

Fig. S1 : Sequence alignment of *MFS1* promoter of *Z. tritici* field strains

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gi|110265120|gb GCCGCAAGGATTCGGACTTGACGACTTTTCGGTGGACAGGACAGATT-----CCGGAC-GGGGTAGGAATGCGAGGAGAGGGTAA-----
12-VM-4J -----GACTTGACGACTTTTCGGTGGACAGGACAGATT-CGTCGGCGCAACTTGCCCGGAC-GGGGTAGGAATGCGAGGAGAGGGTAA-TTGTTTGTGTTTGTGTTTGT
12_VM_5A -----ACAGGACAGATT-CGTCGGCGCAACTTGCCCGGAC-GGGGTAGGAATGCGAGGAGAGGGTAA-TTGTTTGTGTTTGTGTTTGT
12_VM_5C -----GACTTGACGACTTTTCGGTGGACAGGACAGATT-CGTCGGCGCAACTTGCCCGGAC-GGGGTAGGAATGCGAGGAGAGGGTAA-TTGTTTGTGTTTGTGTTTGT
14_STDO_28 -----TTCGACTGACGACTTTTCGGTGGACAGGACAGATT-CGTCGGCGCAACTTGCCCGGAC-GGGGTAGGAATGCGAGGAGAGGGTAA-TTGTTTGTGTTTGTGTTTGT
12_VM_5F -----GCTGACGACTTTTCGGTGGACAGGACAGATT-CGTCGGCGCAACTTGCCCGGAC-GGGGTAGGAATGCGAGGAGAGGGTAA-TTGTTTGTGTTTGTGTTTGT
12_VM_5E -----GCTGACGACTTTTCGGTGGACAGGACAGATT-CGTCGGCGCAACTTGCCCGGAC-GGGGTAGGAATGCGAGGAGAGGGTAA-TTGTTTGTGTTTGTGTTTGT
12_AGC_13C ----CAAGGAATTCGACTTGACGACTTTTCGGTGGACAGGACAGATT-CGTCGGCGCAACTTGCCCGGAC-GGGGTAGGAATGCGAGGAGAGAA-----
12_VM_4F ----CAAGGAATTCGACTTGACGACTTTTCGGTGGACAGGACAGATT-CGTCGGCGCAACTTGCCCGGAC-GGGGTAGGAATGCGAGGAGAGAA-----
ST_5548 ----CAAGGATTCGGACTTGACGACTTTTCGGTGGACAGGACAGATT-CGTCGGCGCAACTTGCCCGGAC-GGGGTAGGAATGCGAGGAGAGAA-----
14_AQ-1 -----GACTTGACGACTTTTCGGTGGACAGGACAGATT-CGTCGGCGCAACTTGCCCGGAC-GGGGTAGGAATGCGAGGAGAGGGTAA-----
14_STIRLO_13 ----CAAGGAATTCGACTTGACGACTTTTCGGTGGACAGGACAGATT-CGTCGGCGCAACTTGCCCGGAC-GGGGTAGGAATGCGAGGAGAG-----
15_PN_3 ----CAAGGATTCGGACTTGACGACTTTTCGGTGGACAGGACAGATT-CGTCGGCGCAACTTGCCCGGAC-GGGGTAGGAATGCGAGGAGAGGGTAA-----
STDP_04915 ----CAAGGATTCGACTTGACGACTTTTCGGTGGACAGGACAGATT-CGTCGGCGCAACTTGCCCGGAC-GGGGTAGGAATGCGAGGAGAGGGTAA-----
15_OU_1D -----GGACTTGACGACTTTTCGGTGGACAGGACAGATT-CGTCGGCGCAACTTGCCCGGAC-GGGGTAGGAATGCGAGGAGAG-----
15-PQ-8B -----GAGGAGAGAGGGTAA-----
15_PQ-2B -----ACTTGACGACTTTTCGGTGGACAGGACAGATT-CGTCGGCGCAACTTGCCCGGAC-GGGGTAGGAATGCGAGGAGAGGGTAA-----
09-ASA-3a GCCGCAAGGATTCGGACTTGACGACTTTTCGGTGGACAGGACAGATT-CGTCGGCGCAACTTGCCCGGAC-GGGGTAGGAATGCGAGGAGAGGGTAA-----
13-AHJ-8C -----PCGAGGAGAGGGTAA-----
14-STDK -----GACTTGCCCGGAC-GGGGTAGGAATGCGAGGAGAGGGTAA-----
10-BNE-35 -----AGAGAG-ATCGGCAGTGCCTTGCCCGGAC-GGGGTAGGAATGCGAGGAGAGGGTAA-----
15-PQ-6A -----AGAGAG-ATCGGCAGTGCCTTGCCCGGAC-GGGGTAGGAATGCGAGGAGAGGGTAA-----
09-ASA-10b.pz -----GAGAG-ATCGGAGTGCCTTGCCCGGAC-GGGGTAGGAATGCGAGGAGAGGGTAA-----
12-VM-7A -----GAGAG-ATCGGAGTGCCTTGCCCGGAC-GGGGTAGGAATGCGAGGAGAGGGTAA-----
14-EG-A1 -----GAGAG-ATCGGAGTGCCTTGCCCGGAC-GGGGTAGGAATGCGAGGAGAGGGTAA-----
09-CB1 GCCGCAAGGATTCGGACTTGACGACTTTTCGGTGGACAGGACAGATT-CGTCGGCGCAACTTGCCCGGAC-GGGGTAGGAATGCGAGGAGAGGGTAA-----
