Supplementary figure 2: Sequence alignment of 58-67kb tb1 upstream region. Sequences are named to reflect their species and origins. The first letter indicates the species (m for maize and t fro teosinte), and followed by maize inbred lines or specific accession of teosinte. Identical sequences are highlighted in deep blue. Conserved sequences are highlighted in deep pink (75%-99%), light blue (50%-75%) and yellow (35%-50%). The retrotransposon inserted 58.8kb upstream of tb1 is removed from alignment, and it’s insertion site is shown in lowercase letters.

```
mCIMBL84                                                                                                                 0
mSi273                                                                   TGGTCCAAGATCACCCCTTTATGTTTAGTAGTAGTTTGA    39
mCML115     TATAAATAAACCGTGCTA.TTTCTAATA........................................................................    27
mGEMS3      TACAA.TAAA.CGTGCTG..TTCTAATAAATTTTTTGTTGCAGTGGTGG..ATTTTTTTTTTGGTCCAAGATCACCCCTTTATGTTTAGTAGTAGTTTGA    94
mHYS        TACAAATAAACCGTGCTG.TTTCTAATAAATTTTTTGTTGCAGTGGTGGATATATATTTTTTTGTCCAAGATCACTCCTTTATTTTTAGTAGTAGTTTGA    99
mCIMBL36    TACA.ATA..GCGTGCTG..TTCTAATAAATT.TTTGTTGCAGTGGTGG..ATTTTTTTTTTGGTCCAAGATCACCCCTTTATGTTTAGTAGTAGTTTGA    92
mCML307     TACAAATAAACCGTGCTG.TTTCTAATAAATTTTTTGTTGCAGTGGTGGATATATATTTTTTTGTCCAAGATCACTCCTTTATTTTTAGTAGTAGTTTGA    99
mCIMBL144   TAC..ATAA..CGTGCTG.TTTCTAATAAATTTTTTGTTGCAGTGGTGG..ATTTTTTTTTTGGTCCAAGATCACCCCTTTATGTTTAGTAGTAGTTTGA    93
mGEMS45     TATAAATAAACCGTGCTA.TTTCTAATA........................................................................    27
mCIMBL60    TACAAATAAACCGTGCTA.TTTCTAATA........................................................................    27
mCIMBL156   TACAA.TAAA.CGTGCTG.GTTCTAATAAATTTTTTGGGGCAGTGGGGG..ATTTTTTTT.GGGTCCAAGATCACCCCTTTATGTTTAGTAGTAGTTTGA    94
mCIMBL72    TACAAATAAACCGGGCTG.TTTTTAATAAATTTTTTGTTGCAGTGGTGG..ATTTTTTTTTTGGTCCAAGATCACCCCTTTATGTTTAGTAGTAGTTTGA    97
mZZ03       TATAAATAAACCGTGCTA.TTTCTAATA........................................................................    27
mJiao51     TACAAATAAACCGTGCTG.TTTCTAATAAATTTTTTGTTGCAGTGGTGGATATATATTTTTTTGTCCAAGATCACTCCTTTATTTTTAGTAGTAGTTTGA    99
mCML486     TACAAATAAACCGTGCTG.TTTTTAATAAATTTTTTGTTGCAGTGGGGGAT...TTTTTTTTGGTCCAAGATCACCCCTTTATGTATAGTAGTAGTTTGA    96
mBZN        TACAAATAAACCGTGCTG.TTTCTAATAAATTTTTTGTTGCAGTGGTGGATATATATTTTTTTGTCCAAGATCACTCCTTTATTTTTAGTAGTAGTTTGA    99
mB73        TACAAATAAACCGTGCTG.TTTCTAATAAATTTTTTGTTGCAGTGGTGG..ATTTTTTTTTTGGTCCAAGATCACCCCTTTATGTTTAGTAGTAGTTTGA    97
mW22        TACAAATAAACCGTGCTG.TTTCTAATAAATTTTTTGTTGCAGTGGTGG..ATTTTTTTTTTGGTCCAAGATCACCCCTTTATGTTTAGTAGTAGTTTGA    97
m87-1       TACAAATAAACCGTGCTG.TTTCTAATAAATTTTTTGTTGCAGTGGTGGAT.TTTTTTTTTTGGTCCAAGATCACCCCTTTATGTTTAGTAGTAGTTTGA    98
t384061     TACAAACAAACCGTGCTG.TTTCTAATAAATTTGTTGTTGCAGTGGTGG..ATATTTTTTGTTGTCCAAGATCACCCCTTTATTTTTAGTAGTAGTTTGA    97
t8766       TACAAATAAACCGTGCTG.TTTCTAATAAATTTTTTGTTGCAGTGGTGGATATATATTTTTTTGTCCAAGATCACTCCTTTATTTTTAGTAGTAGTTTGA    99
t13554      TAAAATTAAACCGTGGTGTTTTTTAAAAAATTTTTTGGTGGCAGGGGGGGATATTTTTTTTTTGTCCAAGATCACTCCTTTATTTTTAGCAGTAGTTTGA   100
t29080      TACAAATAAACCGTGCTA.TTTCTAATA........................................................................    27
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mCML51                                                                                                                   0
mSi273.2                                                                                                                 0
mCIMBL96                                                                                                                 0
mYe478                                                                                                                   0
m7327                                                                                                                    0

mCIMBL84                                                  CACCACCATTAATCAAAGTTTAT.ACCAAACTTAATTG.GGGGCGCCGTCGATTCTCACGTG    60
mSi273      GCTTGCGG.AT..GTAATAACGATGGACAAAGTACG.ACACCACCATTAATCAAAGTTTTA.TACAAACATAATTT.GGGGCGCCGTCGAATCTCACGTG   133
mCML115     ....................................................AAAGTTTTA.TACAAACATAATTT.GGGGCGCCGTCGAATCTCACGTG    73
mGEMS3      GCTTGCGG.AT..GTAATAACGATGGACAAAGTACG.ACACCACCATTAATCAAAGTTTTA.TACAAACATAATTT.GGGGCGCCGTCGAATCTCACGTG   188
mHYS        GCTTGCGG.AT..GTAATAACGATGGACAAAGTACG.ACACCACCATTAATCAAAGTTTTA.TACAAACATAATTT.GGGGCGCCGTTGATTCTCACGTG   193
mCIMBL36    GCTTGCGG.AT..GTAATAACGATGGACAAAGTACG.ACACCACCATTAATCAAAGTTTTA.TACAAACATAATTT.GGGGCGCCGTCGAATCTCACGTG   186
mCML307     GCTTGCGG.AT..GTAATAACGATGGACAAAGTACG.ACACCACCATTAATCAAAGTTTTA.TACAAACATAATTT.GGGGCGCCGTTGATTCTCACGTG   193
mCIMBL144   GCTTGCGG.AT..GTAATAACGATGGACAAAGTACG.ACACCACCATTAATCAAAGTTTTA.TACAAACATAATTTGGGGGCGCCGTCGAATCTCACGTG   188
mGEMS45     ....................................................AAAGTTTTA.TACAAACATAATTT.GGGGCGCCGTCGAATCTCACGTG    73
mCIMBL60    ....................................................AAAGTTTTA.TACAAACATAATTT.GGGGCGCCGTCGAATCTCACGTG    73
mCIMBL156   GCTTGCGGAAT..GTAATAACGATGGACAAAGTACGAACACCACCATTAATCAAAGTTTTATTACAAACATAATTT.GGGGCGCCGTCGAATCTCACGTG   191
mCIMBL72    GCTTGCGG.AT..GTAATAACGATGGACAAAGTACG.ACACCACCATTAATCAAAGTTTTA.TACAAACATAATTT.GGGGCGCCGTCGAATCTCACGTG   191
mZZ03       ....................................................AAAGTTTTA.TACAAACATAATTT.GGGGCGCCGTCGAATCTCACGTG    73
mJiao51     GCTTGCGGTAT..GTAATAACGATGGACAAAGTACG.ACACCACCATTAATCAAAGTTTTA.TACAAACATAATTT.GGGGCGCCGTTGATTCTCACGTG   194
mCML486     GCTTGCGG.AT..GTAATAACGATGGACAAAGTACG.ACACCACCATTAATCAAAGTTTTA.TACAAACATAATTT.GGGGCGCCGTCGAATCTCACGTG   190
mBZN        GCTTGCGG.AT..GTAATAACGATGGACAAAGTACG.ACACCACCATTAATCAAAGTTTTA.TACAAACATAATTT.GGGGCGCCGTTGATTCTCACGTG   193
mB73        GCTTGCGG.AT..GTAATAACGATGGACAAAGTACG.ACACCACCATTAATCAAAGTTTTA.TACAAACATAATTT.GGGGCGCCGTCGAATCTCACGTG   191
mW22        GCTTGCGGAT...GTAATAACGATGGACAAAGTACG.ACACCACCATTAATCAAAGTTTTA.TACAAACATAATTT.GGGGCGCCGTCGAATCTCACGTG   191
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m87-1        GCTTGCGGAT...GTAATAACGATGGACAAAGTACG.ACACCACCATTAATCAAAGTTTTA.TACAAACATAATTT.GGGGCGCCGTCGAATCTCACGTG    192
t384061      GCTTGCGGAT...GTAATAACGATGGACAAAGTACG.ACACCACCATTAATCAAAGTTTGA.TACAAACATAATTT.GGGGCGCCGTCGATTCTCACGTG    191
t8766        GCTTGCGGAT...GTAATAACGATGGACAAAGTACG.ACACCACCATTAATCAAAGTTTTA.TACAAACATAATTT.GGGGCGCCGTTGATTCTCACGTG    193
t13554       GCTTGCGGATGTAATAATAACGATGGACAAAGTACG.ACACCACCATTAATCAAAGTTTTA.TACAAACATAATTTGGGGCGCCGTTCGATTCTCACGTG    198
t29080       ....................................................AAAGTTTTA.TACAAACATAATTT.GGGGCGCCGTCGAATCTCACGTG     73
t29085       ...............................................TAATAAAAGTTTTA.TACAAACATAATTT.GGGGCGCCGTCGAATCTCACGTG     73
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mSi273       AAGAGACAGTTTTGTTGACAATTT.AAAAGCACGCATATCTCTCACAGATTCAAC.AACAAATC..AGCAACT.ACCAGC...GAAGAAGAGGCTAATAT    225
mCML115      AAGAGACAGTTTTGTTGACAATTT.AAAAGCATGCATATCTCTCACAGATTGAAC.AACAAATC..AACAACT.ACCAGCGAAGAAGAAGAGGCTAATGT    168
mGEMS3       AAGAGACAGTTTTGTTGACAATTT.AAAAGCACGCATATCTCTCACAGATTCAAC.AACAAATC..AGCAACT.ACCAGCGAAGAAGAAGAGGCTAATAT    283
mHYS         AAGAGACAGTTTTGTTGACAATTT.AAAAGCATGC..ATCTCTCACAGATTCAAC.AACAAATC..AACAACT.ACCAGCGAAGAAGAAGAGGCTAATGT    286
mCIMBL36     AAGAGACAGTTTTGTTGACAATTT.AAAAGCACGCATATCTCTCACAGATTCAAC.AACAAATC..AGCAACT.ACCAGC...GAAGAAGAGGCTAATAT    278
mCML307      AAGAGACAGTTTTGTTGACAATTT.AAAAGCATGC..ATCTCTCACAGATTCAAC.AACAAATC..AACAACT.ACCAGCGAAGAAGAAGAGGCTAATGT    286
