Supplementary File 1. Plasmid sequencing results

1. M0827.0479-RIP3-RIP3_C1R_F09

TAAAGGAAAGGAAAGGGAAGGTATTAGATGAAGGGGGGGGTCAGAGATTTTTCCCTCTCTTGCTCCCCAGAAGATGCAGC
AGCCTCAGCTTTTTGGAAGGTGTTATGGAGGACCAGAGGGAAGGTAAAGTCATTGAGAACTTAGCAGGAGATCTGAGTTG
CTGATGGGCAGGCCTGAGATAAGTCAGCCGGATCCCCTCGAGGGACCTAATAACTTCGTATAGCATACATTATACGAAGT
TATATTAAGGGTTATTGAATATGATCGGAATTGGGCTGCAGGAATTCGTCGACTGGGTCCGTGAGGGTGCATTAGGCCTG
TGGAACTGAGCCAGGGGGTTAAGAAGGGCGTCTGGTAAGGAGGGTCACCTGGTATGACTAGAAATAAAACTCCTAGTTGG
GTCTTGTCATGTGTGTAGTCTTGTATTCAGAGGGACAGGTACTCAACATGGTCCCAAGTCTACACTAGGTTGTAGATGGA
CTAACCTTGGCGTGGAGCTCTGGATCCAGCAGAATGTTAGAGGGCTTGAGGTCCCGGTGCAGGAGCGGAGGGTTCAAGCT
GTGTAGGTAGCACATCCCCAGCACCACTTCCTGCAGCAGGCGACAGAGGAGTGGCCAGGGCCGAGGGCACTCGGGTTGCA
GCAGCCCTGCGAGGGAGCCATTCTCCATGAATCTTGTCACCAGAGCCTGCCCGGACACGAAGTCCCACTGGAGGTCCTCA
GTGACCCCCAGCAGGAGCAGAACGTTCTCATTACGAAGATTAACCATAGCCTTCACCTCCCAGGATATCTTCTTCCTACA
CGCCGAAAGGGGGCCAAAATTGGATTGCGCTCTGGAAGACCCCACCCTTGCCCCACTCAGCTCGTGACCACACTCTGACT
ACAGCTGGGGTCACTCACGAGTTCACGATCTTGACTGCTACATCATGGTTCCATG

2. M0827.0480-RIP3-NEO_R_G09

CGCTCACCTGGCACGACGCGAGCTGCGGGGCGGGGGGGACTTCCTGACTAGGGGAGGAGTAGAAGGTGGCGCGAAGGGGC
CACCAAAGAACGGAGCCGGTTGGCGCCTACCGGTGGATGTGGAATGTGTGCGAGGCCAGAGGCCACTTGTGTAGCGCCAA
GTGCCCAGCGGGGCTGCTAAAGCGCATGCTCCAGACTGCCTTGGGAAAAGCGCCTCCCCTACCCGGTAGAATTTCGACGA
CCTGCAGCCAAGCTAGCTTGGCTGGACGTAAACTCCTCTTCAGACCTGAAGTTCCTATACTTTCTAGAGAATAGGAACTT
CGGAATTCTGCTGTTTGGGTGTCTTTGATGGGAGACCTTCTGGACTTGCTTATCAATAAAGGAACTGTGGGGGCTCACAG
ACTCTGTGCTGGGAAAAGTCAGCCAATCCCGACTTTCTTTCGTTGTGTGACCTCAGTGGGATCCTCTCCTAGTGGATGTC
ATGTTCCTCGTCTTAAACGAGGCAGATCGGGTTAGATGATCTCTAGTCATTCCTTCCCACCTCCAGAGTAACTCATGTCT
ATAGATAAGTGCTGAGGAGGAAGGTGATGGGAGAGCTGAGCGGGGAGAGCAAGAGAGAATGAAGAATGGGTACCTGTCAT
TGGATTCGGTGGGGTCCAGGGATACCAAGGAGTGCCGTGTCTTCCATCTCCCTGCAAACAACACAGAGCTCTCAGGCTTT
CTATTCAAGAGCCTAATCTCATCACCGTGCAGTTCTCCTGGGTAAGAGGGTGTGCTCTAGTCTTGCCAGTGTCTCACCTG
ATTCCTTTGGGGGTGAGGACCGGGAGTCTCAGTAAAGACTGGCCCAGGTGTTGTGCCTCTGAAGGGTAAAGTATGTGGAA
TCTGAGGAGTGCCAGCCACGGGGTCAGAAGATGTCCTTGCTGGTGTGGCAGGCCCAACTGATGTGTCCTGTGCTTGCCTC
TCAGGACATTTTCCAGGAACTGGTCCGGAGGGTTCCTCCAAATGCA

