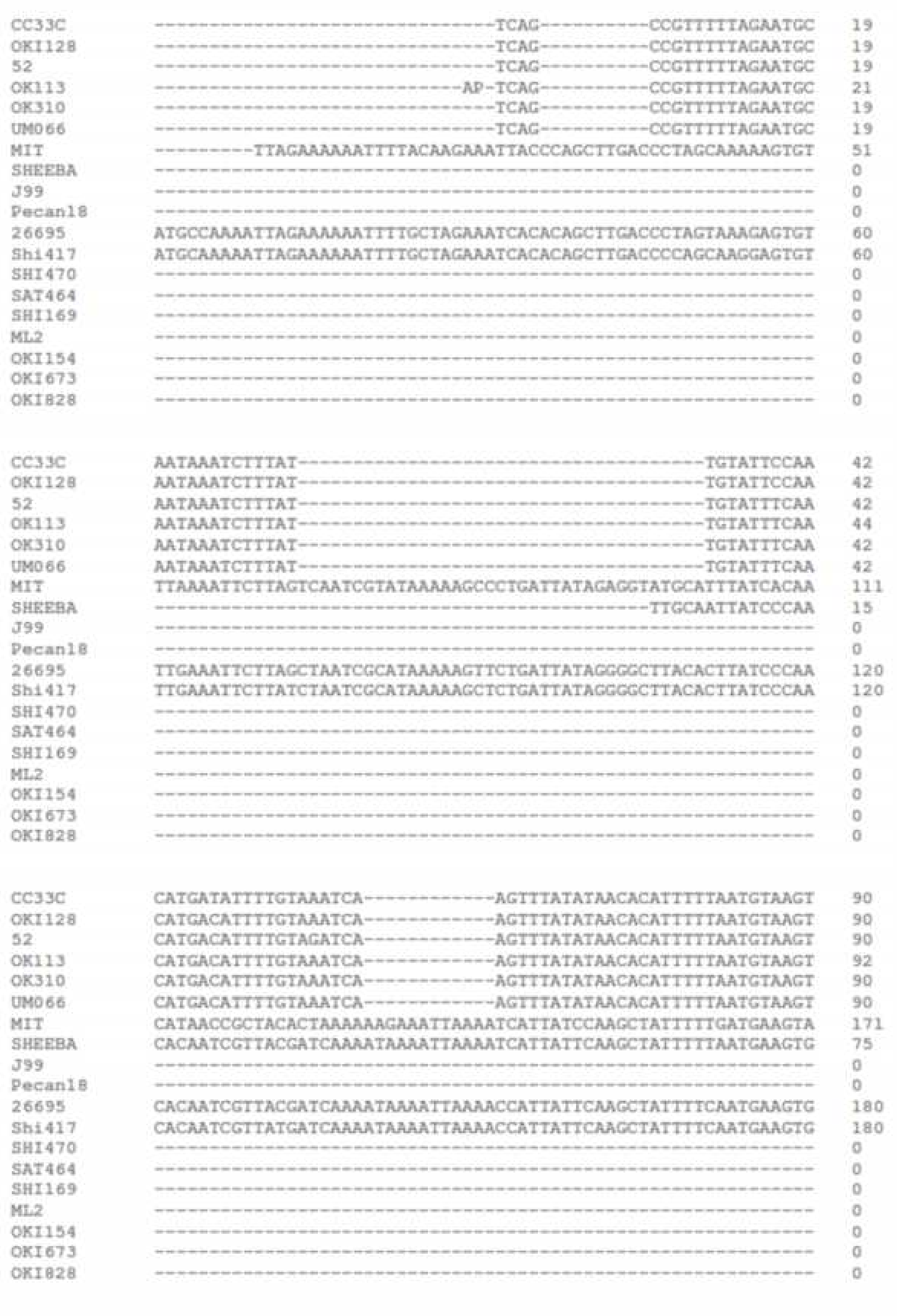
Figure S1



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CC33C           -------------------------------TCAG----------CCGTTTTTAGAATGC   19
OKI128          -------------------------------TCAG----------CCGTTTTTAGAATGC   19
52              -------------------------------TCAG----------CCGTTTTTAGAATGC   19
OK113           ----------------------------AP-TCAG----------CCGTTTTTAGAATGC   21
OK310           -------------------------------TCAG----------CCGTTTTTAGAATGC   19
UM066           -------------------------------TCAG----------CCGTTTTTAGAATGC   19
MIT             ---------TTAGAAAAAATTTTACAAGAAATTACCCAGCTTGACCCTAGCAAAAAGTGT   51
SHEEBA          ------------------------------------------------------------   0
J99             ------------------------------------------------------------   0
Pecan18         ------------------------------------------------------------   0
26695           ATGCCAAAATTAGAAAAAATTTTGCTAGAAATCACACAGCTTGACCCTAGTAAAGAGTGT   60
Shi417          ATGCAAAAATTAGAAAAAATTTTGCTAGAAATCACACAGCTTGACCCCAGCAAGGAGTGT   60
SHI470          ------------------------------------------------------------   0
SAT464          ------------------------------------------------------------   0
SHI169          ------------------------------------------------------------   0
ML2             ------------------------------------------------------------   0
OKI154          ------------------------------------------------------------   0
OKI673          ------------------------------------------------------------   0
OKI828          ------------------------------------------------------------   0


CC33C           AATAAATCTTTAT-------------------------------------TGTATTCCAA   42
OKI128          AATAAATCTTTAT-------------------------------------TGTATTCCAA   42
52              AATAAATCTTTAT-------------------------------------TGTATTTCAA   42
OK113           AATAAATCTTTAT-------------------------------------TGTATTTCAA   44
OK310           AATAAATCTTTAT-------------------------------------TGTATTTCAA   42
UM066           AATAAATCTTTAT-------------------------------------TGTATTTCAA   42
MIT             TTAAAATTCTTAGTCAATCGTATAAAAAGCCCTGATTATAGAGGTATGCATTTATCACAA   111
SHEEBA          ---------------------------------------------TTGCAATTATCCCAA   15
J99             ------------------------------------------------------------   0
Pecan18         ------------------------------------------------------------   0
26695           TTGAAATTCTTAGCTAATCGCATAAAAAGTTCTGATTATAGGGGCTTACACTTATCCCAA   120
Shi417          TTGAAATTCTTATCTAATCGCATAAAAAGCTCTGATTATAGGGGCTTACACTTATCCCAA   120
SHI470          ------------------------------------------------------------   0
SAT464          ------------------------------------------------------------   0
SHI169          ------------------------------------------------------------   0
ML2             ------------------------------------------------------------   0
OKI154          ------------------------------------------------------------   0
OKI673          ------------------------------------------------------------   0
OKI828          ------------------------------------------------------------   0


CC33C           CATGATATTTTGTAAATCA------------AGTTTATATAACACATTTTTAATGTAAGT   90
OKI128          CATGACATTTTGTAAATCA------------AGTTTATATAACACATTTTTAATGTAAGT   90
52              CATGACATTTTGTAGATCA------------AGTTTATATAACACATTTTTAATGTAAGT   90
OK113           CATGACATTTTGTAAATCA------------AGTTTATATAACACATTTTTAATGTAAGT   92
OK310           CATGACATTTTGTAAATCA------------AGTTTATATAACACATTTTTAATGTAAGT   90
UM066           CATGACATTTTGTAAATCA------------AGTTTATATAACACATTTTTAATGTAAGT   90
MIT             CATAACCGCTACACTAAAAAAGAAATTAAAATCATTATCCAAGCTATTTTTGATGAAGTA   171
SHEEBA          CACAATCGTTACGATCAAAATAAAATTAAAATCATTATTCAAGCTATTTTTAATGAAGTG   75
J99             ------------------------------------------------------------   0
Pecan18         ------------------------------------------------------------   0
26695           CACAATCGTTACGATCAAAATAAAATTAAAACCATTATTCAAGCTATTTTCAATGAAGTG   180
Shi417          CACAATCGTTATGATCAAAATAAAATTAAAACCATTATTCAAGCTATTTTCAATGAAGTG   180
SHI470          ------------------------------------------------------------   0
SAT464          ------------------------------------------------------------   0
SHI169          ------------------------------------------------------------   0
ML2             ------------------------------------------------------------   0
OKI154          ------------------------------------------------------------   0
OKI673          ------------------------------------------------------------   0
OKI828          ------------------------------------------------------------   0
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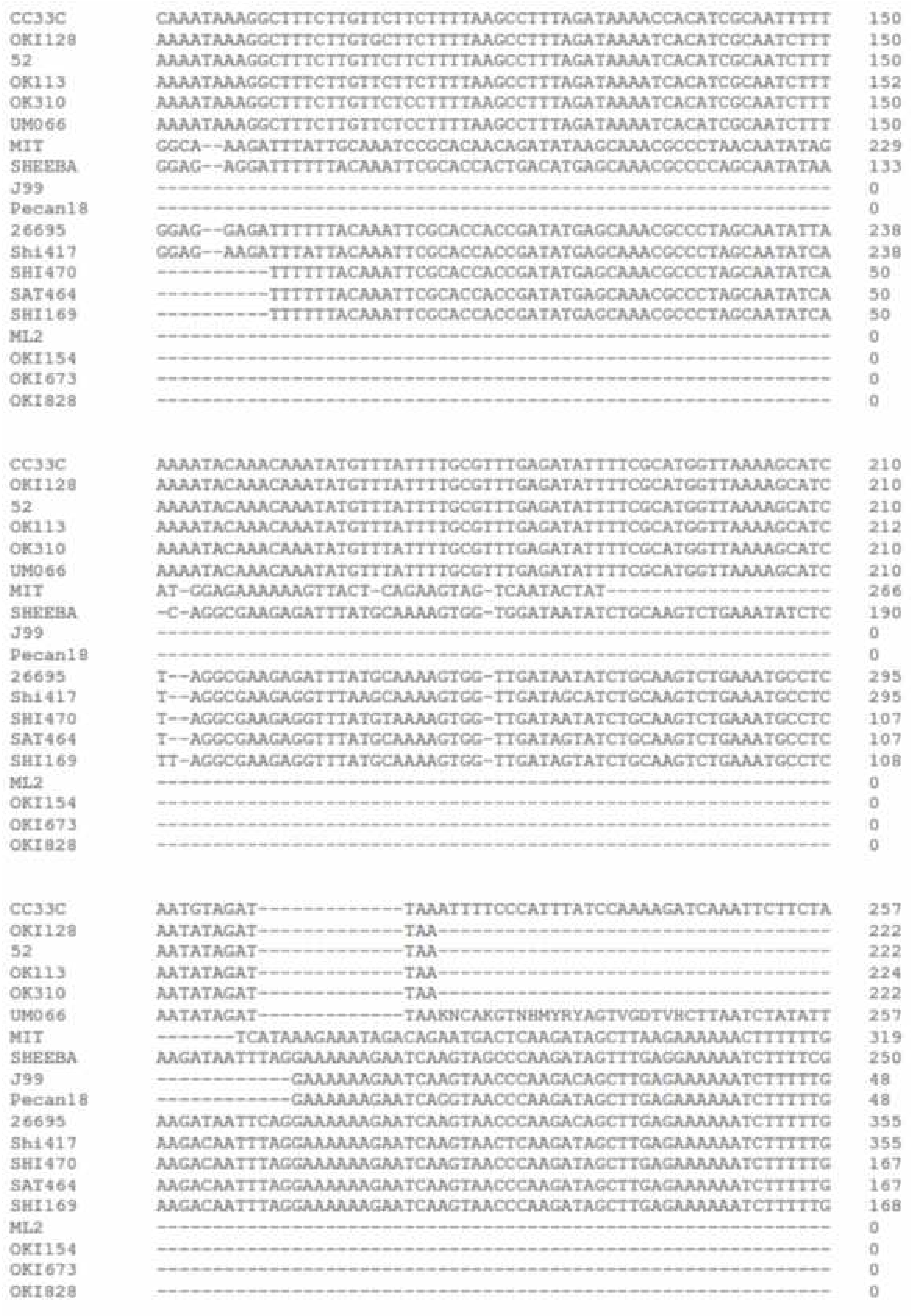
Figure S1