14-AK1b -----ACTTGACGACTTTTCGGTGGACAGGACAGATT-----CCGGAC-GGGGTAGGAATGCGAGGAGAGGGTAA-GGTAGTTGTTTGTGTTTGT
consensus ..... 370..... 380..... 390..... 400..... 410..... 420..... 430..... 440..... 450..... 460..... 470..... 480
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gi|110265120|gb
12-VM-4J TGTTTGTGTTGTTCCATTTACGTCTGTAGGAGTCTATGACTATGTAGGACGGCCTTGC----AAGCAAGGCAATGATGATCTATTACAATCAAATTCCTTCAGTATTCTTTGACCTTAGG
12_VM_5A TGTTTGTGTTGTTCCATTTACGTCTGTAGGAGTCTATGACTATGTAGGACGGCCTTGC----AAGCAAGGCAATGATGATCTATTACAATCAAATTCCTTCAGTATTCTTTGACCTTAGG
12_VM_5C TGTTTGTGTTGTTCCATTTACGTCTGTAGGAGTCTATGACTATGTAGGACGGCCTTGC----AAGCAAGGCAATGATGATCTATTACAATCAAATTCCTTCAGTATTCTTTGACCTTAGG
14_STDO_28 TGTTTGTGTTGTTCCATTTACGTCTGTAGGAGTCTATGACTATGTAGGACGGCCTTGC----AAGCAAGGCAATGATGATCTATTACAATCAAATTCCTTCAGTATTCTTTGACCTTAGG
12_VM_5F TGTTTGTGTTGTTCCATTTACGTCTGTAGGAGTCTATGACTATGTAGGACGGCCTTGC----AAGCAAGGCAATGATGATCTATTACAATCAAATTCCTTCAGTATTCTTTGACCTTAGG
12_VM_5E TGTTTGTGTTGTTCCATTTACGTCTGTAGGAGTCTATGACTATGTAGGACGGCCTTGC----AAGCAAGGCAATGATGATCTATTACAATCAAATTCCTTCAGTATTCTTTGACCTTAGG
12_AGC_13C -----GGTAGAAC-----
12_VM_4F -----GGTAGAAC-----
ST_5548 -----GGTAGAAC-----
14_AQ-1 -----GGTAGAAC-----
14_STIRLO_13 -----GGTAGAAC-----
15_PN_3 -----GGTAGAAC-----
STDP_04915 -----GGTAGAAC-----
15_OU_1D -----GGTAGAAC-----
15-PQ-8B -----GGTAGAAC-----
15_PQ-2B -----GGTAGAAC-----
09-ASA-3a -----GGTAGAAC-----
13-AHJ-8C -----GGTAGAAC-----
14-STDK -----GGTAGAAC-----
10-BNE-35 -----GGTAGAAC-----
15-PQ-6A -----GGTAGAAC-----
09-ASA-10b.pz -----GGTAGAAC-----
12-VM-7A -----GGTAGAAC-----
14-EG-A1 -----GGTAGAAC-----
09-CB1 -----GGTAGAAC-----
14-AK1b TGTTTGTGTTGTTCCATTTACGTCTGTAGGAGTCTAAGACTATGTAGGACGGCCTTGCCTTAAAGGCAAAGCAATGATGATCTATTACAATCAGATTCTTTAGTATTCTTTGACCTTAGG
consensus ..... 490..... 500..... 510..... 520..... 530..... 540..... 550..... 560..... 570..... 580..... 590..... 600
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gi|110265120|gb
12-VM-4J GGAAACCCCGTGCCTAAGGCAGTGCCAAAGGACTTTAAACAAATGCAAGACAAAGGAATCGAACGAGTGTCTGTGCTGCTGAGCTGGGGCTGCAGAAATTTTCGTTGTCTGCAG
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12_VM_5A      GGAAACCCCGTGCCTAAGGCAGTGCCAAAGGACTTTAAACAAATGCAAGACAAAGGAAATCGAACGAGTGTCTGTGTCTGTCTGCAGCTGGGGCTGCAGAATTTTCGTTGTCTGCAG
12_VM_5C      GGAAACCCCGTGCCTAAGGCAGTGCCAAAGGACTTTAAACAAATGCAAGACAAAGGAAATCGAACGAGTGTCTGTGTCTGTCTGCAGCTGGGGCTGCAGAATTTTCGTTGTCTGCAG
14_STDO_28    GGAAACCCCGTGCCTAAGGCAGTGCCAAAGGACTTTAAACAAATGCAAGACAAAGGAAATCGAACGAGTGTCTGTGTCTGTCTGCAGCTGGGGCTGCAGAATTTTCGTTGTCTGCAG
12_VM_5F      GGAAACCCCGTGCCTAAGGCAGTGCCAAAGGACTTTAAACAAATGCAAGACAAAGGAAATCGAACGAGTGTCTGTGTCTGTCTGCAGCTGGGGCTGCAGAATTTTCGTTGTCTGCAG
12_VM_5E      GGAAACCCCGTGCCTAAGGCAGTGCCAAAGGACTTTAAACAAATGCAAGACAAAGGAAATCGAACGAGTGTCTGTGTCTGTCTGCAGCTGGGGCTGCAGAATTTTCGTTGTCTGCAG
