**Appendix 8**

**Inverse PCR and Genome walking results**

***Inverse PCR***

MseI restriction site

EcoRI restriction site

F11135 and R11076 binding sites

**mi2004 sequence**

ttaacgtgagttttcgttccactgagcgtcagaccccgtagaaaagatcaaaggatcttcttgagatcctttttttctgcgcgtaatctgctgcttgcaaacaaaaaaaccaccgctaccagcggtggtttgtttgccggatcaagagctaccaactctttttccgaaggtaactggcttcagcagagcgcagataccaaatactgtccttctagtgtagccgtagttaggccaccacttcaagaactctgtagcaccgcctacatacctcgctctgctaatcctgttaccagtggctgctgccagtggcgataagtcgtgtcttaccgggttggactcaagacgatagttaccggataaggcgcagcggtcgggctgaacggggggttcgtgcacacagcccagcttggagcgaacgacctacaccgaactgagatacctacagcgtgagctatgagaaagcgccacgcttcccgaagggagaaaggcggacaggtatccggtaagcggcagggtcggaacaggagagcgcacgagggagcttccagggggaaacgcctggtatctttatagtcctgtcgggtttcgccacctctgacttgagcgtcgatttttgtgatgctcgtcaggggggcggagcctatggaaaaacgccagcaacgcggcctttttacggttcctggccttttgctggccttttgctcacatgttctttcctgcgttatcccctgattctgtggataaccgtattaccgccatgcattagttattactagcgctaccggactcagatctcgag

**F11135 predicted sequence**

tcctgttaccagtggctgctgccagtggcgataagtcgtgtcttaccgggttggactcaagacgatagttaccggataaggcgcagcggtcgggctgaacggggggttcgtgcacacagcccagcttggagcgaacgacctacaccgaactgagatacctacagcgtgagctatgagaaagcgccacgcttcccgaagggagaaaggcggacaggtatccggtaagcggcagggtcggaacaggagagcgcacgagggagcttccagggggaaacgcctggtatctttatagtcctgtcgggtttcgccacctctgacttgagcgtcgatttttgtgatgctcgtcaggggggcggagcctatggaaaaacgccagcaacgcggcctttttacggttcctggccttttgctggccttttgctcacatgttctttcctgcgttatcccctgattctgtggataaccgtattaccgccatgcattagttattactagcgctaccggactcagatctcgag

----3’ downstream flanking region-------

ttaacgtgagttttcgttccactgagcgtcagaccccgtagaaaagatcaaaggatcttcttgagatcctttttttctgcgcgtaatctgctgcttgcaaacaaaaaaaccaccgctaccagcggtggtttgtttgccggatcaagagctaccaactctttttccgaaggtaactggcttcagcagagcgcagataccaaatactgtccttctagtgtagccg

**R11076 predicted sequence**

cggctacactagaaggacagtatttggtatctgcgctctgctgaagccagttaccttcggaaaaagagttggtagctcttgatccggcaaacaaaccaccgctggtagcggtggtttttttgtttgcaagcagcagattacgcgcagaaaaaaaggatctcaagaagatcctttgatcttttctacggggtctgacgctcagtggaacgaaaactcacgttaa

----3’ downstream flanking region-------

ctcgagatctgagtccggtagcgctagtaataactaatgcatggcggtaatacggttatccacagaatcaggggataacgcaggaaagaacatgtgagcaaaaggccagcaaaaggccaggaaccgtaaaaaggccgcgttgctggcgtttttccataggctccgcccccctgacgagcatcacaaaaatcgacgctcaagtcagaggtggcgaaacccgacaggactataaagataccaggcgtttccccctggaagctccctcgtgcgctctcctgttccgaccctgccgcttaccggatacctgtccgcctttctcccttcgggaagcgtggcgctttctcatagctcacgctgtaggtatctcagttcggtgtaggtcgttcgctccaagctgggctgtgtgcacgaaccccccgttcagcccgaccgctgcgccttatccggtaactatcgtcttgagtccaacccggtaagacacgacttatcgccactggcagcagccactggtaacagga

**Sequencing Results**

>custom1
NTATGTGTNTACGGGNTNGGACTCAGNACGATAGTTTACCGGATAAGGCGCAGCGGTCGGGCTGANCCCNTTAANANNCGNTGCACACAGCCCAGCTTGGAGCGAACGACCTACACCGAACTGAGATACCTACAGCGTGAGCTATGAGAAAGCGCCACGCTTCCCGAAGGGAGAAAGGCGGACAGGTATCCGGTAAGCGGCAGGGTCGGAACAGGAGAGCGCACGAGGGAGCTTCCAGGGGGAAACGCCTGGTATCTTTATAGTCCTGTCGGGTTTCGCCACCTCTGACTTGAGCGTCGATTTTTGTGATGCTCGTCAGGGGGGCGGAGCCTATGGAAAAACGCCAGCAACGCGGCCTTTTTACGGTTCCTGGCCTTTTGCTGGCCTTTTGCTCACATGTTCTTTCCTGCGTTATCCCCTGATTCTGTGGATAACCGTATTACCGCCTTTGAGTGAGCTGATACCGCTCGCCGCAGCCGAACNACCGAGCGCAGCTGAGTCAGTGAGCGAGGAAGCGGAANANCNCCCAATACGCAAACCGCCTCTCCCCGNNCGNTGGCCGATTCATTAACGTGAGTTTTCGTTCCACTGAGCGTCAGACCCCGTAGAAAANATCAAAGGATCTTCTTGANATCCTTTTTTTCTGCNCGTAATCTGCTGCTTGCAAACAAAAAAACCACCGCTACCAGCGGTGGTTTTGTTTGCNGGATCAANAGCTACCAANTNTTTTTCCGAACGTAANCTGGCTTCAGCCAGAGCGCAGATACCAAATNNCTGTCCCTTCTAGNGTATTNNGATTTCATTTNNGNNCGGGTNTATTTTTTATCNNNCTCCCCCNTNTANCTNNNNATNTNCCTCNTTTTTTNTTTTNNANANTANNATNCNNNNN

>custom2
TGGCNNCNTAGCAGATTCCTTCGGAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCCCCNTTAAAGGGGGTTTTTTTGTTTGCAAGCAGCAGATTACGCGCAGAAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGGTCTGACGCTCAGTGGAACGAAAACTCACGTTAATGAATCGGCCAACGCGCGGGGAGAGGCGGTTTGCNTATTGGGCGCTCTTCCGCTTCCTCGCTCACTGACTCGCTGCGCTCGGTCGTTCGGCTGCGGCGAGNGGTATCAGCTCACTCAAAGGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGCANGAAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGNCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCCTGACGAGNATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAANCCCGACNGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGNTCTCCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGGGCTGTGTGCACNAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTTAAGACACGACTTATCGCCACTGGCAGCAGCCANNTGGTAAACAGGAAATTTTTTTTTCTTTCTGCNCGNTTANANTTNTTTNTNTTTCCGCTATAGGTTTTTTTTNTNNTCNTNNTTTNTATTTTNNTTTNCGTNCCTTTGA