mCIMBL144    AAGAGACAGTTTTGTTGACAATTT.AAAAGCACGCATATCTCTCACAGATTCAAC.AACAAATC..AGCAACT.ACCAGC...GAAGAAGAGGCTAATAT    280
mGEMS45      AAGAGACAGTTTTGTTGACAATTT.AAAAGCATGCATATCTCTCACAGATTGAAC.AACAAATC..AACAACT.ACCAGCGAAGAAGAAGAGGCTAATGT    168
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mCIMBL156    AAGAGACAGTTTTGTTGACAATTT.AAAAGCACGCATATCTCTCACAGATTCAAC.AACAAATC..AGCAACT.ACCAGCGAAAAAAAAAAGGCTAATAT    286
mCIMBL72     AAGAGACAGTTTTGTTGACAATTT.AAAAGCACGCATATCTCTCACAGATTCAAC.AACAAATC..AGCAACT.ACCAGCGAAGAAGAAGAGGCTAATAT    286
mZZ03        AAGAGACAGTTTTGTTGACAATTT.AAAAGCATGCATATCTCTCACAGATTGAAC.AACAAATC..AACAACT.ACCAGCGAAGAAGAAGAGGCTAATGT    168
mJiao51      AAGAGACAGTTTTGTTGACAATTT.AAAAGCATGC..ATCTCTCACAGATTCAAC.AACAAATC..AACAACT.ACCAGCGAAGAAGAAGAGGCTAATGT    287
mCML486      AAGAGACAGTTTTGTTGACAATTT.AAAAGCACGCATATCTCTCACAGATTCAAC.AACAAATC..AGCAACT.ACCAGCGAAGAAGAAGAGGCTAATAT    285
mBZN         AAGAGACAGTTTTGTTGACAATTT.AAAAGCATGC..ATCTCTCACAGATTCAAC.AACAAATC..AACAACT.ACCAGCGAAGAAGAAGAGGCTAATGT    286
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m87-1        AAGAGACAGTTTTGTTGACAATTT.AAAAGCACGCATATCTCTCACAGATTCAAC.AACAAATC..AGCAACT.ACCAGCGAAGAAGAAGAGGCTAATAT    287
t384061      AAG..ACAGTTTTGTTGACAATTT.GAAAGCATGC..ATCTCTCACAGATTCAACAAACAAATC..AGCAACT.ACCAGCGAAGAAGAAGAGGCTAATGT    283
t8766        AAGAGACAGTTTTGTTGACAATTT.AAAAGCATGC..ATCTCTCACAGATTCAAC.AACAAATC..AACAACT.ACCAGCGAAGAAGAAGAGGCTAATGT    286
t13554       AAG..ACAGTTTTGTTGACAATTTAAAAAGCATGC..ATCTCTCACAGATTCAACAACAAATCAACAACTACGTACCAGCGAAGAAGGAGAGGCTAATGT    294
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t29085       AAGAGACAGTTTTGTTGACAATTT.AAAAGCATGCATATCTCTCACAGATTCAAC.AACAAATC..AACAACT.ACCAGCGAAGAAGAAGAGGCTAATGT    168
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mGy220                                                                                                                 0
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mSi273.2                                                                                                               0
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mYe478                                                                                                                 0
m7327                                                                                                                  0


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mSi273        AATAACTAGCCTGCTGAAGCTCAGGAGGCTGTACA......ATGCTGTGGTCCATGGTCCCTGT....CCTGCTCG.CCGCAACTGAACTGAGTTTGGG.    313
mCML115       AATAACTAGACTGCTGAAGCTCAGCAGGCTGTACAATGCATATGCTGTGGTCCATGGTCCCTGT....CCTGCTCG.CCGCAACTGAACTGAGTTTGGG.    262
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mCIMBL36      AATAACTAGCCTGCTGAAGCTCAGGAGGCTGTACA......ATGCTGTGGTCCATGGTCCCTGT....CCTGCTCG.CCGCAACTGAACTGAGTTTGGG.    366
mCML307       AATAACTAGCCTGCTGAAGCTCAGCAGGCTGTACA....AAATGCTGTGGTCCATGGTCCCTGT....CCTGCTCG.CCGCAACTGAACTGAGTTTGGG.    376
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mGEMS45       AATAACTAGACTGCTGAAGCTCAGCAGGCTGTACAATGCATATGCTGTGGTCCATGGTCCCTGT....CCTGCTCG.CCGCAACTGAACTGAGTTTGGG.    262
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mZZ03         AATAACTAGACTGCTGAAGCTCAGCAGGCTGTACAATGCATATGCTGTGGTCCATGGTCCCTGT....CCTGCTCG.CCGCAACTGAACTGAGTTTGGG.    262
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mW22          AATAACTAGCCTGCTGAAGCTCAGGAGGCTGTACA......ATGCTGTGGTCCATGGTCCCTGT....CCTGCTCG.CCGCAACTGAACTGAGTTTGGG.    374
m87-1         AATAACTAGCCTGCTGAAGCTCAGGAGGCTGTACA......ATGCTGTGGTCCATGGTCCCTGT....CCTGCTCG.CCGCAACTGAACTGAGTTTGGG.    375
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mGy220                                                                                                                 0
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mSi273.2                                                                                                               0
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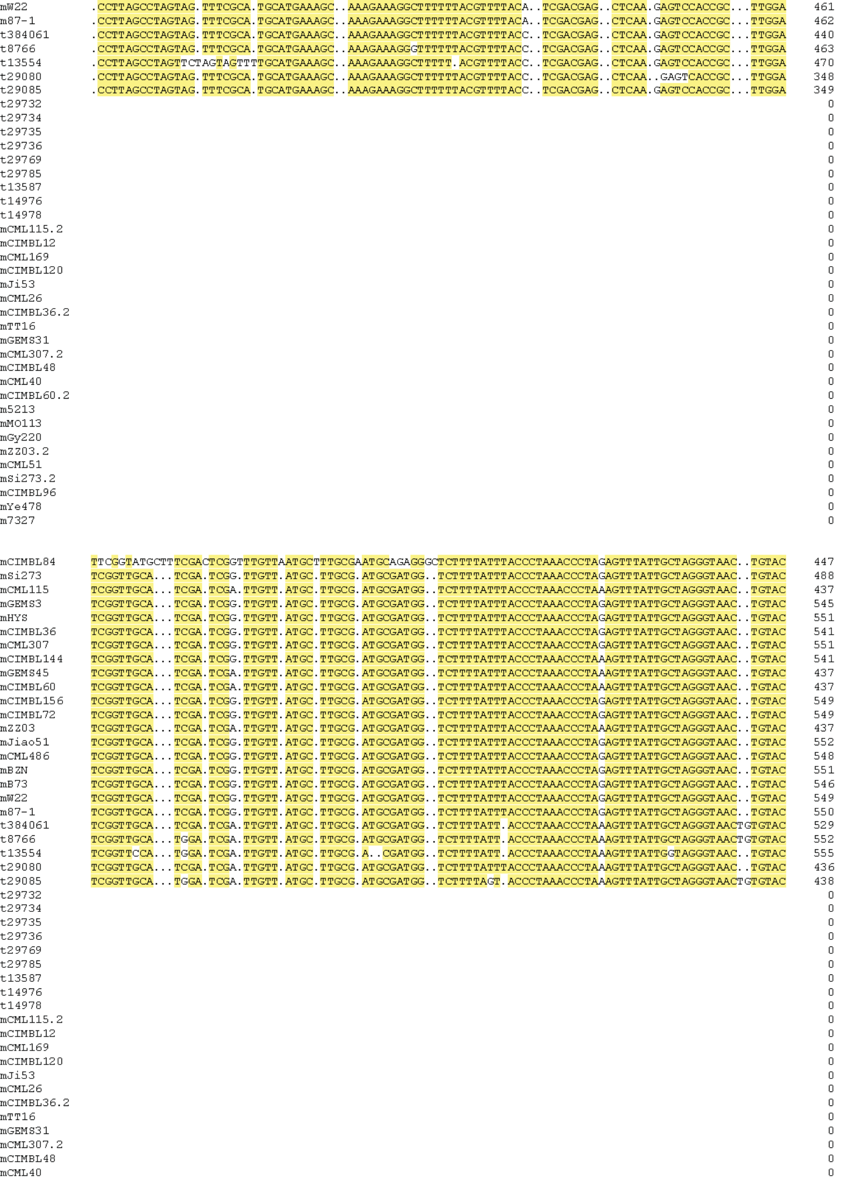

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mSi273.2                                                                                                               0
mCIMBL96                                                                                                               0
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mGEMS3        TCGGTTGCA...TCGA.TCGG.TTGTT.ATGC.TTGCG.ATGCGATGG..TCTTTTATTTACCCTAAACCCTAGAGTTTATTGCTAGGGTAAC..TGTAC     545
mHYS          TCGGTTGCA...TCGA.TCGG.TTGTT.ATGC.TTGCG.ATGCGATGG..TCTTTTATTTACCCTAAACCCTAGAGTTTATTGCTAGGGTAAC..TGTAC     551
mCIMBL36      TCGGTTGCA...TCGA.TCGG.TTGTT.ATGC.TTGCG.ATGCGATGG..TCTTTTATTTACCCTAAACCCTAGAGTTTATTGCTAGGGTAAC..TGTAC     541
mCML307       TCGGTTGCA...TCGA.TCGG.TTGTT.ATGC.TTGCG.ATGCGATGG..TCTTTTATTTACCCTAAACCCTAGAGTTTATTGCTAGGGTAAC..TGTAC     551
mCIMBL144     TCGGTTGCA...TCGA.TCGG.TTGTT.ATGC.TTGCG.ATGCGATGG..TCTTTTATTTACCCTAAACCCTAAAGTTTATTGCTAGGGTAAC..TGTAC     541
mGEMS45       TCGGTTGCA...TCGA.TCGA.TTGTT.ATGC.TTGCG.ATGCGATGG..TCTTTTATTTACCCTAAACCCTAAAGTTTATTGCTAGGGTAAC..TGTAC     437
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mZZ03         TCGGTTGCA...TCGA.TCGA.TTGTT.ATGC.TTGCG.ATGCGATGG..TCTTTTATTTACCCTAAACCCTAAAGTTTATTGCTAGGGTAAC..TGTAC     437
mJiao51       TCGGTTGCA...TCGA.TCGG.TTGTT.ATGC.TTGCG.ATGCGATGG..TCTTTTATTTACCCTAAACCCTAGAGTTTATTGCTAGGGTAAC..TGTAC     552
mCML486       TCGGTTGCA...TCGA.TCGG.TTGTT.ATGC.TTGCG.ATGCGATGG..TCTTTTATTTACCCTAAACCCTAGAGTTTATTGCTAGGGTAAC..TGTAC     548
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t384061       TCGGTTGCA...TCGA.TCGA.TTGTT.ATGC.TTGCG.ATGCGATGG..TCTTTTATT.ACCCTAAACCCTAAAGTTTATTGCTAGGGTAACTGTGTAC     529
t8766         TCGGTTGCA...TGGA.TCGA.TTGTT.ATGC.TTGCG.ATGCGATGG..TCTTTTATT.ACCCTAAACCCTAAAGTTTATTGCTAGGGTAACTGTGTAC     552
t13554        TCGGTTCCA...TGGA.TCGA.TTGTT.ATGC.TTGCG.A..CGATGG..TCTTTTATT.ACCCTAAACCCTAAAGTTTATTGGTAGGGTAAC..TGTAC     555
t29080        TCGGTTGCA...TCGA.TCGA.TTGTT.ATGC.TTGCG.ATGCGATGG..TCTTTTATTTACCCTAAACCCTAAAGTTTATTGCTAGGGTAAC..TGTAC     436
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mCML115       GTGTTGTTACTCGTTA....CATATATGCAGCACGCCCATGGAAACGAAGACAAAGATGCTGTGCTCTAAAGCGTTTGCCCAGATCCCCATCGGGTGCCT    533
mGEMS3        GTGTTCTTACTCGTTACATGCATATATGCAGCACGCCCATGGAAACGAAGACAAAGATGCTGTGCTCTAAAGCGTTTGCCCAGATCCCCATCGGGTGCCT    645
mHYS          GTGTTGTTACTCGTTA....CATATATGCAGCACGCCCATGGAAACGAAGACAAAGATGCTGTGCTCTAAAGCGTTTGCCCAGATCCCCATCGGGTGCCT    647
mCIMBL36      GTGTTCTTACTCGTTACATGCATATATGCAGCACGCCCATGGAAACGAAGACAAAGATGCTGTGCTCTAAAGCGTTTGCCCAGATCCCCATCGGGTGCCT    641
mCML307       GTGTTCTTACTCGTTACATGCATATATGCAGCACGCCCATGGAAACGAAGACAAAGATGCTGTGCTCTAAAGCGTTTGCCCAGATCCCCATCGGGTGCCT    651
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mW22          GTGTTCTTACTCGTTACATGCATATATGCAGCACGCCCATGGAAACGAAGACAAAGATGCTGTGCTCTAAAGCGTTTGCCCAGATCCCCATCGGGTGCCT    649
m87-1         GTGTTCTTACTCGTTACATGCATATATGCAGCACGCCCATGGAAACGAAGACAAAGATGCTGTGCTCTAAAGCGTTTGCCCAGATCCCCATCGGGTGCCT    650
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t8766         GTGTTGTTACTCGTTA....CATATATGCAGCACGCCCATGGAAACGAAGACAAAGATGCTGTGCTCTAAAGCGTTTGCCCAGATCCCCATCGGGTGCCT    648
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t29080        GTGTTCTTACTCGTTACATGCATATATGCAGCACGCCCATGGAAACGAAGACAAAGATGCTGTGCTCTAGAGCGTTTGCCCAGATCCCCATCGGGTGCCT    536
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mSi273.2                                                                                                                    0