12_AGC_13C   -----
12_VM_4F      -----
ST_5548      -----
14_AQ-1      -----
14_STIRLO_13 -----
15_PN_3      -----
STDP_04915   -----
15_OU_1D     -----
15_PQ-8B     -----
15_PQ-2B     -----
09-ASA-3a    -----
13-AHJ-8C    -----
14-STDK      -----
10-BNE-35    -----
15-PQ-6A     -----
09-ASA-10b.pz -----
12-VM-7A     -----
14-EG-A1     -----
09-CB1       -----
14-AK1b      GGAGACCCCGTGCCTAAGGCAGTGCCAAAGGACTTCAAACAGCGCAAGACAAAGGAAATCAAACGAGTGTCTGTGTCTGCAGCCGG-----GGCTGCAGAATTTTCGCGCCAAGCTTTT
consensus    .....610.....620.....630.....640.....650.....660.....670.....680.....690.....700.....710.....720

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gi|110265120|gb -----GGTAGGT
12-VM-4J      CTGGGGCTGCAGAATTTTCGTTGTCTGCAGCTAAGGCTGCAGAATTTTTTTCGCGCCAAGCTTTTTCGAGAATTTTCAGCGGATCCTTCCGCTTCGAGGAGAGGGTAATAATAAGGTAGGT
12_VM_5A      CTGGGGCTGCAGAATTTTCGTTGTCTGCAGCTAAGGCTGCAGAATTTTTTTCGCGCCAAGCTTTTTCGAGAATTTTCAGCGGATCCTTCCGCTTCGAGGAGAGGGTAATAATAAGGTAGGT
12_VM_5C      CTGGGGCTGCAGAATTTTCGTTGTCTGCAGCTAAGGCTGCAGAATTTTTTTCGCGCCAAGCTTTTTCGAGAATTTTCAGCGGATCCTTCCGCTTCGAGGAGAGGGTAATAATAAGGTAGGT
14_STDO_28    CTGGGGCTGCAGAATTTTCGTTGTCTGCAGCTAAGGCTGCAGAATTTTTTTCGCGCCAAGCTTTTTCGAGAATTTTCAGCGGATCCTTCCGCTTCGAGGAGAGGGTAATAATAAGGTAGGT
12_VM_5F      CTGGGGCTGCAGAATTTTCGTTGTCTGCAGCTAAGGCTGCAGAATTTTTTTCGCGCCAAGCTTTTTCGAGAATTTTCAGCGGATCCTTCCGCTTCGAGGAGAGGGTAATAATAAGGTAGGT
12_VM_5E      CTGGGGCTGCAGAATTTTCGTTGTCTGCAGCTAAGGCTGCAGAATTTTTTTCGCGCCAAGCTTTTTCGAGAATTTTCAGCGGATCCTTCCGCTTCGAGGAGAGGGTAATAATAAGGTAGGT
12_AGC_13C   -----TGGGT
12_VM_4F      -----TGGGT
ST_5548      -----TGGGT
14_AQ-1      -----TAGGT
14_STIRLO_13 -----TGGGT
15_PN_3      -----TAGGT
STDP_04915   -----TAGGT
15_OU_1D     -----TGGGT
15_PQ-8B     -----GGTAGGT
15_PQ-2B     -----GGTAGGT
09-ASA-3a    -----GGTAGGT
13-AHJ-8C    -----GGTAGGT
14-STDK      -----GGTAGGT
10-BNE-35    -----GGTAGGT
15-PQ-6A     -----GGTAGGT
09-ASA-10b.pz -----GGTAGGT
12-VM-7A     -----GGTAGGT
14-EG-A1     -----GGTAGGT
09-CB1       -----GGTAGGT
14-AK1b      GCAGAATTTTCAGAGTGTCTGTCTGCAGCCCAAGGCTGCAGAATTTTCGCGCCAAGCTTTTTCGAGAATTTTCAGGGTAA-----GGTAGGT
consensus    .....730.....740.....750.....760.....770.....780.....790.....800.....810.....820.....830.....840

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gi|110265120|gb GAACACCTTATACTCCGTTCTTTCCCATTTCTCTCCCTCCATCATCACAGTCATCAGAT-----
12-VM-4J GAACACCTTATACTCCGTTCTTTCCCATTTCTCTCCCTCCATCATCACAGTCATCAGAT-----
12_VM_5A GAACACCTTATACTCCGTTCTTTCCCATTTCTCTCCCTCCATCATCACAGTCATCAGAT-----
12_VM_5C GAACACCTTATACTCCGTTCTTTCCCATTTCTCTCCCTCCATCATCACAGTCATCAGAT-----
14_STDO_28 GAACACCTTATACTCCGTTCTTTCCCATTTCTCTCCCTCCATCATCACAGTCATCAGAT-----