**Custom1 vs F11135 predicted sequence alignment**

custom1 -----------------------------------NTATGTGTNTACGGGNTNGGACTCA

F11135 TCCTGTTACCAGTGGCTGCTGCCAGTGGCGATAAGTCGTGT-CTTACCGGGTTGGACTCA

 \*\*\* \*\*\* \*\* \* \*\*\*\*\*\*\*

custom1 GNACGATAGTTTACCGGATAAGGCGCAGCGGTCGGGCTGANCCCNTTAANANNCGNTGCA

F11135 AGACGATAGTT-ACCGGATAAGGCGCAGCGGTCGGGCTGAACGGG----GGGTTCGTGCA

 \*\*\*\*\*\*\*\*\* \*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\* \* \*\*\*\*

custom1 CACAGCCCAGCTTGGAGCGAACGACCTACACCGAACTGAGATACCTACAGCGTGAGCTAT

F11135 CACAGCCCAGCTTGGAGCGAACGACCTACACCGAACTGAGATACCTACAGCGTGAGCTAT

 \*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*

custom1 GAGAAAGCGCCACGCTTCCCGAAGGGAGAAAGGCGGACAGGTATCCGGTAAGCGGCAGGG

F11135 GAGAAAGCGCCACGCTTCCCGAAGGGAGAAAGGCGGACAGGTATCCGGTAAGCGGCAGGG

 \*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*

custom1 TCGGAACAGGAGAGCGCACGAGGGAGCTTCCAGGGGGAAACGCCTGGTATCTTTATAGTC

F11135 TCGGAACAGGAGAGCGCACGAGGGAGCTTCCAGGGGGAAACGCCTGGTATCTTTATAGTC

 \*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*

custom1 CTGTCGGGTTTCGCCACCTCTGACTTGAGCGTCGATTTTTGTGATGCTCGTCAGGGGGGC

F11135 CTGTCGGGTTTCGCCACCTCTGACTTGAGCGTCGATTTTTGTGATGCTCGTCAGGGGGGC

 \*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*

custom1 GGAGCCTATGGAAAAACGCCAGCAACGCGGCCTTTTTACGGTTCCTGGCCTTTTGCTGGC

F11135 GGAGCCTATGGAAAAACGCCAGCAACGCGGCCTTTTTACGGTTCCTGGCCTTTTGCTGGC

 \*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*

custom1 CTTTTGCTCACATGTTCTTTCCTGCGTTATCCCCTGATTCTGTGGATAACCGTATTACCG

F11135 CTTTTGCTCACATGTTCTTTCCTGCGTTATCCCCTGATTCTGTGGATAACCGTATTACCG

 \*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*

custom1 CCTTTGAGTGAGCTGATACCGCTCGCCGCAGCCGAACNACCGAGCGCAGCTGAGTCAGTG

F11135 CCAT-GCATTAGTTATTACTAG----CGCTACCGGACT-CAGATCTC----GAGTTAA--

 \*\* \* \* \* \*\* \* \*\*\* \*\*\* \*\*\* \*\* \* \*\* \* \* \*\*\*\* \*

custom1 AGCGAGGAAGCGGAANANCNCCCAATACGCAAACCGCCTCTCCCCGNNCGNTGGCCGATT

F11135 ---AAGGATCTAGGTGAAGATCCTTTTTGATAATCTCAT------GACCAA-----AATC

 \*\*\*\* \* \* \*\* \* \* \*\* \* \* \* \* \* \*\*

custom1 CATTAACGTGAGTTTTCGTTCCACTGAGCGTCAGACCCCGTAGAAAANATCAAAGGATCT

F11135 CCTTAACGTGAGTTTTCGTTCCACTGAGCGTCAGACCCCGTAGAAAAGATCAAAGGATCT

 \* \*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\* \*\*\*\*\*\*\*\*\*\*\*\*

custom1 TCTTGANATCCTTTTTTTCTGCNCGTAATCTGCTGCTTGCAAACAAAAAAACCACCGCTA

F11135 TCTTGAGATCCTTTTTTTCTGCGCGTAATCTGCTGCTTGCAAACAAAAAAACCACCGCTA

 \*\*\*\*\*\* \*\*\*\*\*\*\*\*\*\*\*\*\*\*\* \*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*

custom1 CCAGCGGTGGTTTTGTTTGCNGGATCAANAGCTACCAANTNTTTTTCCGAACGTAANCTG

F11135 CCAGCGGTGGTTT-GTTTGCCGGATCAAGAGCTACCAACTCTTTTTCCGAAGGTAAC-TG

 \*\*\*\*\*\*\*\*\*\*\*\*\* \*\*\*\*\*\* \*\*\*\*\*\*\* \*\*\*\*\*\*\*\*\* \* \*\*\*\*\*\*\*\*\*\* \*\*\*\* \*\*

custom1 GCTTCAGCCAGAGCGCAGATACCAAATNNCTGTCCCTTCTAGNGTATTNNGATTTCATTT

F11135 GCTTCAGC-AGAGCGCAGATACCAAATAC-TGTCC-TTCTAGTGTAGCCG----------

 \*\*\*\*\*\*\*\* \*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\* \*\*\*\*\* \*\*\*\*\*\* \*\*\*

custom1 NNGNNCGGGTNTATTTTTTATCNNNCTCCCCCNTNTANCTNNNNATNTNCCTCNTTTTTT

F11135 ------------------------------------------------------------

custom1 NTTTTNNANANTANNATNCNNNNN

F11135 ------------------------

**Possible flanking genomic sequence (custom1 vs F11135 alignment)** TTTGAGTGAGCTGATACCGCTCGCCGCAGCCGAACNACCGAGCGCAGCTGAGTCAGTGAGCGAGGAAGCGGAANANCNCCCAATACGCAAACCGCCTCTCCCCGNNCGNTGGCCGATTCA

