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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
TGAGTACAATTAAAAATCAATACTTTTACTTTTACTTAATTACATTTTTTTAGAAAAAAAAGTACTTTTTACTCCTTACAA
TTTTATTTACAGTCAAAAAGTACTTATTTTTTGGAGATCACTTCATTCTATTTTCCCTTGCTATTACCAAACCAATTGAAT
TGCGCTGATGCCCAGTTTAATTTAAAT**AGATCT**GCAGGTTTAAACGAATTCGCCCTTCATCCCTCAAATCTCTCATTCAC
GTCCCCCTCCCCATCTGCACACTTTATCTCATTTTCCACCCTGCTGGAATCTGAGCACTTGTGCAGTTATCAGGGCTCCTG
TATTTAGGAGGCTCTGGGTGTCCATGTAGGGGACGAACAGAAACACTGCAGACCTTTATAGAAGAACAAATGATAAGA
GTCCTCATACATAAAGACTCCATTAGAAACGTCAGTGACCCAGGAGCCCAGACCAACAGCAAAGCAGACAGTGAACAT
GGTGAGTAGACAAAGCAAGGGCGAATTCCGGCCGCTAAAT**AGATCT**GGCCA**TCTAGA**GCGGCCGCGCGCACTAGTGAA
TTCCATGGCCAGCTCCGAGGATGTCATCAAAGAGTTTATGAGATTTAAGGTCAAGATGGAGGGAAGCGTCAACGGACA
CGAGTTCGAGATTGAGGGAGAAGGAGAAGGCCGGCCTTACGAGGGCACACAAACCGCTAAGCTCAAGGTCACAAAAG
GAGGACCCCTCCCCTTCTCCTGGGATATTCTGAGCCCTCAGTTCCAGTACGGAAGCAAAGCCTATGTTAAACACCCTGCC
GACATCCCTGACTATCTGAAGCTCTCCTTCCCTGAAGGCTTCAAGTGGGAGAGATTCATGAACTTCGAGGACGGAGGCG
TGGTGACAGTCACACAAGATAGCACCCTCCAGGACGGAGAGTTTATTTATAAGTGAAACTCAGAGGACCAACTTCCCCT
CCGATGGCCCTGTCATGCAAAAAAACATGGGATGGCAGCTCCACCGAAAGATGTATCCTGAAGATGCGCTCTGAAGGC
GAATTAAATGAGACTGAAACTCAAGACGGAGGACTACCGATGCGAGTCAAACA

Clone 2, I.D.:LM_304 sequencing results with SSB-P1195
>LM304_p1195.ab1
GGGATTGTCGTTGAGCTTCCTCCATCTTGACCTTAAATCTCATAAACTCTTTGATGACATCCTCGGAGCTGGCCATGGAA
TTCACTAGTGCGCGCGGCCGC**TCTAGA**TGGCC**AGATCT**ATTTAGCGGCCGGAATTCGCCCTTGCTTTGTCTACTCACCAT
GTTCACTGTCTGCTTTGCTGTTGGTCTGGGCTCCTGGGTCACTGACGTTTCTAATGGAGTCTTTATGTATGAGGACTCTTA
TCATTTGTTCTTCTATAAAGGTCTGCAGTGTTTCTGTTCGTCCCCTACATGGACACCCAGAGCCTCCTAAATACAGGAGC
CCTGATAACTGCACAAGTGCTCAGATTCCAGCAGGGTGGAAAATGAGATAAAGTGTGCAGATGGGGAGGGGGACGTGA
ATGAGAGATTTGAGGGATGAAGGGCGAATTCGTTTAAACCTGC**AGATCT**ATTTAAATTAAACTGGGCATCAGCGCAATT
CAATTGGTTTGGTAATAGCAAGGGAAAATAGAATGAAGTGATCTCCAAAAAATAAGTACTTTTTGACTGTAAATAAAAT
TGTAAGGAGTAAAAAGTACTTTTTTTTCTAAAAAAATGTAATTAAGTAAAAGTAAAAGTATTGATTTTTAATTGTACTCA
AGTAAAGTAAAAATCCCCAAAAATAATACTTAAGTACAGTAATCAAGTAAAATTACTCAAGTACTTTACACCTCTGGGC
CCAATTCGCCCTATAGTGAGTCGTATTACAATTCACTGGCCGTCGTTTTACAACGTCGTGACTGGGAAAACCCTGGCGTT