12_VM_5F GAACACCTTATACTCCGTTCTTTCCCATTTCTCTCCCTCCATCATCACAGTCATCAGAT-----
12_VM_5E GAACACCTTATACTCCGTTCTTTCCCATTTCTCTCCCTCCATCATCACAGTCATCAGAT-----
12_AGC_13C GAA-----TATACTCCGATTCTTTCCCTTTTCTCTCCCTTCATCATCACAGTCATCAGAT-----
12_VM_4F GAA-----TATACTCCGATTCTTTCCCTTTTCTCTCCCTTCATCATCACAGTCATCAGAT-----
ST_5548 GAA-----TATACTCCGATTCTTTCCCTTTTCTCTCCCTTCATCATCACAGTCATCAGAT-----
14_AQ-1 GAACACCTTATACTCCGTTCTTTCCCATTTCTCTCCCTCCATCATCACAGTCATCAGAT-----
14_STIRLO_13 GAA-----TATACTCCGATTCTTTCCCATTTCTCTCCCTCCATCATCACAGTCATCAGAT-----
15_PN_3 GAACACCTTATACTCCGATTCTTTCCCATTTCTCTCCCTCCATCATCACAGTCATCAGAT-----
STDP_04915 GAACACCTTATACTCCGTTCTTTCCCATTTCTCTCCCTCCATCATCACAGTCATCAGAT-----
15_OU_1D GAA-----TATACTCCGATTCTTTCCCTTTTCTCTCCCTTCATCATCACAGTCATCAGAT-----
15-PQ-8B GAACACCTTATACTCCGTTCTTTCCCATTTCTCTCCCTCCATCATCACAGTCATCAGAT-----
15_PQ-2B GAACACCTTATACTCCGTTCTTTCCCATTTCTCTCCCTCCATCATCACAGTCATCAGAT-----
09-ASA-3a GAACACCTTATACTCCGATTCTTTCCCTTTTCTCTCCCTTCATCATCACAGTCATCAGATCCGCATGTTGAAAAA
13-AHJ-8C GAACACCTTATACTCCGATTCTTTCCCTTTTCTCTCCCTTCATCATCACAGTCATCAGATCCGCATGTTGAAAAA
14-STDK GAACACCTTATACTCCGATTCTTTCCCTTTTCTCTCCCTTCATCATCACAGTCATCAGATCCGCATGTTGAAAAA
10-BNE-35 GAACACCTTATACTCCGATTCTTTCCCTTTTCTCTCCCTTCATCATCACAGTCATCAGATCCGCATGTTGAAAAA
15-PQ-6A GAACACCTTATACTCCGATTCTTTCCCTTTTCTCTCCCTTCATCATCACAGTCATCAGATCCGCATGTTGAAAAA
09-ASA-10b.pz GAACACCTTATACTCCGATTCTTTCCCTTTTCTCTCCCTTCATCATCACAGTCATCAGATCCGCATGTTGAAAAA
12-VM-7A GAACACCTTATACTCCGATTCTTTCCCTTTTCTCTCCCTTCATCATCACAGTCATCAGATCCGCATGTTGAAAAA
14-EG-A1 GAACACCTTATACTCCGATTCTTTCCCTTTTCTCTCCCTTCATCATCACAGTCATCAGATCCGCATGTTGAAAAA
09-CB1 GAACACCTTATACTCCGATTCTTTCCCTTTTCTCTCCCTTCATCATCACAGTCATCAGATCCGCATGTTGAAAAA
14-AK1b GAACACCTTATACTCCGTTCTTTCCCATTTCTCTCCCTCCATCATCACAGTCATCAGAT-----
consensus *****
.....850.....860.....870.....880.....890.....900.....910.....920.....930.....940.....950.....960
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gi|110265120|gb -----
12-VM-4J -----
12_VM_5A -----
12_VM_5C -----
14_STDO_28 -----
12_VM_5F -----
12_VM_5E -----
12_AGC_13C -----
12_VM_4F -----
ST_5548 -----
14_AQ-1 -----
14_STIRLO_13 -----
15_PN_3 -----
STDP_04915 -----
15_OU_1D -----
15-PQ-8B -----
15_PQ-2B -----
09-ASA-3a AGTGGATTCTGAACCCGGCGTTGGTCGACGATCTTTTACCCGATTAGGACTAGCGCGGAATCGTACC
13-AHJ-8C AGTGGATTCTGAACCCGGCGTTGGTCGACGATCTTTTACCCGATTAGGACTAGCGCGGAATCGTACC
14-STDK AGTGGATTCTGAACCCGGCGTTGGTCGACGATCTTTTACCCGATTAGGACTAGCGCGGAATCGTACC
10-BNE-35 AGTGGATTCTGAACCCGGCGTTGGTCGACGATCTTTTACCCGATTAGGACTAGCGCGGAATCGTACC
15-PQ-6A AGTGGATTCTGAACCCGGCGTTGGTCGACGATCTTTTACCCGATTAGGACTAGCGCGGAATCGTACC
09-ASA-10b.pz AGTGGATTCTGAACCCGGCGTTGGTCGACGATCTTTTACCCGATTAGGACTAGCGCGGAATCGTACC