**Custom2 vs F11135 predicted sequence alignment**

custom2 TCAAAGGNACGNAAANNAAAATANAAANNANGANNANAAAAAAAACCTATAGCGGAAANA

F11135 ------------------------------------------------------------

custom2 NAAANAANTNTAANCGNGCAGAAAGAAAAAAAAATTTCCTGTTTACCANNTGGCTGCTGC

F11135 ------------------------------------TCCTGTT-ACCAGT-GGCTGCTGC

 \*\*\*\*\*\*\* \*\*\*\* \*\*\*\*\*\*\*\*\*

custom2 CAGTGGCGATAAGTCGTGTCTTAACCGGGTTGGACTCAAGACGATAGTTACCGGATAAGG

F11135 CAGTGGCGATAAGTCGTGTCTTA-CCGGGTTGGACTCAAGACGATAGTTACCGGATAAGG

 \*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\* \*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*

custom2 CGCAGCGGTCGGGCTGAACGGGGGGTTNGTGCACACAGCCCAGCTTGGAGCGAACGACCT

F11135 CGCAGCGGTCGGGCTGAACGGGGGGTTCGTGCACACAGCCCAGCTTGGAGCGAACGACCT

 \*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\* \*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*

custom2 ACACCGAACTGAGATACCTACAGCGTGAGCTATGAGAAAGCGCCACGCTTCCCGAAGGGA

F11135 ACACCGAACTGAGATACCTACAGCGTGAGCTATGAGAAAGCGCCACGCTTCCCGAAGGGA

 \*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*

custom2 GAAAGGCGGACAGGTATCCGGTAAGCGGCAGGGTCGGAACAGGAGANCGCACGAGGGAGC

F11135 GAAAGGCGGACAGGTATCCGGTAAGCGGCAGGGTCGGAACAGGAGAGCGCACGAGGGAGC

 \*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\* \*\*\*\*\*\*\*\*\*\*\*\*\*

custom2 TTCCAGGGGGAAACGCCTGGTATCTTTATAGTCCNGTCGGGNTTCGCCACCTCTGACTTG

F11135 TTCCAGGGGGAAACGCCTGGTATCTTTATAGTCCTGTCGGGTTTCGCCACCTCTGACTTG

 \*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\* \*\*\*\*\*\* \*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*

custom2 AGCGTCGATTTTTGTGATNCTCGTCAGGGGGGCGGAGCCTATGGAAAAACGCCAGCAACG

F11135 AGCGTCGATTTTTGTGATGCTCGTCAGGGGGGCGGAGCCTATGGAAAAACGCCAGCAACG

 \*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\* \*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*

custom2 CGNCCTTTTTACGGTTCCTGGCCTTTTGCTGGCCTTTTGCTCACATGTTCTTTCNTGCGT

F11135 CGGCCTTTTTACGGTTCCTGGCCTTTTGCTGGCCTTTTGCTCACATGTTCTTTCCTGCGT

 \*\* \*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\* \*\*\*\*\*

custom2 TATCCCCTGATTCTGTGGATAACCGTATTACCGCCTTTGAGTGAGCTGATACCNCTCGCC

F11135 TATCCCCTGATTCTGTGGATAACCGTATTACCG**CC**AT-GCATTAGTTATTACTAG----C

 \*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\* \* \* \* \*\* \* \*\*\* \*

custom2 GCAGCCGAACGACCGAGCGCAGCGAGTCAGTGAGCGAGGAAGCGGAAGAGCGCCCAATAN

F11135 GCTACCGGACT-CAGATCT---CGAGTTAA-----AAGGATCTAGGTGAAGATCCTTTTT

 \*\* \*\*\* \*\* \* \*\* \* \*\*\*\*\* \* \*\*\*\* \* \*\* \*\* \*

custom2 GCAAACCGCCTCTCCCCGCGCGTTGGCCGATTCA**TTAA**CGTGAGTTTTCGTTCCACTGAG

F11135 GATAATCTCATGACCAA-----------AATCCC**TTAA**CGTGAGTTTTCGTTCCACTGAG

 \* \*\* \* \* \* \*\* \*\* \* \*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*

custom2 CGTCAGACCCCGTAGAAAAGATCAAAGGATCTTCTTGAGATCCTTTTTTTCTGCGCGTAA

F11135 CGTCAGACCCCGTAGAAAAGATCAAAGGATCTTCTTGAGATCCTTTTTTTCTGCGCGTAA

 \*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*

custom2 TCTGCTGCTTGCAAACAAAAAAACCCCCTTTAANGGGGCGGTGGTTTGTTTGCCGGATCA

F11135 TCTGCTGCTTGCAAACAAAAAAACCACCGCTACCA--GCGGTGGTTTGTTTGCCGGATCA

 \*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\* \*\* \*\* \*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*

custom2 AGAGCTACCAACTCTTTT-CCGAAGGAATCTG-CTANGNNGCCA----------------

F11135 AGAGCTACCAACTCTTTTTCCGAAGGTAACTGGCTTCAGCAGAGCGCAGATACCAAATAC

 \*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\* \*\*\*\*\*\*\* \* \*\*\* \*\*

custom2 -------------------

F11135 TGTCCTTCTAGTGTAGCCG

**Possible flanking genomic sequence (custom2 vs F11135 alignment)**

TTTGAGTGAGCTGATACCNCTCGCCGCAGCCGAACGACCGAGCGCAGCGAGTCAGTGAGCGAGGAAGCGGAAGAGCGCCCAATANGCAAACCGCCTCTCCCCGCGCGTTGGCCGATTCA

**Possible genomic custom1 vs Possible genomic custom2**

Possiblegenomiccustom1 TTTGAGTGAGCTGATACCGCTCGCCGCAGCCGAACNACCGAGCGCAGCTG

Possiblegenomiccustom2 TTTGAGTGAGCTGATACCNCTCGCCGCAGCCGAACGACCGAGCGCAGCG-

 \*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*.\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*.\*\*\*\*\*\*\*\*\*\*\*\*

Possiblegenomiccustom1 AGTCAGTGAGCGAGGAAGCGGAANANCNCCCAATACGCAAACCGCCTCTC

Possiblegenomiccustom2 AGTCAGTGAGCGAGGAAGCGGAAGAGCGCCCAATANGCAAACCGCCTCTC

 \*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*.\*.\*.\*\*\*\*\*\*\* \*\*\*\*\*\*\*\*\*\*\*\*\*\*

Possiblegenomiccustom1 CCCGNNCGNTGGCCGATTCA

Possiblegenomiccustom2 CCCGCGCGTTGGCCGATTCA

 \*\*\*\* .\*\*.\*\*\*\*\*\*\*\*\*\*\*

 or **T**

Possiblegenomiccustom1 TTTGAGTGAGCTGATACCGCTCGCCGCAGCCGAAC**G**ACCGAGCGCAGC**~~T~~**G

Possiblegenomiccustom2 TTTGAGTGAGCTGATACC**G**CTCGCCGCAGCCGAACGACCGAGCGCAGCG-

 \*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*.\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*.\*\*\*\*\*\*\*\*\*\*\*\*

Possiblegenomiccustom1 AGTCAGTGAGCGAGGAAGCGGAA**G**A**G**C**G**CCCAATACGCAAACCGCCTCTC

Possiblegenomiccustom2 AGTCAGTGAGCGAGGAAGCGGAAGAGCGCCCAATA**C**GCAAACCGCCTCTC

 \*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*.\*.\*.\*\*\*\*\*\*\* \*\*\*\*\*\*\*\*\*\*\*\*\*\*