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mSi273        GACCATTCATTATCAACAGCAGCAGGCGGCC.GGGGGGGAAGCTAGTAGCTAGTAGCTAGCGCGCACGCA...GCTGGTGGCCGCTGGCCTGGGTGGGCA    684
mCML115       GACCATTCATTATCAACAGCAGCAGGCGGCC.GGGGGGCAAGCTAGTAGC...TAGCTAGCGCGCACGCAGCTGCTGGTGGCCGCTGGCCTGGGTGGGCA    629
mGEMS3        GACCATTCATTATCAACAGCAGCAGGCGGCC.GGGGGGGAAGCTAGTAGCTAGTAGCTAGCGCGCACGCA...GCTGGTGGCCGCTGGCCTGGGTGGGCA    741
mHYS          GACCATTCATTATCAACAGCAGCAGGCGGCC.GGGGGGCAAGCTAGTAGC...TAGCTAGCGCGCACGCAGCTGCTGGTGGCCGCTGGCCTGGGTGGGCA    743
mCIMBL36      GACCATTCATTATCAACAGCAGCAGGCGGCC.GGGGGGGAAGCTAGTAGCTAGTAGCTAGCGCGCACGCA...GCTGGTGGCCGCTGGCCTGGGTGGGCA    737
mCML307       GACCATTCATTATCAACAGCAGCAGGCGGCC.GGGGGGGAAGCTAGTAGCTAGTAGCTAGCGCGCACGCA...GCTGGTGGCCGCTGGCCTGGGTGGGCA    747
mCIMBL144     GACCATTCATTATCAACAGCAGCAGGCGGCC.GGGGGGGAAGCTAGTAGCTAGTAGCTAGCGCGCACGCA...GCTGGTGGCCGCTGGCCTGGGTGGGCA    737
mGEMS45       GACCATTCATTATCAACAGCAGCAGGCGGCC.GGGGGGCAAGCTAGTAGC...TAGCTAGCGCGCACGCAGCTGCTGGTGGCCGCTGGCCTGGGTGGGCA    629
mCIMBL60      GACCATTCATTATCAACAGCAGCAGGCGGCC.GGGGGGCAAGCTAGTAGC...TAGCTAGCGCGCACGCAGCTGCTGGTGGCCGCTGGCCTGGGTGGGCA    629
mCIMBL156     GACCATTCATTATCAACAGCAGCAGGCGGCC.GGGGGGGAAGCTAGTAGCTAGTAGCTAGCGCGCACGCA...GCTGGTGGCCGCTGGCCTGGGTGGGCA    745
mCIMBL72      GACCATTCATTATCAACAGCAGCAGGCGGCCGGGGGGGAAGCTAGTAGCTAGTAGCTAGCGCGCACGCA...GCTGGTGGCCGCTGGCCTGGGTGGGCA    746
mZZ03         GACCATTCATTATCAACAGCAGCAGGCGGCC.GGGGGGCAAGCTAGTAGC...TAGCTAGCGCGCACGCAGCTGCTGGTGGCCGCTGGCCTGGGTGGGCA    629
mJiao51       GACCATTCATTATCAACAGCAGCAGGCGGCC.GGGGGGCAAGCTAGTAGC...TAGCTAGCGCGCACGCAGCTGCTGGTGGCCGCTGGCCTGGGTGGGCA    744
mCML486       GACCATTCATTATCAACAGCAGCAGGCGGCC.GGGGGGGAAGCTAGTAGCTAGTAGCTAGCGCGCACGCA...GCTGGTGGCCGCTGGCCTGGGTGGGCA    744
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m87-1           GACCATTCATTATCAACAGCAGCAGGCGGCC.GGGGGGGAAGCTAGTAGCTAGTAGCTAGCGCGCACGCA...GCTGGTGGCCGCTGGCCTGGGTGGGCA    746
t384061         GACCATTCATTATCAACAGCAGCAGGCGGCCGGGGGGGGAAGCTAGTAGC...TAGCTAGCGCGCACGCA...GCTGGTGGCCGCTGGCCTGGGTGGGCA    719
t8766           GACCATTCATTATCAACAGCAGCAGGCGGCC.GGGGGGGAAGCTAGTAGCTAGTAGCTAGCGCGCACGCA...GCTGGTGGCCGCTGGCCTGGGTGGGCA    744
t13554          GACCATTCATTATCAACAGCAGCAGGCGGCC.GGGGGGGAAGCTAGTAGCTAGTAGCTAGCGCGCACGCA...GCTGGTGGCCGCTGGCCTGGGTGGGCA    747
t29080          GACCATTCATTATCAACAGCAGCAGGCGGCC.GGGGGGGAAGCTAGTAGCTAGTAGCTAGCGCGCACGCA...GCTGGTGGCCGCTGGCCTGGGTGGGCA    632
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mGy220                                                                                                                 0
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mSi273.2                                                                                                               0
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mSi273          CAGCAGCAGCGTCAGATATTTGCCACCA.CGATGTGGATGCGTGGTTGCACTTTGCAAG.CAAGGACTAGGGAGAGCCGGCCGCTACCTGAGCGAGAGGT    782
mCML115         CAGCAGCAGCGTCAGATATTTGCCACCA.CGATGTGGATGCGTGGTTGCACTTTGCAAG.CAAGGACTAGGGAGAGCCGGCCGCTACCTGAGCGAGAGGT    727
mGEMS3          CAGCAGCAGCGTCAGATATTTGCCACCA.CGATGTGGATGCGTGGTTGCACTTTGCAAG.CAAGGACTAGGGAGAGCCGGCCGCTACCTGAGCGAGAGGT    839
mHYS            CAGCAGCAGCGTCAGATATTTGCCACCA.CGATGTGGATGCGTGGTTGCACTTTGCAAG.CAAGGACTAGGGAGAGCCGGCCGCTACCTGAGCGAGAGGT    841
mCIMBL36        CAGCAGCAGCGTCAGATATTTGCCACCA.CGATGTGGATGCGTGGTTGCACTTTGCAAG.CAAGGACTAGGGAGAGCCGGCCGCTACCTGAGCGAGAGGT    835
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mCIMBL60        CAGCAGCAGCGTCAGATATTTGCCACCA.CGATGTGGATGCGTGGTTGCACTTTGCAAG.CAAGGACTAGGGAGAGCCGGCCGCTACCTGAGCGAGAGGT    727
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m87-1           CAGCAGCAGCGTCAGATATTTGCCACCA.CGATGTGGATGCGTGGTTGCACTTTGCAAG.CAAGGACTAGGGAGAGCCGGCCGCTACCTGAGCGAGAGGT    844
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t8766           CAGCAGCAGCGTCAGATATTTGCCACCA.CGATGTGGATGCGTGGTTGCACTTTGCAAG.CAAGGACTAGGGAGAGCCGGCCGCTACCTGAGCGAGAGGT    842
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t29080          CAGCAGCAGCGTCAGATATTTGCCACCA.CGATGTGGATGCGTGGTTGCACTTTGCAAG.CAAGGACTAGGGAGAGCCGGCCGCTACCTGAGCGACAGGT    730
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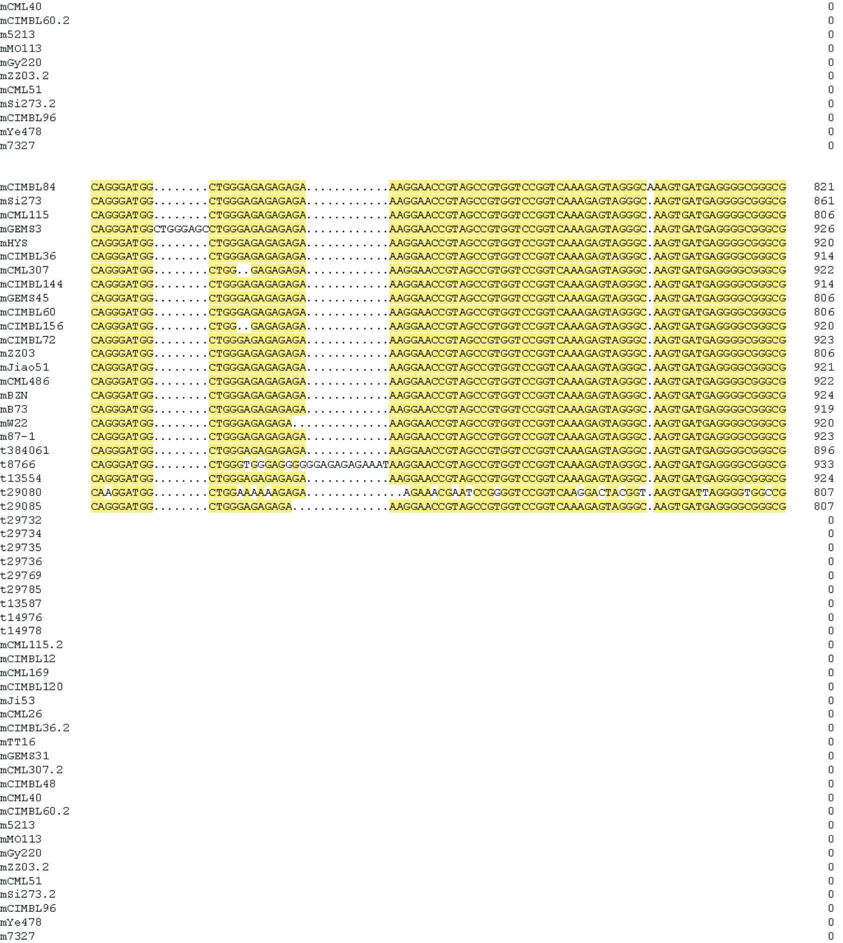

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mSi273.2                                                                                                             0
mCIMBL96                                                                                                             0
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mCML115      CAGGGATGG........CTGGGAGAGAGAGA..........AAGGAACCGTAGCCGTGGTCCGGTCAAAGAGTAGGGC.AAGTGATGAGGGGCGGGCG     806
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mHYS         CAGGGATGG........CTGGGAGAGAGAGA..........AAGGAACCGTAGCCGTGGTCCGGTCAAAGAGTAGGGC.AAGTGATGAGGGGCGGGCG     920
mCIMBL36     CAGGGATGG........CTGGGAGAGAGAGA..........AAGGAACCGTAGCCGTGGTCCGGTCAAAGAGTAGGGC.AAGTGATGAGGGGCGGGCG     914
mCML307      CAGGGATGG........CTGG..GAGAGAGA..........AAGGAACCGTAGCCGTGGTCCGGTCAAAGAGTAGGGC.AAGTGATGAGGGGCGGGCG     922
mCIMBL144    CAGGGATGG........CTGGGAGAGAGAGA..........AAGGAACCGTAGCCGTGGTCCGGTCAAAGAGTAGGGC.AAGTGATGAGGGGCGGGCG     914
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mCIMBL60     CAGGGATGG........CTGGGAGAGAGAGA..........AAGGAACCGTAGCCGTGGTCCGGTCAAAGAGTAGGGC.AAGTGATGAGGGGCGGGCG     806
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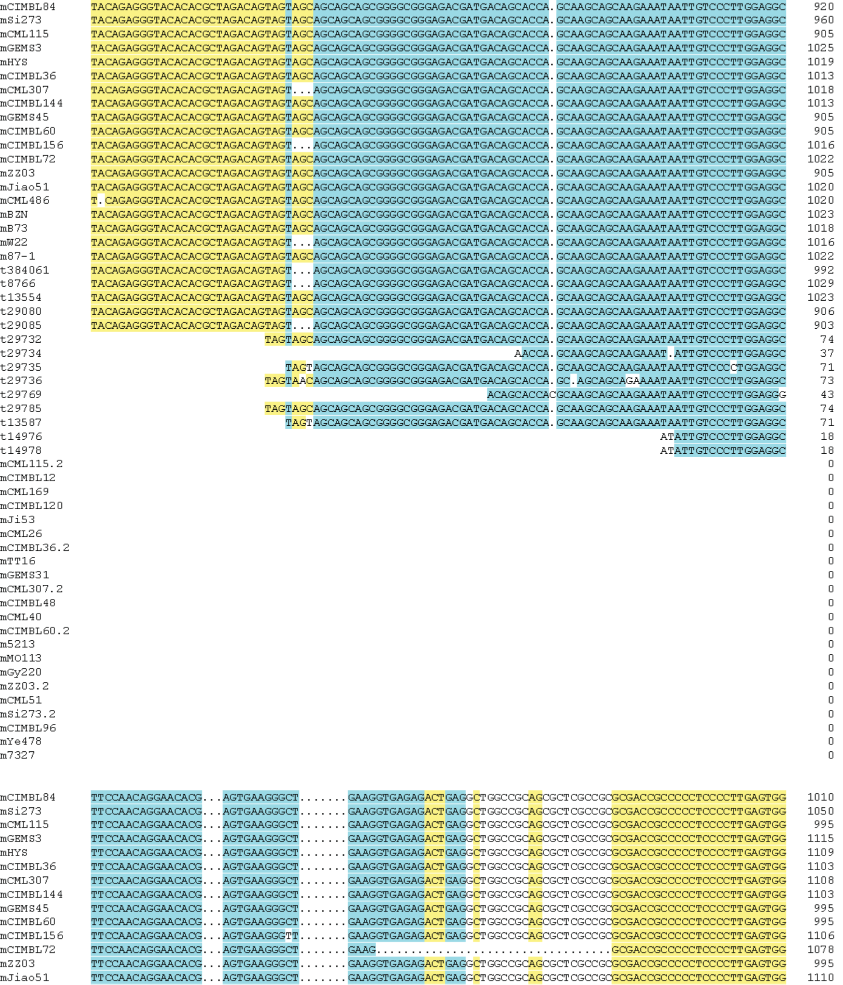

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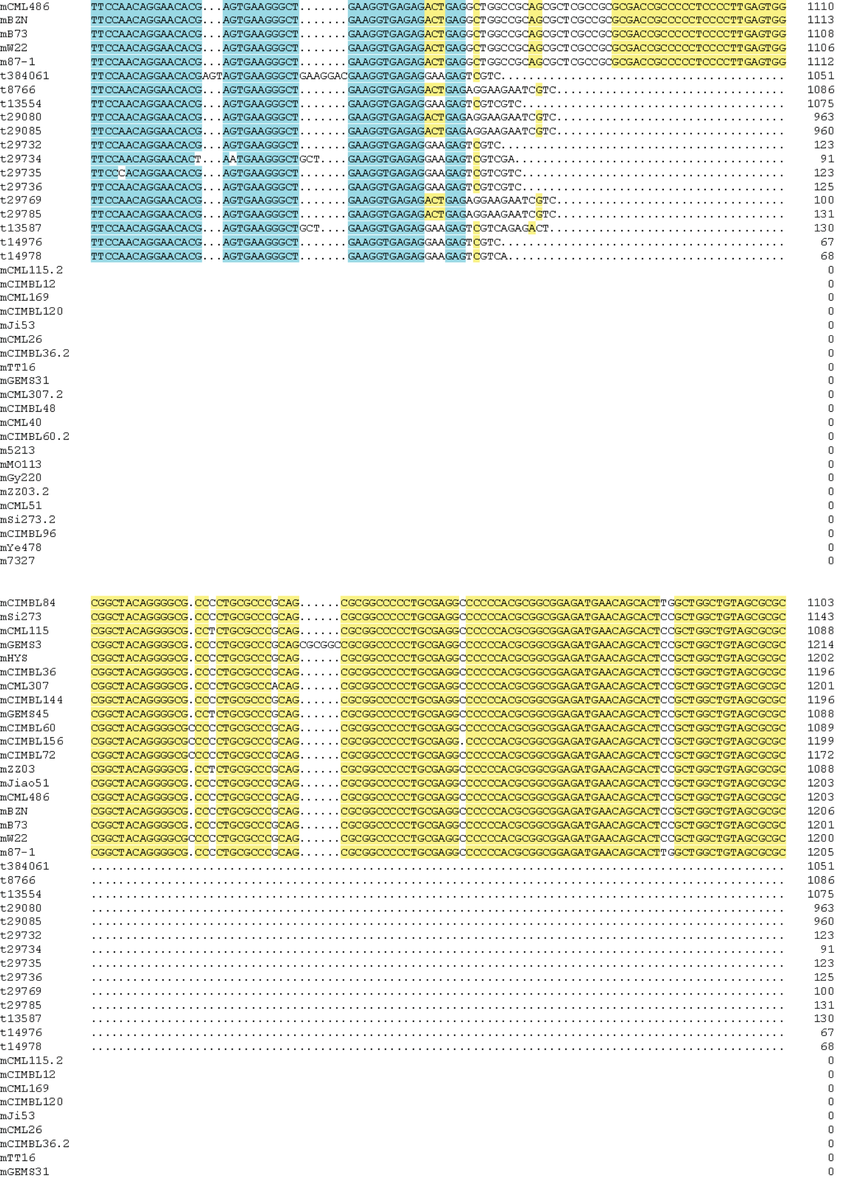

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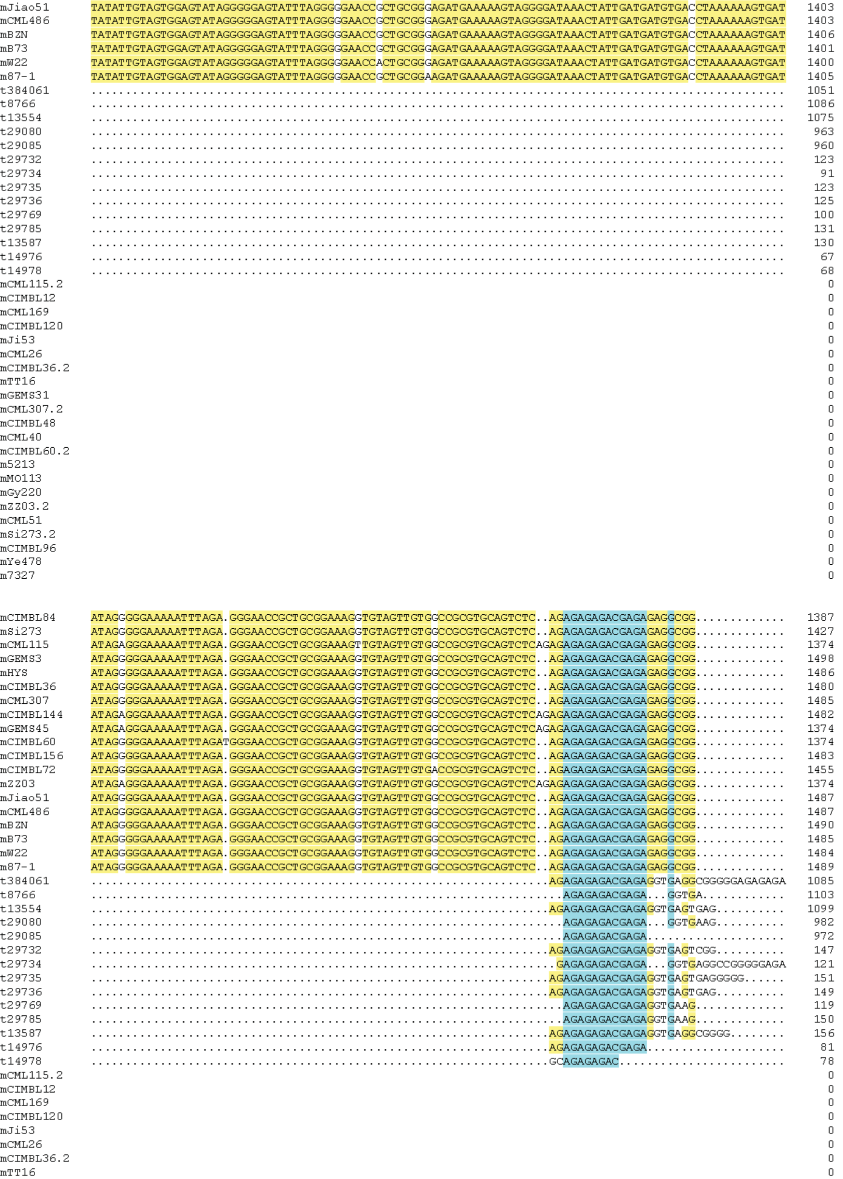

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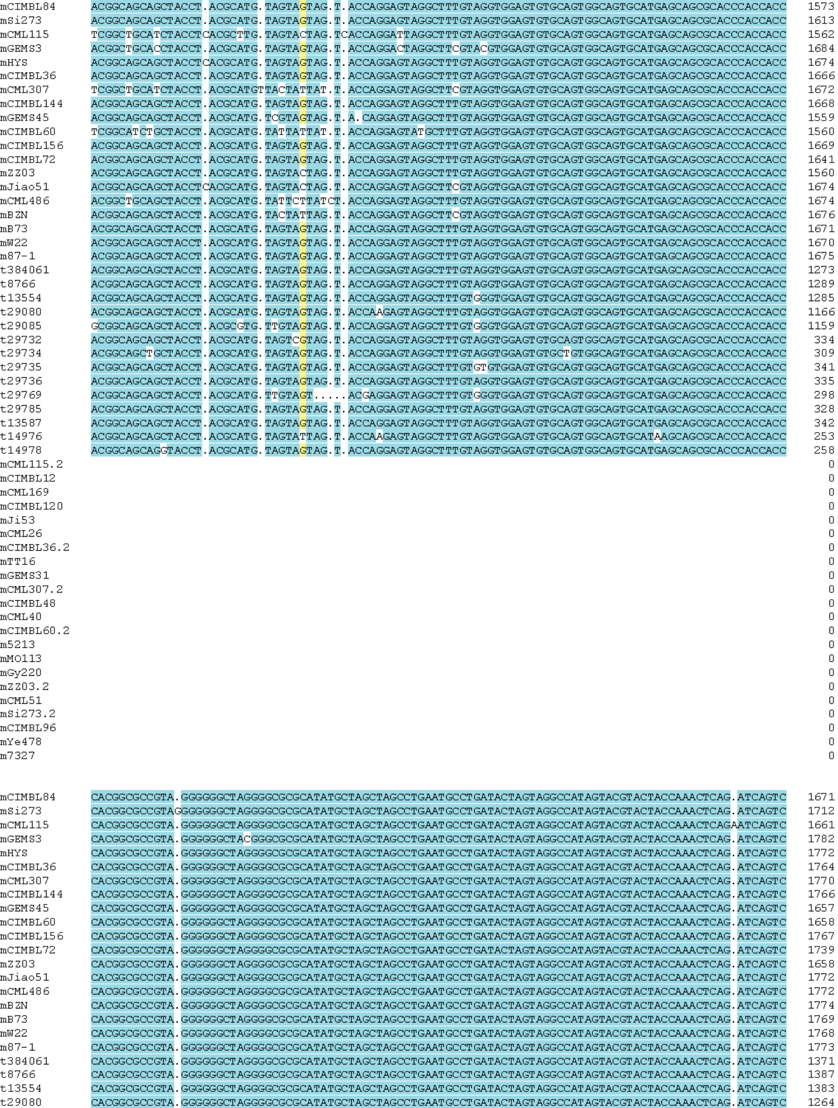

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mZZ03         CACGGCGCCGTA.GGGGGGCTAGGGGCGCGCATATGCTAGCTAGCCTGAATGCCTGATACTAGTAGGCCATAGTACGTACTACCAAACTCAG.ATCAGTC   1658
mJiao51       CACGGCGCCGTA.GGGGGGCTAGGGGCGCGCATATGCTAGCTAGCCTGAATGCCTGATACTAGTAGGCCATAGTACGTACTACCAAACTCAG.ATCAGTC   1772
mCML486       CACGGCGCCGTA.GGGGGGCTAGGGGCGCGCATATGCTAGCTAGCCTGAATGCCTGATACTAGTAGGCCATAGTACGTACTACCAAACTCAG.ATCAGTC   1772
mBZN          CACGGCGCCGTA.GGGGGGCTAGGGGCGCGCATATGCTAGCTAGCCTGAATGCCTGATACTAGTAGGCCATAGTACGTACTACCAAACTCAG.ATCAGTC   1774
mB73          CACGGCGCCGTA.GGGGGGCTAGGGGCGCGCATATGCTAGCTAGCCTGAATGCCTGATACTAGTAGGCCATAGTACGTACTACCAAACTCAG.ATCAGTC   1769
mW22          CACGGCGCCGTA.GGGGGGCTAGGGGCGCGCATATGCTAGCTAGCCTGAATGCCTGATACTAGTAGGCCATAGTACGTACTACCAAACTCAG.ATCAGTC   1768
m87-1         CACGGCGCCGTA.GGGGGGCTAGGGGCGCGCATATGCTAGCTAGCCTGAATGCCTGATACTAGTAGGCCATAGTACGTACTACCAAACTCAG.ATCAGTC   1773
t384061       CACGGCGCCGTA.GGGGGGCTAGGGGCGCGCATATGCTAGCTAGCCTGAATGCCTGATACTAGTAGGCCATAGTACGTACTACCAAACTCAG.ATCAGTC   1371
t8766         CACGGCGCCGTA.GGGGGGCTAGGGGCGCGCATATGCTAGCTAGCCTGAATGCCTGATACTAGTAGGCCATAGTACGTACTACCAAACTCAG.ATCAGTC   1387
t13554        CACGGCGCCGTA.GGGGGGCTAGGGGCGCGCATATGCTAGCTAGCCTGAATGCCTGATACTAGTAGGCCATAGTACGTACTACCAAACTCAG.ATCAGTC   1383
t29080        CACGGCGCCGTA.GGGGGGCTAGGGGCGCGCATATGCTAGCTAGCCTGAATGCCTGATACTAGTAGGCCATAGTACGTACTACCAAACTCAG.ATCAGTC   1264
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t29085         CACGGCGCCGTG.GGGGGGCTAGGGGCGCGCATATGCTAGCTAGCCTGAATGCCTGATACTAGTAGGCCATAGTACGTACTACCAAACTCAG.ATCAGTC   1257
t29732         CACGGCGCCGTA.GGGGGGCTAGGGGCGCGCATATGCTAGCTAGCCTGAATGCCTGATACTAGTAGGCCATAGTACGTACTACCAAACTCAG.ATCAGTC    432
t29734         CACGGCGCCGTA.GGGGGGCTAGGGGCGCGCATATGCTAGCTAGCCTGAATGCCTGATAATACTATGCCATAATACGTACTACCAAACTCAG.ATCACTC    407
t29735         CACGGCGCCGTA.GGGGGGCTAGGGGCGCGCATATGCTAGCTAGCCTGAATGCCTGATACTAGTAGGCCATAGTACGTACTACCAAACTCAG.ATCAGTC    439