12-VM-7A AGTGGATTCTGAACCCGGCGTTGGTCGACGATCTTTTACCCGATTAGGACTAGCGCGGAATCGTACC
14-EG-A1 AGTGGATTCTGAACCCGGCGTTGGTCGACGATCTTTTACCCGATTAGGACTAGCGCGGAATCGTACC
09-CB1 AGTGGATTCTGAACCCGGCGTTGGTCGACGATCTTTTACCCGATTAGGACTAGCGCGGAATCGTACC
14-AK1b -----
consensus .....970.....980.....990.....1000.....1010.....1020.....1030.....1040.....1050.....1060.....1070.....1080
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gi|110265120|gb ----- CCGCACAAACAATCATTCCGGTT
12-VM-4J ----- CCGCACAAACAATCATTCCGGTT
12_VM_5A ----- CCGCACAAACAATCATTCCGGTT
12_VM_5C ----- CCGCACAAACAATCATTCCGGTT
14_STDO_28 ----- CCGCACAAACAATCATTCCGGTT
12_VM_5F ----- CCGCACAAACAATCATTCCGGTT
12_VM_5E ----- CCGCACAAACAATCATTCCGGTT
12_AGC_13C ----- CCGCACAAACAATCATTCCGGTT
12_VM_4F ----- CCGCACAAACAATCA-----TT
ST_5548 ----- CCGCACAAACAATCATTCCGGTT
14_AQ-1 ----- CCGCACAAACAATCATTCCGGTT
14_STIRLO_13 ----- CCGCACAAACAATCATTCCGGTT
15_PN_3 ----- CCGCACAAACAATCATTCCGGTT
STDP_04915 ----- CCGCACAAACAATCATTCCGGTT
15_OU_1D ----- CCGCACAAACAATCA-----TT
15-PQ-8B ----- CCGCACAAACAATCATTCCGGTT
15_PQ-2B ----- CCGCACAAACAATCATTCCGGTT
09-ASA-3a GGCATATAAGGGTTAGAAACGTC CGTAGAATCGATAGCAAGCAATTGAACACTTCTACCTCTTTACCCCTTGGCTATTTCTTCCACTTTTTCATA CCGCACAAACAATCA-----TT
13-AHJ-8C GGCATATAAGGGTTAGAAACGTC CGTAGAATCGATAGCAAGCAATTGAACACTTCTACCTCTTTACCCCTTGGCTATTTCTTCCACTTTTTCATA CCGCACAAACAATCA-----TT
14-STDK GGCATATAAGGGTTAGAAACGTC CGTAGAATCGATAGCAAGCAATTGAACACTTCTACCTCTTTACCCCTTGGCTATTTCTTCCACTTTTTCATA CCGCACAAACAATCA-----TT
10-BNE-35 GGCATATAAGGGTTAGAAACGTC CGTAGAATCGATAGCAAGCAATTGAACACTTCTACCTCTTTACCCCTTGGCTATTTCTTCCACTTTTTCATA CCGCACAAACAATCA-----TT
15-PQ-6A GGCATATAAGGGTTAGAAACGTC CGTAGAATCGATAGCAAGCAATTGAACACTTCTACCTCTTTACCCCTTGGCTATTTCTTCCACTTTTTCATA CCGCACAAACAATCA-----TT
09-ASA-10b.pz GGCATATAAGGGTTAGAAACGTC CGTAGAATCGATAGCAAGCAATTGAACACTTCTACCTCTTTACCCCTTGGCTATTTCTTCCACTTTTTCATA CCGCACAAACAATCA-----TT
12-VM-7A GGCATATAAGGGTTAGAAACGTC CGTAGAATCGATAGCAAGCAATTGAACACTTCTACCTCTTTACCCCTTGGCTATTTCTTCCACTTTTTCATA CCGCACAAACAATCA-----TT
14-EG-A1 GGCATATAAGGGTTAGAAACGTC CGTAGAATCGATAGCAAGCAATTGAACACTTCTACCTCTTTACCCCTTGGCTATTTCTTCCACTTTTTCATA CCGCACAAACAATCA-----TT
09-CB1 GGCATATAAGGGTTAGAAACGTC CGTAGAATCGATAGCAAGCAATTGAACACTTCTACCTCTTTACCCCTTGGCTATTTCTTCCACTTTTTCATA CCGCACAAACAATCA-----TT
14-AK1b ----- CCGCACAAACAATCA-----TT
consensus *****
.....1330.....1340.....1350.....1360.....1370.....1380.....1390.....1400.....1410.....1420.....1430.....1440**

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gi|110265120|gb CCGTTCCCTCCCGTCATACTCATTGCCATTGGAGCTGAAAGGTCGAAATGCTGCTGCCCTGGGTCCTCGCTTCGCTTCTGTGATTC GACTTGTTCGCGCGTTGGATCTGGTGGAAACGGAG