3. M0827.0481-RIP3-NEO_L_H09

CCCAGCCTGGGGGTGCGGTGGGGCAGGAAGCAGGGGGAGGATTGGGAAGACAATAGCAGGCATGCTGGGGATGCGGTGGG
CTCTATGGCTTCTGAGGCGGAAAGAACCAGCTGGGGCTCGACTAGAGCTTGCGGAACCCTTCGAAGTTCCTATTCTCTAG
AAAGTATAGGAACTTCATCAGTCAGGTACATAATATAACTTCGTATAATGTATGCTATACGAAGTTATTAGGTGGATCCC
CCTCCACAGACTAAGACATCCCTAATGGAATGGGCTCAGGAGATGAATGGCACTACTCTTTGAGCTTCTACAAGACTAAT
TCTGAAGAGGCACAGCTCATACTGGGACGCAGTAGCTAGCAGGTGAAGACCCTGCATTTGCATTCCCCAGGGAGATCACA
AGGTGTCGCTGCCCCTTTCCCCAAAGTGCTTGTCAACTTCATCTTTCTAACCTCTGAACCCTCTCACCATCACCTCCTCC
TTTCCTCTTAAAGGGCCACCGGCTCTCGTCTTCAACAACTGTTCTGAAGTGCAGATTGGGAACTACAACTCCTTGGTAGC
ACCACCAAGAACTACTGCCTCAAGTTCGGCCAAGTATGACCAAGCACAGTTCGGCAGGGGTAGGGGCTGGCAGCCCTTCC
ACAAGTAGACTTCAGAGAATCACTGCAAGAGCCTGAAGTGTGCCATTCAGCGTGGCAATAAAAAGCACGTTTTAAGCAAC
CTGGACTGGCTAAGACAGTCCTTGCCACTTCCTGAAGCTCACAACATTCTGTGAGGACAGTTGGACCTACACCCAAACTG
ACTCTTGACCCATCTCCTTAAAGTCAATAAACATAGCATGTTAACTGTGAGAGAGTCTGAGGTGTCAATCCAGGGCATCA
GGGATGGACAGCCAGGAGCTGGCTACCCTGCAGGGGGGGGGTGAGGTGTGTGTGGGGGGGAGTT

Supplementary File 2. ES sequencing results

1. M0928.3699-2_5R_C11-NEO_R_A03

TGAATACTCTCAAGACGCGAGCTGCGGGGCGGGGGGGGACTTCCTGACTAGGGGAGGAGTAGAAGGTGGCGCGAAGGGGCC
ACCAAAGAACGGAGCCGGTTGGCGCCTACCGGTGGATGTGGAATGTGTGCGAGGCCAGAGGCCACTTGTGTAGCGCCAAG
TGCCCAGCGGGGCTGCTAAAGCGCATGCTCCAGACTGCCTTGGGAAAAGCGCCTCCCCTACCCGGTAGAATTTCGACGAC
CTGCAGCCAAGCTAGCTTGGCTGGACGTAAACTCCTCTTCAGACCTGAAGTTCCTATACTTTCTAGAGAATAGGAACTTC
GGAATTCTGCTGTTTGGGTGTCTTTGATGGGAGACCTTCTGGACTTGCTTATCAATAAAGGAACTGTGGGGGCTCACAGA
CTCTGTGCTGGGAAAAGTCAGCCAATCCCGACTTTCTTTCGTTGTGTGACCTCAGTGGGATCCTCTCCTAGTGGATGTCA
TGTTCCTCGTCTTAAACGAGGCAGATCGGGTTAGATGATCTCTAGTCATTCCTTCCCACCTCCAGAGTAACTCATGTCTA
TAGATAAGTGCTGAGGAGGAAGGTGATGGGAGAGCTGAGCGGGGAGAGCAAGAGAGAATGAAGAATGGGTACCTGTCATT
GGATTCGGTGGGGTCCAGGGATACCAAGGAGTGCCGTGTCTTCCATCTCCCTGCAAACAACACAGAGCTCTCAGGCTTTC
TATTCAAGAGCCTAATCTCATCACCGTGCAGTTCTCCTGGGTAAGAGGGTGTGCTCTAGTCTTGCCAGTGTCTCACCTGA
TTCCTTTGGGGGTGAGGACCGGGAGTCTCAGTAAAGACTGGCCCAGGTGTTGTGCCTCTGAGGGGTAAAGTATGTGGAAT
CTGAGGAGTGCCAGCCACCGGCGTCAAAGATGTCCTTGCTGGTGTGGCAGGCCCAACTGATGTGTCCTGTGCTTGCTCTC
ACGACATTTTCAAGGAACTGGTCCGGAGGGTTCTCCAAATGCAGCGGTCCAGCATTTTATAACCATTGGTTTCCTTCGGG
CAAT