ACCCAACTTAATCGCCTTGCAGCACATCCCCCTTTCGCCAGCTGGCGTAATAGCGAAGAAGGCCCGCACCGATCGCCCT
TCCCAACAGTTGCGCAGCCTTGAATGGCGAATGGACGCGCCCTGTAGCGGGCGCATTAAGCGCGCGGGTGTGGTGGTTT
ACGCGCAGCGTGAACGCTACACTTTGCAGCGCCCTAGCGCCCGCTCATTCGCTTTCCTTCCCTCCTTTCTCGCCACGTCG
CAGGCTTCCCGGTCAGCTCTAATCGGGGCTCCCTTAGTCGATTATGCTACCGACCTTGACAAAAACCTGAATAAGGTTA
ATGGTCAGCAGGTGAGATG

ClustalW analysis for Cmlc2

```
CLUSTAL 2.0.11 multiple sequence alignment


1               TGCAGGTTTAAACGAATTCGCCCTTCATCCCTCAAATCTCTCATTCACGTCCCCCTCCCC 60
2               -----ATGCATTCATCCATCCTTTTCATCCCTCAAATCTCTCATTCACGTCCCCCTCCCC 55
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1               ATCTGCACACTTTATCTCATTTTCCACCCTGCTGGAATCTGAGCACTTGTGCAGTTATCA 120
2               ATCTGCACACTTTATCTCATTTTCCACCCTGCTGGAATCTGAGCACTTGTGCAGTTATCA 115
                ************************************************************

1               GGGCTCCTGTATTTAGGAGGCTCTGGGTGTCCATGTAGGGGACGAACAGAAACACTGCAG 180
2               GGGCTCCTGTATTTAGGAGGCTCTGGGTGTCCATGTAGGGGACGAACAGAAACACTGCAG 175
                ************************************************************

1               ACCTTTATAGAAGAACAAATGATAAGAGTCCTCATACATAAAGACTCCATTAGAAACGTC 240
2               ACCTTTATAGAAGAACAAATGATAAGAGTCCTCATACATAAAGACTCCATTAGAAACGTC 235
                ************************************************************

1               AGTGACCCAGGAGCCCAGACCAACAGCAAAGCAGACAGTGAACATGGTGAGTAGACAAAG 300
2               AGTGACCCAGGAGCCCAGACCAACAGCAAAGCAGACAGTGAACATGGTGAGTAGACAAAG 295
                ************************************************************

1               CAAGGGCG----AATTCCGGCCGCTAAATAGATCTGG----------- 333
2               CTATACTTTTTTGGTTTTGAATATAATATTAATGTGAAAATAAAAAGC 343
                * *           **  *      * **  ** **
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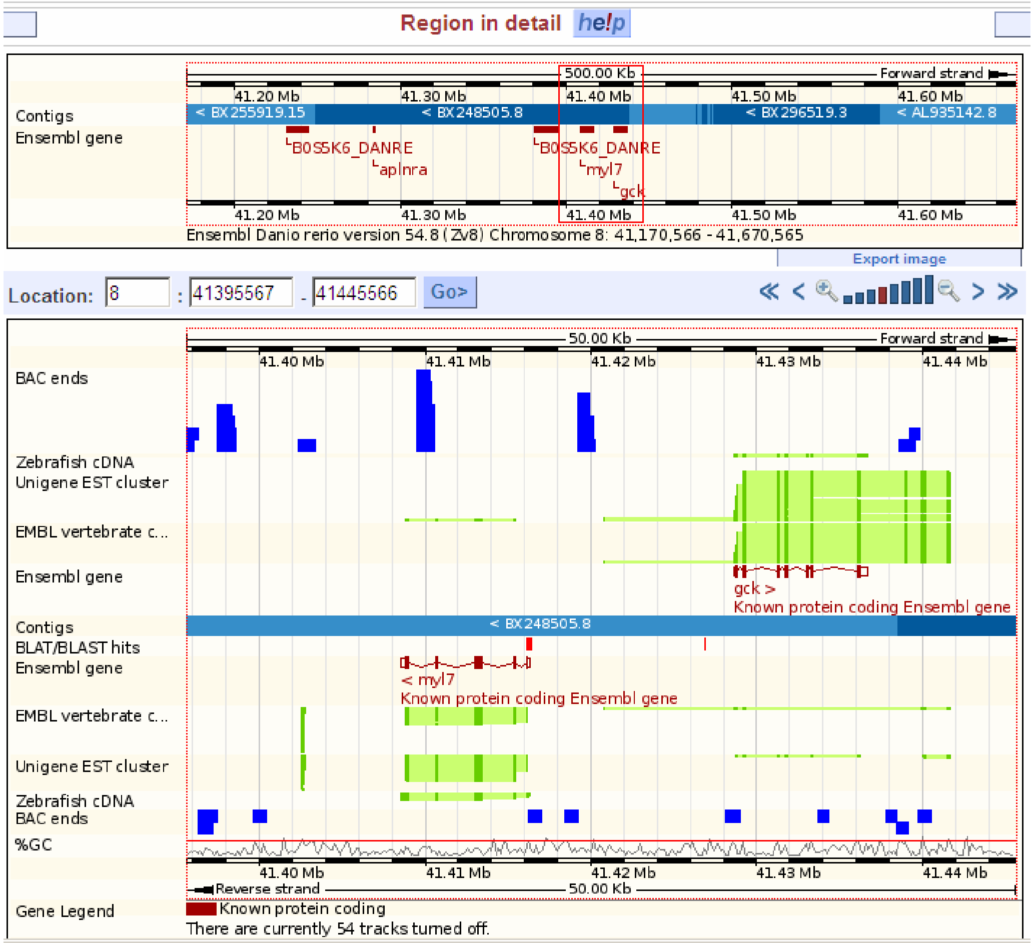
1 is the *cmlc2* gene sequence from Ensembl
2 is the query sequence (cloned product)

Figure S1. Screen shot of ClustalW analysis.



Ensembl Danio rerio version 54.8 (Zv8) Chromosome 8: 41,170,566 - 41,670,565

Location: 8 : 41395567 - 41445566

There are currently 54 tracks turned off.