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CC33C          CAAATAAAGGCTTTCTTGTTCTTCTTTTAAGCCTTTAGATAAAACCACATCGCAATTTTT    150
OKI128         AAAATAAAGGCTTTCTTGTGCTTCTTTTAAGCCTTTAGATAAAATCACATCGCAATCTTT    150
52             AAAATAAAGGCTTTCTTGTTCTTCTTTTAAGCCTTTAGATAAAATCACATCGCAATCTTT    150
OK113          AAAATAAAGGCTTTCTTGTTCTTCTTTTAAGCCTTTAGATAAAATCACATCGCAATCTTT    152
OK310          AAAATAAAGGCTTTCTTGTTCTCCTTTTAAGCCTTTAGATAAAATCACATCGCAATCTTT    150
UM066          AAAATAAAGGCTTTCTTGTTCTCCTTTTAAGCCTTTAGATAAAATCACATCGCAATCTTT    150
MIT            GGCA--AAGATTTATTGCAAATCCGCACAACAGATATAAGCAAACGCCCTAACAATATAG    229
SHEEBA         GGAG--AGGATTTTTTACAAATTCGCACCACTGACATGAGCAAACGCCCCAGCAATATAA    133
J99            ------------------------------------------------------------    0
Pecan18        ------------------------------------------------------------    0
26695          GGAG--GAGATTTTTTACAAATTCGCACCACCGATATGAGCAAACGCCCTAGCAATATTA    238
Shi417         GGAG--AAGATTTATTACAAATTCGCACCACCGATATGAGCAAACGCCCTAGCAATATCA    238
SHI470         ----------TTTTTTACAAATTCGCACCACCGATATGAGCAAACGCCCTAGCAATATCA    50
SAT464         ----------TTTTTTACAAATTCGCACCACCGATATGAGCAAACGCCCTAGCAATATCA    50
SHI169         ----------TTTTTTACAAATTCGCACCACCGATATGAGCAAACGCCCTAGCAATATCA    50
ML2            ------------------------------------------------------------    0
OKI154         ------------------------------------------------------------    0
OKI673         ------------------------------------------------------------    0
OKI828         ------------------------------------------------------------    0


CC33C          AAAATACAAACAAATATGTTTATTTTGCGTTTGAGATATTTTCGCATGGTTAAAAGCATC    210
OKI128         AAAATACAAACAAATATGTTTATTTTGCGTTTGAGATATTTTCGCATGGTTAAAAGCATC    210
52             AAAATACAAACAAATATGTTTATTTTGCGTTTGAGATATTTTCGCATGGTTAAAAGCATC    210
OK113          AAAATACAAACAAATATGTTTATTTTGCGTTTGAGATATTTTCGCATGGTTAAAAGCATC    212
OK310          AAAATACAAACAAATATGTTTATTTTGCGTTTGAGATATTTTCGCATGGTTAAAAGCATC    210
UM066          AAAATACAAACAAATATGTTTATTTTGCGTTTGAGATATTTTCGCATGGTTAAAAGCATC    210
MIT            AT-GGAGAAAAAAGTTACT-CAGAAGTAG-TCAATACTAT--------------------    266
SHEEBA         -C-AGGCGAAGAGATTTATGCAAAAGTGG-TGGATAATATCTGCAAGTCTGAAATATCTC    190
J99            ------------------------------------------------------------    0
Pecan18        ------------------------------------------------------------    0
26695          T--AGGCGAAGAGATTTATGCAAAAGTGG-TTGATAATATCTGCAAGTCTGAAATGCCTC    295
Shi417         T--AGGCGAAGAGGTTTAAGCAAAAGTGG-TTGATAGCATCTGCAAGTCTGAAATGCCTC    295
SHI470         T--AGGCGAAGAGGTTTATGTAAAAGTGG-TTGATAATATCTGCAAGTCTGAAATGCCTC    107
SAT464         T--AGGCGAAGAGGTTTATGCAAAAGTGG-TTGATAGTATCTGCAAGTCTGAAATGCCTC    107
SHI169         TT-AGGCGAAGAGGTTTATGCAAAAGTGG-TTGATAGTATCTGCAAGTCTGAAATGCCTC    108
ML2            ------------------------------------------------------------    0
OKI154         ------------------------------------------------------------    0
OKI673         ------------------------------------------------------------    0
OKI828         ------------------------------------------------------------    0


CC33C          AATGTAGAT-------------TAAATTTTCCCATTTATCCAAAAGATCAAATTCTTCTA    257
OKI128         AATATAGAT-------------TAA-----------------------------------    222
52             AATATAGAT-------------TAA-----------------------------------    222
OK113          AATATAGAT-------------TAA-----------------------------------    224
OK310          AATATAGAT-------------TAA-----------------------------------    222
UM066          AATATAGAT-------------TAAKNCAKGTNHMYRYAGTVGDTVHCTTAATCTATATT    257
MIT            -------TCATAAAGAAATAGACAGAATGACTCAAGATAGCTTAAGAAAAAACTTTTTTG    319
SHEEBA         AAGATAATTTAGGAAAAAAGAATCAAGTAGCCCAAGATAGTTTGAGGAAAAATCTTTTCG    250
J99            ------------GAAAAAAGAATCAAGTAACCCAAGACAGCTTGAGAAAAAATCTTTTTG    48
Pecan18        ------------GAAAAAAGAATCAGGTAACCCAAGATAGCTTGAGAAAAAATCTTTTTG    48
26695          AAGATAATTCAGGAAAAAAGAATCAAGTAACCCAAGACAGCTTGAGAAAAAATCTTTTTG    355
Shi417         AAGACAATTTAGGAAAAAAGAATCAAGTAACTCAAGATAGCTTGAGAAAAAATCTTTTTG    355
SHI470         AAGACAATTTAGGAAAAAAGAATCAAGTAACCCAAGATAGCTTGAGAAAAAATCTTTTTG    167
SAT464         AAGACAATTTAGGAAAAAAGAATCAAGTAACCCAAGATAGCTTGAGAAAAAATCTTTTTG    167
SHI169         AAGACAATTTAGGAAAAAAGAATCAAGTAACCCAAGATAGCTTGAGAAAAAATCTTTTTG    168
ML2            ------------------------------------------------------------    0
OKI154         ------------------------------------------------------------    0
OKI673         ------------------------------------------------------------    0
OKI828         ------------------------------------------------------------    0
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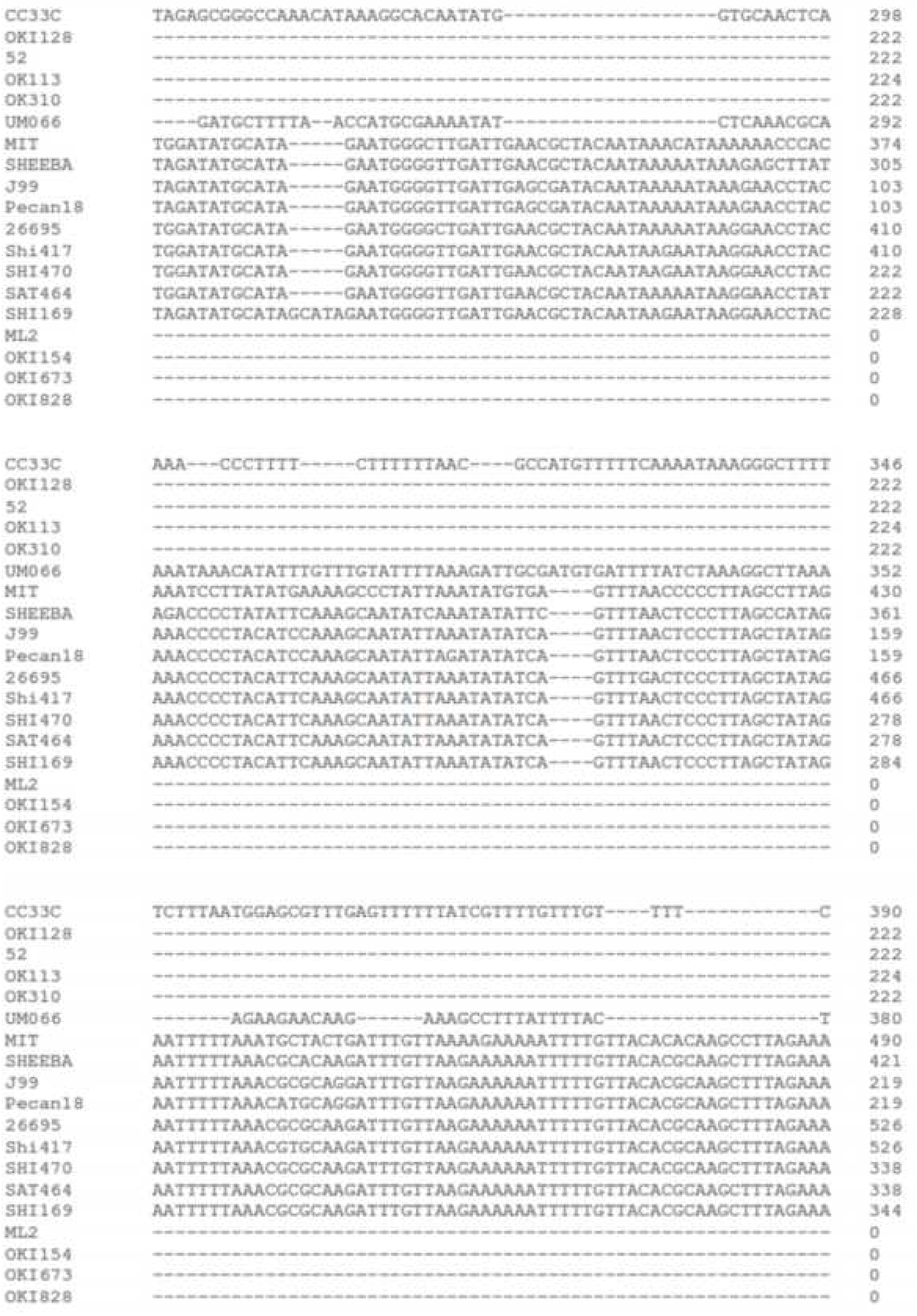
Figure S1



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CC33C           TAGAGCGGGCCAAACATAAAGGCACAATATG-------------------GTGCAACTCA    298
OKI128          ------------------------------------------------------------    222
52              ------------------------------------------------------------    222
OK113           ------------------------------------------------------------    224
OK310           ------------------------------------------------------------    222
UM066           ----GATGCTTTTA--ACCATGCGAAAATAT-------------------CTCAAACGCA    292
MIT             TGGATATGCATA-----GAATGGGCTTGATTGAACGCTACAATAAACATAAAAAACCCAC    374
SHEEBA          TAGATATGCATA-----GAATGGGGTTGATTGAACGCTACAATAAAAATAAAGAGCTTAT    305
J99             TAGATATGCATA-----GAATGGGGTTGATTGAGCGATACAATAAAAATAAAGAACCTAC    103
Pecan18         TAGATATGCATA-----GAATGGGGTTGATTGAGCGATACAATAAAAATAAAGAACCTAC    103
26695           TGGATATGCATA-----GAATGGGGCTGATTGAACGCTACAATAAAAATAAGGAACCTAC    410
Shi417          TGGATATGCATA-----GAATGGGGTTGATTGAACGCTACAATAAGAATAAGGAACCTAC    410
SHI470          TGGATATGCATA-----GAATGGGGTTGATTGAACGCTACAATAAGAATAAGGAACCTAC    222
SAT464          TGGATATGCATA-----GAATGGGGTTGATTGAACGCTACAATAAAAATAAGGAACCTAT    222
SHI169          TAGATATGCATAGCATAGAATGGGGTTGATTGAACGCTACAATAAGAATAAGGAACCTAC    228
ML2             ------------------------------------------------------------    0
OKI154          ------------------------------------------------------------    0
OKI673          ------------------------------------------------------------    0
OKI828          ------------------------------------------------------------    0