Possiblegenomiccustom1 CCCG**CG**CG**T**TGGCCGATTCA

Possiblegenomiccustom2 CCCGCGCGTTGGCCGATTCA

 \*\*\*\* .\*\*.\*\*\*\*\*\*\*\*\*\*\*

**Genomic sequence from inverse PCR**

TTTGAGTGAGCTGATACCGCTCGCCGCAGCCGAACGACCGAGCGCAGCGAGTCAGTGAGCGAGGAAGCGGAAGAGCGCCCAATACGCAAACCGCCTCTCCCCGCGCGTTGGCCGATTCA

**Genomic sequence from inverse PCR, reverse complement**

TGAATCGGCCAACGCGCGGGGAGAGGCGGTTTGCGTATTGGGCGCTCTTCCGCTTCCTCGCTCACTGACTCGCTGCGCTCGGTCGTTCGGCTGCGGCGAGCGGTATCAGCTCACTCAAA

**Zv8NA7791 (hit from Zv8)**

GGGGGGGGGGAAAAACGGGTGAAAAAAGGGGGGAAAATTAAATTCCGCACTTTGGGGGGCATTTTCTGTCAAATGATTTAGGAAGCACGGCTTTTTTTTCAAGGGGTTATTATTTTTTTCAGGGAGTGGGATTACCTTTTTCTCGAAAGGTATTTTAGGAGTGATAAAACAAACTGGGGGGGTCCCGGGTCCCTTTTCCCCCGGGGAAGTCCCCGCGAGACGGTAAGGTTGCCACTTCATTCTTGTCATTATCCTATAATAATGGGGCAATTATGAGGCCTATTGTTTTAGGGGGGGATGGATATGTGGATGTACACATATGACTCATGCAGTTCGGGGTGAGGGTACAAGTCCGTCTAAAATCCGACGCGGGGTGTAAGCAAGCACGTCAGTGAGGGTAAGAGCGTGTAGAAGTAGGTTAGTGCTGAGGTCATTTTGTGGCATGAGAGTCAGATGATGATGAGAGAGCCTATGACGCAGTGCAGATTCCGGAGCCGATGAGAGAGGATAAGTTAGCGGATGAGGGGAGAATAGAGACGTCAGCAGGGGGAATTAGTGGGAATTGGCATGTGTGGGGGCCTGTTTGATTATGCGGCATCTGAGCAGATGGGAATGAGATTGAAGCAGATTAAGTTGGAAATCGCGAGGAGATGCGCAGGGAGAAAATTGTAGCATCAGGTGCCATTCCACAGTTAGATTGCGTGCAGGTTGTTAAGGGGGATCCGAGTGGTCCTCGTTGTGTTTGCTTCAGGCAGTAATTCGTGGACGTGTTGTAAGTTTGAGACATTAGTTCATCGGGCAGGGGTTTGGCTGGCGCGAGATTTTATGAGGGTGGTCTGTGTCAGGCTTGAATTCTTGCAGGTTTGGTTGTTGAGGGCACTAGTTCCTCGGCGTTTGGTCGGTTTGTGCCTTAAAGGCTCTGGGTTTTGTCTGTTTTTTGCATTAGTTCCTCTAAGGATGTCGTTTTTTGCATTAGTTCCTATGCGTTTTGTCTGTTTGTTGCATTATTTCCTCTGCGTTTTGTCGGGTAGCGAGATCGAATCTTGCAGCTCTGTGTGTAGTGTGTCTTCATGATGCTCAAGCTGCTATCTCGGTCTGCTATTCCGCACTACCTCTGAGCCGTAACCGTAAATTGTTAAGTCCGTGGTGCCTAATGATGGATCTAACTCTCATTAATTGCGCTCGCCCTCATGGCCCGCTTTCCAATCGGGAAACCTGTCGTGCCAGCTGCATTAA**TGAATCTGCCAACGCGCTGGGAGAGGCGGTTTGCATATTGGGCGCTCTTCCGCTTCCTCGCTCACTGACTCGCTGCGCTCGGTCGTTCAGCTGCGGCGAGCGGTATCAGCTCACTCAAA**GGCGGTAATACAGTTATCCACACAATCATGGGATAACGCAGGAAAGAACATGTGACCAAAAGGCCAGCAAAAGGCCATGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCCTGACGAGCATCACAAAAATCTACGCTCATGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCGCGTGCGCTCTCCTGTTACCACCCTGCCGCTTACCGGATACCTGTCCGCCATATCACCCTTCGGGAAGCGAGGCGCTTTCTCAAACCTCACGCTGAAGGTATCTCAGTACGGTGAAGGATCGATCGCTCCAAGCAGGGCTGCGTGTAAACCTATGAAAGCCAGAAAGTATGAATACGAACAGTGAGAAACTGAAAAAGACAAGGAAAAGCAACAATCCAAACGAGTCATTCTGAACGAGGCGCGCATACCCAACAGCTAGCAGCAAAACCCAATAATAACCCCCGAACCTCAACGGAATAAAGCCGGGGAGAAAAAACCCAAAAAAGGCGAAAGGAGAAAAAACCCCAAACAGAAAATGAAAGCGAAAAATAACCACCACCCCAAAAGACTGGAGAAGCTGCCGAAAGAAAGAAACCCCCAAGAGGCCCGAAGNACCGCAAACCAAACCAAGCCACGGAATCAAGGGAACGGGCCAAGAAGAACATAGACCCAGCAAAATCTCACAGGGGCCGCACGCGAAACAATTAAATGGGAAAAACCCCCCAAAAATAACAAAAAAAGGCGTCAAAAAGAAAATACCCGACACCCAAAAA