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

Sequencing results for Pak2a/pSS536

>LM314_T7.ab1
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AGTCAAAAAGTACTTATTTTTTGGAGATCACTTCATTCTATTTTCCCTTGCTATTACCAAACCAATTGAATTGCGCTGATGC
CCAGTTTAATTTAAAT**AGATCT**AGTACCTCGAGGCTGTGAGATTCATGAAAGCAGTAGACTAACTATTTCTGATGCAGAAA
CCCGAAACTCAGGCTCTCAAGAAAAAAAAAAATCTTCTGAAATGGACCATGTAGAAGTGCGTTTAAGCCTATAAAACACTG
TGTGCTTGAAGAGAGCCACTCCCATCTCAAATCACTGTCATTACGGGGAAAACAAGTTGAGACTTGATTATTCCAAATAAC
ATTCCTTAAGGAAAAATGGAAAACCTTTGACTGAAATCAGTAAATATCTGGCAGTCAGTGTAGCGTTATTCAGTACAGAA
AGAAGATATAAAAATTAGTTATACCTACAATTCTTGAGAAATTGTGATGTTAAAAGGCTCTAATCAAGCTCTTAAAACACC
TCCTATAATCCTGCTACATTCCTAGTAGTGTGATTGTTATGTGATGGTGGTGATTGGTTATTTTTGAGCAAGAGGCAGTGGT
GTGTAAAGGTATTTTTGGTCCTGTGTTCCCGCTGTAGGGCCTTACATCAAGCCCGAGGGGTGGTAC

>LM314_p1195.ab1
AAGGACTGTCGTTGAGCTTCCTCCATCTTGACCTTAAATCTCATAAACTCTTTGATGACATCCTCGGAGCTGGCCATGGA
ATTCACTAGTGCGCGCGGCCGC**TCTAGA**AATGATGCAATCAGCGCCCAACGACATCACTTTAACCATCTCACCCTGAGG
AACCCTGATGGAAAGCTCCAGCTCACAGCCCTGGCTCTGGTCTGGCACACTACTGAAACATTGAGGGTCTTCACTATCG
TGTGTCCACAGTCTCTTTCTTCCTGTGCTTCCACTGAACTGCACCGAGATAGAGGCATGTTGATGCAGGCATGCTTCATT
CCACAGTAGGATGAACTGCTGCGAGTGCAGTCATGCCTTTGCGCTGCGAATTGCTATAGATGTACCACCCCTCGGGCTT
GATGTAAGGCCCTACAGCGGAGACACAGGACTGAAAATACCTTTACACACCACTGCCTCTTGCTCAAAAATAACCAATC
ACCACCATCACATAACAATCACACTACTAGGAATGTAGCAGGATTATAGGAGGTGTTTTAAGAGCTTGATTAGAGCCTT
TTAACATCACAATTTCTCAAGAATTGTAGGTATAACTAATTTTTATATCTTCTTTCTGTACTGAATAACGCTACACTGACT
GCCAGATATTTACTGATTTCAGTCAAAGGTTTTCCATTTTTCCTTAAGGAATGTTATTTGGAATAATCAAGTCTCAACTTG
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TACATGGTCCATTTCAGAAGATTTTTTTTTTCTTGAGAGCCTGAGTTTCGGGTTTCTGCATCAGAAATAGTTAGTCTACTG
CTTTCATGAATCTCACAGCCTCGAAGTACT**AGATCT**ATTTAAATTAAACTGGGCATCAGCGCATTCAATTGGTTTGGTAA
TAGCAAGGGAAAATAAAATGAAGTGATCTCAAAAAATAAGTACTTTTTGACTGTAAATAAAATTGTAAGGAGTAAAAG
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CGATATACATTACGTGGGGCGGCGTTCAAGGCTTGGACTGAAAACGTGGTATACCATAATCGCTGGGAGCCA

ClustalW analysis of Pak2a/pSS536

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CLUSTAL 2.0.11 multiple sequence alignment


1               ------------AGTACTTCGAGGCTGTGAGATTCATGAAAGCAGTAGACTAACTATTTC 48
2               AGTTGTGGAATCAGTACCTCGAGGCTGTGAGATTCATGAAAGCAGTAGACTAACTATTTC 60
                            ***** ******************************************

1               TGATGCAGAAACCCGAAACTCAGGCTCTCAAGAAAAAAAAAATCTTCTGAAATGGACCAT 108
2               TGATGCAGAAACCCGAAACTCAGGCTCTCAAGAAAAAAAAAATCTACTGAAATGGACCAT 120
                ********************************************* **************

1               GTAGAAGTGCGTTTAAGCCTATAAAACACTGTGTGCTTGAAGAGAGCCACTCCCATCTCA 168
2               GTAGAAGTGCGTTTAAGCCTATAAAACACTGTGTGCTTGAAGAGAGCCACTCCCATCTCA 180
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1               AATCACTGTCATTACGGGGAAAACAAGTTGAGACTTGATTATTCCAAATAACATTCCTTA 228