CC33C           AAA---CCCTTTT-----CTTTTTTAAC----GCCATGTTTTTCAAAATAAAGGGCTTTT    346
OKI128          ------------------------------------------------------------    222
52              ------------------------------------------------------------    222
OK113           ------------------------------------------------------------    224
OK310           ------------------------------------------------------------    222
UM066           AAATAAACATATTTGTTTGTATTTTAAAGATTGCGATGTGATTTTATCTAAAGGCTTAAA    352
MIT             AAATCCTTATATGAAAAGCCCTATTAAATATGTGA----GTTTAACCCCCTTAGCCTTAG    430
SHEEBA          AGACCCCTATATTCAAAGCAATATCAAATATATTC----GTTTAACTCCCTTAGCCATAG    361
J99             AAACCCCTACATCCAAAGCAATATTAAATATATCA----GTTTAACTCCCTTAGCTATAG    159
Pecan18         AAACCCCTACATCCAAAGCAATATTAGATATATCA----GTTTAACTCCCTTAGCTATAG    159
26695           AAACCCCTACATTCAAAGCAATATTAAATATATCA----GTTTGACTCCCTTAGCTATAG    466
Shi417          AAACCCCTACATTCAAAGCAATATTAAATATATCA----GTTTAACTCCCTTAGCTATAG    466
SHI470          AAACCCCTACATTCAAAGCAATATTAAATATATCA----GTTTAACTCCCTTAGCTATAG    278
SAT464          AAACCCCTACATTCAAAGCAATATTAAATATATCA----GTTTAACTCCCTTAGCTATAG    278
SHI169          AAACCCCTACATTCAAAGCAATATTAAATATATCA----GTTTAACTCCCTTAGCTATAG    284
ML2             ------------------------------------------------------------    0
OKI154          ------------------------------------------------------------    0
OKI673          ------------------------------------------------------------    0
OKI828          ------------------------------------------------------------    0


CC33C           TCTTTAATGGAGCGTTTGAGTTTTTTATCGTTTTGTTTGT----TTT------------C    390
OKI128          ------------------------------------------------------------    222
52              ------------------------------------------------------------    222
OK113           ------------------------------------------------------------    224
OK310           ------------------------------------------------------------    222
UM066           -------AGAAGAACAAG------AAAGCCTTTATTTTAC-------------------T    380
MIT             AATTTTTAAATGCTACTGATTTGTTAAAAGAAAAATTTTGTTACACACAAGCCTTAGAAA    490
SHEEBA          AATTTTTAAACGCACAAGATTTGTTAAGAAAAAATTTTTGTTACACGCAAGCTTTAGAAA    421
J99             AATTTTTAAACGCGCAGGATTTGTTAAGAAAAAATTTTTGTTACACGCAAGCTTTAGAAA    219
Pecan18         AATTTTTAAACATGCAGGATTTGTTAAGAAAAAATTTTTGTTACACGCAAGCTTTAGAAA    219
26695           AATTTTTAAACGCGCAAGATTTGTTAAGAAAAAATTTTTGTTACACGCAAGCTTTAGAAA    526
Shi417          AATTTTTAAACGTGCAAGATTTGTTAAGAAAAAATTTTTGTTACACGCAAGCTTTAGAAA    526
SHI470          AATTTTTAAACGCGCAAGATTTGTTAAGAAAAAATTTTTGTTACACGCAAGCTTTAGAAA    338
SAT464          AATTTTTAAACGCGCAAGATTTGTTAAGAAAAAATTTTTGTTACACGCAAGCTTTAGAAA    338
SHI169          AATTTTTAAACGCGCAAGATTTGTTAAGAAAAAATTTTTGTTACACGCAAGCTTTAGAAA    344
ML2             ------------------------------------------------------------    0
OKI154          ------------------------------------------------------------    0
OKI673          ------------------------------------------------------------    0
OKI828          ------------------------------------------------------------    0
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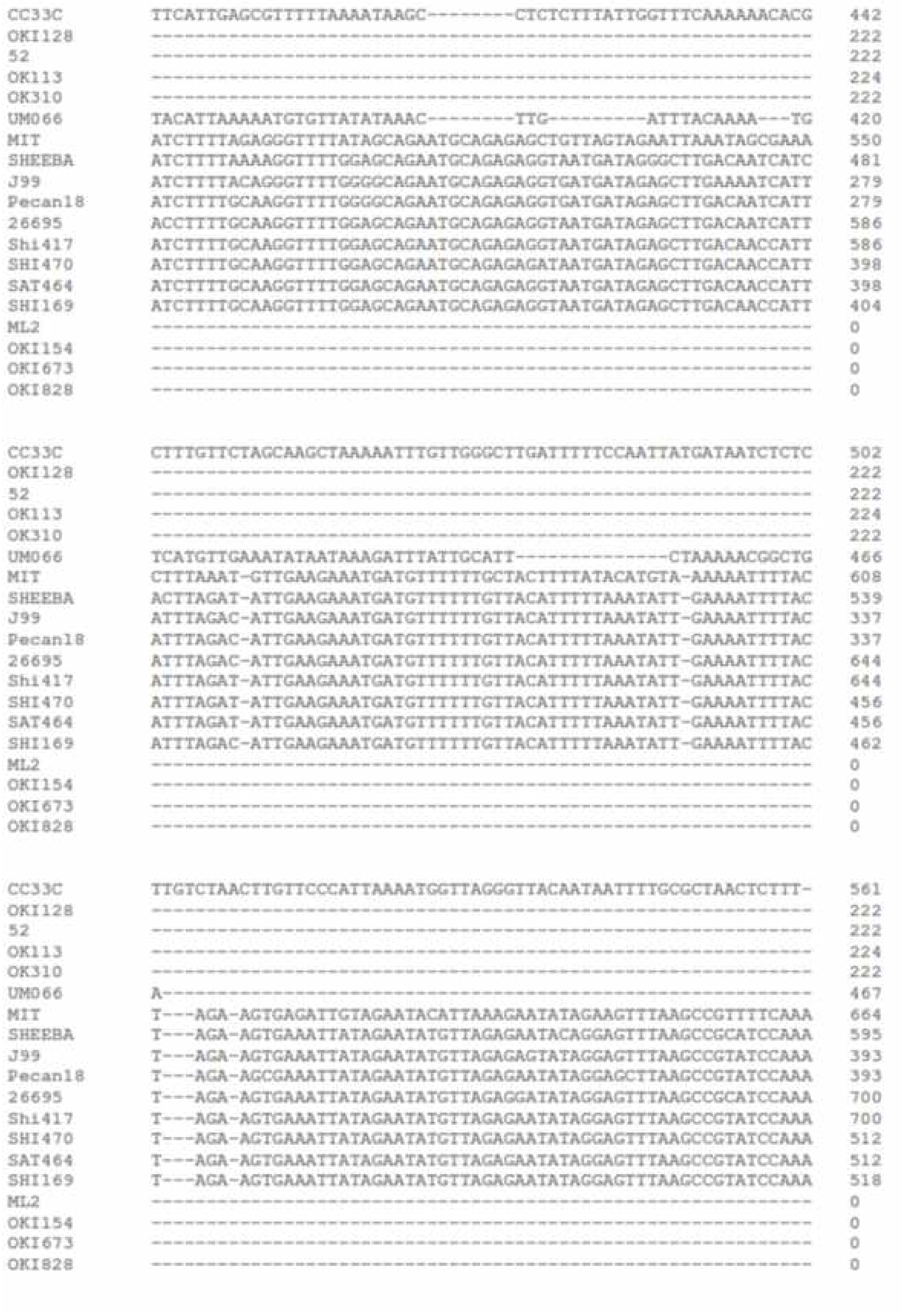
Figure S1



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CC33C           TTCATTGAGCGTTTTTAAAATAAGC--------CTCTCTTTATTGGTTTCAAAAAACACG      442
OKI128          ------------------------------------------------------------      222
52              ------------------------------------------------------------      222
OK113           ------------------------------------------------------------      224
OK310           ------------------------------------------------------------      222
UM066           TACATTAAAAATGTGTTATATAAAC--------TTG---------ATTTACAAAA---TG      420
MIT             ATCTTTTAGAGGGTTTTATAGCAGAATGCAGAGAGCTGTTAGTAGAATTAAATAGCGAAA      550
SHEEBA          ATCTTTTAAAAGGTTTTGGAGCAGAATGCAGAGAGGTAATGATAGGGCTTGACAATCATC      481
J99             ATCTTTTACAGGGTTTTGGGGCAGAATGCAGAGAGGTGATGATAGAGCTTGAAAATCATT      279
Pecan18         ATCTTTTGCAAGGTTTTGGGGCAGAATGCAGAGAGGTGATGATAGAGCTTGACAATCATT      279
26695           ACCTTTTGCAAGGTTTTGGAGCAGAATGCAGAGAGGTAATGATAGAGCTTGACAATCATT      586
Shi417          ATCTTTTGCAAGGTTTTGGAGCAGAATGCAGAGAGGTAATGATAGAGCTTGACAACCATT      586
SHI470          ATCTTTTGCAAGGTTTTGGAGCAGAATGCAGAGAGATAATGATAGAGCTTGACAACCATT      398
SAT464          ATCTTTTGCAAGGTTTTGGAGCAGAATGCAGAGAGGTAATGATAGAGCTTGACAACCATT      398
SHI169          ATCTTTTGCAAGGTTTTGGAGCAGAATGCAGAGAGGTAATGATAGAGCTTGACAACCATT      404
ML2             ------------------------------------------------------------      0
OKI154          ------------------------------------------------------------      0
OKI673          ------------------------------------------------------------      0
OKI828          ------------------------------------------------------------      0


CC33C           CTTTGTTCTAGCAAGCTAAAAATTTGTTGGGCTTGATTTTTCCAATTATGATAATCTCTC      502
OKI128          ------------------------------------------------------------      222
52              ------------------------------------------------------------      222
OK113           ------------------------------------------------------------      224
OK310           ------------------------------------------------------------      222
UM066           TCATGTTGAAATATAATAAAGATTTATTGCATT--------------CTAAAAACGGCTG      466
MIT             CTTTAAAT-GTTGAAGAAATGATGTTTTTTGCTACTTTTATACATGTA-AAAAATTTTAC      608
SHEEBA          ACTTAGAT-ATTGAAGAAATGATGTTTTTTGTTACATTTTTAAATATT-GAAAATTTTAC      539
J99             ATTTAGAC-ATTGAAGAAATGATGTTTTTTGTTACATTTTTAAATATT-GAAAATTTTAC      337
Pecan18         ATTTAGAC-ATTGAAGAAATGATGTTTTTTGTTACATTTTTAAATATT-GAAAATTTTAC      337
26695           ATTTAGAC-ATTGAAGAAATGATGTTTTTTGTTACATTTTTAAATATT-GAAAATTTTAC      644
Shi417          ATTTAGAT-ATTGAAGAAATGATGTTTTTTGTTACATTTTTAAATATT-GAAAATTTTAC      644
SHI470          ATTTAGAT-ATTGAAGAAATGATGTTTTTTGTTACATTTTTAAATATT-GAAAATTTTAC      456
SAT464          ATTTAGAT-ATTGAAGAAATGATGTTTTTTGTTACATTTTTAAATATT-GAAAATTTTAC      456
SHI169          ATTTAGAC-ATTGAAGAAATGATGTTTTTTGTTACATTTTTAAATATT-GAAAATTTTAC      462
ML2             ------------------------------------------------------------      0
OKI154          ------------------------------------------------------------      0
OKI673          ------------------------------------------------------------      0
OKI828          ------------------------------------------------------------      0