2. M0928.3700-2_5R_C11-RIP3_C1R_B03

CGAAAATCGGATCTGATCTGATCCTGACCCTGACTGGGACCCTCCCTGAAACGTGGACAGGCCAAAATCTGCTAGCTGTA
AAGGAAAGGAAAGGGAAGGTATTAGATGAAGGGGGGGGTCAGAGATTTTTCCCTCTCTTGCTCCCCAGAAGATGCAGCAG
CCTCAGCTTTTTGGAAGGTGTTATGGAGGACCAGAGGGAAGGTAAAGTCATTGAGAACTTAGCAGGAGATCTGAGTTGCT
GATGGGCAGGCCTGAGATAAGTCAGCCGGATCCCCTCGAGGGACCTAATAACTTCGTATAGCATACATTATACGAAGTTA
TATTAAGGGTTATTGAATATGATCGGAATTGGGCTGCAGGAATTCGTCGACTGGGTCCGTGAGGGTGCATTAGGCCTGTG
GAACTGAGCCAGGGGGTTAAGAAGGGCGTCTGGTAAGGAGGGTCACCTGGTATGACTAGAAATAAAACTCCTAGTTGGGT
CTTGTCATGTGTGTAGTCTTGTATTCAGAGGGACAGGTACTCAACATGGTCCCAAGTCTACACTAGGTTGTAGATGGACT
AACCTTGGCGTGGAGCTCTGGATCCAGCAGAATGTTAGAGGGCTTGAGGTCCCGGTGCAGGAGCGGAGGGTTCAAGCTGT
GTAGGTAGCACATCCCCAGCACCACTTCCTGCAGCAGGCGACAGAGGAGTGGCCAGGGCCGAGGGCACTCGGGTTGCAGC
AGCCCTGCGAGGGAGCCATTCTCCATGAATCTTGTCACCAGAGCCTGCCCGGACACGAAGTCCCACTGGAGGTCCTCAGT
GACCCCCAGCAGGAGCAGAACGTTCTCATTACGAAGATTAACCATAGCCTTCACCTCCCAGGATATCTTCTTCCTACACG
CCGAAAGGGGGCCAAAATTGGATTGCGCTCTGGAAGACCCCACCCTTGCCCCACTCAGCTCGTGACCACACTCTGACTAC
AGCTGGGGTCACTCACGAGTTCACGATCTTGACTGCTACATCATGGTTCCATGTTCTGTGGTGTGCCCGGAACACGACTC
CGAACCCTCCTTTACCCACAAACTCCAGCTTCTTCAGTTCTTCACGGCTCACCAGAGGAACCGCCTGACGCCCCAGTAGC
CTGAAGAAAGGTTCTTGTCCGTAGGGGCCCATCCCCCAGCCTACGCATTCTCTGTCTCCAGCTCCGGATTCCTTGACTGC
CGCGTGGCCAGCGTAGGCAGCGAG

3. M0928.3701-2_5R_H11-5RIP_111_C03

TGGGTCTTATTGGTGAGTTCAGGACAGCCAGGCTACACAGAGAAACCCTGTCTCGGGGGAAAAAAAAAAAAGAAAGAAAG
ATTTCAGGAACTCTGAAGTGCAGCAAGGAAAGCATGTTTTCCAGCACACTCAACCCAAATAACTGAGCATCCTTCCAAAC
CCTCGCTGATGAAAGGGGTGACTCTCTTTTTCCAAACAGCATCTGCTGTGAGCACTTCTACCTCCGAAAAAAACTAAAAG
CTGGGACTCAAATAACTTCTGTACAATAATGTTCACAGCACTGTCATTTACAATGTTTGAAAGGAAAAAACCAACCAATG
CCCAGGATGGATGAATGGGCATAAAGGTGTGGTATGCACTGTGCTAAAATATTTTCAGCATTTATGGATATTATTTAACC
TTAATAAAATTCAAAAACATCCCATAACATAATTTACCTCGAAAATGTTGTGTCTGAATCCAAATGAATTAAACCAGTCA
AATAAAATAGCATATGGTTCTTCCTCCTCCTCCTCCTCCTCCTTTTTTTTTCTTTTTGAAACAGGGTTTCTCTATGTAGC
CCTGTCCGTAAACCAGGCTGGTCTAACTCTGCCTCCAAAGTATTGGAATTAATGGTGTGTCTCTTTTATAAGGCATCTGA
AGTGTTCGTCAGTGAAGGTTGGGGAGTAGGAATGAGGTGGGAATGGTGTTTTACTGGGCCTGGGAAGAAGGAATGGGGAG
TAACTATGAAATTGCTCCAGAGTGTTACCTTGAGGTTGGATCTTCTTACTAAGGACTGAATGCTAGGGCTGACTATCCAG
TTATTTTCTACCTCCAGCCACAACTATGCCCTGAGTGATAAA

