACATTTTTTTAGAAAAAAAAGTACTTTTACTCCTTAC
AATTTTATTTACAGTCAAAAAGTACTTATTTTTTTGGAGATCACTTCATTCTATTTTCCCTTGCTATTACCAAACCAATTGA
ATTGCGCTGATGCCAGTTTAATTTAAATAGATCTGGCCATCTAGACTTCGCATATGCGCATCTTCTCCTTGAATTGTCTT
ATCCATTTACTTCTTATCGTGAGAAATACAATGTGTGGCGTGCAGTTTTTAAATGCGTGTGATTGTGAATGTGTGAAT
GAGAGCCTGAATTATGTAGATATTTTTGGCGGGTGTGTTTGTGCACCCATGTTATTTCAAAGAGCACAGCATTCTCCGA
GTTCTTATTTTCTTGCTGACGCTGCCATGTTGTTTGTGAGTGTCTATGGCAAATCGGGGGGGGGACTATGGGACCGTGT
AGGGAGCGTCTGTATTAGGGTAAAACCAATTTACATTTCGAATAAATCGATGTAAACTTCAACTGAGTTAAATCAA
ACCAGCCCAAGTTGACAGTTTCTTAATATATTTAGGAGAATTGTTTTATTCTTAAAATCTGTATTAATTCATTGTTTTAAA
ACTAAATATGGGACATTTAGTCCATCTATTTTTGAGCCACGTTATTATTGCTTTCCCTCCCGGTGTTTTGTCCCTGTACAC
TGGTGCTTCCACACTGACACACACACACACACATGACAGTTAGTGG

>LM335_p1195.ab1

GGAATTTTCGTTGAGCTTCCTCCATCTTGACCTTAAATCTCATAAACTCTTTGATGACATCCTCGGAGCTGGCCATGGAA
TTCCTAGTGCAGCGCGGCCGCTCTAGACGTTGGTACATATTCGGAGGGGAATTTATTAGTTGTATAGGAGATTAATAGA
CAGGTTTTACCCTGACCCATCACCAACAACGACGCACCTTGATCGTCTGCATAGCTGTGCTTTTATAAATCCACTGCTC
TCATTCAAGATCTGCAAAGAAAAACAAGAGCGTTCACACAGGAGAAACATTACTCGGTCATAGCTGGCTCTTCGGTCTC
AAGTTCAAAGGTGTAAATAGACCCACTATAACACGTGGCATTACACAACACCTCCATGTCCACTACTGTCATGTGTGT
GTGTGTGTGTGTGTGTGAAGCAACAGTGTACAGGACAAACACCGGAGGAAAGCAATAATAACGTGGCTCAAAAATA
GATGGACTAAATGTCCATATTTAGTTTTTAAAACAATGAATTAATACAGATTTAAGAATAAAAACAATTCTCCTAAATATAT
TAAGAAACTGTCAACTTGGGCTGGTTTTGATTTAACTCAAGTTGAAGTTTACATCGATTTATTTCGAATGTAAATGGTTT
TCACCCTAATACACGACGCTCCCTAACACGGTCCCATAGTCCCCCCCCGATTTGCCATAGAAACACTCAAACAACATG
GCAGCGTCAGCAAGAAAATAAGAACTCGGAGAAATGCTGTGCTCTTTGAAATAACATGGGTGCACAAACACACCCGCC
AAAAATATCTACATAATTCAGGCTCTCATTACACATTCAACAATCAAACACGCATTTAAAAACTGCACGCCACACATTG
TATTTCTCACGATAAGAAGTAAATGGATAGACAATTCAAGGAGAAGATGCGCATATGCGAAGTCTAGATGGCCAGATC
TATTTAAATTAACCTGGGCATCAGCGCAATTCAGTTGGTTTGGTAATAGCAAGGAAAATAGAATGAGTGATCTCCAAAA
TAAGTACTTTTTGACTGTAAATAAACTTGTAAACGAGTAAAAGTACTTTTTTTTTCTAAAAAATGTATTAGGTAAAAGTA
AGTATTGATTTTATTGTACTCAGTTAGTAAATCCAAAATAATATCTAAGGTACGGTATTTCAGTAAATACTCCAGTACCTT
ACCTTGCCATTCCCTTATGTGAGTGGTATCAAATTCCTGGCGCGCC