12-VM-4J CCGTTCCCTCCCGTCATACTCATTGCCATTGGAGCTGAAAGGTCGAAATGCTGCTGCCCTGGGTCCTCGCTTCGCTTCTGTGATTC GACTTGTTCGCGCGTTGGATCTGGTGGAAACGGAG
12_VM_5A CCGTTCCCTCCCGTCATACTCATTGCCATTGGAGCTGAAAGGTCGAAATGCTGCTGCCCTGGGTCCTCGCTTCGCTTCTGTGATTC GACTTGTTCGCGCGTTGGATCTGGTGGAAACGGAG
12_VM_5C CCGTTCCCTCCCGTCATACTCATTGCCATTGGAGCTGAAAGGTCGAAATGCTGCTGCCCTGGGTCCTCGCTTCGCTTCTGTGATTC GACTTGTTCGCGCGTTGGATCTGGTGGAAACGGAG
14_STDO_28 CCGTTCCCTCCCGTCATACTCATTGCCATTGGAGCTGAAAGGTCGAAATGCTGCTGCCCTGGGTCCTCGCTTCGCTTCTGTGATTC GACTTGTTCGCGCGTTGGATCTGGTGGAAACGGAG
12_VM_5F CCGTTCCCTCCCGTCATACTCATTGCCATTGGAGCTGAAAGGTCGAAATGCTGCTGCCCTGGGTCCTCGCTTCGCTTCTGTGATTC GACTTGTTCGCGCGTTGGATCTGGTGGAAACGGAG
12_VM_5E CCGTTCCCTCCCGTCATACTCATTGCCATTGGAGCTGAAAGGTCGAAATGCTGCTGCCCTGGGTCCTCGCTTCGCTTCTGTGATTC GACTTGTTCGCGCGTTGGATCTGGTGGAAACGGAG
12_AGC_13C CCGTTCCCTCCCGTCATACTCATTGCCATTGGAGCTGAAAGGTCGAAATGCTGCTGCCCTGGGTCCTCGCTTCGCTTCTGTGATTC GACTTGTTCGCGCGTTGGATCTGGTGGAAACGGAG
12_VM_4F CCGTTCCCTCCCGTCATACTCATTGCCATTGGAGCTGAAAGGTCGAAATGCTGCTGCCCTGGGTCCTCGCTTCGCTTCTGTGATTC GACTTGTTCGCGCGTTGGATCTGGTGGAAACGGAG
ST_5548 CCGTTCCCTCCCGTCATACTCATTGCCATTGGAGCTGAAAGGTCGAAATGCTGCTGCCCTGGGTCCTCGCTTCGCTTCTGTGATTC GACTTGTTCGCGCGTTGGATCTGGTGGAAACGGAG
14_AQ-1 CCGTTCCCTCCCGTCATACTCATTGCCATTGGAGCTGAAAGGTCGAAATGCTGCTGCCCTGGGTCCTCGCTTCGCTTCTGTGATTC GACTTGTTCGCGCGTTGGATCTGGTGGAAACGGAG
14_STIRLO_13 CCGTTCCCTCCCGTCATACTCATTGCCATTGGAGCTGAAAGGTCGAAATGCTGCTGCCCTGGGTCCTCGCTTCGCTTCTGTGATTC GACTTGTTCGCGCGTTGGATCTGGTGGAAACGGAG
15_PN_3 CCGTTCCCTCCCGTCATACTCATTGCCATTGGAGCTGAAAGGTCGAAATGCTGCTGCCCTGGGTCCTCGCTTCGCTTCTGTGATTC GACTTGTTCGCGCGTTGGATCTGGTGGAAACGGAG
STDP_04915 CCGTTCCCTCCCGTCATACTCATTGCCATTGGAGCTGAAAGGTCGAAATGCTGCTGCCCTGGGTCCTCGCTTCGCTTCTGTGATTC GACTTGTTCGCGCGTTGGATCTGGTGGAAACGGAG
15_OU_1D CCGTTCCCTCCCGTCATACTCATTGCCATTGGAGCTGAAAGGTCGAAATGCTGCTGCCCTGGGTCCTCGCTTCGCTTCTGTGATTC GACTTGTTCGCGCGTTGGATCTGGTGGAAACGGAG
15-PQ-8B CCGTTCCCTCCCGTCATACTCATTGCCATTGGAGCTGAAAGGTCGAAATGCTGCTGCCCTGGGTCCTCGCTTCGCTTCTGTGATTC GACTTGTTCGCGCGTTGGATCTGGTGGAAACGGAG
15_PQ-2B CCGTTCCCTCCCGTCATACTCATTGCCATTGGAGCTGAAAGGTCGAAATGCTGCTGCCCTGGGTCCTCGCTTCGCTTCTGTGATTC GACTTGTTCGCGCGTTGGATCTGGTGGAAACGGAG
09-ASA-3a CCGTTCCCTCCCGTCATACTCATTGCCATTGGAGCTGAAAGGTCGAAATGCTGCTGCCCTGGGTCCTCGCTTCGCTTCTGTGATTC GACTTGTTCGCGCGTTGGATCTGGTGGAAACGGAG
13-AHJ-8C CCGTTCCCTCCCGTCATACTCATTGCCATTGGAGCTGAAAGGTCGAAATGCTGCTGCCCTGGGTCCTCGCTTCGCTTCTGTGATTC GACTTGTTCGCGCGTTGGATCTGGTGGAAACGGAG
14-STDK CCGTTCCCTCCCGTCATACTCATTGCCATTGGAGCTGAAAGGTCGAAATGCTGCTGCCCTGGGTCCTCGCTTCGCTTCTGTGATTC GACTTGTTCGCGCGTTGGATCTGGTGGAAACGGAG
10-BNE-35 CCGTTCCCTCCCGTCATACTCATTGCCATTGGAGCTGAAAGGTCGAAATGCTGCTGCCCTGGGTCCTCGCTTCGCTTCTGTGATTC GACTTGTTCGCGCGTTGGATCTGGTGGAAACGGAG
15-PQ-6A CCGTTCCCTCCCGTCATACTCATTGCCATTGGAGCTGAAAGGTCGAAATGCTGCTGCCCTGGGTCCTCGCTTCGCTTCTGTGATTC GACTTGTTCGCGCGTTGGATCTGGTGGAAACGGAG