4. M0928.3714-2_3R_C11-3RIP_212_H04

CGCCCACATCATCTTGAGGAGGCAATGATTACCCTGAGCCTCTTATAAAGAAGGTGCTAAGAAGCTGCTCTTTCTGAGCT
GCTGTCCCTTTCTGCCTCTTAGGTCCTACTGACCTGGTGCTTTTTCTCAGTGTCCAGCCTCCGGCGTGAGTGCATAGAGC
TAAGAGCCTCCCGGAACGTGGCCCGCAATGCTCGCTCCATCAGGGCCTTGTGGTACCCTCCCACCACGTTCCCACACAGG
AACAATACCGCGTTTGCTGCCAACTGTGGGCAAAGGCCAGACTTAAAAAGTGTACTACTCCCCTATCTCTACTCTGTGGG
GGAGTCTATCTGTGTAGCTGGAGTTGGTTGCAAACACAGGTCGAGGAGAGCTGGCTCTATGGTTAAGGACCTAGGTATCT
CAGAACAATAGGAGCCACTTTGTGACATCCATCCGGAAGAGTTGGTTGCTTTCCTTCTCTGCTCTCTGCTATAGACTCTT
TCTTGGCTGTGGAACCAACCTGACCGCTTAGGCCTAGCTATCTTGCATGTATATTTCCTCTGTCTACAGTGCTATTCTTC
CATATTCATCTCCTGAGCCCATTCCAGCTGCAAGAAACTACTCCAGTTCTGATTCACGTTTTCCACTAATGCTCCTCGGT
TTACTTCTGTACCCGCGAGAGAATCTTGACTGATTTCCCAATGGCTATAGTGCCCTCTTCTGACAAAGGTAGGCATGATG
CACTGATGTACCAACGACACTAGAGGTCGCTATAGGGGTGTTATCAATGCTTGGCTCCTGCGAGGGCCGAGCCATGTCTT
GGATAATGCTCACAGCATTACTAAACAGCTGACCCAGCTCTGGGCACACTATCGACACCACTTGCATTTTTACCTGTGGT
AGCAGAGCTCTCTGTGACTCAAGCTGCCACCCAAGATACAGTCCAAGGACCAGCACGTGCGAGAGGGATGAGATGACTCC
CGCAGCAGCAGCATCCCGCATGCCCAAGGCAGCATGGCGTACACGGTGAAGATGATGAAGAGGAAAAAAAGACACCTGGA
GAAGGGTGTGGGAAGCTGAATGCCCGTGATGTTGCGCCCAGGGTCTAAATTTGAAGGTTCAACTTCCCTCAAGCCTTGAT
TTTCCTCACCTGGATCCAAGGCGCTCACCACACCCCCCAGTGCACAAGAAAATTCCATAGGCCAAAGGCGGTAATGCCAC
CCGATATTGC

5. M0928.3715-2_3R_C11-NEO_L_A05

TACAATTCTCGCTGGGGGGGTGGGGAGGAAGCAGGGGGAGGATTGGGAAGACAATAGCAGGCATGCTGGGGATGCGGTGG
GCTCTATGGCTTCTGAGGCGGAAAGAACCAGCTGGGGCTCGACTAGAGCTTGCGGAACCCTTCGAAGTTCCTATTCTCTA
GAAAGTATAGGAACTTCATCAGTCAGGTACATAATATAACTTCGTATAATGTATGCTATACGAAGTTATTAGGTGGATCC
CCCTCCACAGACTAAGACATCCCTAATGGAATGGGCTCAGGAGATGAATGGCACTACTCTTTGAGCTTCTACAAGACTAA
TTCTGAAGAGGCACAGCTCATACTGGGACGCAGTAGCTAGCAGGTGAAGACCCTGCATTTGCATTCCCCAGGGAGATCAC
AAGGTGTCGCTGCCCCTTTCCCCAAAGTGCTTGTCAACTTCATCTTTCTAACCTCTGAACCCTCTCACCATCACCTCCTC
CTTTCCTCTTAAAGGGCCACCGGCTCTCGTCTTCAACAACTGTTCTGAAGTGCAGATTGGGAACTACAACTCCTTGGTAG
CACCACCAAGAACTACTGCCTCAAGTTCGGCCAAGTATGACCAAGCACAGTTCGGCAGGGGTAGGGGCTGGCAGCCCTTC
CACAAGTAGACTTCAGAGAATCACTGCAAGAGCCTGAAGTGTGCCATTCAGCGTGGCAATAAAAAGCACGTTTTAAGCAA
CCTGGACTGGCTAAGACAGTCCTTGCCACTTCCTGAAGCTCACAACATTCTGTGAGGACAGTTGGACCTACACCCAAACT
GACTCTTGACCCATCTCCTTAAAGTCAATAAACATAGCATGTTAACTGTGAGAGAGTCTGAGGTGTCAATCCAGGGCATC
AGGGATGGACAGCCAGGAGCTGGCTACCCTGGAGGGGGGGGGGTGAGGTGTGTGTGGGGGGA