t29736         CACGGCGCCGTA.GGGGGGCTAGGGGCGCGCATATGCTAGCTAGCCTGAATGCCTGATACTAGTAGGCCATAGTACGTACTACCAAACTCAG.ATCAGTC    433
t29769         CACGGCGCCGTA.GGGGGGC............TATGCTAGCTAGCCTGAATGCCTGATACTAGTAGGCCATAGTACGTACTACCAAACTCAG.ATCAGTC    384
t29785         CACGGCGCCGTA.GGGGGGCTAGGGGCGCGCATATGCTAGCTAGCCTGAATGCCTGATACTAGTAGGCCATAGTACGTACTACCAAACTCAG.ATCAGTC    426
t13587         CACGGCGCCGTA.GGGGGGCTAGGGGCGCGCATATGCTAGCTAGCCTGAATGCCTGATACTAGTAGGCCATAGTACGTACTACCAAACTCAG.ATCAGTC    440
t14976         CACGGCGCCGTA.TGGGGGCTAGGGGCGCGCATATGCTAGCTAGCCTGAATGCCTGATACTAGTAGGCCATAGTACGTACTACCAAACTCAG.ATCAGTC    351
t14978         CACGGCGCCGTA.GGGGGGCTAGGGGCGCGCATATGCTAGCTAGCCTGAATGCCTGATACTAGTAGGCCATAGTACGTACTACCAAACTCAG.ATCAGTC    356
mCML115.2                                                                                                                  0
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mCML169                                                                                                                    0
mCIMBL120                                                                                                                  0
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mCML26                                                                                                                     0
mCIMBL36.2                                                                                                                 0
mTT16                                                                                                                      0
mGEMS31                                                                                                                    0
mCML307.2                                                                                                                  0
mCIMBL48                                                                                                                   0
mCML40                                                                                                                     0
mCIMBL60.2                                                                                                                 0
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mMO113                                                                                                                     0
mGy220                                                                                                                     0
mZZ03.2                                                                                                                    0
mCML51                                                                                                                     0
mSi273.2                                                                                                                   0
mCIMBL96                                                                                                                   0
mYe478                                                                                                                     0
m7327                                                                                                                      0


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mSi273         ACTGCTCACCTATAGCGACAAGTGAATGCGGAACAGACGCACACGCAGGGGAGGGGG.......GCAGCCGCAGCCGCAGGCGCGCGCGG.....GGGAA   1800
mCML115        ACTGCTCACCTATAGCGACAAGTGAATGCGGAACAGACGCACACGCAGGGGAGGGGG.......GCAGCCGCAGCCGCGGGCGCGCGCGGG....GGGAA   1750
mGEMS3         ACTGCTCACCTATAGCGACAAGTGAATGCGGAACAGACGCACACGCAGGGGAGGGGG.......GCAGCCGCAGCCGCAGGCGCGCGCGG.....GGGAA   1870
mHYS           ACTGCTCACCTATAGCGACAAGTGAATGCGGAACAGACGCACACGCAGGGGAGGGGG.......GCAGCCGCAGCCGCAGGCGCGCGCGG.....GGGAA   1860
mCIMBL36       ACTGCTCACCTATAGCGACAAGTGAATGCGGAACAGACGCACACGCAGGGGAGGGGG.......GCAGCCGCAGCCGCAGGCGCGCGCGG.....GGGAA   1852
mCML307        ACTGCTCACCTATAGCGACAAGTGAATGCGGAACAGACGCACACGCAGGGGAGGGGG.......GCAGCCGCAGCCGCAGGCGCGCGCGG.....GGGAA   1858
mCIMBL144      ACTGCTCACCTATAGCGACAAGTGAATGCGGAACAGACGCACACGCAGGGGAGGGGG.......GCAGCCGCAGCCGCAGGCGCGCGCGG.....GGGAA   1854
mGEMS45        ACTGCTCACCTATAGCGACAAGTGAATGCGGAACAGACGCACACGCAGGGGAGGGGG.......GCAGCCGCAGCCGCAGGCGCGCGCGG.....GGGAA   1745
mCIMBL60       ACTGCTCACCTATAGCGACAAGTGAATGCGGAACAGACGCACACGCAGGGGAGGGGG.......GCAGCCGCAGCCGCAGGCGCGCGCGG.....GGGAA   1746
mCIMBL156      ACTGCTCACCTATAGCGACAAGTGAATGCGGAACAGACGCACACGCAGGGGAGGGGG.......GCAGCCGCAGCCGCAGGCGCGCGCGG.....GGGAA   1855
mCIMBL72       ACTGCTCACCTATAGCGACAAGTGAATGCGGAACAGACGCACACGCAGGGGAGGGGG.......GCAGCCGCAGCCGCAGGCGCGCGCGG.....GGGAA   1827
mZZ03          ACTGCTCACCTATAGCGACAAGTGAATGCGGAACAGACGCACACGCAGGGGAGGGGG.......GCAGCCGCAGCCGCAGGCGCGCGCGG.....GGGAA   1746
mJiao51        ACTGCTCACCTATAGCGACAAGTGAATGCGGAACAGACGCACACGCAGGGGAGGGGG.......GCAGCCGCAGCCGCAGGCGCGCGCGG.....GGGAA   1860
mCML486        ACTGCTCACCTATAGCGACAAGTGAATGCGGAACAGACGCACACGCAGGGGAGGGGG.......GCAGCCGCAGCCGCAGGCGCGCGCGG.....GGGAA   1860
mBZN           ACTGCTCACCTATAGCGACAAGTGAATGCGGAACAGACGCACACGCAGGGGAGGGGG.......GCAGCCGCAGCCGCAGGCGCGCGCGG.....GGGAA   1862
mB73           ACTGCTCACCTATAGCGACAAGTGAATGCGGAACAGACGCACACGCAGGGGAGGGGG.......GCAGCCGCAGCCGCAGGCGCGCGCGG.....GGGAA   1857
mW22           ACTGCTCACCTATAGCGACAAGTGAATGCGGAACAGACGCACACGCAGGGGAGGGGG.......GCAGCCGCAGCCGCAGGCGCGCGCGG.....GGGAA   1856
m87-1          ACTGCTCACCTATAGCGACAAGTGAATGCGGAACAGACGCACACGCAGGGGAGGGGG.......GCAGCCGCAGCCGCAGGCGCGCGCGG.....GGGAA   1861
t384061        ACTGCTCACCTATAGCGACAAGTGAATGCGGAACAGACGCACACGCAGGGGAGGGGG.......GCAGCCGCAGCCGCAGGCGCAGGCGCGCGCGGGGAA   1464
t8766          ACTGCTCACCTATAGCGACAAGTGAATGCGGAACAGACGCACACGCAGGGGAGGGGG.......GCAGCCGCAGCCGCACCCGCACGCGCGCGCGGGGAA   1480
t13554         ACTGCTCACCTATAGCGACAAGTGAATGCGGAACAGACGCACACGCAGGGGGGG..........GCAGCCGCAGCCGCAGGCGCGCGCGG.....GGGAA   1468
t29080         ACTGCTCACCTATAGCGACAAGTGAATGCGGAACAGACGCACACGCAGGGGAGGGGG.GCAGCCGCAGCCGCAGGCGCAGGCGCGCGCGGGGAA.GGGAA   1362
t29085         ACTGCTCACCTATAGCGACAAGTGAATGCGGAACAGACGCACACGCAGGGGAGGGGGGGCAGCCGCAGCCGCAGCCGCAGGCGCGCGCG......GGGAA   1351
t29732         ACTGCTCACCTATAGCGACAAGTGAATGCGGAACAGACGCACACGCAGGGGAGGGGGG......GCAGCCGCAGCCGCAGGCGCGCGCG......GGGAA    520
t29734         ACTGCTCACCTATATCGACAAGTGAATGCGGAACAGACGCACACGCAGGGGGGG..........GCAGCCGCAGCCGCAGGCGCGCGCG......GGGAA    491
t29735         ACTGCTCACCTATAGCGACAAGTGAATGCGGAACAGACGCACACGCAGGGGAGGGGGGGCAGCCGCAGCCGCAGGCGCAGGCGCGCGCGGGAAA.GGGAA    538
t29736         ACTGCTCACCTATAGCGACAAGTGAATGCGGAACAGACGCACACGCAGGGGGGG..........GCAGCCGCAGCCGCAGGCGCGCGCGG.....GGGAA    518
t29769         ACTGCTCACCTATAGCGACAAGTGAATGCGGAACAGACGCACACGCAGGGGGG...........GCAGCCGCAGCCGCAGGCGCGCGCG......GGGAA    467
t29785         ACTGCTCACCTATAGCGACAAGTGAATGCGGAACAGACGCACACGCAGGGGAGGGGGGGCAGCCGCAGCCGCAGGCGCAGGCGCGCGCGGGGAA.GGGAA    525
t13587         ACTGCTCACCTATAGCGACAAGTGAATGCGGAACAGACGCACACGCAGGGGGGG..........GCAGCCGCAGCCGCAGGCGCGCGCGGGGAA.GGGAA    529
t14976         ACTGCTCACCTATAGCGACAAGTGAATGCGGAACAGACGCACACGCAGGGGAGGGGGG......GCAGCCGCAGCCGCAGGCGCGCGCGG.....GGGAA    440
t14978         ACTGCTCACCTATAGCGACAAGTGAATGCGGAACAGACGCACACGCAGGGGAGGGGGG......GCAGCCGCAGCCGCAGGCGCGCGCGG.....GGGAA    445
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mCML169                                                                                                                    0
mCIMBL120                                                                                                                  0
mJi53                                                                                                                      0