09-ASA-10b.pz CCGTTCCCTCCCGTCATACTCATTGCCATTGGAGCTGAAAGGTCGAAATGCTGCTGCCCTGGGTCCTCGCTTCGCTTCTGTGATTC GACTTGTTCGCGCGTTGGATCTGGTGGAAACGGAG
12-VM-7A CCGTTCCCTCCCGTCATACTCATTGCCATTGGAGCTGAAAGGTCGAAATGCTGCTGCCCTGGGTCCTCGCTTCGCTTCTGTGATTC GACTTGTTCGCGCGTTGGATCTGGTGGAAACGGAG
14-EG-A1 CCGTTCCCTCCCGTCATACTCATTGCCATTGGAGCTGAAAGGTCGAAATGCTGCTGCCCTGGGTCCTCGCTTCGCTTCTGTGATTC GACTTGTTCGCGCGTTGGATCTGGTGGAAACGGAG
09-CB1 CCGTTCCCTCCCGTCATACTCATTGCCATTGGAGCTGAAAGGTCGAAATGCTGCTGCCCTGGGTCCTCGCTTCGCTTCTGTGATTC GACTTGTTCGCGCGTTGGATCTGGTGGAAACGGAG
14-AK1b CCGTTCCCTCCCGTCATACTCATTGCCATTGGAGCTGAAAGGTCGAAATGCTGCTGCCCTGGGTCCTCGCTTCGCTTCTGTGATTC GACTTGTTCGCGCGTTGGATCTGGTGGAAACGGAG
consensus *****
.....1450.....1460.....1470.....1480.....1490.....1500.....1510.....1520.....1530.....1540.....1550.....1560**

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gi|110265120|gb CACTTCTCAGGTTTGTAGCATTCAACCACTTCGACCAGGTCAGGTCAGGCCCACCCCGTCAACCCCTCAACAACCATACCTGGTAGTTCTACCCATCCACCGACTTCGTCATCGACGATA
12-VM-4J -----TC-----AAGCATTCAACCACTTCGACCAGGTCAGGTCAGGCCCACCCCGTCAACCATCAACAACCATACCGGGTAGT-----
12_VM_5A -----TC-----AAGCATTCAACCACTTCGACCAGGTCAGGTCAGGCCCACCCCGTCAACCATCAACAACCATACCGGGTAGTTCTACCCATCCACCGACTTCGTCATCGACGATA
12_VM_5C -----TC-----AAGCATTCAACCACTTCGACCAGGTCAGGTCAGGCCCACCCCGTCAACCATCAACAACCATACCGGGTAGTTCTACCCATCCACCGACTTCGTCATCGACGATA
14_STDO_28 -----TC-----AAGCATTCAACCACTTCGACCAGGTCAGGTCAGGCCCACCCCGTCAACCATCAACAACCATACCGGGTAGTTCTACCCATCCACCGACTTCGTCACGAC-----
12_VM_5F -----TC-----AAGCATTCAACCACTTCGACCAGGTCAGGTCAGGCCCACCCCGTCAACCATCAACAACCATACCGGGTAGTTCTACCCATCCACCGACTTCGTCATCA-----
12_VM_5E -----TC-----AAGCATTCAACCACTTCGACCAGGTCAGGTCAGGCCCACCCCGTCAACCATCAACAACCATACCGGGTAGTTCTACCCATCCACCGACTTCGTCATCGACGATA
12_AGC_13C -----TC-----AAGCATTCAACCACTTCGACCAGGTCAGGTCAGGCCCACCCCGTCAACCATCAACAACCATACCGGGTAGTTCTACCCATCCACCGACTTCGTCATCGAATTAC
12_VM_4F -----TC-----AAGCATTCAACCACTTCGACCAGGTCAGGTCAGGCCCACCCCGTCAACCATCAACAACCATACCGGGTAGTTCTACCCATCCACCGACTTCGTCATCGACGATA
ST_5548 -----TC-----AAGCATTCAACCACTTCGACCAGGTCAGGTCAGGCCCACCCCGTCAACCATCAACAACCATACCGGGTAGTTCTACCCATCCACCGACTTCGTCATCGACATA
14_AQ-1 CACTTCTCAGGTTTGTAGCATTCAACCACTTCGACCAGGTCAGGTCAGGCCCACCCCGTCAACCCCTCAACAACCATACCTGGTAGTTCTACCCATCCACCGACTTCGTCATCGAC-----
14_STIRLO_13 -----TC-----AAGCATTCAACCACTTCGACCAGGTCAGGTCAGGCCCACCCCGTCAACCATCAACAACCATACCGGGTAGTTCTACCCATCCACCGACTTCGTCATCGACATA
15_PN_3 CACTTCTCAGGTTTGTAGCATTCAACCACTTCGACCAGGTCAGGTCAGGCCCACCCCGTCAACCCCTCAACAACCATACCTGGTAGTTCTACCCATCCACCGACTTCGTCATCGAC-----
STDP_04915 -----TC-----AAGCATTCAACCACTTCGACCAGGTCAGGTCAGGCCCACCCCGTCAACCATCAACAACCATACCGGGTAGTTCTACCCATCCACCGACTTCGTCATCGA-----