CC33C           TTGTCTAACTTGTTCCCATTAAAATGGTTAGGGTTACAATAATTTTGCGCTAACTCTTT-      561
OKI128          ------------------------------------------------------------      222
52              ------------------------------------------------------------      222
OK113           ------------------------------------------------------------      224
OK310           ------------------------------------------------------------      222
UM066           A-----------------------------------------------------------      467
MIT             T---AGA-AGTGAGATTGTAGAATACATTAAAGAATATAGAAGTTTAAGCCGTTTTCAAA      664
SHEEBA          T---AGA-AGTGAAATTATAGAATATGTTAGAGAATACAGGAGTTTAAGCCGCATCCAAA      595
J99             T---AGA-AGTGAAATTATAGAATATGTTAGAGAGTATAGGAGTTTAAGCCGTATCCAAA      393
Pecan18         T---AGA-AGCGAAATTATAGAATATGTTAGAGAATATAGGAGCTTAAGCCGTATCCAAA      393
26695           T---AGA-AGTGAAATTATAGAATATGTTAGAGGATATAGGAGTTTAAGCCGCATCCAAA      700
Shi417          T---AGA-AGTGAAATTATAGAATATGTTAGAGAATATAGGAGTTTAAGCCGTATCCAAA      700
SHI470          T---AGA-AGTGAAATTATAGAATATGTTAGAGAATATAGGAGTTTAAGCCGTATCCAAA      512
SAT464          T---AGA-AGTGAAATTATAGAATATGTTAGAGAATATAGGAGTTTAAGCCGTATCCAAA      512
SHI169          T---AGA-AGTGAAATTATAGAATATGTTAGAGAATATAGGAGTTTAAGCCGTATCCAAA      518
ML2             ------------------------------------------------------------      0
OKI154          ------------------------------------------------------------      0
OKI673          ------------------------------------------------------------      0
OKI828          ------------------------------------------------------------      0
```

```
CC33C       TAATTTTTCTTTTTGGATACGGCTTAAACTCCTATACTCTCTAACATATT-CTATAATTT    620
OKI128      ------------------------------------------------------------    222
52          ------------------------------------------------------------    222
OK113       ------------------------------------------------------------    224
OK310       ------------------------------------------------------------    222
UM066       ------------------------------------------------------------    467
MIT         GAGAAAAACTTCTTGAATTAGTGCAAAATTATTGTAACCCTAAAAATTTTGATGGGGATA    724
SHEEBA      AAGAAAAATTAAAAGAGTCAGTGCAAAATTATTGCAACCCTAACCATTTTAGTGGGAACA    655
J99         AAGAAAAATTAAAAGAGTTAGCGCAAGATTATTGCAATCCTAATCATTTTAATGGGAATA    453
Pecan18     AAGAAAAATTAAAAGAGTTAGTGCAAAATTATTGCAACCCTAACCATTTTAACGGGAATA    453
26695       AAGAAAAATTAAAAGAGTTAGTGCAAGATTATTGCAACCCTAACCATTTTAATGGGAATA    760
Shi417      AAGAAAAATTAAAAGAGTTAGTGCAAGATTATTGCAACCCTAACCATTTTAACGGAAATA    760
SHI470      AAGAAAAATTAAAAGAGTTAGTGCAAGATTATTGTAACCCTAACCATTTTAACGGAAATA    572
SAT464      AAGAAAAATTAAAAGAGTTAGTGCAAGATTATTGCGACCCTAACCATTTTAACGGAAATA    572
SHI169      AAGAAAAATTAAAAGAGTTAGTGCAAGATTATTGCGACCCTAACCATTTTAACGGAAATA    578
ML2         ------------------------------------------------------------    0
OKI154      ------------------------------------------------------------    0
OKI673      ------------------------------------------------------------    0
OKI828      ------------------------------------------------------------    0


CC33C       CGCTTCT--AGTAAAATTTTCAATATTTAA-AAACGTAACAAAAAACATCATTTCTTCA-    676
OKI128      ------------------------------------------------------------    222
52          ------------------------------------------------------------    222
OK113       ------------------------------------------------------------    224
OK310       ------------------------------------------------------------    222
UM066       ------------------------------------------------------------    467
MIT         AAACACA--TAAGAGACTATCATAATTGGAAAAATGAAACAGACCAAATTTTTACTTTAC    782
SHEEBA      AGTTAAATAAAAGAGATTATCATAATTGGAAAAATCAAGCCCAACAAATTTTTAGCTTGC    715
J99         AGTTAGACAAGAGAGATTATCATAATTGGAAAAATCAAGCCCAACAAATTTTTAGCTTGC    513
Pecan18     AGCTAGAAAAGAGAGATTATCATAATTGGAAAAATCAAGCCCAACAAATTTTTAGCTTGC    513
26695       AGCTAGAAAAGAGAGATTATCATAATTGGAAAAATCAAGCCCAACAAATTTTTAGCTTGC    820
Shi417      AGCTAGAAAAGAGAGATTATCATAATTGGAAAAATCAAGCCCAACAAATTTTTAGCTTGC    820
SHI470      AGCTAGAAAAGAGAGATTATCATAATTGGAAAAATCAAGCCCAACAAATTTTTAGCTTGC    632
SAT464      AGCTAGAAAAGAGAGATTATCATAATTGGAAAAATCAAGCCCAACAAATTTTTAGCTTGC    632
SHI169      AGTTAGAAAAGAGAGATTATCATAATTGGAAAAATCAAGCCCAACAAATTTTTAGCTTGC    638
ML2         ------------------------------------------------------------    0
OKI154      ------------------------------------------------------------    0
OKI673      ------------------------------------------------------------    0
OKI828      ------------------------------------------------------------    0


CC33C       ATGTCTAAATAATGATTTTCAAGCTCTATCATCACCT--------------CTCTGCATT    722
OKI128      ------------------------------------------------------------    222
52          ------------------------------------------------------------    222
OK113       ------------------------------------------------------------    224
OK310       ------------------------------------------------------------    222
UM066       ------------------------------------------------------------    467
MIT         TAGAACAAAGCGTATTTTTTGAAAGAGATAAAAACAAGCTTATTTTAAGAATGCTAGACA    842
SHEEBA      TAGAACAAAGCGTATTTTTTGAAACCAATAAAGAGAGGCTTATTTTGAAAACGATCAGTG    775
J99         TAGAACAAAGCGTGTTTTTTGAAACCAATAAAGAGAGGCTTATTTTAAAAACGCTCAATG    573
Pecan18     TAGAACAAAGCGTGTTTTTTGAAACCAATAAAGAGAGGCTTATTTTAAAAACGCTCAATG    573
26695       TAGAACAAAGCGTGTTTTTTGAAACCAATAAAGAGAGGCTTATTTTAAAAGCGCTCAATG    880
Shi417      TAGAACAAAGCGTGTTTTTTGAAACCAATAAAGAGAGGCTTATTTTAAAAACGCTCAATG    880
SHI470      TAGAACAAAGCGTGTTTTTTGAAACCAATAAAGAGAGGCTTATTTTAAAAACGCTCAATG    692
SAT464      TAGAACAAAGCGTGTTTTTTGAAACCAATAAAGAGAGGCTTATTTTAAAAACGCTCAATG    692
SHI169      TAGAACAAAGCGTGTTTTTTGAAACCAATAAAGAGAGGCTTATTTTAAAAACGCTCAATG    698
ML2         ------------------------------------------------------------    0
OKI154      ------------------------------------------------------------    0
OKI673      ------------------------------------------------------------    0
OKI828      ------------------------------------------------------------    0
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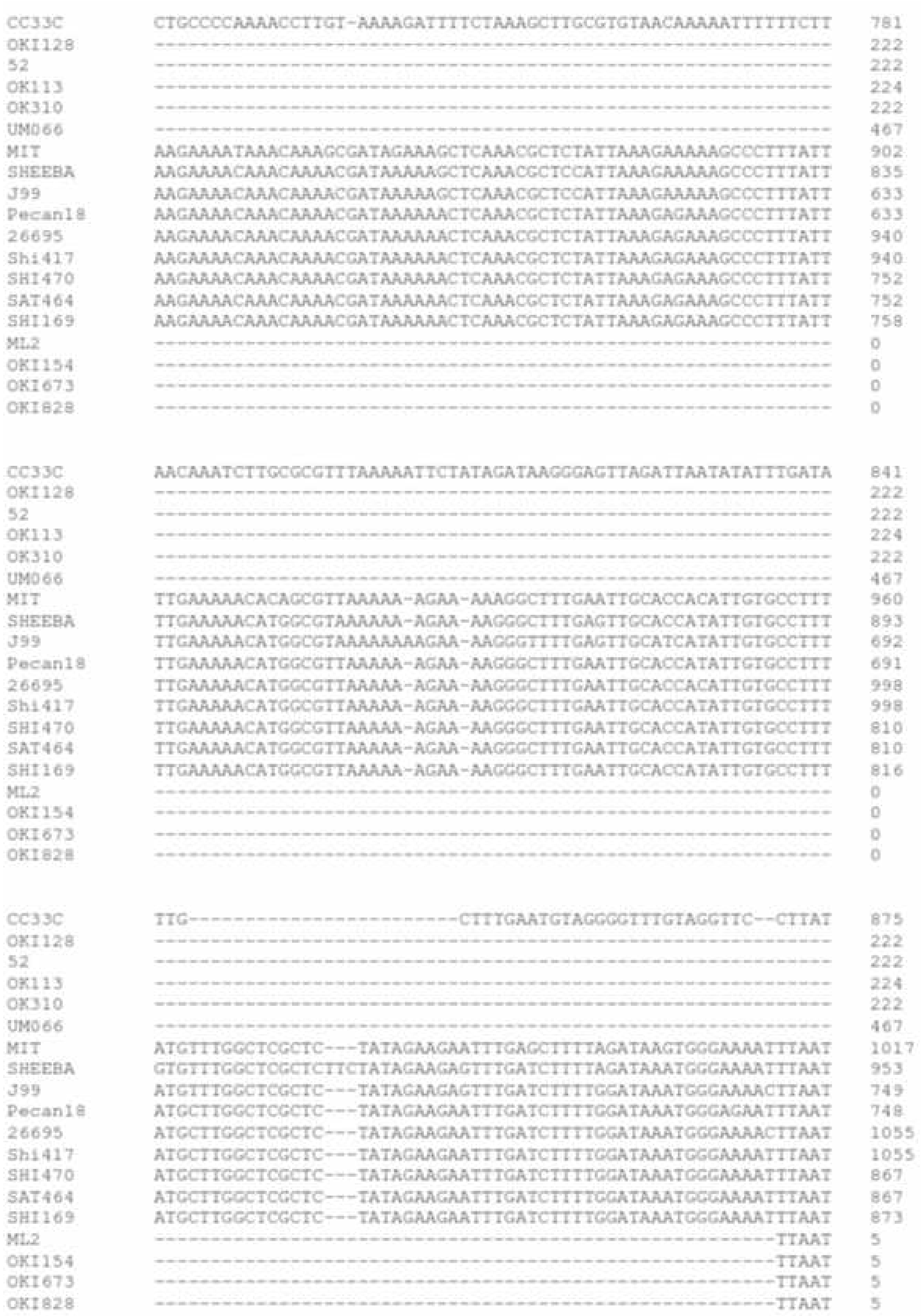