inversePCRrevcomp ------------------------------------------------------------

Zv8NA7791 GGGGGGGGGGAAAAACGGGTGAAAAAAGGGGGGAAAATTAAATTCCGCACTTTGGGGGGC

inversePCRrevcomp ------------------------------------------------------------

Zv8NA7791 ATTTTCTGTCAAATGATTTAGGAAGCACGGCTTTTTTTTCAAGGGGTTATTATTTTTTTC

inversePCRrevcomp ------------------------------------------------------------

Zv8NA7791 AGGGAGTGGGATTACCTTTTTCTCGAAAGGTATTTTAGGAGTGATAAAACAAACTGGGGG

inversePCRrevcomp ------------------------------------------------------------

Zv8NA7791 GGTCCCGGGTCCCTTTTCCCCCGGGGAAGTCCCCGCGAGACGGTAAGGTTGCCACTTCAT

inversePCRrevcomp ------------------------------------------------------------

Zv8NA7791 TCTTGTCATTATCCTATAATAATGGGGCAATTATGAGGCCTATTGTTTTAGGGGGGGATG

inversePCRrevcomp ------------------------------------------------------------

Zv8NA7791 GATATGTGGATGTACACATATGACTCATGCAGTTCGGGGTGAGGGTACAAGTCCGTCTAA

inversePCRrevcomp ------------------------------------------------------------

Zv8NA7791 AATCCGACGCGGGGTGTAAGCAAGCACGTCAGTGAGGGTAAGAGCGTGTAGAAGTAGGTT

inversePCRrevcomp ------------------------------------------------------------

Zv8NA7791 AGTGCTGAGGTCATTTTGTGGCATGAGAGTCAGATGATGATGAGAGAGCCTATGACGCAG

inversePCRrevcomp ------------------------------------------------------------

Zv8NA7791 TGCAGATTCCGGAGCCGATGAGAGAGGATAAGTTAGCGGATGAGGGGAGAATAGAGACGT

inversePCRrevcomp ------------------------------------------------------------

Zv8NA7791 CAGCAGGGGGAATTAGTGGGAATTGGCATGTGTGGGGGCCTGTTTGATTATGCGGCATCT

inversePCRrevcomp ------------------------------------------------------------

Zv8NA7791 GAGCAGATGGGAATGAGATTGAAGCAGATTAAGTTGGAAATCGCGAGGAGATGCGCAGGG

inversePCRrevcomp ------------------------------------------------------------

Zv8NA7791 AGAAAATTGTAGCATCAGGTGCCATTCCACAGTTAGATTGCGTGCAGGTTGTTAAGGGGG

inversePCRrevcomp ------------------------------------------------------------

Zv8NA7791 ATCCGAGTGGTCCTCGTTGTGTTTGCTTCAGGCAGTAATTCGTGGACGTGTTGTAAGTTT

inversePCRrevcomp ------------------------------------------------------------

Zv8NA7791 GAGACATTAGTTCATCGGGCAGGGGTTTGGCTGGCGCGAGATTTTATGAGGGTGGTCTGT

inversePCRrevcomp ------------------------------------------------------------

Zv8NA7791 GTCAGGCTTGAATTCTTGCAGGTTTGGTTGTTGAGGGCACTAGTTCCTCGGCGTTTGGTC

inversePCRrevcomp ------------------------------------------------------------

Zv8NA7791 GGTTTGTGCCTTAAAGGCTCTGGGTTTTGTCTGTTTTTTGCATTAGTTCCTCTAAGGATG

inversePCRrevcomp ------------------------------------------------------------

Zv8NA7791 TCGTTTTTTGCATTAGTTCCTATGCGTTTTGTCTGTTTGTTGCATTATTTCCTCTGCGTT

inversePCRrevcomp ------------------------------------------------------------

Zv8NA7791 TTGTCGGGTAGCGAGATCGAATCTTGCAGCTCTGTGTGTAGTGTGTCTTCATGATGCTCA

inversePCRrevcomp ------------------------------------------------------------

Zv8NA7791 AGCTGCTATCTCGGTCTGCTATTCCGCACTACCTCTGAGCCGTAACCGTAAATTGTTAAG

inversePCRrevcomp ------------------------------------------------------------

Zv8NA7791 TCCGTGGTGCCTAATGATGGATCTAACTCTCATTAATTGCGCTCGCCCTCATGGCCCGCT

inversePCRrevcomp ------------------------------------TGAATCGGCCAACGCGCGGGGAGA

Zv8NA7791 TTCCAATCGGGAAACCTGTCGTGCCAGCTGCATTAATGAATCTGCCAACGCGCTGGGAGA

 \*\*\*\*\*\* \*\*\*\*\*\*\*\*\*\* \*\*\*\*\*\*

inversePCRrevcomp GGCGGTTTGCGTATTGGGCGCTCTTCCGCTTCCTCGCTCACTGACTCGCTGCGCTCGGTC

Zv8NA7791 GGCGGTTTGCATATTGGGCGCTCTTCCGCTTCCTCGCTCACTGACTCGCTGCGCTCGGTC

 \*\*\*\*\*\*\*\*\*\* \*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*

inversePCRrevcomp GTTCGGCTGCGGCGAGCGGTATCAGCTCACTCAAA-------------------------

Zv8NA7791 GTTCAGCTGCGGCGAGCGGTATCAGCTCACTCAAAGGCGGTAATACAGTTATCCACACAA

 \*\*\*\* \*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*

inversePCRrevcomp ------------------------------------------------------------

Zv8NA7791 TCATGGGATAACGCAGGAAAGAACATGTGACCAAAAGGCCAGCAAAAGGCCATGAACCGT

inversePCRrevcomp ------------------------------------------------------------

Zv8NA7791 AAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCCTGACGAGCATCACAAA

inversePCRrevcomp ------------------------------------------------------------

Zv8NA7791 AATCTACGCTCATGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTT

inversePCRrevcomp ------------------------------------------------------------

Zv8NA7791 CCCCCTGGAAGCTCCCGCGTGCGCTCTCCTGTTACCACCCTGCCGCTTACCGGATACCTG

inversePCRrevcomp ------------------------------------------------------------

Zv8NA7791 TCCGCCATATCACCCTTCGGGAAGCGAGGCGCTTTCTCAAACCTCACGCTGAAGGTATCT

inversePCRrevcomp ------------------------------------------------------------

Zv8NA7791 CAGTACGGTGAAGGATCGATCGCTCCAAGCAGGGCTGCGTGTAAACCTATGAAAGCCAGA

inversePCRrevcomp ------------------------------------------------------------

Zv8NA7791 AAGTATGAATACGAACAGTGAGAAACTGAAAAAGACAAGGAAAAGCAACAATCCAAACGA

inversePCRrevcomp ------------------------------------------------------------

Zv8NA7791 GTCATTCTGAACGAGGCGCGCATACCCAACAGCTAGCAGCAAAACCCAATAATAACCCCC

inversePCRrevcomp ------------------------------------------------------------

Zv8NA7791 GAACCTCAACGGAATAAAGCCGGGGAGAAAAAACCCAAAAAAGGCGAAAGGAGAAAAAAC

inversePCRrevcomp ------------------------------------------------------------

Zv8NA7791 CCCAAACAGAAAATGAAAGCGAAAAATAACCACCACCCCAAAAGACTGGAGAAGCTGCCG

inversePCRrevcomp ------------------------------------------------------------

Zv8NA7791 AAAGAAAGAAACCCCCAAGAGGCCCGAAGNACCGCAAACCAAACCAAGCCACGGAATCAA

inversePCRrevcomp ------------------------------------------------------------

Zv8NA7791 GGGAACGGGCCAAGAAGAACATAGACCCAGCAAAATCTCACAGGGGCCGCACGCGAAACA

inversePCRrevcomp ------------------------------------------------------------

Zv8NA7791 ATTAAATGGGAAAAACCCCCCAAAAATAACAAAAAAAGGCGTCAAAAAGAAAATACCCGA

inversePCRrevcomp ----------

Zv8NA7791 CACCCAAAAA

***Genome walking***

F11423 and F11592 binding sites

**mi2004 sequence**

ttaacgtgagttttcgttccactgagcgtcagaccccgtagaaaagatcaaaggatcttcttgagatcctttttttctgcgcgtaatctgctgcttgcaaacaaaaaaaccaccgctaccagcggtggtttgtttgccggatcaagagctaccaactctttttccgaaggtaactggcttcagcagagcgcagataccaaatactgtccttctagtgtagccgtagttaggccaccacttcaagaactctgtagcaccgcctacatacctcgctctgctaatcctgttaccagtggctgctgccagtggcgataagtcgtgtcttaccgggttggactcaagacgatagttaccggataaggcgcagcggtcgggctgaacggggggttcgtgcacacagcccagcttggagcgaacgacctacaccgaactgagatacctacagcgtgagctatgagaaagcgccacgcttcccgaagggagaaaggcggacaggtatccggtaagcggcagggtcggaacaggagagcgcacgagggagcttccagggggaaacgcctggtatctttatagtcctgtcgggtttcgccacctctgacttgagcgtcgatttttgtgatgctcgtcaggggggcggagcctatggaaaaacgccagcaacgcggcctttttacggttcctggccttttgctggccttttgctcacatgttctttcctgcgttatcccctgattctgtggataaccgtattaccgccatgcattagttattactagcgctaccggactcagatctcgag

**F11423 predicted sequence**

atagtcctgtcgggtttcgccacctctgacttgagcgtcgatttttgtgatgctcgtcaggggggcggagcctatggaaaaacgccagcaacgcggcctttttacggttcctggccttttgctggccttttgctcacatgttctttcctgcgttatcccctgattctgtggataaccgtattaccgccatgcattagttattactagcgctaccggactcagatctcgag

----3’ downstream flanking region-------

ggtcgccgtgtaccgtcctcgcat

**Sequencing Results**

**Aligns with inverse PCR sequence**

>custom1
GACATTGAGCGTCGATTTTTGTGATGCTCGTCGGGGGGCGGAGCCTATGGAAAAACGCCAGCAACGCGGCCTTTTTACGGTTCCTGGCCTTTTGCTGGCCTTTTGCTCACATGTTCTTTCCTGCGTTATCCCCTGATTCTGTGGATAACCGTATTACCGCC**TTTGAGTGAGCTGATACCGCTCGCCGCAGCTCGAACGACCGAGCGCAGCGAGTCAGTGAGCAAGGAAGCGGANGAGCGCNCAA**ATNTGTTNNNGCCTCTCNACGCGCGTGNGAAGACTCANTNATGCTGCTGNAACGNCNGGTTTCCCGNCNGAAAAAAGAGCNATGAGCCCTCAGNAATTCCCTNTAANCTNGNGTCGCANGTTTTTNGAAAAAAAANAATTTAAAACATAAAAAAAAACNNTNGNNTNNACCNNTNTTTTTGTAAGGGAAAGAAAAANNNNNGCTTNNNNGGTTTTTGNCGCCCNTTTTTTTAGATACNGNGGANTCCNAANTTTCNGAAAAATGANTNTTNGTNCAACCATTTTTTNNNGGCGCCAAAAAATNTTCNCANGCNCCANCNGCCNGTNAGTCNTTTTTATTNANCNNTNNNTNCCTCCTGTNNTTNTNTGGGGGANANCAAANCTCCANNCNANAAAAAAAAGNGTTNCNCCGNCCCCCCCCTCCAAAAAAAAATTTTNTTCNCAAGATTNNTAAAACCCNGNNNCNGCCNGTTAACGTTAAATTTGANGNNNTAAAAAAAAAAGTANGGGGTGGGNGNTNNCCCTNCCNNGTATNANNTNTGCCANTNGGNCCGTTCCCCAATTTGTGTNNNTTCCCATGNGCCNNNTNTGAANGCNAAAAAAANTAAGNNNNANNTGNAAAANANCCNANACNNNCTTTTNAANNCNTTTTTNCCCGGGTGTTCCANGNNAAAAAGNAAACAANAACGNAGNGNAAATGGNANNNNCCAANCCCCCCCTCCNTTNNGTGNAANANNNNNNNGGGATGAACACTTNANNCTTANCNTNNNAANNGGTAANAAATNTNNGGAACCNCNAANGNNCNAAACNGNTNCCNANANCNGNNNNNCCAAGNNTGAAAANTTNTGNTTTNANNCCNGNNNNNTCCNANNNNNCNCCNNANANTNTCNNTNCCTCCAAAANNCNCAGGAAANCCACCNNNAAGANCCTTTNNCNCAANANNTNNCTNNTAGACCAAANATNGCTTNTAAAANATCCTCCCCCGNNTTNGNCGGGNAGANTNNNTGTNGAAANNCTCNTNCNCCNNG

**F11423 predicted vs custom 1 sequence alignment**

F11423pred 1 atagtcctgtcgggtttcgccacctctgac-ttgagcgtcgatttttgtg 49

 ||| |||||||||||||||||||

custom1 1 ---------------------------GACATTGAGCGTCGATTTTTGTG 23

F11423pred 50 atgctcgtcaggggggcggagcctatggaaaaacgccagcaacgcggcct 99

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custom1 24 ATGCTCGTC-GGGGGGCGGAGCCTATGGAAAAACGCCAGCAACGCGGCCT 72

F11423pred 100 ttttacggttcctggccttttgctggccttttgctcacatgttctttcct 149

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custom1 73 TTTTACGGTTCCTGGCCTTTTGCTGGCCTTTTGCTCACATGTTCTTTCCT 122

F11423pred 150 gcgttatcccctgattctgtggataaccgtattaccgccatgcattagtt 199

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custom1 123 GCGTTATCCCCTGATTCTGTGGATAACCGTATTACCGCCTT---TGAGTG 169

F11423pred 200 a--ttactagcgct----------------accggactcagatctcgag- 230

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custom1 170 AGCTGA-TACCGCTCGCCGCAGCTCGAACGACCGAGCGCAG----CGAGT 214