2               AATCACTGTCATTATGGGGAAAACAAGTTGAGACTTGATTATCCCAAATAACATTCCTTG 240
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1               AGGAAAAATGGAAAACCTTTGACTGAAATCAGTAAATATCTGGCAGTCAGTGTAGCGTTA 288
2               AGAAAAAATGGAAAACCTTTGACTAAAATCAGTAAATATCTGGACGTCAGTGTAGCGTTA 300
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1               TTCAGTACAGAAAGAAGATATA----AAAATTAGTTATACCTACAATTCTTGAGAAATTG 344
2               TTCAGTACAGAAAGAAGATATACTCCAAAACTAGTTATACCTACAATTCTCGAGAAATTG 360
                **********************    **** ******************* *********

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2               TGATGTTAAAATGCTCTAATCAAGCTCTTAAAACACCTCCTATAATCCTGCTTCATTCCT 420
                *********** **************************************** *******

1               AGTAGTGTGATTGTTATGTGATGGTGGTGATTGGTTATTTTTGAGCAAGAGGCAGTGGTG 464
2               AGTAGTGTGATTGTTATGTGATGGTGGTGATTAGTTATTTT-GAGCAAGAGGCAGTGGTG 479
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1               TGTAAAGGTATTTTCAGTCCTGTGTCTCCGCTGTAGGGCCTTACATCAAGCCCGAGGGGT 524
2               TGTAAAGGTATTTTCAGTCCTGTGTCTCCGCTGTAGGGCCTTACATCAAGCCCGAGGGGT 539
                ************************************************************

1               GGTACATC--TATAGCAATTCGCAGCGCAAAGGCATGACTGCACTCGCAGCAGTTCATCC 582
2               GGTACATCACTATAGCAATTCGCAGCGCAAAGGCATGACTGCACTCGCAGCAGTTCATCC 599
                ********  **************************************************

1               TACTGTGGAATGAAGCATGCCTGCATCAACATGCCTCTATCTCGGTGCAGTTCAGTGGAA 642
2               TACTGTGGAATGAAGCATGCCTGCATCAACATGCCTCTATCTCGGTGCAGTTCAGTGGAA 659
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1               GCACAGGAAGAAAGAGACTGTGGACACACGATAGTGAAGACCCTCAATGTTTCAGTAGTG 702
2               GCACAGGAAGAAAGAGACTGTGGACACACGATAGTGAAGACCCTTAATGTTTCAGTAGTG 719
                ******************************************** ***************

1               TGCCAGACCAGAGCCAGGGCTGTGAGCTGGAGCTTTCCATCAGGGTTCCTCAGGGTGAGA 762
2               TGCCAGACCAGAGCCAGGGCTGTGAGCTGGAGCTTTCCATCAGGGTTCCTCAGGGTGAGA 779
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1               TGGTTAAAGTGATGTCGTTGGGCGCTGATTGCATCATT---------------------- 800
2               TGGTTAAAGTGATGTCGTTGGGCGCTGATTGCATCATTTTCCTTTACTTTTTGGAGTTTC 839
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1               ------------------------------------------------------------
2               GATGTTGATTGTGACTGTTTCTTACATGCTCAAATGTATGGTGGCTATTATACAGCTAAA 899


1               -
2               C 900
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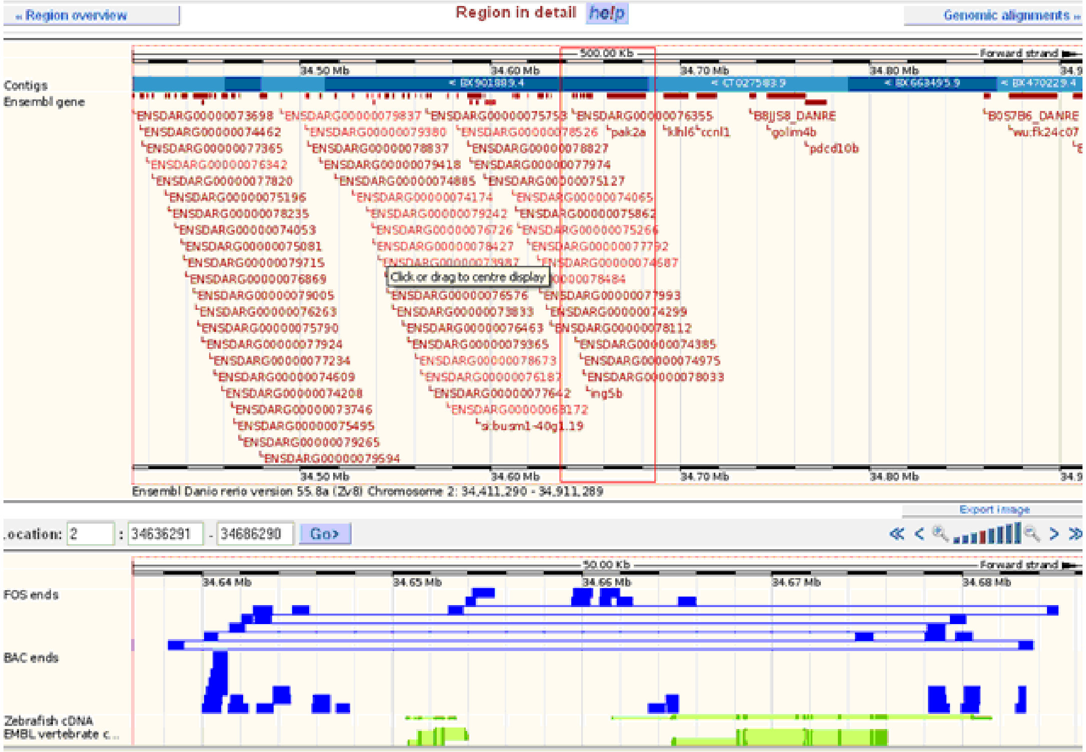
1 is the gene sequence of *Pak2a* from ensembl
2 is the query sequence (cloned product)

Figure S3. Screen shot for ClustalW analysis.