Supplementary File 3. Sequencing results of F1 generation

Results of no. 1:

```
Query  12342  GAGTTCCAGGACAGCCAAGGCTACACAGAGAAACCCTGTCTCGGGGGaaaaaaaaaaaaG  12401
              |||||  ||||||||||| | |||  ||||||||||||||||||||||||||||||||||
Sbjct  17     GAGTT-CAGGACAGCCAGGTCTATGCAGAGAAACCCTGTCTCGGGGGAAAAAAAAAAAA-  74

Query  12402  AAAGAAAGATTTCAGGAACTCTGAAGTGCAGCAAGGAGAGCATGTTTTCCAGCACACTCA  12461
              |||||||  |||||  |||||||  |||||||||  | |||  ||  ||||||||||||  ||||||
Sbjct  75     AAAGAAATATTTCCGGAACTCGGAAGTGCAGAATGGAAAGAGTGTTTTCCAGCCCACTCA  134

Query  12462  ACCCAAATAACTGAGCATCCTTCCAAACCCTCGCTGATGAGAGGGGTGACTCTCTTTTTC  12521
              |||||||||||||  ||||||||||||||| ||||||  ||  |||||  ||||||||||||||
Sbjct  135    ACCCAAATAACTGGTCATCCTTCCAAACCCCCGCTGAGGAAAGGGGGGACTCTCTTTTTC  194

Query  12522  CAAACAGCATCTGCTGTGAGCACTTCTACCTCCGAAAAGAACTAGAAGCTGGGACTCAAA  12581
              |||||||||||||||||| ||||||||||||| |||| |||||  ||||||||||||||||
Sbjct  195    CAAACAGCATCTGCTGTGATCACTTCTACCTCCAAAAAAAACTAAAAGCTGGGACTCAAA  254

Query  12582  TAACTTCTGTACAATAATGTTCACAGCACTGTCATTTACAATGTTTGAAAGGAGAAAACC  12641
              |||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Sbjct  255    TAACTTCTGTACAATAATGTTCACAGCACTGTAATTTACAATGTTTGAAAGGAGAAAACC  314

Query  12642  AACCAATGCCCAGGATGGATGAATGGGCATAGAGGTGTGGTATGCACTGTGCTAGAATAT  12701
              |||||||||||||||||||||||||||||| ||||| ||||||||||||||| |||||
Sbjct  315    AACCAATGCCCAGGATGGATGAATGGGCATAAAGGTGGGGTATGCACTGTGCTAAAATAT  374

Query  12702  TTTCAGCATTTATGGATATTATTTAACCTTAATAAAATTCAGAAACATCCCATAACATAA  12761
              |||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Sbjct  375    TTTCAGCATTTATGGATATTATTTAACCTTAATAAAATTCAAAAACATCCCATAACATAA  434

Query  12762  TTTACCTCGAAGATGTTGTGTCTGAATCCAAATGAAGTAAACCAGTCAAATAAGATAGCA  12821
              |||||||||| ||||||||||||||||||||||||||||||||||||||||||||| |||||||
Sbjct  435    TTTACCTCGAAAATGTTGTGTCTGAATCCAAATGAAGTAAACCAGTCAAATAAAATAGCA  494

Query  12822  TATGGTTCTtcctcctcctcctcctcctcctttttttttctttttGAGACAGGGTTTCTC  12881
              |||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Sbjct  495    TATGGTTCTTCCTCCTCCTCCTCCTCCTTTTTTTTTCTTTTTGAAACAGGGTTTCTC  554

Query  12882  TATGTAGCCCTGTCCGTAGACCAGGCTGGTCTAACTCTGCCTCCAGAGTATTGGAATTAA  12941
              |||||||||||||||||| |||||||||||||||||||||||| ||||||||||||||
Sbjct  555    TATGTAGCCCTGTCCGTAAACCAGGCTGGTCTAACTCTGCCTCCAAAGTATTGGAATTAA  614

Query  12942  TGGTGTGTCTCTTTTATAAGGCATCTGAAGTGTTCGTCAGTGAAGGTTGGGGAGTAGGAA  13001
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  615    TGGTGTGTCTCTTTTATAAGGCATCTGAAGTGTTCGTCAGTGAAGGTTGGGGAGTAGGAA  674

Query  13002  TGAGGTGGGAATGGTGTTTTACTGGGCCTGGGAAGAAGGAATGGGGAGTAACTATGAAAT  13061
              |||||||||||||||||||||||||||||||| |||||||||||||||||||||||||||
Sbjct  675    TGAGGTGGGAATGGTGTTTTACTGGGCCTGGGAAAAAGGAATGGGGAGTAACTATGAAAT  734

Query  13062  TGCTCCAGAGTGTTAGCTTGAGGTTGGATCTTCCTACTAAGGACTGAATGCTAGGGCTGA  13121
              ||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  735    TGCTCCAAAGTGTTAGCTTGAGGTTGGATCTTCCTACTAAGGACTGAATGCTAGGGCTGA  794
```

Query is the Target sequence (RIPK3 cko recombinated genomic DNA sequence), Subject is the result of sequencing.