F11423pred 231 -------------------------------------------------- 230

custom1 215 CAGTGAGCAAGGAAGCGGANGAGCGCNCAAATNTGTTNNNGCCTCTCNAC 264

F11423pred 231 -------------------------------------------------- 230

custom1 265 GCGCGTGNGAAGACTCANTNATGCTGCTGNAACGNCNGGTTTCCCGNCNG 314

F11423pred 231 -------------------------------------------------- 230

custom1 315 AAAAAAGAGCNATGAGCCCTCAGNAATTCCCTNTAANCTNGNGTCGCANG 364

F11423pred 231 -------------------------------------------------- 230

custom1 365 TTTTTNGAAAAAAAANAATTTAAAACATAAAAAAAAACNNTNGNNTNNAC 414

F11423pred 231 -------------------------------------------------- 230

custom1 415 CNNTNTTTTTGTAAGGGAAAGAAAAANNNNNGCTTNNNNGGTTTTTGNCG 464

F11423pred 231 -------------------------------------------------- 230

custom1 465 CCCNTTTTTTTAGATACNGNGGANTCCNAANTTTCNGAAAAATGANTNTT 514

F11423pred 231 -------------------------------------------------- 230

custom1 515 NGTNCAACCATTTTTTNNNGGCGCCAAAAAATNTTCNCANGCNCCANCNG 564

F11423pred 231 -------------------------------------------------- 230

custom1 565 CCNGTNAGTCNTTTTTATTNANCNNTNNNTNCCTCCTGTNNTTNTNTGGG 614

F11423pred 231 -------------------------------------------------- 230

custom1 615 GGANANCAAANCTCCANNCNANAAAAAAAAGNGTTNCNCCGNCCCCCCCC 664

F11423pred 231 -------------------------------------------------- 230

custom1 665 TCCAAAAAAAAATTTTNTTCNCAAGATTNNTAAAACCCNGNNNCNGCCNG 714

F11423pred 231 -------------------------------------------------- 230

custom1 715 TTAACGTTAAATTTGANGNNNTAAAAAAAAAAGTANGGGGTGGGNGNTNN 764

F11423pred 231 -------------------------------------------------- 230

custom1 765 CCCTNCCNNGTATNANNTNTGCCANTNGGNCCGTTCCCCAATTTGTGTNN 814

F11423pred 231 -------------------------------------------------- 230

custom1 815 NTTCCCATGNGCCNNNTNTGAANGCNAAAAAAANTAAGNNNNANNTGNAA 864

F11423pred 231 -------------------------------------------------- 230

custom1 865 AANANCCNANACNNNCTTTTNAANNCNTTTTTNCCCGGGTGTTCCANGNN 914

F11423pred 231 -------------------------------------------------- 230

custom1 915 AAAAAGNAAACAANAACGNAGNGNAAATGGNANNNNCCAANCCCCCCCTC 964

F11423pred 231 -------------------------------------------------- 230

custom1 965 CNTTNNGTGNAANANNNNNNNGGGATGAACACTTNANNCTTANCNTNNNA 1014

F11423pred 231 -------------------------------------------------- 230

custom1 1015 ANNGGTAANAAATNTNNGGAACCNCNAANGNNCNAAACNGNTNCCNANAN 1064

F11423pred 231 -------------------------------------------------- 230

custom1 1065 CNGNNNNNCCAAGNNTGAAAANTTNTGNTTTNANNCCNGNNNNNTCCNAN 1114

F11423pred 231 -------------------------------------------------- 230

custom1 1115 NNNNCNCCNNANANTNTCNNTNCCTCCAAAANNCNCAGGAAANCCACCNN 1164

F11423pred 231 -------------------------------------------------- 230

custom1 1165 NAAGANCCTTTNNCNCAANANNTNNCTNNTAGACCAAANATNGCTTNTAA 1214

F11423pred 231 -------------------------------------------------- 230

custom1 1215 AANATCCTCCCCCGNNTTNGNCGGGNAGANTNNNTGTNGAAANNCTCNTN 1264

F11423pred 231 ------- 230

custom1 1265 CNCCNNG 1271

**Custom1 seq vs inverse PCR sequence alignment**

custom1seq 1 GACATTGAGCGTCGATTTTTGTGATGCTCGTCGGGGGGCGGAGCCTATGG 50

inversepcr 1 -------------------------------------------------- 0

custom1seq 51 AAAAACGCCAGCAACGCGGCCTTTTTACGGTTCCTGGCCTTTTGCTGGCC 100

inversepcr 1 -------------------------------------------------- 0

custom1seq 101 TTTTGCTCACATGTTCTTTCCTGCGTTATCCCCTGATTCTGTGGATAACC 150

inversepcr 1 -------------------------------------------------- 0

custom1seq 151 GTATTACCGCCTTTGAGTGAGCTGATACCGCTCGCCGCAGCTCGAACGAC 200

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inversepcr 1 -----------TTTGAGTGAGCTGATACCGCTCGCCGCAGC-CGAACGAC 38

custom1seq 201 CGAGCGCAGCGAGTCAGTGAGCAAGGAAGCGGANGAGCGCNCAAATNTGT 250

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inversepcr 39 CGAGCGCAGCGAGTCAGTGAGCGAGGAAGCGGAAGAGCGCCCAA------ 82

custom1seq 251 TNNNGCCTCTCNACGCGCGTGNGAAGACTCANTNATGCTGCTGNAACGNC 300

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inversepcr 83 -----------TACGC---------------------------------- 87

custom1seq 301 NGGTTTCCCGNCNGAAAAAAGAGCNATGAGCCCTCAGNAATTCCCTNTAA 350

inversepcr 88 -------------------------------------------------- 87

custom1seq 351 NCTNGNGTCGCANGTTTTTNGAAAAAAAANAATTTAAAACATAAAAAAAA 400

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inversepcr 88 ------------------------------------AAAC---------- 91

custom1seq 401 ACNNTNGNNTNNACCNNTNTTTTTGTAAGGGAAAGAAAAANNNNNGCTTN 450

inversepcr 92 -------------------------------------------------- 91

custom1seq 451 NNNGGTTTTTGNCGCCCNTTTTTTTAGATACNGNGGANTCCNAANTTTCN 500

inversepcr 92 -------------------------------------------------- 91

custom1seq 501 GAAAAATGANTNTTNGTNCAACCATTTTTTNNNGGCGCCAAAAAATNTTC 550

inversepcr 92 -------------------------------------------------- 91

custom1seq 551 NCANGCNCCANCNGCCNGTNAGTCNTTTTTATTNANCNNTNNNTNCCTCC 600

inversepcr 92 -------------------------------------------------- 91

custom1seq 601 TGTNNTTNTNTGGGGGANANCAAANCTCCANNCNANAAAAAAAAGNGTTN 650

inversepcr 92 -------------------------------------------------- 91

custom1seq 651 CNCCGNCCCCCCCCTCCAAAAAAAAATTTTNTTCNCAAGATTNNTAAAAC 700

 || |.|.||||

inversepcr 92 ---CGCCTCTCCCC------------------------------------ 102

custom1seq 701 CCNGNNNCNGCCNGTTAACGTTAAATTTGANGNNNTAAAAAAAAAAGTAN 750

inversepcr 103 -------------------------------------------------- 102

custom1seq 751 GGGGTGGGNGNTNNCCCTNCCNNGTATNANNTNTGCCANTNGGNCCGTTC 800

 | .||||.