Ensembl Danio rerio version 55.8a (Zv8) Chromosome 2: 34,411,290 - 34,911,289

Location: 2 : 34636291 - 34686290

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

Sequencing results of Rac1/pSS536

>LM334_T7.ab1
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TTACAGTCAAAAAGTACTTATTTTTTGGAGATCACTTCATTCTATTTTCCCTTGCTATTACCAAACCAATTGAATTGCGCT
GATGCCCAGTTTAATTTAAAT**AGATCT**GAGCAACAGTTGAAGCGGTCTAAACACAAACTCATTTTTTTAAAGCTTGTAGT
ATTATCAAACTTTAAAAAGACATGAAAGTTTTGGATTGTGTTCTCATTTTAAGTGTTATAATAAATATATTTATTGCATTT
TTAATATAATTACGTTATGATTTAAAATACTTATAATGAGACAAAATTTATATGGATTACATGATATTCATTAACACACA
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AAAATAATCTGTTGGGCAGAAAATATTAGTTTAGTAAGTTATCTAGCCAGCACTGTTTACCTGCTGACCTAGAAATGCCC
CTGTTTTTTTAGGATGAACGCAGCTCTTCTCCAGTCCATCAGGAGGCAGCAGAGAGTCTGTTTATTGTTCGGGACGGGAC
GGGATATATATGTGTGTGCGTGCGGACCGGGATCTGAGATTTTTTGGGTGGTGGCTGTTTGTTTAACTGGAAGCAGCGG
CCGTAAATGCGCCGAGAATGCAGGATTCAGCT

>LM334_p1195.ab1
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AATTCACTAGTGCGCGCGGCCGC**TCTAGA**CCGCTAGCTGTATCTGTGAATGAATCAATAAAAGCTGCTGTGCCAGAGAC
ACCCGCCCTCACAATTCAACACGCAAAACAAGAGCGGAGTCGATAGAAGTCGACAGAAAATGAGGAATTTCGCTCAAA
CTCGACGGAGAAAAGTTAGCTGGAATCCTGCATTCCGGCGCATTTACTGCCGCTGCTTCCAGTTAAACAAACAGCCACC
ACCCAAAAAATCTCAGATCCCGGTCCGCACGCACACACATATATATCCCGTCCCGTCCCGAACAATAAACAGACTCTCT
GCTGCCTCCTGATGGACTGGAGAAGAGCTGCGTTCATCCTAAAAAAACAGGGGCATTTCTAGGTCAGCAGGTAAACAGT
GCTGGCTAGATAACTTACTAAACTAATATTTTCTGCCCAACAGATTATTTTTGAGTTATTTTTATTATGTAAACTACATTT
TTAACAAAACACAGAAAAAAGTAGAAGTGTGTGACATACTTGCATATCCAGTGTGTGTTAATGAATATCATGTAATCCA
TATAAATTTTGTCTCATTATAAGTATTTTAAATCATAACGTAATTATATTAAAAATGCAATAAATATATTTATTATAACA
CTTAAAATGAGAACACAATCCAAAACTTTCATGTCTTTTTAAAGTTTGATAATACTACAAGCTTTAAAAAAATGAGTTTG
TGTTTAGACGCTTCAACTGTTGCTC**AGATCT**ATTTAAATTAAACTGGGCATCAGCGCAATTCAATTGGTTTGTATAGCAG
GGAAAATAGAATGAAGTGATCTCAAAAAATAACGTACTTTTTGACTGTCAATGAAATTGTAGAGTAAAAGTACTTTTTT
TTTCTAAAAATGTATAGTAAGTAAGTATGATTTTGATTGAACTCAAGTAGGTAAAATCCCAGAAATAATACTAAGTTAC
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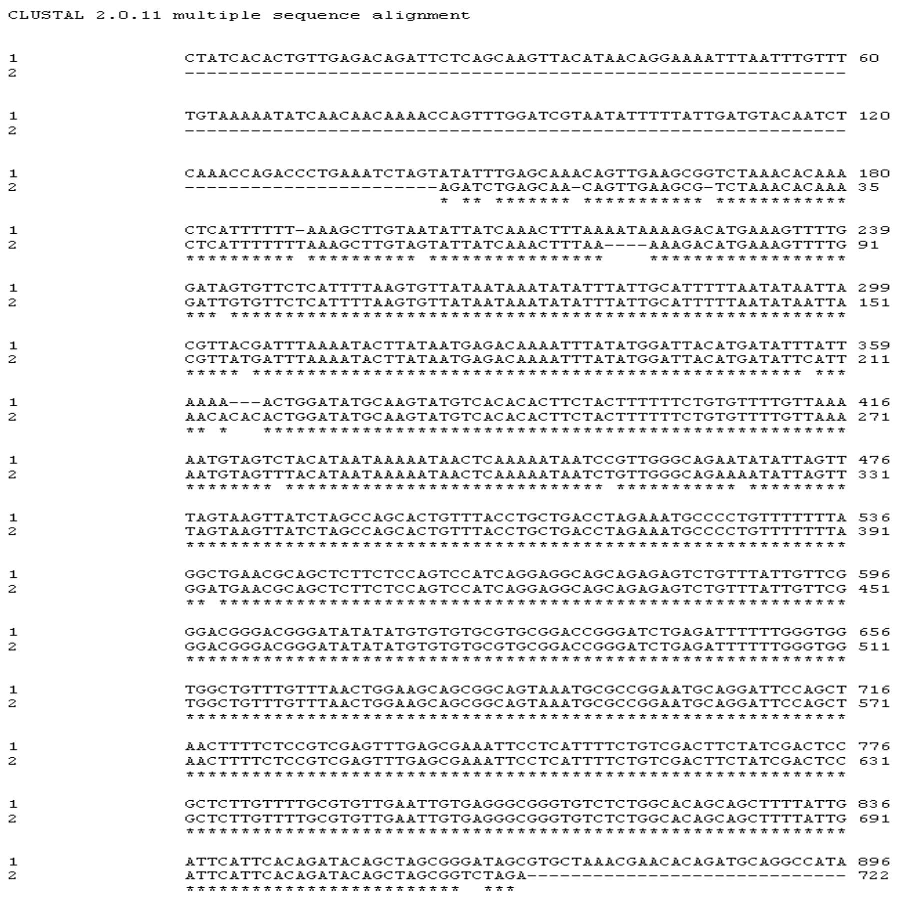
ClustalW analysis of Rac1/pSS536



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CLUSTAL 2.0.11 multiple sequence alignment


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2            ------------------------------------------------------------


1            CAAACCAGACCCTGAAATCTAGTATATTTGAGCAAACAGTTGAAGCGGTCTAAACACAAA 180
2            -----------------------AGATCTGAGCAA-CAGTTGAAGCG-TCTAAACACAAA 35
                                    * ** ******* *********** ************

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2            CTCATTTTTTTAAAGCTTGTAGTATTATCAAACTTTAA----AAAGACATGAAAGTTTTG 91