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CC33C      CTGCCCCAAAACCTTGT-AAAAGATTTTCTAAAGCTTGCGTGTAACAAAAATTTTTTCTT   781
OKI128     ------------------------------------------------------------   222
52         ------------------------------------------------------------   222
OK113      ------------------------------------------------------------   224
OK310      ------------------------------------------------------------   222
UM066      ------------------------------------------------------------   467
MIT        AAGAAAATAAACAAAGCGATAGAAAGCTCAAACGCTCTATTAAAGAAAAAGCCCTTTATT   902
SHEEBA     AAGAAAACAAACAAAACGATAAAAAGCTCAAACGCTCCATTAAAGAAAAAGCCCTTTATT   835
J99        AAGAAAACAAACAAAACGATAAAAAGCTCAAACGCTCCATTAAAGAAAAAGCCCTTTATT   633
Pecan18    AAGAAAACAAACAAAACGATAAAAAACTCAAACGCTCTATTAAAGAGAAAGCCCTTTATT   633
26695      AAGAAAACAAACAAAACGATAAAAAACTCAAACGCTCTATTAAAGAGAAAGCCCTTTATT   940
Shi417     AAGAAAACAAACAAAACGATAAAAAACTCAAACGCTCTATTAAAGAGAAAGCCCTTTATT   940
SHI470     AAGAAAACAAACAAAACGATAAAAAACTCAAACGCTCTATTAAAGAGAAAGCCCTTTATT   752
SAT464     AAGAAAACAAACAAAACGATAAAAAACTCAAACGCTCTATTAAAGAGAAAGCCCTTTATT   752
SHI169     AAGAAAACAAACAAAACGATAAAAAACTCAAACGCTCTATTAAAGAGAAAGCCCTTTATT   758
ML2        ------------------------------------------------------------   0
OKI154     ------------------------------------------------------------   0
OKI673     ------------------------------------------------------------   0
OKI828     ------------------------------------------------------------   0


CC33C      AACAAATCTTGCGCGTTTAAAAATTCTATAGATAAGGGAGTTAGATTAATATATTTGATA   841
OKI128     ------------------------------------------------------------   222
52         ------------------------------------------------------------   222
OK113      ------------------------------------------------------------   224
OK310      ------------------------------------------------------------   222
UM066      ------------------------------------------------------------   467
MIT        TTGAAAAACACAGCGTTAAAAA-AGAA-AAAGGCTTTGAATTGCACCACATTGTGCCTTT   960
SHEEBA     TTGAAAAACATGGCGTAAAAAA-AGAA-AAGGGCTTTGAGTTGCACCATATTGTGCCTTT   893
J99        TTGAAAAACATGGCGTAAAAAAAAGAA-AAGGGTTTTGAGTTGCATCATATTGTGCCTTT   692
Pecan18    TTGAAAAACATGGCGTTAAAAA-AGAA-AAGGGCTTTGAATTGCACCATATTGTGCCTTT   691
26695      TTGAAAAACATGGCGTTAAAAA-AGAA-AAGGGCTTTGAATTGCACCACATTGTGCCTTT   998
Shi417     TTGAAAAACATGGCGTTAAAAA-AGAA-AAGGGCTTTGAATTGCACCATATTGTGCCTTT   998
SHI470     TTGAAAAACATGGCGTTAAAAA-AGAA-AAGGGCTTTGAATTGCACCATATTGTGCCTTT   810
SAT464     TTGAAAAACATGGCGTTAAAAA-AGAA-AAGGGCTTTGAATTGCACCATATTGTGCCTTT   810
SHI169     TTGAAAAACATGGCGTTAAAAA-AGAA-AAGGGCTTTGAATTGCACCATATTGTGCCTTT   816
ML2        ------------------------------------------------------------   0
OKI154     ------------------------------------------------------------   0
OKI673     ------------------------------------------------------------   0
OKI828     ------------------------------------------------------------   0


CC33C      TTG------------------------CTTTGAATGTAGGGGTTTGTAGGTTC--CTTAT   875
OKI128     ------------------------------------------------------------   222
52         ------------------------------------------------------------   222
OK113      ------------------------------------------------------------   224
OK310      ------------------------------------------------------------   222
UM066      ------------------------------------------------------------   467
MIT        ATGTTTGGCTCGCTC---TATAGAAGAATTTGAGCTTTTAGATAAGTGGGAAAATTTAAT   1017
SHEEBA     GTGTTTGGCTCGCTCTTCTATAGAAGAGTTTGATCTTTTAGATAAATGGGAAAATTTAAT   953
J99        ATGTTTGGCTCGCTC---TATAGAAGAGTTTGATCTTTTGGATAAATGGGAAAACTTAAT   749
Pecan18    ATGCTTGGCTCGCTC---TATAGAAGAATTTGATCTTTTGGATAAATGGGAGAATTTAAT   748
26695      ATGCTTGGCTCGCTC---TATAGAAGAATTTGATCTTTTGGATAAATGGGAAAACTTAAT   1055
Shi417     ATGCTTGGCTCGCTC---TATAGAAGAATTTGATCTTTTGGATAAATGGGAAAATTTAAT   1055
SHI470     ATGCTTGGCTCGCTC---TATAGAAGAATTTGATCTTTTGGATAAATGGGAAAATTTAAT   867
SAT464     ATGCTTGGCTCGCTC---TATAGAAGAATTTGATCTTTTGGATAAATGGGAAAATTTAAT   867
SHI169     ATGCTTGGCTCGCTC---TATAGAAGAATTTGATCTTTTGGATAAATGGGAAAATTTAAT   873
ML2        -------------------------------------------------------TTAAT   5
OKI154     -------------------------------------------------------TTAAT   5
OKI673     -------------------------------------------------------TTAAT   5
OKI828     -------------------------------------------------------TTAAT   5
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OKI128      ------------------------------------------------------------   222
52          ------------------------------------------------------------   222
OK113       ------------------------------------------------------------   224
OK310       ------------------------------------------------------------   222
UM066       ------------------------------------------------------------   467
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J99         CTATATTGACGCTTTTAACCATGCGAAGATATCTCAAACGCAAAATAAACATCTTTGTTT   809
Pecan18     CTATATTGATGCTTTTAACCATGCGAAAATATCTCAAACGCAAAATAAACATATTTGTTT   808
26695       CTATATTGACGCTTTTAACCATGCGAAAATATCTCAAACGCAAAATAAACATATTTGTTT   1115
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ML2         CTATATTGATGCTTTTAACCATGCGAAAATATCTCAAACGCAAAATAAACATATTTGTTT   65
OKI154      CTATATTGATGCTTTTAACCATGCGAAAATATCTCAAACGCAAAATAAACATATTTGTTT   65
OKI673      CTATATTGATGCTTTTAACCATGCGAAAATATCTCAAACGCAAAATAAACATATTTGTTT   65
OKI828      CTATATTGATGCTTTTAACCATGCGAAAATATCTCAAACGCAAAATAAACATATTTGTTT   65


CC33C       AGCTGTCTTGGGTTACTTGATTCTTTTTTCGTGAAGTGCCCAA-----------------   978
OKI128      ------------------------------------------------------------   222
52          ------------------------------------------------------------   222
OK113       ------------------------------------------------------------   224
OK310       ------------------------------------------------------------   222
UM066       ------------------------------------------------------------   467
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OKI673      GTATTTTAAAGATTGCGATGTGATTTTATCTAAAGGCTTAAAAGAAGCACAAGAAAGCCT   125
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CC33C       ------------------------------------------------------------   978
OKI128      ------------------------------------------------------------   222
52          ------------------------------------------------------------   222
OK113       ------------------------------------------------------------   224
OK310       ------------------------------------------------------------   222
UM066       ------------------------------------------------------------   467
MIT         TTATTTTACTTATCTTAAAAATGTATTGTATAAACTTGATTTACAAAATATCATGCTGAA   1197
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OKI673      TTATTTTACTTACATTAAAAATGTGTTATATAAACTTGATTTACAAAATGTCATGTTGGA   185
OKI828      TTATTTTACTTACATTAAAAATGTGTTATATAAACTTGATTTACAAAATATCATGTTGGA   185
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Figure S1

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CC33C           ------------------------------------------------      978
OKI128          ------------------------------------------------      222
52              ------------------------------------------------      222
OK113           ------------------------------------------------      224
OK310           ------------------------------------------------      222
UM066           ------------------------------------------------      467
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J99             ATACAATAAAGATTTATTGCATTCTAAAAACGGCTGA-----------      966
Pecan18         ATACAATAAAGATTTATTGCATTCTAAAAACGGCTGA-----------      965
26695           ATACAATAAAGATTTATTGCATTCTAAAAACGGCTGA-----------      1272
Shi417          ATACAATAAAGATTTATTGCATTCTAAAAACGGCTG------------      1271
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SHI169          ATACAATAAAGATTTATTGCATTCTAAAAACGGCTGA-----------      1090
ML2             ATACAATAAAGATTTATTGCATTCTAAAAACGGCTGA-----------      222
OKI154          ATACAATAAAGATTTATTGCATTCTAAAAACGGCTGA-----------      222
OKI673          ATACAATAAAGATTTATTGCATTCTAAAAACGGCTGA-----------      222
OKI828          ATACAATAAAGATTTATTGCACTCTAAAAACGGCTGA                 233
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Figure S1. Multiple DNA sequence alignment of *R.hpyAII* gene in the sequenced *H. pylori* strains which lack the cognate *M1.hpyAII* and *M2.hpyAII or M1.hpyAII alone* methyltransferases in their genomes. *H. pylori* 26695 strain contains the full length active copy of *R.hpyAII* gene (1272 bp) while in other strains truncated versions are present. 16 strains which are negative for *M1.hpyAII* and *M2.hpyAII* genes and 2 strains (Pecan18 and CC33C) which are positive for *R.hpyAII* and *M2.hpyAII* but negative for *M1.hpyAII* were used for the alignment. Gene sequences were downloaded from NCBI database and alignment performed using CLUSTAL Omega server.