mCML26                                                                                                                     0
mCIMBL36.2                                                                                                                 0
mTT16                                                                                                                      0
mGEMS31                                                                                                                    0
mCML307.2                                                                                                                  0
mCIMBL48                                                                                                                   0
mCML40                                                                                                                     0
mCIMBL60.2                                                                                                                 0
m5213                                                                                                                      0
mMO113                                                                                                                     0
mGy220                                                                                                                     0
mZZ03.2                                                                                                                    0
mCML51                                                                                                                     0
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mSi273.2                                                                                                          0
mCIMBL96                                                                                                          0
mYe478                                                                                                            0
m7327                                                                                                             0


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mSi273       GGCAATGGCCGGCCACTGTTGCCATACGCGCGCCCGTGCCAGTTGCAGTTGCAGCAG......GGCT....CCCCCGCCCCGTCGTTGATGCTTTGATGG   1890
mCML115      GGCAATGGCCGGCCACTGTTGCCATACGCGCGCCCGTGCCAGTTGCAGTTGCAGCAG......GGCT....CCCCCGCCCCGTCGTTGATGCTTTGATGG   1840
mGEMS3       GGCAATGGCCGGCCACTGTTGCCATACGCGCGCCCGTGCCAGTTGCAGTTGCAGCAG......GGCT....CCCCCGCCCCGTCGTTGATGCTTTGATGG   1960
mHYS         GGCAATGGCCGGCCACTGTTGCCATACGCGCGCCCGTGCCAGTTGCAGTTGCAGCAG......GGCTC...CCCCCGCCCCGTCGTTGATGCTTTGATGG   1951
mCIMBL36     GGCAATGGCCGGCCACTGTTGCCATACGCGCGCCCGTGCCAGTTGCAGTTGCAGCAG......GGCT....CCCCCGCCCCGTCGTTGATGCTTTGATGG   1942
mCML307      GGCAATGGCCGGCCACTGTTGCCATACGCGCGCCCGTGCCAGTTGCAGTTGCAGCAG......GGCT....CCCCCGCCCCGTCGTTGATGCTTTGATGG   1948
mCIMBL144    GGCAATGGCCGGCCACTGTTGCCATACGCGCGCCCGTGCCAGTTGCAGTTGCAGCAG......GGCT....CCCCCGCCCCGTCGTTGATGCTTTGATGG   1944
mGEMS45      GGCAATGGCCGGCCACTGTTGCCATACGCGCGCCCGTGCCAGTTGCAGTTGCAGCAG......GGCT....CCCCCGCCCCGTCGTTGATGCTTTGATGG   1835
mCIMBL60     GGCAATGGCCGGCCACTGTTGCCATACGCGCGCCCGTGCCAGTTGCAGTTGCAGCAG......GGCT....CCCCCGCCCCGTCGTTGATGCTTTGATGG   1836
mCIMBL156    GGCAATGGCCGGCCACTGTTGCCATACGCGCGCCCGTGCCAGTTGCAGTTGCAGCAG......GGCT....CCCCCGCCCCGTCGTTGATGCTTTGATGG   1945
mCIMBL72     GGCAATGGCCGGCCACTGTTGCCATACGCGCGCCCGTGCCAGTTGCAGTTGCAGCAG......GGCT....CCCCCGCCCCGTCGTTGATGCTTTGATGG   1917
mZZ03        GGCAATGGCCGGCCACTGTTGCCATACGCGCGCCCGTGCCAGTTGCAGTTGCAGCAG......GGCT....CCCCCGCCCCGTCGTTGATGCTTTGATGG   1836
mJiao51      GGCAATGGCCGGCCACTGTTGCCATACGCGCGCCCGTGCCAGTTGCAGTTGCAGCAG......GGCT....CCCCCGCCCCGTCGTTGATGCTTTGATGG   1950
mCML486      GGCAATGGCCGGCCACTGTTGCCATACGCGCGCCCGTGCCAGTTGCAGTTGCAGCAG......GGCT....CCCCCGCCCCGTCGTTGATGCTTTGATGG   1950
mBZN         GGCAATGGCCGGCCACTGTTGCCATACGCGCGCCCGTGCCAGTTGCAGTTGCAGCAG......GGCT....CCCCCGCCCCGTCGTTGATGCTTTGATGG   1952
mB73         GGCAATGGCCGGCCACTGTTGCCATACGCGCGCCCGTGCCAGTTGCAGTTGCAGCAG......GGCT....CCCCCGCCCCGTCGTTGATGCTTTGATGG   1947
mW22         GGCAATGGCCGGCCACTGTTGCCATACGCGCGCCCGTGCCAGTTGCAGTTGCAGCAG......GGCT....CCCCCGCCCCGTCGTTGATGCTTTGATGG   1946
m87-1        GGCAATGGCCGGCCACTGTTGCCATACGCGCGCCCGTGCCAGTTGCAGTTGCAGCAG......GGCT....CCCCCGCCCCGTCGTTGATGCTTTGATGG   1951
t384061      GGCAATGGCCGGCCACTGTTGCCATA....CGCCCGTGCCAGTTGCAGTTGCAGCAG......GGCTTCCTCCCCCGGCCCGTCGTTGATGCTTTGATGG   1554
t8766        GGCAATGGCCGGCCACTGTTGCCATA....CGCCCGTGCCAGTTGCAGTTGCAGCAG......GGCT....CCCCCGCCCCGTCGTTGATGCTTTGATGG   1566
t13554       GGCAATGGCCGGCCACTGTTGCCATACGCGCGCCCGTGCCAGTTGCAGTTGCAGCTGCAGCAGCCT....CCCCCGGCCCGTCGTTGATGCTTTGATGG   1564
t29080       GGCAATGGCCGGCCACTGTTGCCATA....CGCCCGTGCCAGTTGCAGTTGCAGCAG......GGCT....CCCGCGGCCCGTCGTTGATGCTTTGATGG   1448
t29085       GGCAATGGCCGGCCACTGTTGCCATA....CGCCCGTGCCAGTTGCAGTTGCAGCAG......GGCT....CCCCCGGCCCGTCGTTGATGCTTTGATGG   1437
t29732       GGCAATGGCCGGCCACTGTTGCCATA....CGCCCGTGCCAGTTGCAGTTGCAGCTGCAGCAGGGCT....CCCCCGCCCCGTCGTTGATGCTTTGATGG    612
t29734       GGCAATGGCCGGCCACTGTTGCCATACGCGCGCCCGTGCCAGTTGCAGTTGCAGCTGCAGCACGGCT....CCCCCGCCCCGTCGTTGATGCTTTGATGG    587
t29735       GGCAATGGCCGGCCACTGTTGCCATA....CGCCCGTGCCAGTTGCAGTTGCAGCAG......GGCT....CCCCCGGCCCGTCGTTGATGCTTTGATGG    624
t29736       GGCAATGGCCGGCCACTGTTGCCATACGCGCGCCCGTGCCAGTTGCAGTTGCAGCTGCAGCAGCCT....CCCCCGGCCCGTCGTTGATGCTTTGATGG    614
t29769       GGCAATGGCCGGCCACTGTTGCCATA....CGCCCGTGCCAGTTGCAGTTGCAGCAG......GGCT....CCCCCGGCCCGTCGTTGATGCTTTGATGG    553
t29785       GGCAATGGCCGGCCACTGTTGCCATA....CGCCCGTGCCAGTTGCAGTTGCAGCAG......GACT....CCCCCGGCCCGTCGTTGATGCTTTGATGG    611
t13587       GGCAATGGCCGGCCACTGTTGCCATA....CGCCCGTGCCAGTTGCAGTTGCAGCAG......GGCTCCCTCCCCCGGCCCGTCGTTGATGCTTTGATGG    619
t14976       GGCAATGGCCGGCCACTGTTGCCATA....CGCCCGTGCCAGTTGCAGTTGCAGCTGCAGCAGGGCT....CCCCCGGCCCGTCGTTGATGCTTTGATGG    532
t14978       GGCAATGGCCGGCCACTGTTGCCATA....CGCCCGTGCCAGTTGCAGGTGCAGCTGCATCAAGGCT....CCCCCGGCCCGTCGTTGATGCTTTGATGG    537
mCML115.2                                                                                                         0
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mCML169                                                                                                           0
mCIMBL120                                                                                                         0
mJi53                                                                                                             0
mCML26                                                                                                            0
mCIMBL36.2                                                                                                        0
mTT16                                                                                                             0
mGEMS31                                                                                                           0
mCML307.2                                                                                                         0
mCIMBL48                                                                                                          0
mCML40                                                                                                            0
mCIMBL60.2                                                                                                        0
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mMO113                                                                                                            0