             ********** ********** ****************    ******************

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2            GATTGTGTTCTCATTTTAAGTGTTATAATAAATATATTTATTGCATTTTTAATATAATTA 151
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1            CGTTACGATTTAAAATACTTATAATGAGACAAAATTTATATGGATTACATGATATTTATT 359
2            CGTTATGATTTAAAATACTTATAATGAGACAAAATTTATATGGATTACATGATATTCATT 211
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1            AAAA---ACTGGATATGCAAGTATGTCACACACTTCTACTTTTTTCTGTGTTTTGTTAAA 416
2            AACACACACTGGATATGCAAGTATGTCACACACTTCTACTTTTTTCTGTGTTTTGTTAAA 271
             ** *   *****************************************************

1            AATGTAGTCTACATAATAAAAATAACTCAAAAATAATCCGTTGGGCAGAATATATTAGTT 476
2            AATGTAGTTTACATAATAAAAATAACTCAAAAATAATCTGTTGGGCAGAAAATATTAGTT 331
             ******** ***************************** *********** *********

1            TAGTAAGTTATCTAGCCAGCACTGTTTACCTGCTGACCTAGAAATGCCCCTGTTTTTTTA 536
2            TAGTAAGTTATCTAGCCAGCACTGTTTACCTGCTGACCTAGAAATGCCCCTGTTTTTTTA 391
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1            GGCTGAACGCAGCTCTTCTCCAGTCCATCAGGAGGCAGCAGAGAGTCTGTTTATTGTTCG 596
2            GGATGAACGCAGCTCTTCTCCAGTCCATCAGGAGGCAGCAGAGAGTCTGTTTATTGTTCG 451
             ** *********************************************************

1            GGACGGGACGGGATATATATGTGTGTGCGTGCGGACCGGGATCTGAGATTTTTTGGGTGG 656
2            GGACGGGACGGGATATATATGTGTGTGCGTGCGGACCGGGATCTGAGATTTTTTGGGTGG 511
             ************************************************************

1            TGGCTGTTTGTTTAACTGGAAGCAGCGGCAGTAAATGCGCCGGAATGCAGGATTCCAGCT 716
2            TGGCTGTTTGTTTAACTGGAAGCAGCGGCAGTAAATGCGCCGGAATGCAGGATTCCAGCT 571
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1            AACTTTTCTCCGTCGAGTTTGAGCGAAATTCCTCATTTTCTGTCGACTTCTATCGACTCC 776
2            AACTTTTCTCCGTCGAGTTTGAGCGAAATTCCTCATTTTCTGTCGACTTCTATCGACTCC 631
             ************************************************************

1            GCTCTTGTTTTGCGTGTTGAATTGTGAGGGCGGGTGTCTCTGGCACAGCAGCTTTTATTG 836
2            GCTCTTGTTTTGCGTGTTGAATTGTGAGGGCGGGTGTCTCTGGCACAGCAGCTTTTATTG 691
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1            ATTCATTCACAGATACAGCTAGCGGGATAGCGTGCTAAACGAACACAGATGCAGGCCATA 896
2            ATTCATTCACAGATACAGCTAGCGGTCTAGA----------------------------- 722
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1 is gene sequence of *Rac1* from ensembl
2 is the query sequence (cloned product)

Figure S5. Screen shot for ClustalW analysis.

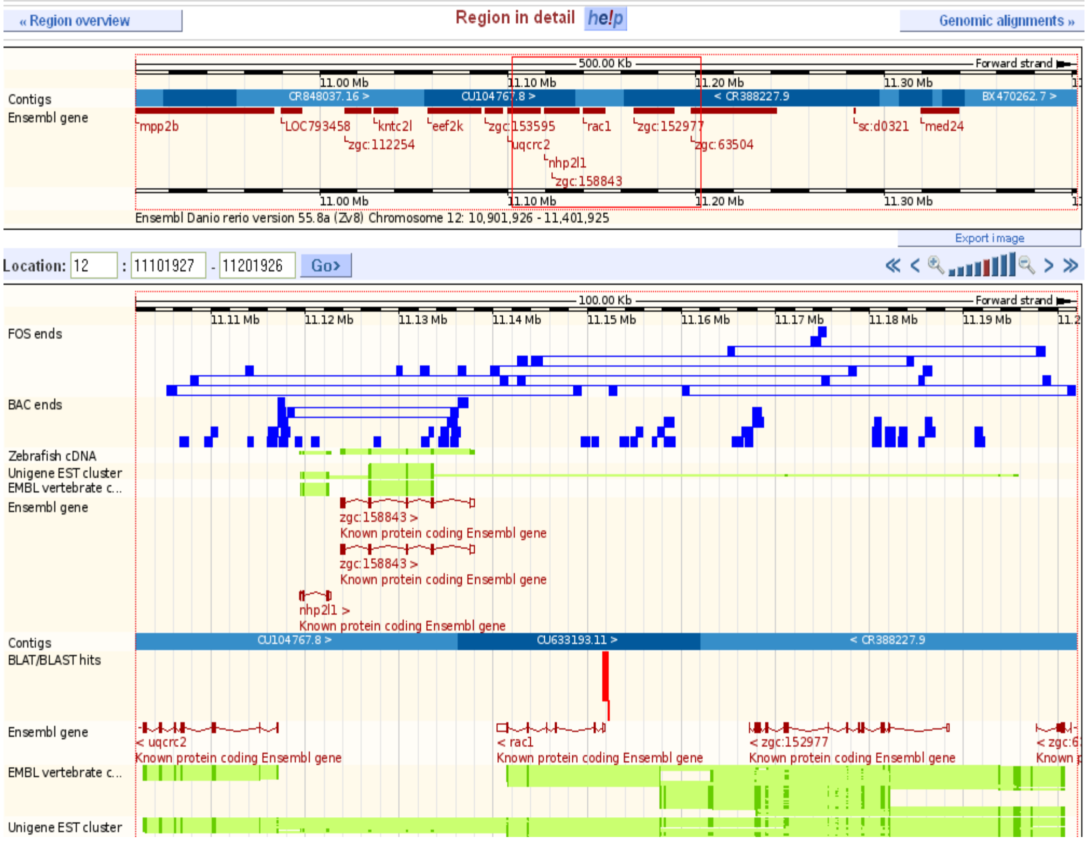

Figure S6. Screen shot for BLAST results of *Rac1*.