Results of no. 2:

```
Query  15603  AGTCAAGA-TCGTGAACTCGTGAGTGACCCC-AGCTGT-AGTCAG-AGTGTGGTCACGAG  15658
              ||||||||  |||  |||  ||||||  |  |||||  ||||||  |  ||||  ||||||||||  |
Sbjct  1011   AGTCAAGATTCG-GAATTCGTGAATAACCCCCAGCTGTAATTCAGAAGTGTGGTCACAAC  953

Query  15659  CCTGAGTGGGGCAA-GGGTG-GGGTCTTCCAGAGCGCAATCCAATTTTGGC-C-CCCTTT  15714
              |||||  ||||||||  |||||  |||||||||  |   ||||  ||||||||||  |  ||||||
Sbjct  952    CCTGAATGGGGCAAAGGGTGAAGGTCTTCCAAAAGGCAAACCAATTTTGGCACACCCTTT  893

Query  15715  CGGCGTGTA-GGAAGAAGATATCCT-GGGAGGTGAAGGCTATGGTTAATCTTCGTAATGA  15772
              |||  |||||  ||||||||||||||  ||  ||  |||||  ||||||||||||||  ||||  ||
Sbjct  892    CGGTGTGTAAGGAAGAAGATATCCTTGGAAGATGAAGACTATGGTTAATCTTAGTAAAGA  833

Query  15773  GAA-CGTTCTGCTCCTG-CTGGGGGTCACTGAGGACCTCCAGTGGGACTTCGTGTCC-GG  15829
              |||  |  ||  ||||  |||  |||||||||  ||||||||||||  |  |  |||||  |||  |
Sbjct  832    GAAACATTTTGCTACTGGTTGGGGGTCAATGAGGACCTCCAGAGAAATTTCGTATCCAGA  773

Query  15830  GCA-GGCTCTGGTGACAAGATTCATGGAGAATGGCTCCCTCGCAGGGCTGCTGCAACCCG  15888
              |||  ||  ||||||||||||||||||  |||||||||  |||||||||  |||||  |||||||||
Sbjct  772    GCAGGGATCTGGTGACAAGATTCAAGGAGAATGGTTCCCTCGCAAGGCTGATGCAACCCG  713

Query  15889  AGTGCCCTCGGCCCTGGCCACTCCTCTGTCGCCTGCTGCAGGAAGTGGTGCTGGGGATGT  15948
              ||||||  ||||||||||||||||  |  ||||||  ||||||||||||||||||||||||||||
Sbjct  712    AGTGCCATCGGCCCTGGCCACTCTTATGTCGCTTGCTGCAGGAAGTGGTGCTGGGGATGT  653

Query  15949  GCTACCTACACAGCTTGAACCCTCCGCTCCTGCACCGGGACCTCAAGCCCTCTAACATTC  16008
              ||||||||||||||||||||  ||||||||||||||||||||||||||||||||||||||||||||
Sbjct  652    GCTACCTACACAGCTTGAACCATCCGCTCCTGCACCGGGACCTCAAGCCCTCTAACATTA  593

Query  16009  TGCTGGATCCAGAGCTCCACGCCAAGGTTAGTCCATCTACAACCTAGTGTAGACTTGGGA  16068
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  592    TGCTGGATCCAGAGCTCCACGCCAAGGTTAGTCCATCTACAACCTAGTGTAGACTTGGGA  533

Query  16069  CCATGTTGAGTACCTGTCCCTCTGAATACAAGACTACACACATGACAAGACCCAACTAGG  16128
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  532    CCATGTTGAGTACCTGTCCCTCTGAATACAAGACTACACACATGACAAGACCCAACTAGG  473

Query  16129  AGTTTTATTTCTAGTCATACCAGGTGACCCTCCTTACCAGACGCCCTTCTTAACCCCCTG  16188
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  472    AGTTTTATTTCTAGTCATACCAGGTGACCCTCCTTACCAGACGCCCTTCTTAACCCCCTG  413

Query  16189  GCTCAGTTCCACAGGCCTAATGCACCCTCACGGACCCAGTCGACGAATTCCTGCAGCCCA  16248
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  412    GCTCAGTTCCACAGGCCTAATGCACCCTCACGGACCCAGTCGACGAATTCCTGCAGCCCA  353

Query  16249  ATTCCGATCATATTCAATAACCCTTAATATAACTTCGTATAATGTATGCTATACGAAGTT  16308
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  352    ATTCCGATCATATTCAATAACCCTTAATATAACTTCGTATAATGTATGCTATACGAAGTA  293

Query  16309  ATTAGGT  16315
              |||||||
Sbjct  292    ATTAGGT  286
```

Query is the Target sequence (RIPK3 cko recombinated genomic DNA sequence), Subject is the result of sequencing.