Figure S2

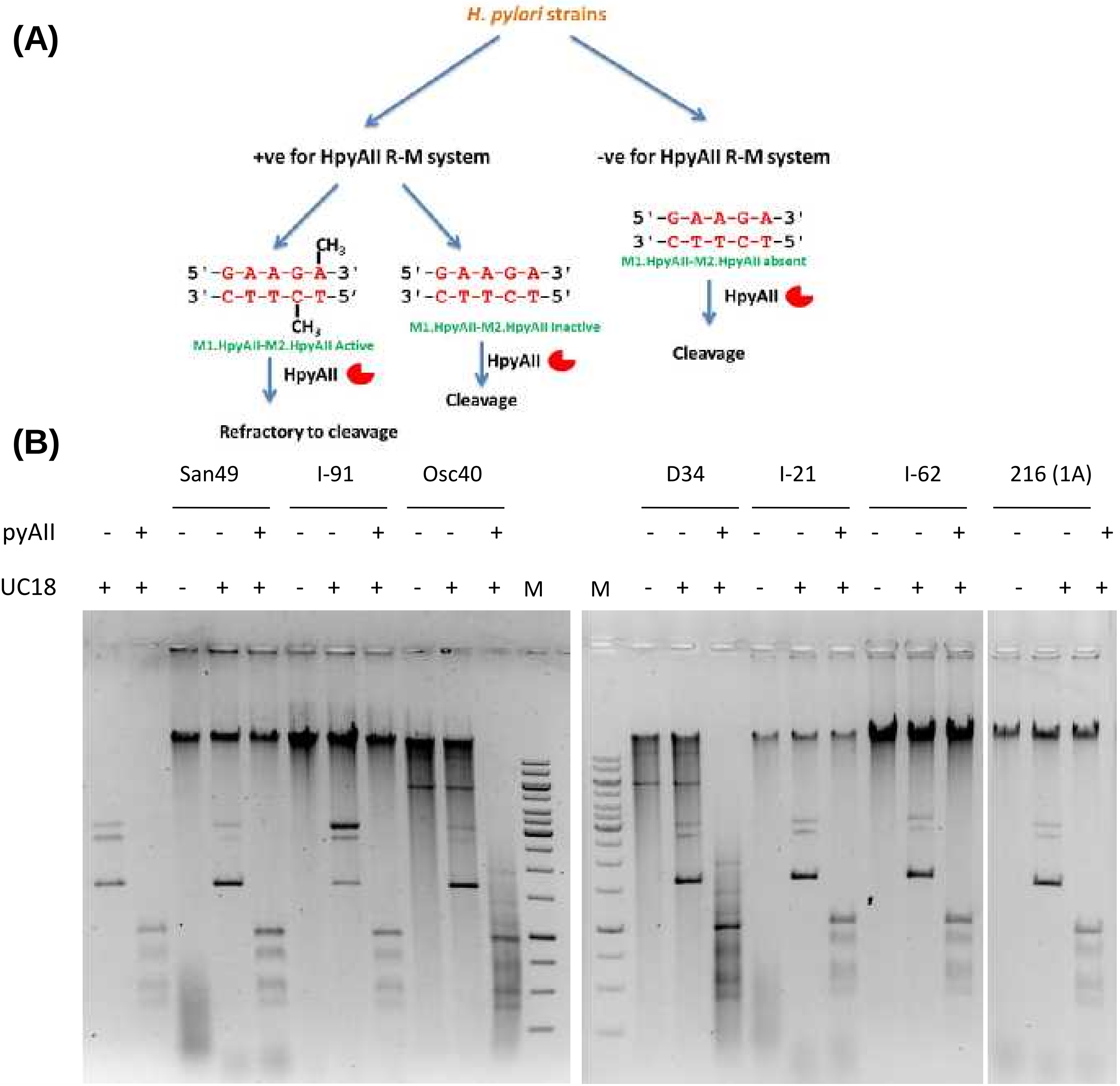

Figure S2. Activity analysis of M1.HpyAII and M2.HpyAII MTases in the Indian *H. pylori* clinical isolates. Genomic DNA was isolated as described in materials and method section. *In vitro* digestion with purified HpyAII was performed to check the activity status of M1.HpyAII and M2.HpyAII MTases. **(A)** Genomic DNA of the strains harboring active M1.HpyAII-M2.HpyAII MTases will be refractory to HpyAII clevage. In constrast the genomic DNA of the strains lacking or harboring inactive M1.HpyAII-M2.HpyAII MTases will be cleaved *in vitro* by HpyAII. **(B)** Genomic DNA from seven Indian isolates was digested to HpyAII cleavage. Two *H. pylori* Indian isolates (D34 and Osc40) which are negative for HpyAII R-M system as expected were found to be susceptible to HpyAII cleavage.

Figure S3

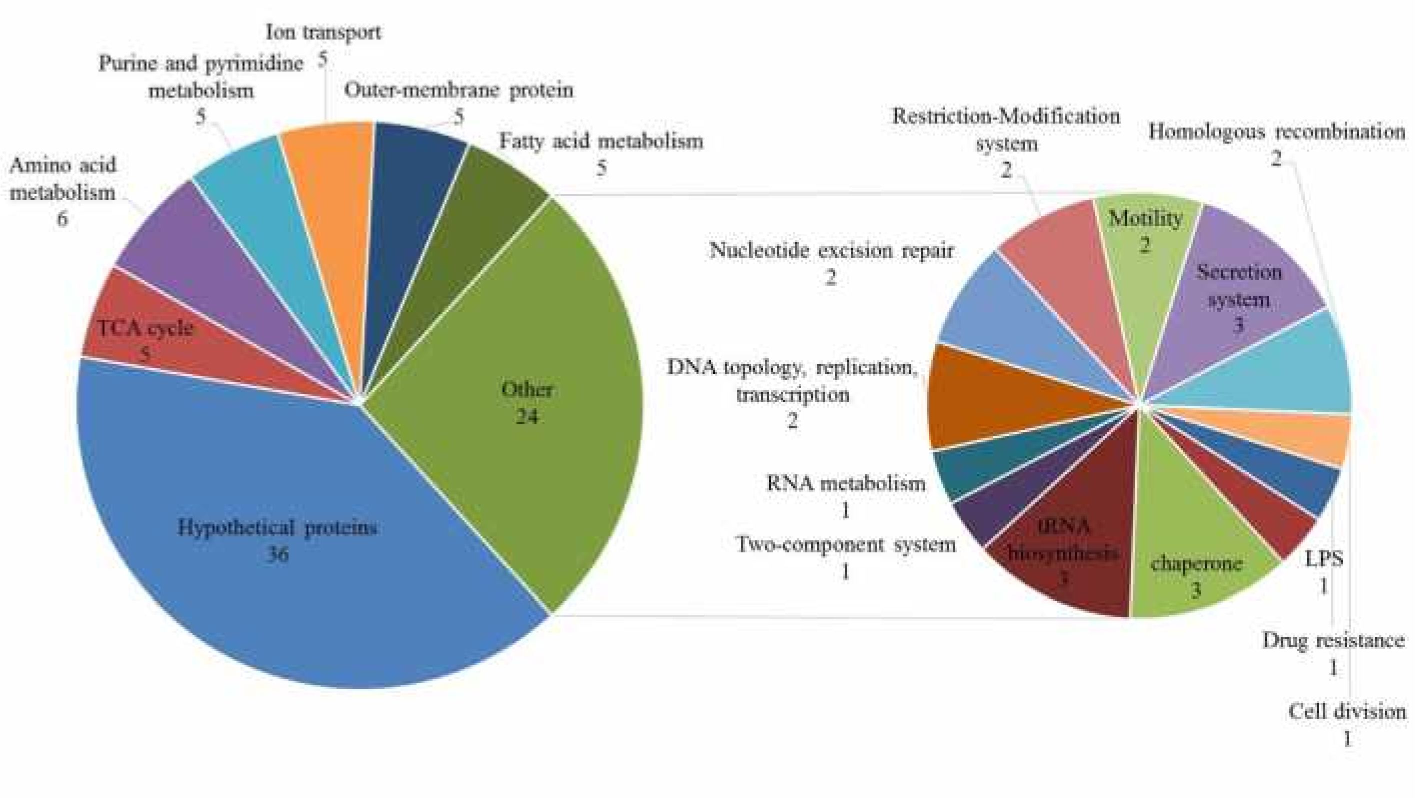

Figure S3 Analysis of 5' TCTTC 3' motifs in the promoter region of *H. pylori* 26695 strain. 50 nucleotides region upstream of the known TSS of *H. pylori* 26695 strain was screened for the distribution of 5' TCTTC 3' sites. Genes which harbor 5' TCTTC 3' motif in the promoter region were classified according to the pathway and shown in the form of pie chart. Pathway classification was performed using gene ontology from KEGG database. Numbers in the pie chart indicate number of genes harboring 5' TCTTC 3' site.

Figure S4

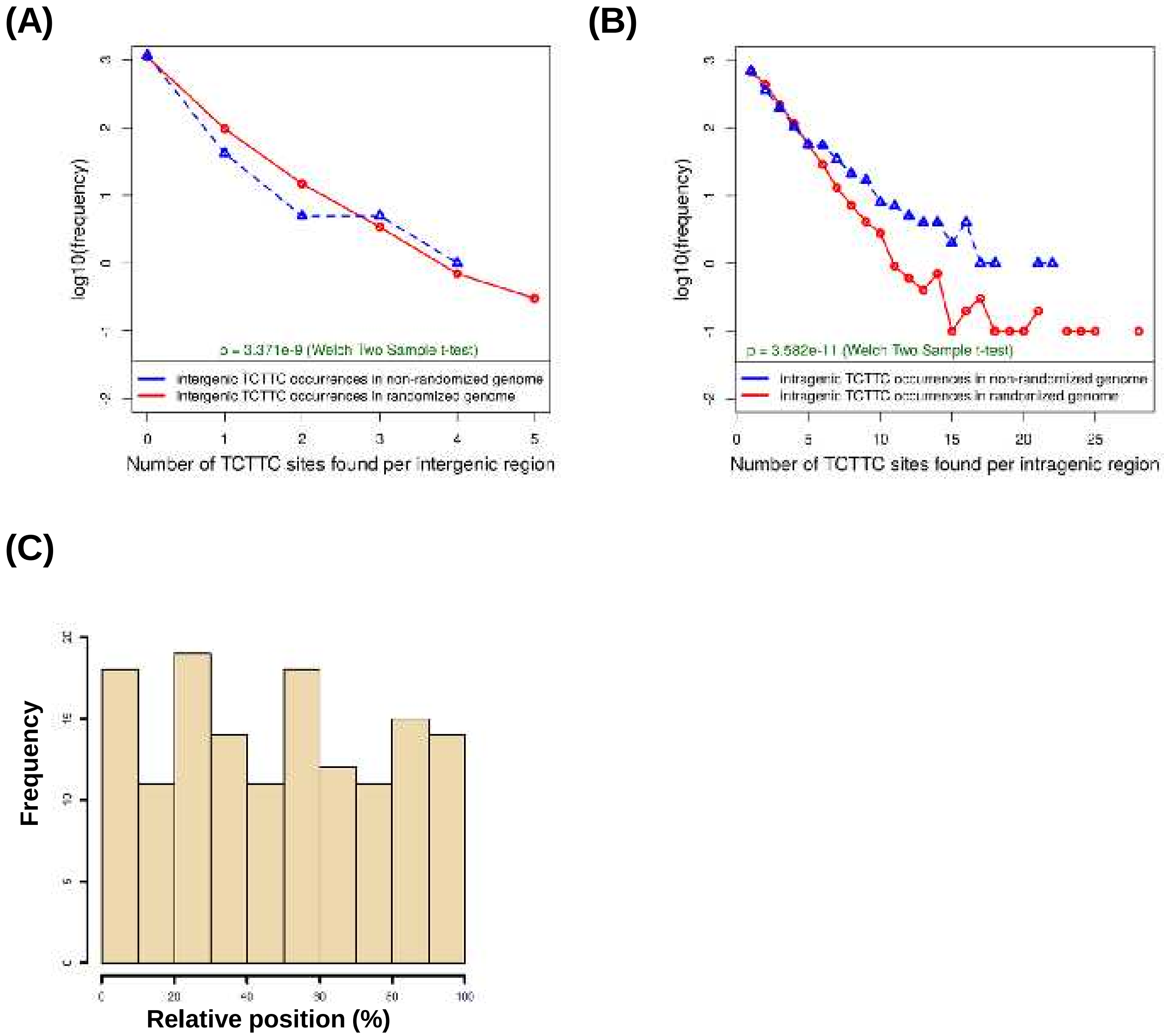

Figure S4. **Analysis of intergenic and intragenic region of *H. pylori* 26695 strain for 5' TCTTC 3' site distribution.** Frequency distribution of TCTTC sites were examined in intergenic and intragenic region of the genome. Blue dotted line indicates the distribution of TCTTC sites in the actual *H. pylori* intergenic or intragenic region. Red solid line indicates the distribution pattern in the randomized data set (n=10). P-values were calculated using Welch Two Sample T- test. Panel **(A)** and **(B)** site distribution in intergenic and intragenic region. **(C)** Frequency distribution of TCTTC sites in the intergenic dsDNA regions containing at least one site.