inversepcr 103 ------------------------------------------GCGCGTTG 110

custom1seq 801 CCCAATTTGTGTNNNTTCCCATGNGCCNNNTNTGAANGCNAAAAAAANTA 850

 .||.|||

inversepcr 111 GCCGATT------------------------------------------- 117

custom1seq 851 AGNNNNANNTGNAAAANANCCNANACNNNCTTTTNAANNCNTTTTTNCCC 900

inversepcr 118 -------------------------------------------------- 117

custom1seq 901 GGGTGTTCCANGNNAAAAAGNAAACAANAACGNAGNGNAAATGGNANNNN 950

inversepcr 118 -------------------------------------------------- 117

custom1seq 951 CCAANCCCCCCCTCCNTTNNGTGNAANANNNNNNNGGGATGAACACTTNA 1000

 ||

inversepcr 118 -CA----------------------------------------------- 119

custom1seq 1001 NNCTTANCNTNNNAANNGGTAANAAATNTNNGGAACCNCNAANGNNCNAA 1050

inversepcr 120 -------------------------------------------------- 119

custom1seq 1051 ACNGNTNCCNANANCNGNNNNNCCAAGNNTGAAAANTTNTGNTTTNANNC 1100

inversepcr 120 -------------------------------------------------- 119

custom1seq 1101 CNGNNNNNTCCNANNNNNCNCCNNANANTNTCNNTNCCTCCAAAANNCNC 1150

inversepcr 120 -------------------------------------------------- 119

custom1seq 1151 AGGAAANCCACCNNNAAGANCCTTTNNCNCAANANNTNNCTNNTAGACCA 1200

inversepcr 120 -------------------------------------------------- 119

custom1seq 1201 AANATNGCTTNTAAAANATCCTCCCCCGNNTTNGNCGGGNAGANTNNNTG 1250

inversepcr 120 -------------------------------------------------- 119

custom1seq 1251 TNGAAANNCTCNTNCNCCNNG 1271

inversepcr 120 --------------------- 119

**Genome-walking and inverse PCR shared region of genome-walking seq**

TTTGAGTGAGCTGATACCGCTCGCCGCAGCTCGAACGACCGAGCGCAGCGAGTCAGTGAGCAAGGAAGCGGANGAGCGCNCAA

**Zv8NA7791 (hit from Zv8)**

GGGGGGGGGGAAAAACGGGTGAAAAAAGGGGGGAAAATTAAATTCCGCACTTTGGGGGGCATTTTCTGTCAAATGATTTAGGAAGCACGGCTTTTTTTTCAAGGGGTTATTATTTTTTTCAGGGAGTGGGATTACCTTTTTCTCGAAAGGTATTTTAGGAGTGATAAAACAAACTGGGGGGGTCCCGGGTCCCTTTTCCCCCGGGGAAGTCCCCGCGAGACGGTAAGGTTGCCACTTCATTCTTGTCATTATCCTATAATAATGGGGCAATTATGAGGCCTATTGTTTTAGGGGGGGATGGATATGTGGATGTACACATATGACTCATGCAGTTCGGGGTGAGGGTACAAGTCCGTCTAAAATCCGACGCGGGGTGTAAGCAAGCACGTCAGTGAGGGTAAGAGCGTGTAGAAGTAGGTTAGTGCTGAGGTCATTTTGTGGCATGAGAGTCAGATGATGATGAGAGAGCCTATGACGCAGTGCAGATTCCGGAGCCGATGAGAGAGGATAAGTTAGCGGATGAGGGGAGAATAGAGACGTCAGCAGGGGGAATTAGTGGGAATTGGCATGTGTGGGGGCCTGTTTGATTATGCGGCATCTGAGCAGATGGGAATGAGATTGAAGCAGATTAAGTTGGAAATCGCGAGGAGATGCGCAGGGAGAAAATTGTAGCATCAGGTGCCATTCCACAGTTAGATTGCGTGCAGGTTGTTAAGGGGGATCCGAGTGGTCCTCGTTGTGTTTGCTTCAGGCAGTAATTCGTGGACGTGTTGTAAGTTTGAGACATTAGTTCATCGGGCAGGGGTTTGGCTGGCGCGAGATTTTATGAGGGTGGTCTGTGTCAGGCTTGAATTCTTGCAGGTTTGGTTGTTGAGGGCACTAGTTCCTCGGCGTTTGGTCGGTTTGTGCCTTAAAGGCTCTGGGTTTTGTCTGTTTTTTGCATTAGTTCCTCTAAGGATGTCGTTTTTTGCATTAGTTCCTATGCGTTTTGTCTGTTTGTTGCATTATTTCCTCTGCGTTTTGTCGGGTAGCGAGATCGAATCTTGCAGCTCTGTGTGTAGTGTGTCTTCATGATGCTCAAGCTGCTATCTCGGTCTGCTATTCCGCACTACCTCTGAGCCGTAACCGTAAATTGTTAAGTCCGTGGTGCCTAATGATGGATCTAACTCTCATTAATTGCGCTCGCCCTCATGGCCCGCTTTCCAATCGGGAAACCTGTCGTGCCAGCTGCATTAATGAATCTGCCAACGCGCTGGGAGAGGCGGTTTGCATA**TTGGGCGCTCTTCCGCTTCCTCGCTCACTGACTCGCTGCGCTCGGTCGTTCAGCTGCGGCGAGCGGTATCAGCTCACTCAAA**GGCGGTAATACAGTTATCCACACAATCATGGGATAACGCAGGAAAGAACATGTGACCAAAAGGCCAGCAAAAGGCCATGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCCTGACGAGCATCACAAAAATCTACGCTCATGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCGCGTGCGCTCTCCTGTTACCACCCTGCCGCTTACCGGATACCTGTCCGCCATATCACCCTTCGGGAAGCGAGGCGCTTTCTCAAACCTCACGCTGAAGGTATCTCAGTACGGTGAAGGATCGATCGCTCCAAGCAGGGCTGCGTGTAAACCTATGAAAGCCAGAAAGTATGAATACGAACAGTGAGAAACTGAAAAAGACAAGGAAAAGCAACAATCCAAACGAGTCATTCTGAACGAGGCGCGCATACCCAACAGCTAGCAGCAAAACCCAATAATAACCCCCGAACCTCAACGGAATAAAGCCGGGGAGAAAAAACCCAAAAAAGGCGAAAGGAGAAAAAACCCCAAACAGAAAATGAAAGCGAAAAATAACCACCACCCCAAAAGACTGGAGAAGCTGCCGAAAGAAAGAAACCCCCAAGAGGCCCGAAGNACCGCAAACCAAACCAAGCCACGGAATCAAGGGAACGGGCCAAGAAGAACATAGACCCAGCAAAATCTCACAGGGGCCGCACGCGAAACAATTAAATGGGAAAAACCCCCCAAAAATAACAAAAAAAGGCGTCAAAAAGAAAATACCCGACACCCAAAAA