Results of no. 3:

```
Query  17755  TTCCTGGAAAATGTCCTGAGAGGCAAGCACAGGACACATCAGTTGGGCCTGCCACACCAG  17814
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  779    TTCCTGGAAAATGTCCTGAGAGGCAAGCACAGGACACATCAGTTGGGCCTGCCACACCAG  720

Query  17815  CAAGG-ACATCTTCTGACCCCGTGGCTGGCACTCCTCAGATTCCACATACTTTACCCTTC  17873
              |||||  |||||||||||||||||||||||||||||  ||||||||||||||||||||||||||
Sbjct  719    CAAGGGACATCTTCTGACCCCGTGGCTGGCACTCATCAGATTCCACATACTTTACCCTTC  660

Query  17874  AGAGGCACAACACCTGGGCCAGTCTTTACTGAGACTCCCGGTCCTCACCCCCAAAGGAAT  17933
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  659    AGAGGCACAACACCTGGGCCAGTCTTTACTGAGACTCCCGGTCCTCACCCCCAAAGGAAT  600

Query  17934  CAGGTGAGACACTGGCAAGACTAGAGCACACCCTCTTACCCAGGAGAACTGCACGGTGAT  17993
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  599    CAGGTGAGACACTGGCAAGACTAGAGCACACCCTCTTACCCAGGAGAACTGCACGGTGAT  540

Query  17994  GAGATTAGGCTCTTGAATAGAAAGCCTGAGAGCTCTGTGTTGTTTGCAGGGAGATGGAAG  18053
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  539    GAGATTAGGCTCTTGAATAGAAAGCCTGAGAGCTCTGTGTTGTTTGCAGGGAGATGGAAG  480

Query  18054  ACACGGCACTCCTTGGTATCCCTGGACCCCACCGAATCCAATGACAGGTACCCATTCTTC  18113
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  479    ACACGGCACTCCTTGGTATCCCTGGACCCCACCGAATCCAATGACAGGTACCCATTCTTC  420

Query  18114  ATTCTCTCTTGCTCTCCCCGCTCAGCTCTCCCATCACCTTCCTCCTCAGCACTTATCTAT  18173
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  419    ATTCTCTCTTGCTCTCCCCGCTCAGCTCTCCCATCACCTTCCTCCTCAGCACTTATCTAT  360

Query  18174  AGACATGAGTTACTCTGGAGGTGGGAAGGAATGACTAGAGATCATCTAACCCGATCTGCC  18233
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  359    AGACATGAGTTACTCTGGAGGTGGGAAGGAATGACTAGAGATCATCTAACCCGATCTGCC  300

Query  18234  TCGTTTAAGACGAGGAACATGACATCCACTAGGAGAGGATCCCACTGAGGTCACACAACG  18293
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  299    TCGTTTAAGACGAGGAACATGACATCCACTAGGAGAGGATCCCACTGAGGTCACACAACG  240

Query  18294  AAAGAAAGTCGGGATTGGCTGACTTTTCCCAGCACAGAGTCTGTGAGCCCCCACAGTTCC  18353
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  239    AAAGAAAGTCGGGATTGGCTGACTTTTCCCAGCACAGAGTCTGTGAGCCCCCACAGTTCC  180

Query  18354  TTTATTGATAAGCAAGTCCAGAAGGTCTCCCATCAAAGACACCCAAACAGCAGAATTCCG  18413
              |||||||||||||||||||||||||||  ||||||||||||||||||||||||||||||||
Sbjct  179    TTTATTGATAAGCAAGTCCAGAAGGTCTTCCATCAAAGACACCCAAACAGCAGAATTCCG  120

Query  18414  AAGTTCCTATTCTCTAGAAAGTATAGGAACTTCATCAGTCAGGTACATAATATAACTTCG  18473
              ||||||  ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  119    AAGTTCTTATTCTCTAGAAAGTATAGGAACTTCATCAGTCAGGTACATAATATAACTTCG  60

Query  18474  TATAATGTATGCTATACGAAGTTATTAGGTGGATCCCCCTCCACAGACTAAGACATC  18530
              |||||||||||||||||||||||||||||||| ||||||||||||| ||  |  ||||
Sbjct  59     TATAATGTATGCTATACGAAGTTATTAGGTGG-TCCCCCTCCACAGATTATGTCATC  4
```

Query is the Target sequence (RIPK3 cko recombinated genomic DNA sequence), Subject is the result of sequencing.

Results of no. 4:

Range 1: 1 to 674 Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Gaps	Strand
1210 bits(655)	0.0	670/676(99%)	5/676(0%)	Plus/Plus

```
Query  18542  GGGCTCAG-GAGATGA-ATGGCACTACTCTTTGAGCTTCTACAAGACTAATTCTGAAGAG  18599
              ||| ||||  ||| || ||||||||||||||||||||||||||||||||||||||||||
Sbjct  1      GGG-TCAGCTAGA-GAGATGGCACTACTCTTTGAGCTTCTACAAGACTAATTCTGAAGAG  58

Query  18600  GCACAGCTCATACTGGGACGCAGTAGCTAGCAGGTGAAGACCCTGCATTTGCATTCCCCA  18659
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  59     GCACAGCTCATACTGGGACGCAGTAGCTAGCAGGTGAAGACCCTGCATTTGCATTCCCCA  118

Query  18660  GGGAGATCACAAGGTGTCGCTGCCCCTTTCCCCAAAGTGCTTGTCAACTTCATCTTTCTA  18719
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  119    GGGAGATCACAAGGTGTCGCTGCCCCTTTCCCCAAAGTGCTTGTCAACTTCATCTTTCTA  178

Query  18720  ACCTCTGAACCCTCTCACCATCACCTCCTCCTTTCCTCTTAAAGGGCCACCGGCTCTCGT  18779
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  179    ACCTCTGAACCCTCTCACCATCACCTCCTCCTTTCCTCTTAAAGGGCCACCGGCTCTCGT  238

Query  18780  CTTCAACAACTGTTCTGAAGTGCAGATTGGGAACTACAACTCCTTGGTAGCACCACCAAG  18839
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  239    CTTCAACAACTGTTCTGAAGTGCAGATTGGGAACTACAACTCCTTGGTAGCACCACCAAG  298

Query  18840  AACTACTGCCTCAAGTTCGGCCAAGTATGACCAAGCACAGTTCGGCAGGGGTAGGGGCTG  18899
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  299    AACTACTGCCTCAAGTTCGGCCAAGTATGACCAAGCACAGTTCGGCAGGGGTAGGGGCTG  358

Query  18900  GCAGCCCTTCCACAAGTAGACTTCAGAGAATCACTGCAAGAGCCTGAAGTGTGCCATTCA  18959
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  359    GCAGCCCTTCCACAAGTAGACTTCAGAGAATCACTGCAAGAGCCTGAAGTGTGCCATTCA  418

Query  18960  GCGTGGCAATAAAAAGCACGTTTTAAGCAACCTGGACTGGCTAAGACAGTCCTTGCCACT  19019
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  419    GCGTGGCAATAAAAAGCACGTTTTAAGCAACCTGGACTGGCTAAGACAGTCCTTGCCACT  478

Query  19020  TCCTGAAGCTCACAACATTCTGTGAGGACAGTTGGACCTACACCCAAACTGACTCTTGAC  19079
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  479    TCCTGAAGCTCACAACATTCTGTGAGGACAGTTGGACCTACACCCAAACTGACTCTTGAC  538

Query  19080  CCATCTCCTTAAAGTCAATAAACATAGCATGTTAACTGTGAGAGAGTCTGAGGTGTCAAT  19139
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  539    CCATCTCCTTAAAGTCAATAAACATAGCATGTTAACTGTGAGAGAGTCTGAGGTGTCAAT  598

Query  19140  CCAGGGCATCAGGGATGGACAGCCAGGAGCTGGCTACCCTGGAggggggggTGAGGTGT  19199
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  599    CCAGGGCATCAGGGATGGACAGCCAGGAGCTGGCTACCCTGGAGGGGGGGGGTGAGGTGT  658

Query  19200  GTGTGGGGGG-AGTTG  19214
              |||||||||  |||||
Sbjct  659    GTGTGGGGGGGAGTTG  674
```