ClustalW analysis of Cdc42/pSS536

```

CLUSTAL 2.0.11 multiple sequence alignment

1          AATTGCGTTC AATAGAGGAAAGCTAGTTTTTTTTTTTACAAAAGCCATT TAAAAAGTAC 60
2          -----

1          GTATTTAGAGCAGTAATTACAATACC GTGAAACTGTGAT TATTTTCTTATCCAAGGTT 120
2          -----

1          AT TATAC CAGCCCATGCCTA TCTTCCCATATGCGCATCTCTCCCTTGAAATTGTCATATC 180
2          -----GGC CAT--CTAGACTTCCCATATGCGCATCTCTCCCTTGAAATTGTC-TATC 48
                * **** *

1          CATTTAC TTC TTATCAT GAGAAATACAATG TGTGGCCTGCCAGTTT- AAATGCCGTGTTG 239
2          CATTTAC TTC TTATCCT GAGAAATACAATG TGTGGCCTGCCAGTTT TAAATGCCGTGTTG 108
                *****

1          ATTCTGAATG TGTGAAT GAGAGCCCTGAATTATGTAGATTTT TTTCGCCGGGTGCTTTGTC 299
2          ATTCTGAATG TGTGAAT GAGAGCCCTGAATTATGTAGATAT TTTCGCCGGGTGCTTTGTC 168
                *****

1          CACCCATGTTATTTCAAAGAGCCGACGATTTC TCCGAGTTCTTATTTGCTCGCTGACGCT 359
2          CACCCATGTTATTTCAAAGAGCAGCAGCATTTC TCCGAGTTCTTATTTTCTTGCTGACGCT 228
                *****

1          GCCATGTTGTTGAGTGTTTCTATGCGCAAATCGGGGGGGA-ACAA TGCGGACCCTGTTAGC 418
2          GCCATGTTGTTGAGTGTTTCTATGCGCAAATCGGGGGGGA-ACAA TGCGGACCCTGTTAGC 288
                *****

1          GAGCGTCTGCTATTAGCGTCAAAAACAATTTCATTCGAA TAAATCGATT TAAACTTCAA 478
2          GAGCGTCTGCTATTAGCGTCAAAAACAATTTCATTCGAA TAAATCGATT TAAACTTCAA 348
                *****

1          CTTGAGT TAAATCAAACCAAGCCCAAGTTGACAGTTTCTTAA TATATTTAGGAGAAT TGT 538
2          CTTGAGT TAAATCAAACCAAGCCCAAGTTGACAGTTTCTTAA TATATTTAGGAGAAT TGT 408
                *****

1          TT TATTTTAAATCTCTATTAA TTCAT TGT TTTAAACTAAA TATGGACATT TAGTCCAT 598
2          TT TATTC TAAATCTCTATTAA TTCAT TGT TTTAAACTAAA TATGGACATT TAGTCCAT 468
                *****

1          CTATTTT TGAGCCACCTTAT TATTGCTTTCCTCCGCTGTT TGTCCGTGACACTGT TGCCT 658
2          CTATTTT TGAGCCACCTTAT TATTGCTTTCCTCCGCTGTT TGTCCGTGACACTGT TGCCT 528
                *****

1          CACACACACACACACACACA --- -TGACAGTAGTGCACATGCAGCTCTTCTGTAAATGC 712
2          CACACACACACACACACACACA --- -TGACAGTAGTGCACATGCAGCTCTTCTGTAAATGC 588
                *****

1          CACGCTTATAGTGGCTCTATT TACACCTTTGAACTTGAGACCGAAGAGCCAGCTATGA 772
2          CACGCTTATAGTGGCTCTATT TACACCTTTGAACTTGAGACCGAAGAGCCAGCTATGA 648
                *****

1          ACGAGTAAATGTTTCTCC TGTGTGAAAGCTCTTGT TTTCTTTCCAGATCTTGAATGAGAG 832
2          ACGAGTAAATGTTTCTCC TGTGTGAAAGCTCTTGT TTTCTTTCCAGATCTTGAATGAGAG 708
                *****

1          CAGTGGATTTATAAAAGCACAGCTATGCAGACGATCAAGTCCGTCCTTGT TGTGATGCT 892
2          CAGTGGATTTATAAAAGCACAGCTATGCAGACGATCAAGTCCGTCCTTGT TGTGATGCT 768
                *****

1          GCAGTGGTAAAACC TGTCTAT TAAATC TCC TATACA ACTAATAAATCCCTCCGAAATAT 952
2          GCAGTGGTAAAACC TGTCTAT TAAATC TCC TATACA ACTAATAAATCCCTCCGAAATAT 828
                *****

1          GTACCAAGCTGAGTACAGCTT TCCGGTTCATTTCCGATTCTCTTACATAAAGTCATGCC 1012
2          GTACCAAGCTGAGTACAGCTT TCCGGTTCATTTCCGATTCTCTTACATAAAGTCATGCC 837
                *****