mGy220                                                                                                            0
mZZ03.2                                                                                                           0
mCML51                                                                                                            0
mSi273.2                                                                                                          0
mCIMBL96                                                                                                          0
mYe478                                                                                                            0
m7327                                                                                                             0


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mSi273       ATGGACATATCCATTCCATTAGTGCTAGTAGCTACGTACTACACGTCCAGTCCAACAAACATTACCG....CTATAGCAGCATCTGGACCAGAAACTGCT   1986
mCML115      ATGGACATATCCATTCCATTAGTGCTAGTAGCTACGTACTACACGTCCAGTCCAACAAACATTACCG....CTATAGCAGCATCTGGACCAGAAACTGCT   1936
mGEMS3       ATGGACATATCCATTCCATTAGTGCTAGTAGCTACGTACTACACGTCCAGTCCAACAAACATTACCG....CTATAGCAGCATCTGGACCAGAAACTGCT   2056
mHYS         ATGGACATATCCATTCCATTAGTGCTAGTAGCTACGTACTACACGTCCAGTCCAACAAACATTACCG....CTATAGCAGCATCTGGACCAGAAACTGCT   2047
mCIMBL36     ATGGACATATCCATTCCATTAGTGCTAGTAGCTACGTACTACACGTCCAGTCCAACAAACATTACCG....CTATAGCAGCATCTGGACCAGAAACTGCT   2038
mCML307      ATGGACATATCCATTCCATTAGTGCTAGTAGCTACGTACTACACGTCCAGTCCAACAAACATTACCG....CTATAGCAGCATCTGGACCAGAAACTGCT   2044
mCIMBL144    ATGGACATATCCATTCCATTAGTGCTAGTAGCTACGTACTACACGTCCAGTCCAACAAACATTACCG....CTATAGCAGCATCTGGACCAGAAACTGCT   2040
mGEMS45      ATGGACATATCCATTCCATTAGTGCTAGTAGCTACGTACTACACGTCCAGTCCAACAAACATTACCG....CTATAGCAGCATCTGGACCAGAAACTGCT   1931
mCIMBL60     ATGGACATATCCATTCCATTAGTGCTAGTAGCTACGTACTACACGTCCAGTCCAACAAACATTACCG....CTATAGCAGCATCTGGACCAGAAACTGCT   1932
mCIMBL156    ATGGACATATCCATTCCATTAGTGCTAGTAGCTACGTACTACACGTCCAGTCCAACAAACATTACCG....CTATAGCAGCATCTGGACCAGAAACTGCT   2041
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mZZ03        ATGGACATATCCATTCCATTAGTGCTAGTAGCTACGTACTACACGTCCAGTCCAACAAACATTACCG....CTATAGCAGCATCTGGACCAGAAACTGCT   1932
mJiao51      ATGGACATATCCATTCCATTAGTGCTAGTAGCTACGTACTACACGTCCAGTCCAACAAACATTACCG....CTATAGCAGCATCTGGACCAGAAACTGCT   2046
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mB73         ATGGACATATCCATTCCATTAGTGCTAGTAGCTACGTACTACACGTCCAGTCCAACAAACATTACCG....CTATAGCAGCATCTGGACCAGAAACTGCT   2043
mW22         ATGGACATATCCATTCCATTAGTGCTAGTAGCTACGTACTACACGTCCAGTCCAACAAACATTACCG....CTATAGCAGCATCTGGACCAGAAACTGCT   2042
m87-1        ATGGACATATCCATTCCATTAGTGCTAGTAGCTACGTACTACACGTCCAGTCCAACAAACATTACCG....CTATAGCAGCATCTGGACCAGAAACTGCT   2047
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t384061       ATGGACATATCCATTCCATTAGTGCTAGTAGCTACGTACTACACGTCCAGTCCAACAAACATTACCG....CTATAGCAGCATCTGGACCAGAAACTGCT  1650
t8766         ATGGACATATCCATTCCATTAGTGCTAGTAGCTACGTACTACACGTCCAGTCCAACAAACATAACCG....CTATAGCAGCATCTGGACCAGAAACTGCT  1662
t13554        ATGGACATATCCATTCCATTAGTGCTAGTAGCTACGTACTACACGTCCAGTCCAGCAAACATTACCG....CTATAGCAGCATCTGGACCAGAAACTGCT  1660
t29080        ATGGACATATCCATTCCATTAGTGCTAGTAGCTACGTACTACACGTCCAGTCCAGCAAACATTACCGCTATCTATAGCAGCATCTGGACCAGAAACTGCT  1548
t29085        ATGGACATATCCATTCCATTAGTGCTAGC.......TACTACACGTCCAGTCCAACAAACATTACCG....CTATAGCAGCATCTGGACCAGAAACTGCT  1526
t29732        ATGGACATATCCATTCCATTAGTGCTAGTAGCTACGTACTACACGTCCAGTCCAACAAACATTACCGCTATCTATAGCAGCATCTGGACCAGAAACTGCT   712
t29734        ATGGACATATCCATTCCATTAGTGCTAGTAGCTACGTACTACACGTCCAGTCCAACAAACATTACCG....CTATAGCAGCATCTGGACCAGAAACTGCT   683
t29735        ATGGACATATCCATTCCATTAGTGCTAGTAGCTACGTACTACACGTCCAGTCCAACAAACATTACCG....CTATAGCAGCATCTGGACCAGAAACTGCT   720
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t29769        ATGGACATATCCATTCCATTAGTGCTAGC.......TACTACACGTCCAGTCCAACAAACATTACCG....CTATAGCAGCATCTGGACCAGAAGCTGCT   642
t29785        ATGGACATATCCATTCCATTAGTGCTAGTAGCTACGTACTACACGTCCAGTCCAACAAACATTACCGCTATCTATAGCAGCATCTGGACCAGAAACTGCT   711
t13587        ATGGACATATCCATTCCATTAGTGCTAGTAGCTACGTACTACACGTCCAGTCCAGCAAACATTACCG....CTATAGCAGCATCTGGACCAGAAACTGCT   715
t14976        ATGGACATATCCATTCCATTAGTGCTAGTAGCTACGTACTACACGTCCAGTCCAACAAACATTACCGCTATCTATAGCAGCATCTGGACCAGAAACTGCT   632
t14978        ATGGACATATCCATTCCATTAGTGCTTGTATCTACGTACTACACGTCCATTCCATCAAACATTACCGCTATCTATAGCAGCATCTGGACCAAAAACTGCT   637
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mCML169                                                                                                                0
mCIMBL120                                                                                                              0
mJi53                                                                                                                  0
mCML26                                                                                                                 0
mCIMBL36.2                                                                                                             0
mTT16                                                                                                                  0
mGEMS31                                                                                                                0
mCML307.2                                                                                                              0
mCIMBL48                                                                                                               0
mCML40                                                                                                                 0
mCIMBL60.2                                                                                                             0
m5213                                                                                                                  0
mMO113                                                                                                                 0
mGy220                                                                                                                 0
mZZ03.2                                                                                                                0
mCML51                                                                                                                 0
mSi273.2                                                                                                               0
mCIMBL96                                                                                                               0
mYe478                                                                                                                 0
m7327                                                                                                                  0


mCIMBL84      GCTGCTGGCTGCTGCCACTGCGATGATGCAAGGAGTACTGTACTGTAGGGGCTCGGT........AAAGAGG..ACACACACAGAGATAAGAAT.AGATA  2034
mSi273        GCTGCTGGCTGCTGCCACTGCGATGATGCAAGGAGTACTGTACTGTAGGGGCTCGGT........AAAGAGG..ACACACACAGAGATAAGAAT.AGATA  2075
mCML115       GCTGCTGGCTGCTGCCACTGCGATGATGCAAGGAGTACTGTACTGTAGGGGCTCGGT........AAAGAGG..ACACACACAGAGATAAGAAT.AGATA  2025
mGEMS3        GCTGCTGGCTGCTGCCACTGCGATGATGCAAGGAGTACTGTACTGTAGGGGCTCGGT........AAAGAGG..ACACACACAGAGATAAGAAT.AGATA  2145
mHYS          GCTGCTGGCTGCTGCCACTGCGATGATGCAAGGAGTACTGTACTGTAGGGGCTCGGT........AAAGAGG..ACACACACAGAGATAAGAAT.AGATA  2136
mCIMBL36      GCTGCTGGCTGCTGCCACTGCGATGATGCAAGGAGTACTGTACTGTAGGGGCTCGGT........AAAGAGG..ACACACACAGAGATAAGAAT.AGATA  2127