Query is the Target sequence (RIPK3 cko recombinated genomic DNA sequence), Subject is the result of sequencing.

Results of no. 5:

```
Query  22673  CGCTGCTACATCAGTGCACCATGCCTACCTTTGTCAGAAGAGGGCACTATAGCCATTGGG  22732
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  739    CGCTGCTACATCAGTGCACCATGCCTACCTTTGTCAGAAGAGGGCACTATAGCCATTGGG  680

Query  22733  AAATCAGTCAAGATTCTCTCGCGGGTACAGAAGTAAACCGAGGAGCATTCGTGGAAAACG  22792
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  679    AAATCAGTCAAGATTCTCTCGCGGGTACAGAAGTAAACCGAGGAGCATTCGTGGAAAACG  620

Query  22793  TGAATCAGAACTGGAGTAGTTTCTTGCAGCTGGAATGGGCTCAGGAGATGAATATGGAAG  22852
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  619    TGAATCAGAACTGGAGTAGTTTCTTGCAGCTGGAATGGGCTCAGGAGATGAATATGGAAG  560

Query  22853  AATAGCACTCTAGACAGAGGAAATATACATGCAAGATAGCTAGGCCTAAGCGGTCAGGTT  22912
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  559    AATAGCACTCTAGACAGAGGAAATATACATGCAAGATAGCTAGGCCTAAGCGGTCAGGTT  500

Query  22913  GGTTCCACAGCCAAGAAAGAGTCTATAGCAGAGAGCAGAGAAGGAAAGCAACCAACTCTT  22972
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  499    GGTTCCACAGCCAAGAAAGAGTCTATAGCAGAGAGCAGAGAAGGAAAGCAACCAACTCTT  440

Query  22973  CCGGATGGATGTCACAAAGTGGCTCCTATTGTTCTGAGATACCTAGGTCCTTAACCATAG  23032
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  439    CCGGATGGATGTCACAAAGTGGCTCCTATTGTTCTGAGATACCTAGGTCCTTAACCATAG  380

Query  23033  AGCCAGCTCTCCTCGACCTGTGTTTGGAACCAACTCCAGCTACACAGATAGACTCCCCCA  23092
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  379    AGCCAGCTCTCCTCGACCTGTGTTTGGAACCAACTCCAGCTACACAGATAGACTCCCCCA  320

Query  23093  CAGACTAGAGATAGGGGAGTGGTACACTTTCTAAGTCTGGCCTTTGCCCACAGTTGGCAG  23152
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  319    CAGACTAGAGATAGGGGAGTGGTACACTTTCTAAGTCTGGCCTTTGCCCACAGTTGGCAG  260

Query  23153  CAAACGCGGTATTGTTCCTGTGTGGGAACGTGGTGGGAGCGTACCACAAGGCCCTGATGG  23212
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  259    CAAACGCGGTATTGTTCCTGTGTGGGAACGTGGTGGGAGCGTACCACAAGGCCCTGATGG  200

Query  23213  AGCGAGCATTGCGGGCCACGTTCCGGGAGGCTCTTAGCTCTCTGCACTCACGCCGGAGGC  23272
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  199    AGCGAGCATTGCGGGCCACGTTCCGGGAGGCTCTTAGCTCTCTGCACTCACGCCGGAGGC  140

Query  23273  TGGACACTGAGAAAAAGCACCAGGTCAGTAGGACCTAAGAGGCAGAAAGGGACAGCAGCT  23332
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  139    TGGACACTGAGAAAAAGCACCAGGTCAGTAGGACCTAAGAGGCAGAAAGGGACAGCAGCT  80

Query  23333  CAGAAAGAGCAGCTTCTTAGCACCTTCTTTCTAAGTGGCTCTGGGTAATTCATTTGCCTT  23392
              |||||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Sbjct  79     CAGAAAGAGCAGCTTCTTAGCACCTTCTTTCTAAGTGGCTCTGGGTAATTCATT-GCCT-  22

Query  23393  CCTCAAGTAT  23402
              ||||||||||
Sbjct  21     CCTCAAGTAT  12
```

Query is the Target sequence (RIPK3 cko recombinated genomic DNA sequence), Subject is the result of sequencing.