```

1 is gene sequence of *cdc42* from Ensembl
2 is the query sequence (cloned product)

Figure S7. ClustalW analysis.

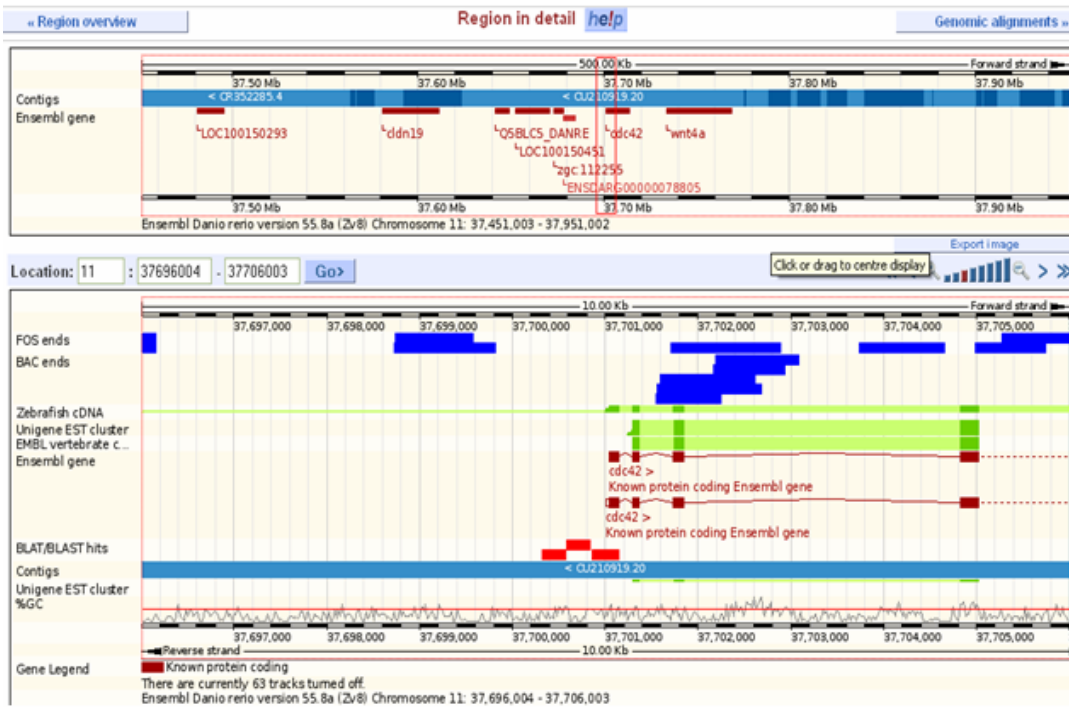


Figure S8. Screen shot for BLAST results of *Cdc42*.