mCML307       GCTGCTGGCTGCTGCCACTGCGATGATGCAAGGAGTACTGTACTGTAGGGGCTCGGT........AAAGAGG..ACACACACAGAGATAAGAAT.AGATA  2133
mCIMBL144     GCTGCTGGCTGCTGCCACTGCGATGATGCAAGGAGTACTGTACTGTAGGGGCTCGGT........AAAGAGG..ACACACACAGAGATAAGAAT.AGATA  2129
mGEMS45       GCTGCTGGCTGCTGCCACTGCGATGATGCAAGGAGTACTGTACTGTAGGGGCTCGGT........AAAGAGG..ACACACACAGAGATAAGAAT.AGATA  2020
mCIMBL60      GCTGCTGGCTGCTGCCACTGCGATGATGCAAGGAGTACTGTACTGTAGGGGCTCGGT........AAAGAGG..ACACACACAGAGATAAGAAT.AGATA  2021
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mCIMBL72      GCTGCTGGCTGCTGCCACTGCGATGATGCAAGGAGTACTGTACTGTAGGGGCTCGGT........AAAGAGG..ACACACACAGAGATAAGAAT.AGATA  2102
mZZ03         GCTGCTGGCTGCTGCCACTGCGATGATGCAAGGAGTACTGTACTGTAGGGGCTCGGT........AAAGAGG..ACACACACAGAGATAAGAAT.AGATA  2021
mJiao51       GCTGCTGGCTGCTGCCACTGCGATGATGCAAGGAGTACTGTACTGTAGGGGCTCGGT........AAAGAGG..ACACACACAGAGATAAGAAT.AGATA  2135
mCML486       GCTGCTGGCTGCTGCCACTGCGATGATGCAAGGAGTACTGTACTGTAGGGGCTCGGT........AAAGAGG..ACACACACAGAGATAAGAAT.AGATA  2135
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m87-1         GCTGCTGGCTGCTGCCACTGCGATGATGCAAGGAGTACTGTACTGTAGGGGCTCGGT........AAAGAGG..ACACACACAGAGATAAGAAT.AGATA  2136
t384061       GCTGCTGGCTGCTGCCACTGCGATGATGCAAGGAGTACTGTACTGTAGGGGCTCGGT........AAAGAGG..ACGCACACAGAGATAAGAAT.AGATA  1739
t8766         GCTGCTGGCTGCTGCCACTGCGATGATGCAAGGAGTACTGTACTGTAGGGGCTCGGT........AAAGAGG....ACACACAGAGATAAGAAT.AGATA  1749
t13554        GCTGCTGGCTGCTGCCACTGCGATGATGCAAGGAGTACTGTACTGTAGGGGCTCGGT........AAAGAGG..ACACACACAGAGTTAAGAATAAGATA  1750
t29080        GCTGCTGGCTGCTGCCACTGCGATGATGCAAGGAGTACTGTACTGTAGGGGCTCGGT........AAAGAGG..ACACACACAGAGATAAGAAT.AGATA  1637
t29085        GCTGCTGGCTGCTGCCACTGCGATGATGCAAGGAGTACTGTACTGTAGGGGCTCGGT........AAAGAGG..ACACACACAGAGATAAGAAT.AGATA  1615
t29732        GCTGCTGGCTGCTGCCACTGCGATGATGCAAGGAGTACTGTACTGTAGGGGCTCGGT........AAAGAGG..ACACACACAGAGATAAGAAT.AGCTA   801
t29734        GCTGCTGGCTGCTGCCACTGCGATGATGCAAGGAGTACTGTACTGTAGGGGCTCGGT........AAAGAGG..ACACACACAGAGTTAAGAAT.AGATA   772
t29735        GCTGCTGGCTGCTGCCACTGCGATGATGCAAGGAGTACTGTACTGTAGGGGCTCGGT.........AAGAGG....ACACACAGAGATAAGAAT.AGATA   806
t29736        GCTGCTGGCTGCTGCCACTGCGATGATGCAAGGAGTACTGTACTGTAGGGGCTCGGT........AAAGAGG..ACACACACAGAGTTAAGAAT.AGATA   799
t29769        GCTG....CTGCTGCCACTGCGATGATGCAAGGAGTACTGTACTGTAGGGGCTCGGT........AAAGAGG....ACACACAGAGATAAGAAT.AGATA   725
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t14976        GCTGCTGGCTGCTGCCACTGCGATGATGCAAGGAGTACTGTACTGTAGGGGCTCGGTAAAGAGCCAAAGAGGACACACACACAGAGATAAGAAT.AGATA   731
t14978        GCTGCTGGCTGCTGCCACTGCGATGATGCAAGGAGTACTGTACTGTAGGGGCTCGGTAAAGAGCCAAAGAGGACACACACACAGAGATAAGAAT.AGATA   736
mCML115.2                                                                                                              0
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mCML169                                                                                                                0
mCIMBL120                                                                                                              0
mJi53                                                                                                                  0
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mCIMBL36.2                                                                                                             0
mTT16                                                                                                                  0
mGEMS31                                                                                                                0
mCML307.2                                                                                                              0
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mCML40                                                                                                                 0
mCIMBL60.2                                                                                                             0
m5213                                                                                                                  0
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mMO113                                                                                                                   0
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mZZ03.2                                                                                                                  0
mCML51                                                                                                                   0
mSi273.2                                                                                                                 0
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mYe478                                                                                                                   0
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mGEMS3        CTGGA.....GTACATATATATATATA..ctacg                                                                   2172
mHYS          CTGGA.....GTACATATATATATATA..ctacg                                                                   2163
mCIMBL36      CTGGA.....GTACATATATATATATA..ctacg                                                                   2154
mCML307       CTGGA.....GTACATATATATATATA..ctacg                                                                   2160
mCIMBL144     CTGGA.....GTACATATATATATATA..ctacg                                                                   2156
mGEMS45       CTGGA.....GTACATATATATATATATActacg                                                                   2049
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mZZ03         CTGGA.....GTACATATATATATATATActacg                                                                   2050
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t384061       CTGGA.....GTACATATATATATATACACTACG.GTCCCATGAAATCA.TACTGTTTCTCTTTCTCCCCCGTGTGTGTGTGTG............TATA  1820
t8766         CTGGA.....GTACATATATATA......CTACG.GTCCCATGAAATCA.TACTGTTTCTCTTTCTCCCC.GTGTGTGTGTGTG............TATA  1823
t13554        CTGGA.....GTACATATATATACA....CTACG.GTCCCATGAAATCA.TACTGTTTCTCTTTCTCCCCCGCGTGTGTGACTGTGTGTG......CATA  1833
t29080        CTGGA.....GTACATATATATATA....CTACG.GTCCCATGAAATCA.TACTGTTTCTCTTTCTCCCC.GTGTGTGTGTG..............TATA  1711
t29085        CTGGA.....GTACATATATATA......CTACG.GTCCCATGAAATCA.TACTGTTTCTCTTTCTCCCC.GTGTGTGTG................TGTA  1685
t29732        CTGGA.....GTACATATATATATATACACTACG.GTCCCATGAAATCA.TACTGTTTCTCTTTCTCCCCCGCGCGTGTGTGTG............TATA   882
t29734        CTGGA.....GTACATATATATACA....CTACGGGTCCCATGAAATCA.TTCTGTCTCTCTTTCTCCCCCTTTTTTTTTTT..............TATA   848
t29735        CTGGA.....GTACATATATATA......CTACG.GTCCCATGAAATCA.TACTGTTTCTCTTTCTCCCC.GTGTGTGTGTGTG............TATA   880
t29736        CTGGA.....GTACATATATATACA....CTACG.GTCCCATGAAATCA.TACTGTTTCTCTTTCTCCCCCGCGTGTGTGACTGTGTGTG......CATA   882
t29769        CTGGA.....GTACCTATATATATA....CTACG.GTCCCATGAAATCA.TACTGTTTCTCTTTCTCCCC.GTGTGTGTGTG..............TATA   799
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t13587        CTGGAGACTCGAGTACATATATATATATACTACG.GTCCCATGAAATCA.TACTGTTTCTCTTTCTCCCCCGTGTGTGTGTGTG............TATA   890
t14976        CTGGA.....GTACATATATATACA....CTACG.GTCCCATGAAATCA.TACTGTTTCTCTTTCTCCCCCGCGTGTGTGACTGTGTGTG......CATA   814
t14978        ATGGA.....GTACATATATATACA....CTACG.GTCCCATGAAATCA.TACTGTCTCTCTTTCTCCCCCGGC.GTGTGTGACTGTGTGTG....CATA   820
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mCIMBL12                                     ctacg.GTCCCATGAAATCA.TACTGTTTCTCTTTCTCCCCCGTGTGTGTGTGTGTGTG........TATA    61