Figure S5

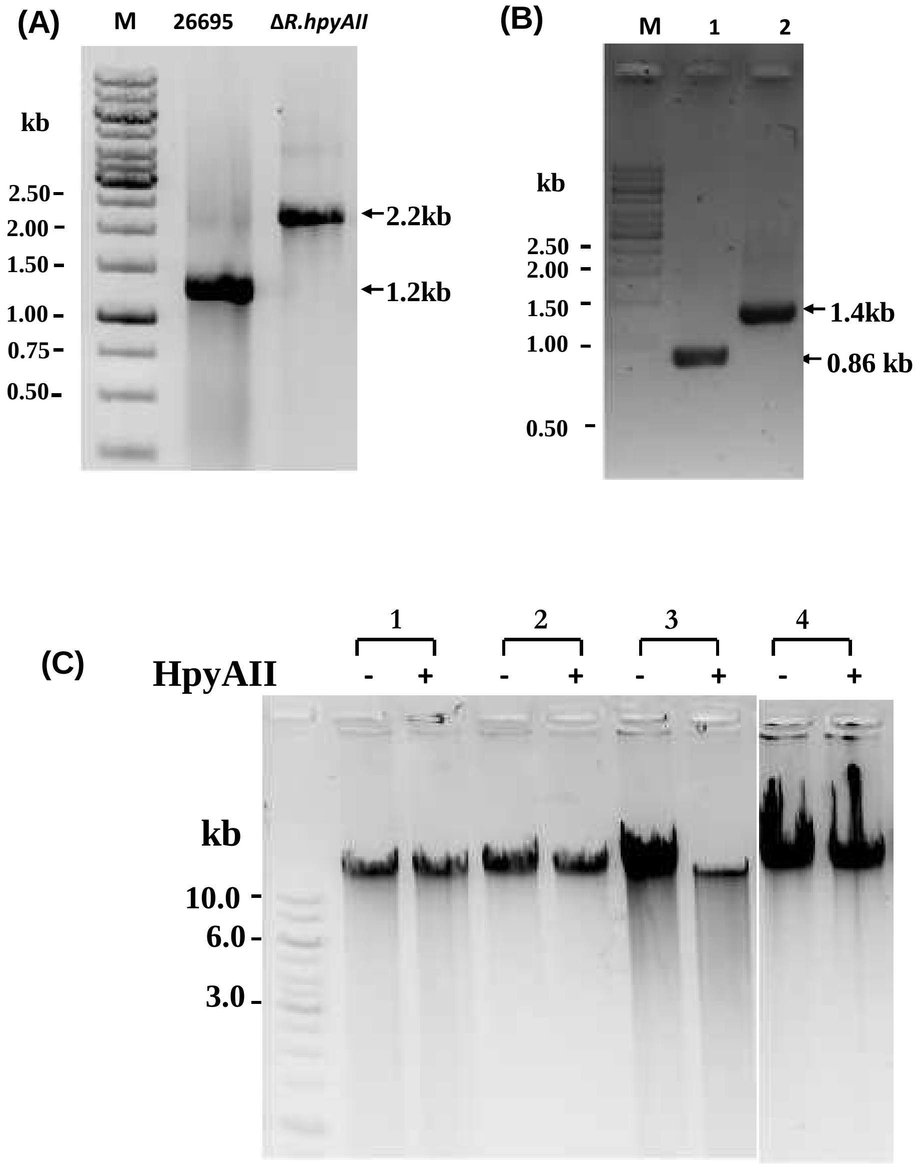

Figure S5. Stepwise deletion of *M2.hpyAII* gene in *H. pylori* 26695 strain. PCR confirmation of *R.hpyAII* gene deletion in **(A)** Strain 26695, PCR amplification using genomic DNA of wild-type and deletion strain was performed to confirm the deletion of *R.hpyAII* using gene specific primers (Table S2). Amplification of 1.27 kb product was observed in the wild type strain as compared to the 2.27 kb product amplified from the deletion strain. **(B)** Deletion of *M1.hpyAII-M2.hpyAII* genes in *H. pylori* strain 26695 was confirmed using primers 3 and 4 (Table S2). PCR product of size 1.637 kb in wild-type and 2.453 kb in deletion strain was observed. Lane 1: Strain 26695, lane 2: Δ*R.hpyAII*, **(C)** Loss of DNA methylation at GAAGA/TCTTC sites was confirmed by *in vitro* digestion with HpyAII endonuclease. Wild-type and deletions strains were subjected to *in vitro* digestion and digestion pattern were compared. Lane 1: wild-type 26695, lane 2: Δ*R.hpyAII*, lane 3: Δ*R.hpyAII-M2.hpyAII*, and lane 4: Δ*R.hpyAII-M2.hpyAII*::*kan*::*M2.hpyAII*,

Figure S6

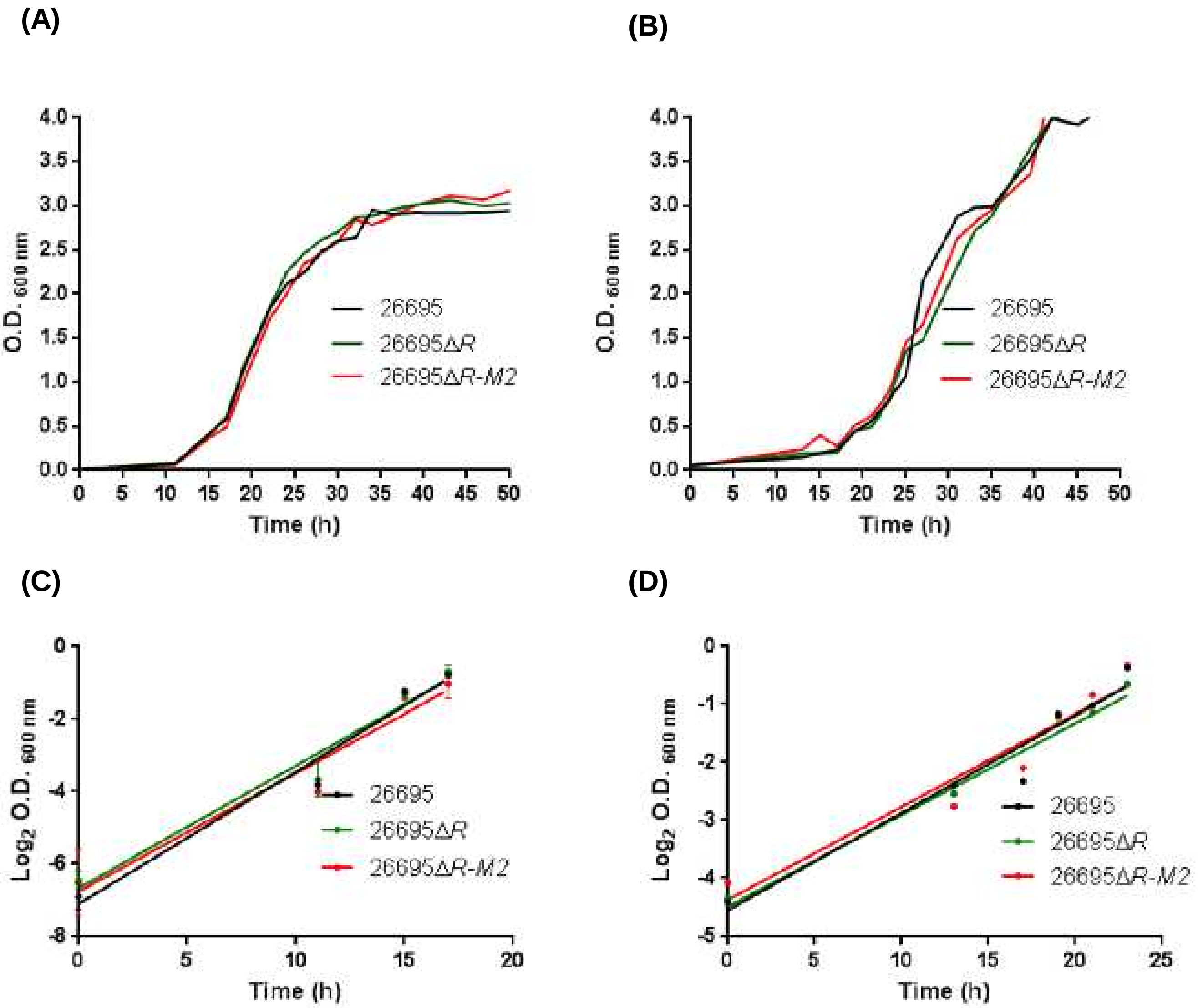

Figure S6. Growth profile analysis of *H. pylori* wild-type and HpyAII R-M system deletion strains in neutral and acidic growth medium . Wild-type and deletion strains were cultured in BHI broth containing 8% horse serum, 0.2% Iso-vitaleX, vancomycin (6 μg ml^{-1}), trimethoprim (8 μg ml^{-1}), and amphotericin B (8 μg ml^{-1}) at pH 7.2 or pH 4.5. The optical density (O.D.) at 600 nm was measured. **(A)** Growth in neutral medium (pH 7.2), **(B)** growth in acidic (pH 4.5) medium. Data represents the median values of 3 independent experiments. Generation time of *H. pylori* strains was estimated by plotting the values of linear range from Log$_2$O.D.$_{600}$ values vs time. Straight line was fitted to the curve and generation time was calculated from the inverse of the slope (growth rate). **(C)** and **(D)** Generation time in neutral and acidic growth conditions.

Figure S7

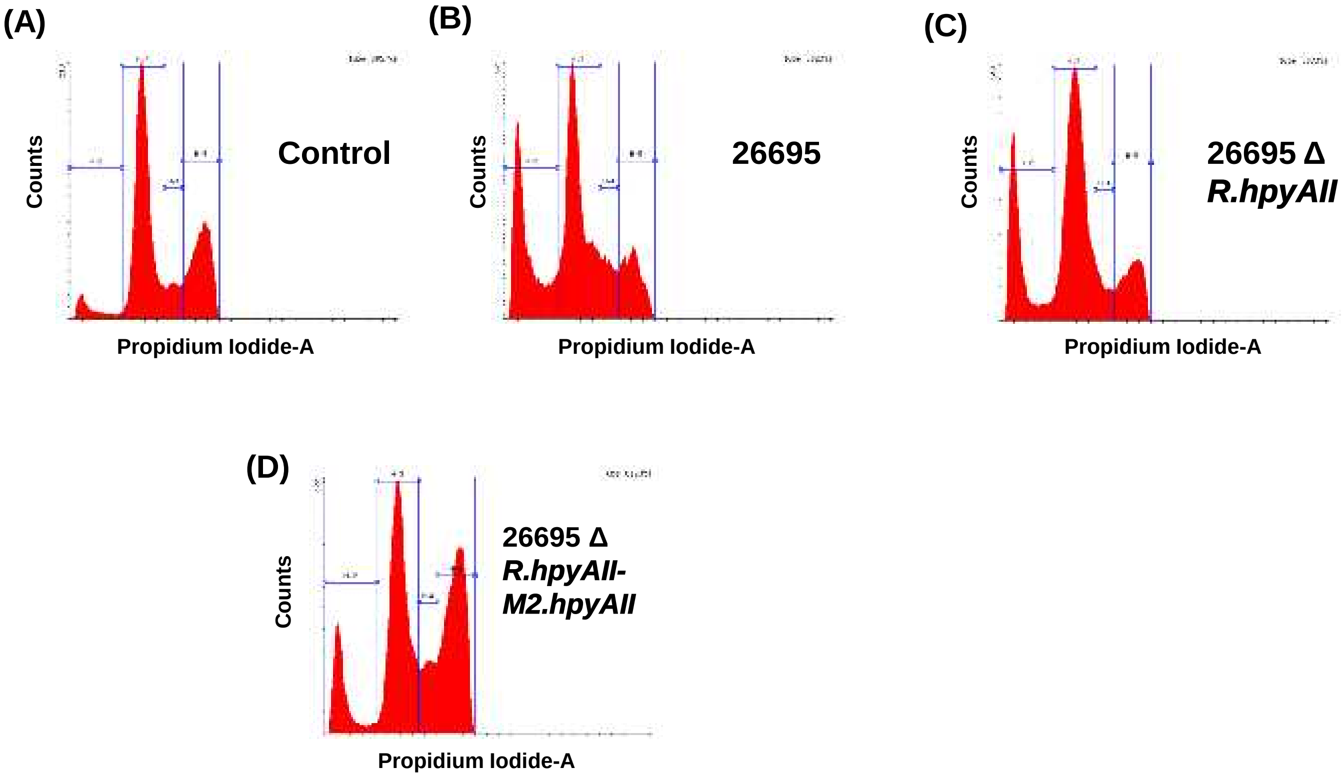

Figure S7. Loss of m4C modification reduces *H. pylori*-induced apoptosis of the host AGS cells. Cell cycle progression of control or *H. pylori* treated (24h coculture) AGS cells was monitored by propidium iodide staining and flow cytometry analysis. Results are presented as histograms showing the distribution of cells in different cell cycle phases (n= 3).