Sequencing results of Cdc42/pSS536

>LM335_T7.ab1

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>LM335_p1195.ab1

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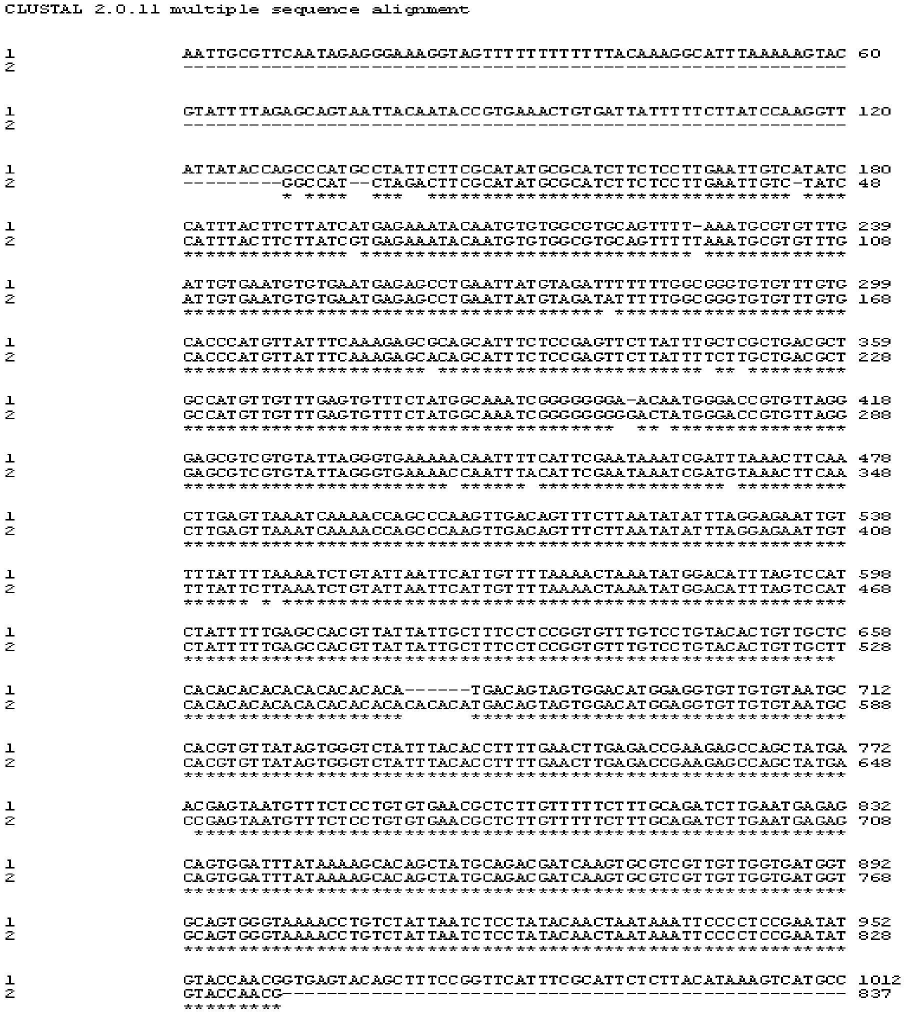
ClustalW analysis of Cdc42/pSS536



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CLUSTAL 2.0.11 multiple sequence alignment

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2               ------------------------------------------------------------


1               ATTATACCAGCCCATGCCTATTCTTCGCATATGCGCATCTTCTCCTTGAATTGTCATATC 180
2               ---------GGCCAT--CTAGACTTCGCATATGCGCATCTTCTCCTTGAATTGTC-TATC 48
                         * ****  ***  ********************************* ****

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2               ATTGTGAATGTGTGAATGAGAGCCTGAATTATGTAGATATTTTTGGCGGGTGTGTTTGTG 168
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1               CACCCATGTTATTTCAAAGAGCGCAGCATTTCTCCGAGTTCTTATTTGCTCGCTGACGCT 359
2               CACCCATGTTATTTCAAAGAGCACAGCATTTCTCCGAGTTCTTATTTTCTTGCTGACGCT 228
                ********************** ************************ ** *********

1               GCCATGTTGTTTGAGTGTTTCTATGGCAAATCGGGGGGGA-ACAATGGGACCGTGTTAGG 418
2               GCCATGTTGTTTGAGTGTTTCTATGGCAAATCGGGGGGGGGACTATGGGACCGTGTTAGG 288
                ***************************************  ** ****************

1               GAGCGTCGTGTATTAGGGTGAAAAACAATTTTCATTCGAATAAATCGATTTAAACTTCAA 478
2               GAGCGTCGTGTATTAGGGTGAAAACCAATTTACATTCGAATAAATCGATGTAAACTTCAA 348
                ************************ ****** ***************** **********

1               CTTGAGTTAAATCAAAACCAGCCCAAGTTGACAGTTTCTTAATATATTTAGGAGAATTGT 538
2               CTTGAGTTAAATCAAAACCAGCCCAAGTTGACAGTTTCTTAATATATTTAGGAGAATTGT 408
                ************************************************************

1               TTTATTTTAAAATCTGTATTAATTCATTGTTTTAAAACTAAATATGGACATTTAGTCCAT 598
2               TTTATTCTTAAATCTGTATTAATTCATTGTTTTAAAACTAAATATGGACATTTAGTCCAT 468
                ****** * ***************************************************