15_OU_1D CACTTCTCAGGTTTGTAGCATTCAACCACTTCGACCAGGTCAGGTCAGGCCCACCCCGTCAACCCCTCAACAACCATACCTGGTAGTTCTACCCATCCACCGACTTCGTCATCGAC-----
09-ASA-3a -----TC-----AAGCATTCAACCACTTCGACCAGGTCAGGTCAGGCCCACCCCGTCAACCCCTCAACAACCATACCTGGTAGTTCTACCCATCCACCGACTTCGTCATCGACATA
13-AHJ-8C -----TC-----AAGCATTCAACCACTTCGACCAGGTCAGGTCAGGCCCACCCCGTCAACCCCTCAACAACCATACCTGGTAGTTCTACCCATCCACCGACTTCGTCATCGAC-----
14-STDK -----TC-----AAGCATTCAACCACTTCGACCAGGTCAGGTCAGGCCCACCCCGTCAACCCCTCAACAACCATACCTGGTAGTTCTACCCATCCACCGACTTCGTCATCGAC-----
10-BNE-35 -----TC-----AAGCATTCAACCACTTCGACCAGGTCAGGTCAGGCCCACCCCGTCAACCCCTCAACAACCATACCTGGTAGTTCTACCCATCCACCGACTTCGTCATCGAC-----
15-PQ-6A -----TC-----AAGCATTCAACCACTTCGACCAGGTCAGGTCAGGCCCACCCCGTCAACCCCTCAACAACCATACCTGGTAGTTCTACCCATCCACCGACTTCGTCATCGA-----
09-ASA-10b.pz -----TC-----AAGCATTCAACCACTTCGACCAGGTCAGGTCAGGCCCACCCCGTCAACCCCTCAACAACCATACCTGGTAGTTCTACCCATCCACCGACTTCGTCATCGAC-----
12-VM-7A -----TC-----AAGCATTCAACCACTTCGACCAGGTCAGGTCAGGCCCACCCCGTCAACCCCTCAACAACCATACCTGGTAGTTCTACCCATCCACCGACTTCGTCATCGAC-----
14-EG-A1 -----TC-----AAGCATTCAACCACTTCGACCAGGTCAGGTCAGGCCCACCCCGTCAACCCCTCAACAACCATACCTGGTAGTTCTACCCATCCACCGACTTCGTCATCGA-----
09-CB1 -----TC-----AAGCATTCAACCACTTCGACCAGGTCAGGTCAGGCCCACCCCGTCAACCCCTCAACAACCATACCTGGTAGTTCTACCCATCCACCGACTTCGTCATCGAC-----
14-AK1b CACTTCTCAGGTTTGTAGCATTCAACCACTTCGACCAGGTCAGGTCAGGCCCACCCCGTCAACCCCTCAACAACCATACCTGGTAGTTCTACCCATCCACCGACTTCGTCATCGAC-----
consensus .....1810.....1820.....1830.....1840.....1850.....1860.....1870.....1880.....1890.....1900.....1910.....1920

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gi|110265120|gb CCGGCAGATCGCTCATACGAGCAGGACTTCACCTCTCATCACCACCCACACCCGCCACCACAACCCCGCTTCTCAGCAAGAAGTCGCCGGCCGGGTCGTCGACTCCACCGACCCCT
12-VM-4J -----TC-----
12_VM_5A -----TC-----
12_VM_5C -----TC-----
14_STDO_28 -----TC-----
12_VM_5F -----TC-----
12_VM_5E -----TC-----
12_AGC_13C CCGGCA-----
12_VM_4F CCGGCA-----
ST_5548 -----TC-----
14_AQ-1 -----TC-----
14_STIRLO_13 CCGGCA-----
15_PN_3 -----TC-----
STDP_04915 -----TC-----
15_OU_1D -----TC-----
15-PQ-8B -----TC-----
15_PQ-2B -----TC-----
09-ASA-3a CCGGCAGATCGCTCATACGAAACAGGACTTCACCTCTCATCACCACCCACACCCGCCACCACAACCATGCGCTTCTTCAGCAAGAAGTCGCCGGCCGGGTCGTCGACTCCACCGACCCCT
13-AHJ-8C -----TC-----
14-STDK -----TC-----
10-BNE-35 -----TC-----
15-PQ-6A -----TC-----
09-ASA-10b.pz -----TC-----
12-VM-7A -----TC-----
14-EG-A1 -----TC-----
09-CB1 CCGGCAGATCGCTCATACGAAACAGGACTTCACCTCTCATCACCACCCACACCCGCCACCACAACCATGCGCTTCTTCAGCAAGAAGTCGCCGGCCGGGTCGTCGACTCCACCGACCCCT
14-AK1b -----TC-----
consensus .....1930.....1940.....1950.....1960.....1970.....1980.....1990.....2000.....2010.....2020.....2030.....2040

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