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mCIMBL120                                    ctacg.GTCCCATGAAATCA.TACTGTTTCTCTTTCTCCCCCGTGTGTGTGTGTG..........TATA    59
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mCML40                                       caacg.GTCCCATGATATAT.TACTGTTTCTCTGTCTCCCCCGCGTGTGTGTGTGTGTGTGTG....TATA    65
mCIMBL60.2                                   ctacg.GTCCCACGAAATCA.TACTGTTTCTCTTTCTCCCCCGTGTGTGTGTGTGTGTG........TATA    61
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mMO113                                       ctacg.GTCCCATGAAATCA.TACTGTTTCTCTTTCTCCCCCGTGTGTGT.....................    48
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mZZ03.2                                      ctacg.GTCCCATGAAATCA.TACTGTTTCTCTTTCTCCCCCGTGTGTGTGTGTGTGTG........TATA    61
mCML51                                       caacgCTCCCACGAAATATTACTGTGTCTCTCTCTCTCCCCCGTGTGTGTGTGTGTGTGTGTGTGTGTATA    71
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m7327                                        ctacg.GTCCCATGAAATCA.TACTGTTTCTCTTTCTCCCCCGTGTGTGTGTGTG..........TATA    59


mCIMBL84
mSi273
mCML115
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mHYS
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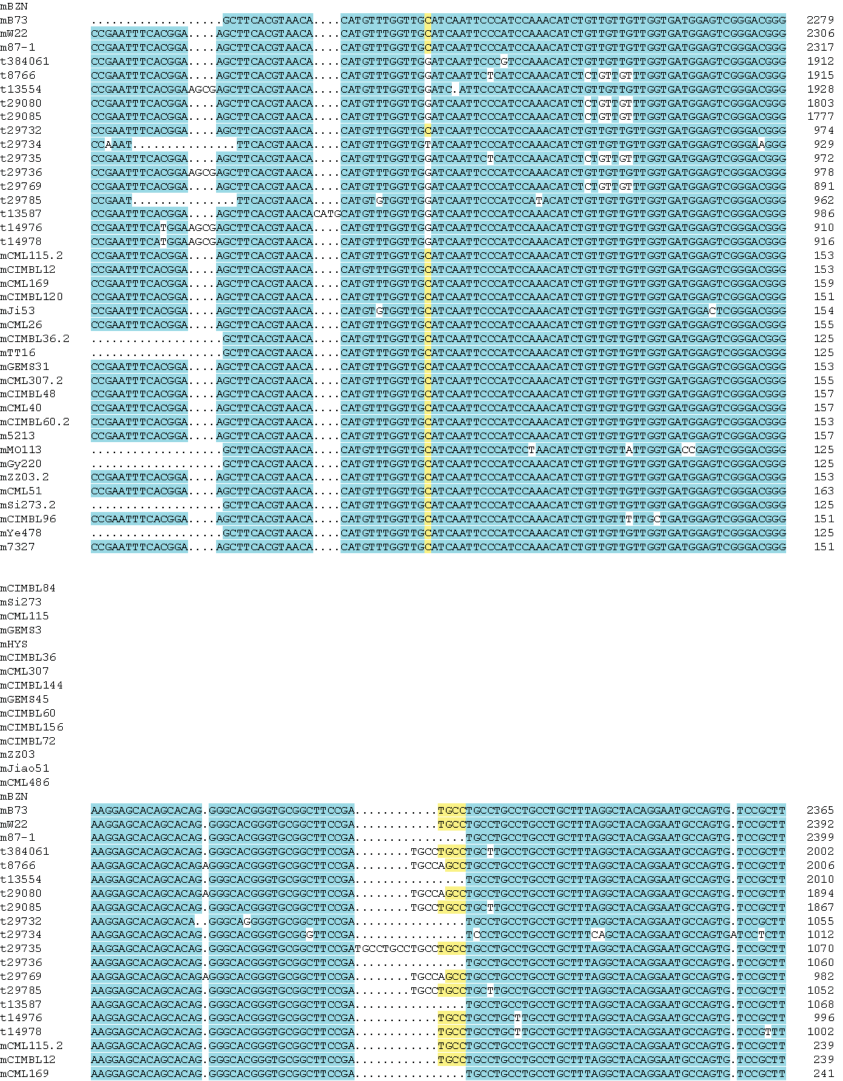

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mW22         CCGAATTTCACGGA....AGCTTCACGTAACA....CATGTTTGGTTGCATCAATTCCCATCCAAACATCTGTTGTTGTTGGTGATGGAGTCGGGACGGG   2306
m87-1        CCGAATTTCACGGA....AGCTTCACGTAACA....CATGTTTGGTTGCATCAATTCCCATCCAAACATCTGTTGTTGTTGGTGATGGAGTCGGGACGGG   2317
t384061      CCGAATTTCACGGA....AGCTTCACGTAACA....CATGTTTGGTTGGATCAATTCCCGTCCAAACATCTGTTGTTGTTGGTGATGGAGTCGGGACGGG   1912
t8766        CCGAATTTCACGGA....AGCTTCACGTAACA....CATGTTTGGTTGGATCAATTCTCATCCAAACATCTCTGTTGTTTGGTGATGGAGTCGGGACGGG   1915
t13554       CCGAATTTCACGGAAGCGAGCTTCACGTAACA....CATGTTTGGTTGGATC.ATTCCCATCCAAACATCTGTTGTTGTTGGTGATGGAGTCGGGACGGG   1928
t29080       CCGAATTTCACGGA....AGCTTCACGTAACA....CATGTTTGGTTGGATCAATTCCCATCCAAACATCTCTGTTGTTTGGTGATGGAGTCGGGACGGG   1803
t29085       CCGAATTTCACGGA....AGCTTCACGTAACA....CATGTTTGGTTGGATCAATTCCCATCCAAACATCTCTGTTGTTTGGTGATGGAGTCGGGACGGG   1777
t29732       CCGAATTTCACGGA....AGCTTCACGTAACA....CATGTTTGGTTGCATCAATTCCCATCCAAACATCTGTTGTTGTTGGTGATGGAGTCGGGACGGG    974
t29734       CCAAAT...............TTCACGTAACA....CATGTTTGGTTGTATCAATTCCCATCCAAACATCTGTTGTTGTTGGTGATGGAGTCGGGAAGGG    929
t29735       CCGAATTTCACGGA....AGCTTCACGTAACA....CATGTTTGGTTGGATCAATTCTCATCCAAACATCTCTGTTGTTTGGTGATGGAGTCGGGACGGG    972
t29736       CCGAATTTCACGGAAGCGAGCTTCACGTAACA....CATGTTTGGTTGGATCAATTCCCATCCAAACATCTGTTGTTGTTGGTGATGGAGTCGGGACGGG    978
t29769       CCGAATTTCACGGA....AGCTTCACGTAACA....CATGTTTGGTTGGATCAATTCCCATCCAAACATCTCTGTTGTTTGGTGATGGAGTCGGGACGGG    891
t29785       CCGAAT...............TTCACGTAACA....CATGTGTGGTTGGATCAATTCCCATCCATACATCTGTTGTTGTTGGTGATGGAGTCGGGACGGG    962
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t14978       CCGAATTTCATGGAAGCGAGCTTCACGTAACA....CATGTTTGGTTGGATCAATTCCCATCCAAACATCTGTTGTTGTTGGTGATGGAGTCGGGACGGG    916
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mCIMBL120    CCGAATTTCACGGA....AGCTTCACGTAACA....CATGTTTGGTTGCATCAATTCCCATCCAAACATCTGTTGTTGTTGGTGATGGAGTCGGGACGGG    151
mJi53        CCGAATTTCACGGA....AGCTTCACGTAACA....CATGTGTGGTTGCATCAATTCCCATCCAAACATCTGTTGTTGTTGGTGATGGACTCGGGACGGG    154
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mGEMS31      CCGAATTTCACGGA....AGCTTCACGTAACA....CATGTTTGGTTGCATCAATTCCCATCCAAACATCTGTTGTTGTTGGTGATGGAGTCGGGACGGG    153
mCML307.2    CCGAATTTCACGGA....AGCTTCACGTAACA....CATGTTTGGTTGCATCAATTCCCATCCAAACATCTGTTGTTGTTGGTGATGGAGTCGGGACGGG    155
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mCIMBL60.2   CCGAATTTCACGGA....AGCTTCACGTAACA....CATGTTTGGTTGCATCAATTCCCATCCAAACATCTGTTGTTGTTGGTGATGGAGTCGGGACGGG    153
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mMO113       ...................GCTTCACGTAACA....CATGTTTGGTTGCATCAATTCCCATCCTAACATCTGTTGTTATTGGTGACCGAGTCGGGACGGG    125
mGy220       ...................GCTTCACGTAACA....CATGTTTGGTTGCATCAATTCCCATCCAAACATCTGTTGTTGTTGGTGATGGAGTCGGGACGGG    125
mZZ03.2      CCGAATTTCACGGA....AGCTTCACGTAACA....CATGTTTGGTTGCATCAATTCCCATCCAAACATCTGTTGTTGTTGGTGATGGAGTCGGGACGGG    153
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mBZN
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t384061      AAGGAGCACAGCACAG.GGGCACGGGTGCGGCTTCCGA........TGCCTGCCTGCTTGCCTGCCTGCTTTAGGCTACAGGAATGCCAGTG.TCCGCTT   2002
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mCIMBL36.2    AAGGAGCACAGCACAG.GGGCACGGGTGCGGCTTCCGA............TGCCTGCCTGCCTGCCTGCTTTAGGCTACAGGAATGCCAGTG.TCCGCTT    211
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m7327         AAGGAGCACAGCACAG.GGGCACGGGTGCGGCTTCCGA................TGCCTGCCTGCCTGCTTTAGGCTACAGGAATGCCAGTG.TCCGCTT    233


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mGEMS3
mHYS
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mZZ03
mJiao51
mCML486
mBZN
mB73          CTCTCTGG.CATCCCGAAA.CGTGTGCCCCAATAACGGCATGCA.TTGAGACCAGAGGCAAATTCCA.CTTTGGTGGCGAAAGGTCT....GCTG.GCTG   2456
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t29085        CTCTCTGG.CATCCCGAAA.CGTGTGCCCCAATAACGGCATGCA.TTGAGACCAGAGGCAAATTCCA.CTTTGGTGGCGAAAGGTCTGCTGGCTG.GCTG   1962
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t29736        CTCTCTGG.CATCCCGAAA.CGTGTGCCCCAATAACGGCATGCA.TTGAGACCAGAGGCAAATTCCA.CTTTGGTGGCGAAAGGTCT....GCTG.GCTG   1151
t29769        CTCTCTGG.CATCCCGAAA.CGTGTGCCCCAATAACGGCATGCA.TTGAGACCAGAGGCAAATTCCA.CTTTGGTGGCGAAAGGTCT.........GCTG   1069
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mYe478        CTCTCTGG.CATCCCGAAA.CGTGTGCCCCAATAACGGCATGCA.TTGAGACCAGAGGCAAATTCCA.CTTTGGTGGCGAAAGGTCT....GCTG.GCTG    302
m7327         CTCTCTGG.CATCCCGAAA.CGTGTGCCCCAATAACGGCATGCA.TTGAGACCAGAGGCAAATTCCA.CTTTGGTGGCGAAAGGTCT....GCTG.GCTG    324


mCIMBL84
mSi273
mCML115
mGEMS3
mHYS
mCIMBL36
mCML307
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mCIMBL144
mGEMS45
mCIMBL60
mCIMBL156
mCIMBL72
mZZ03
mJiao51
mCML486
mBZN
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t29736        GCTGG.CTGGCATGCATCA.GCGCTGTGC........CTGCGCTCGC...........TGGCCCCTCGCCTC.ACTAG.........CAGCAGCAGGCA   1220
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t29785        GCTGG.CTGGCATGCATCA.GCGCTGTGC........CTGCGC...............TGGCCCCTCGCCTC.ACTAGCAGGAACAGCAGCAGCAGGCA   1217
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mCIMBL84
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mGEMS3
mHYS
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t8766         GGCCGGC......CGCCCGCGCCCGCGCTACCATTCGATCAC........TCACACGCACGCACTCTTTAGTCTTCTTTCCCAACAAATTAAACGGA      2251
t13554        GGCCAGC......CGCCCGCGCCCGCGCTACCATTCGATCAC............ACGCACGCACTCTTTAGTCTTCTTTCCCAACAAATTAAACGGA      2249
t29080        GGCCGGC......CGCCCGCGCCCGCGCTACCATTCGATCAC........TCACACGCACGCACTCTTTAGTCTTCTTTCCCAACAAATTAAACGGA      2139
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t29732        GGCCGGC......CGCCCGCGCCCGCGCTACCATTCGATCAC........ACACACGCACGCACTCTTTAGTCTTCTTTCCCAACAAATTAAACGGA      1301
t29734        GGCCGGCCGCCCGCGCCCGCGCCCGCGCTACCATTCAATCAC........TCACACGCACACAC..........TCTTTCCCAACAAATTAAACAGA      1258
t29735        GGCCGGCCGCCCGCGCCCGCGCCCGCGCTACCATTCGATCAC........TCACACGCACGCACTCTTTATTCTTCTTTCCCAACAAATTAAACGGA      1318
t29736        GGCCAGC......CGCCCGCGCCCGCGCTACCATTCGATCAC............ACGCACGCACTCTTTATTCTTCTTTCCCAACAAATTAAACGGA      1299
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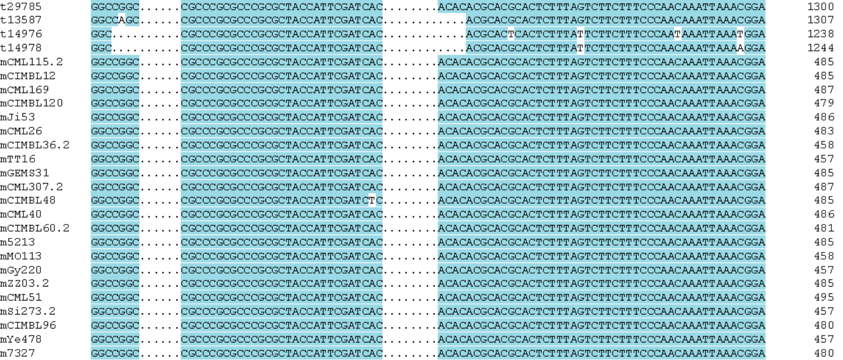

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