1               CTATTTTTGAGCCACGTTATTATTGCTTTCCTCCGGTGTTTGTCCTGTACACTGTTGCTC 658
2               CTATTTTTGAGCCACGTTATTATTGCTTTCCTCCGGTGTTTGTCCTGTACACTGTTGCTT 528
                *********************************************************** 

1               CACACACACACACACACACA------TGACAGTAGTGGACATGGAGGTGTTGTGTAATGC 712
2               CACACACACACACACACACACACACATGACAGTAGTGGACATGGAGGTGTTGTGTAATGC 588
                ********************      **********************************

1               CACGTGTTATAGTGGGTCTATTTACACCTTTTGAACTTGAGACCGAAGAGCCAGCTATGA 772
2               CACGTGTTATAGTGGGTCTATTTACACCTTTTGAACTTGAGACCGAAGAGCCAGCTATGA 648
                ************************************************************

1               ACGAGTAATGTTTCTCCTGTGTGAACGCTCTTGTTTTTCTTTGCAGATCTTGAATGAGAG 832
2               CCGAGTAATGTTTCTCCTGTGTGAACGCTCTTGTTTTTCTTTGCAGATCTTGAATGAGAG 708
                 ***********************************************************

1               CAGTGGATTTATAAAAGCACAGCTATGCAGACGATCAAGTGCGTCGTTGTTGGTGATGGT 892
2               CAGTGGATTTATAAAAGCACAGCTATGCAGACGATCAAGTGCGTCGTTGTTGGTGATGGT 768
                ************************************************************

1               GCAGTGGGTAAAACCTGTCTATTAATCTCCTATACAACTAATAAATTCCCCTCCGAATAT 952
2               GCAGTGGGTAAAACCTGTCTATTAATCTCCTATACAACTAATAAATTCCCCTCCGAATAT 828
                ************************************************************

1               GTACCAACGGTGAGTACAGCTTTCCGGTTCATTTCGCATTCTCTTACATAAAGTCATGCC 1012
2               GTACCAACG--------------------------------------------------- 837
                *********
```
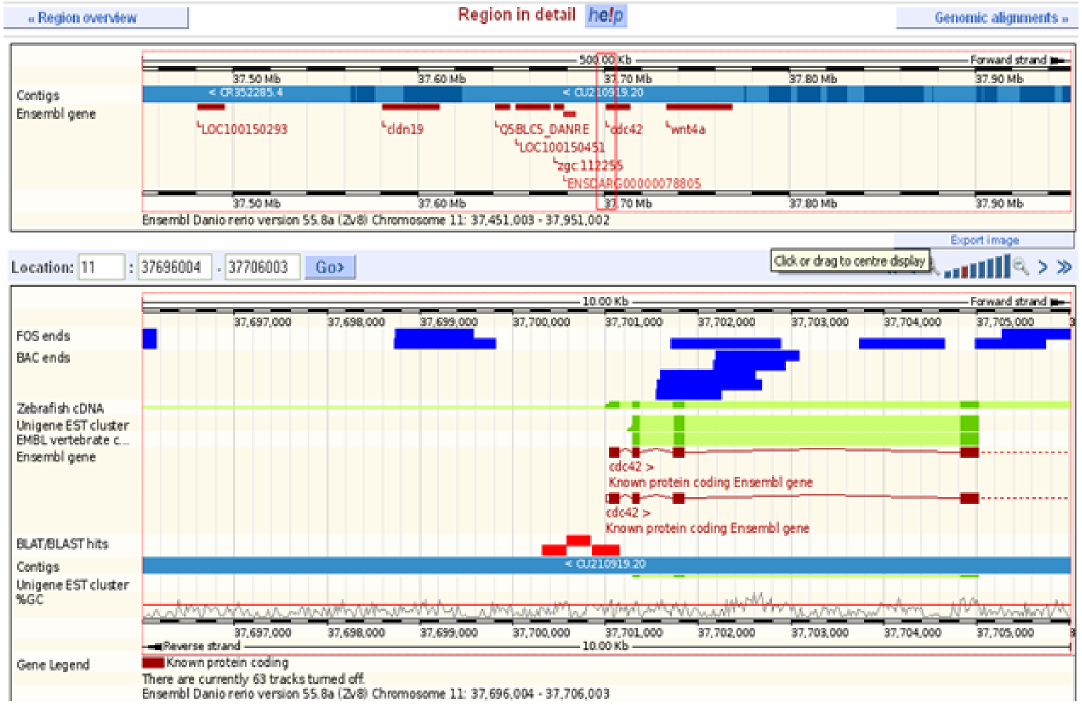

1 is gene sequence of *cdc42* from Ensembl

2 is the query sequence (cloned product)

Figure S7. ClustalW analysis.



Ensembl Danio rerio version 55.8a (Zv8) Chromosome 11: 37,451,003 - 37,951,002

There are currently 63 tracks turned off.

Ensembl Danio rerio version 55.8a (Zv8) Chromosome 11: 37,696,004 - 37,706,003

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