Figure S8

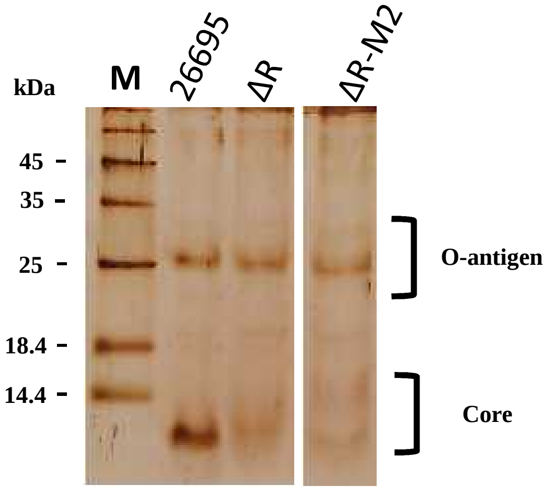

Figure S8. Effect of m4C modification on lipopolysaccharide profile of *H. pylori.* lipopolysaccharide profile of *H. pylori* 26695, *R.hpyAII*, *R.hpyAII-M2.hpyAII* gene deletion strains. Lipopolysaccharide (LPS) was isolated from the *H. pylori* strains and detected by silver-staining on 15 % SDS-PAGE.

Figure S9

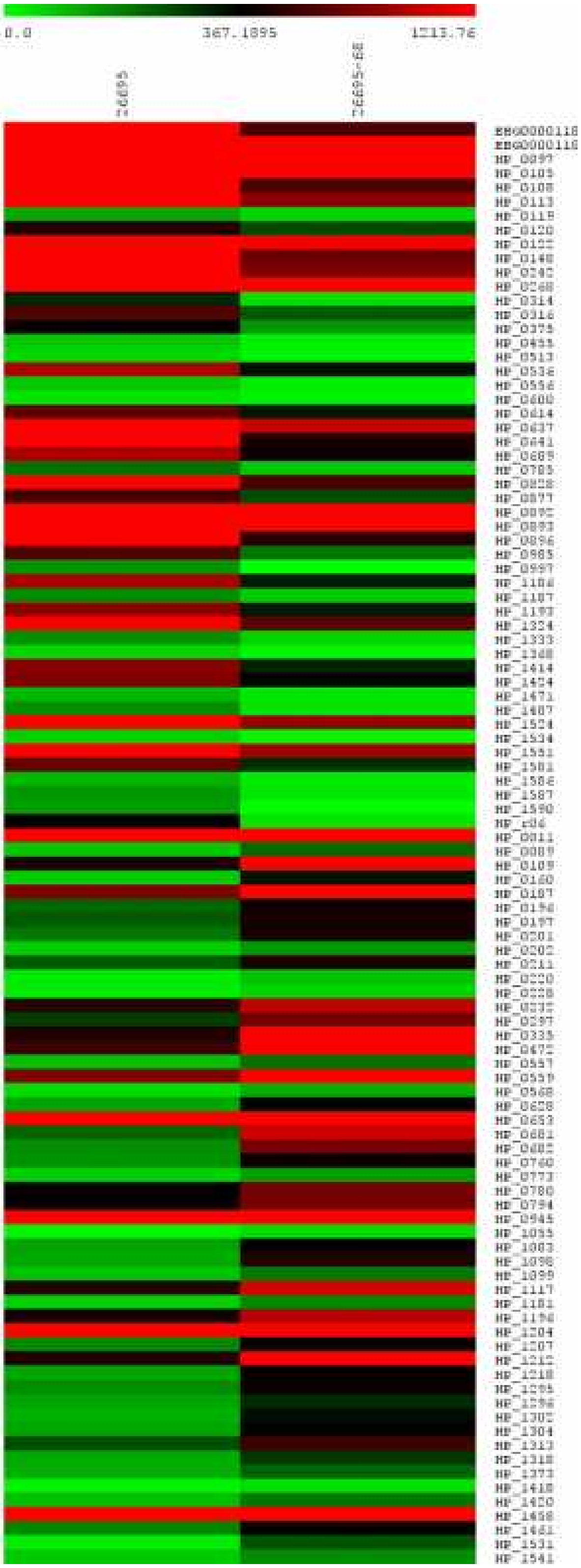

Figure S9.Global transcription regulation in *H. pylori* 26695 strain by N-^{4} cytosine methylation. Heat map depicting the differential gene expression in *R.hpyAII-M2.hpyAII* deletion strain compared to 26695 wild-type strain. Left panel indicates the transcripts expressed in the 26695 wild-type strain, right panel indicates the transcripts expressed in the *R.hpyAII-M2.hpyAII* deletion strain.

Table S1. **List of primers used in the study**

Primer number	Primer	Nucleotide Sequence 5’-3’
1	hpyAII F	CATATGATGCCAAAATTAGAAAAAATTTTGC
2	hpyAII R	GGATCC TCAGCCGTTTTTAGAATGCAAT
3	M1.hpyAII F	TTGATTTTGAATAAGATTTATATAG
4	M1.hpyAII R	TTATTCGCATTCATTATAC
5	M2.hpyAII F	TTGAATATCAATAAAGTGTTTTA
6	M2.hpyAII R	TTATTCAAAATCAAACAAGTTTCC
7	P1hpyAII	CAATATTAAATATATCAGTTTGACTCCCTTAG
8	P2hpyAII	AGAAAAGCCTTGCCATGGAGGCCCGCCAATCACGCTTTGTTCTAGCAAGCTAAAAATTTG
9	P3hpyAII	TGCGCTAAAGGCTATTTTTTAGAA GAGAAAGCCCTTTATTTTGAAAAAC
10	P4hpyAII	GTATTTTAACATGGCATTTTGTAAATC
11	P1M1.M2	GAAGAGTTTTTAACATTTTCTTACG
12	P2M1.M2	GGATCGGGCCTTGATGTTACCCGAGAGCTTTTGTGAAGTGATTTCCCAC
13	P3M1.M2	GTTAACTGTTAATTGTCCTTGTTCAAGG GGTAAGTTATGCATTAATGTGCCTTTAATG
14	P4M1.M2	CCTTAAGGTTGTCCCGCTC
15	P1M2	CCTTAAGGTTGTCCCGCTC
16	P2M2	GGATCGGGCCTTGATGTTACCCGAGAGCTGAACATTTTAGGTTTGTTTTTTAGC
17	P3M2	GTTAACTGTTAATTGTCCTTGTTCAAGG CTAGATGTCTATATTTGG
18	Cam F	ATTGGCGGGCCTCCATGGCAAGGCTTTTCT
19	Cam R	TTCTAAAAAATAGCCTTTAGCGCA
20	Gen F	AGCTCTCGGGTAACATCAAGG
21	Gen R	CCTTGAACAAGGACAATTAACAGTTA
22	Sm1	GGATCCATTATAACGCTCCTTAAAAAACATAGG
23	Sm2	CTCGAGTTATTCAAAATCAAACAAGTTTCCTAGTTTTTGC
24	Sm3	AGGAGCGTTATAATGGATCCTTATTCCTCCTAGTTAGTCAGGTACC
25	Sm4	GTTTGATTTTGAATAACTCGAGATGGCTAAAATGAGAATATCACCGG
26	Rdx F (-100)	ATTTGAGCATGGGGCAGATTTTAAG
27	Rdx R (-100)	CCCTAAAAGAGCGATTAAAACCATTC

Table S2 Summary of the protein spots identified by LC-MS/MS analysis from the 2D PAGE gel. Proteins spots which are differentially expressed in *R.hpyAII-M2.hpyAII* deletion strain compared to *R.hpyAII* and *R.hpyAII-M1.hpyAII-M2.hpyAII* gene deletion *H. pylori* 26695 strains.

Spot	S.No	Protein name	Molecular weight (kDA)	pI	Coverage (percentage)
1-2	1	Co-chaperone GroES	13.0	6.6	25.42
	2	Thiol peroxidase	18.3	5.7	34.94
	3	peptidyl-prolyl cis-trans isomerase B	17.6	7.53	36.20
3-4	4	3-hydroquinate dehydrogenase	18.5	5.26	47.90
	5	Ferritin non-heme binding	19.3	5.67	49.10
	6	DNA protection during starvation protein (dps)	16.9	5.94	53.47
	7	flagellar protein FlaG	13.4	5.6	31.09
	8	Ni-responsive regulator	17.1	5.36	27.7
11	9	molecular chaperone GroEL	58.2	5.59	51.47
	10	Cytosol aminopeptidase	54.4	7.09	43.55
	11	acetone carboxylase subunit beta			28.19
	12	hydrogenase 2 large subunit	64.3	7.14	26.12
	13	IMP dehydrogenase	51.8	7.97	15.38
	14	fumarate hydratase	50.9	7.27	20.30
	15	cell division protein FtsA	54.6	6.65	20.28
	16	ATP-dependent protease subunit HslV	20.0	6.55	41.67
	17	Acid stress response factor HP1286	20.6	9.22	45.05

12	18	urease subunit alpha	26.6	8.47	26.05
	19	peroxidase	22.2	6.30	30.30
	20	transcription termination/antitermination protein NusG	20.2	7.61	28.98
	21	zinc ABC transporter substrate-binding protein	18.1	8.91	23.72
19	22	flavodoxin FldA	17.5	4.59	85.37
29	23	Catalase (KatA)	58.6	8.66	44.36
	24	serine endoprotease DegQ	51.6	9.19	46.01
	25	DEAD/DEAH box family RNA helicase	55.9	8.02	33.54
	26	malate:quinone oxidoreductase	50.7	7.36	17.33
	27	cag pathogenicity island protein cag3	55.0	9.92	37.84
32	28	urease subunit alpha	26.5	8.47	69.75
	29	protein-disulfide isomerase	29.4	9.04	57.36
	30	beta-lactamase HcpC	31.6	8.47	31.38
	31	2-dehydro-3-deoxyphosphooctonate aldolase	30.3	8.19	27.9
33	32	peroxidase	22.2	6.30	64.14
	33	superoxide dismutase	24.6	6.21	56.81
	34	2-keto-3-deoxy-6-phosphogluconate aldolase	22.6	8.05	30.77
	35	2-oxoglutarate-acceptor oxidoreductase subunit OorC	20.2	5.72	29.03
	36	succinyl-CoA--3-ketoacid-CoA transferase	22.2	5.59	30.43
	37	nucleotide exchange factor GrpE	22.6	5.53	32.14

	38	Clp protease	21.5	5.41	23.47
	39	elongation factor P	20.8	5.62	19.79
	40	Cag-specific translocation protein CagZ	23.0	5.37	13.57
35	41	molecular chaperone DnaK	67.0	5.14	50.81
	42	molecular chaperone GroEL	58.2	5.76	33.52
49	43	CagA	132.3	8.82	53.79
50	44	elongation factor Tu	43.6	5.26	83.71
	45	trigger factor	52.0	5.41	57.87
	46	ATP synthase subunit beta	51.4	5.41	37.53
X	47	thioredoxin reductase	33.5	6.32	72.03
	48	fructose-bisphosphate aldolase	33.8	6.30	43.97
	49	UTP--glucose-1-phosphate uridylyltransferase	31.0	6.57	45.79
	50	zinc ribbon domain-containing protein	29.7	5.87	35.04
	51	malonyl CoA-ACP transacylase	34.46	6.79	37.86
	52	iron-dependent superoxide dismutase	24.6	6.21	18.78
	53	protein HP1451	30.1	6.57	26.14
	54	hydrogenase/urease nickel incorporation protein HypB	27.3	5.78	25.62
	55	fumarate reductase	27.6	5.54	22.45