**Figure S9. Alignment of nucleotide sequences corresponding to *mxa* and *mxb*.**

1 50

mxa\_U66475 (1) GGCACGAGGGGACACGCAGGTCGATCAGATAGCAGAACACCTTGCTGTTT

mxb\_BT044881 (1) ---------------------------------AGTTGCAGTTGCAGTGT

51 100

mxa\_U66475 (51) ATTTAAGTTTTATCACTAAATAATAATTCACAATGAATAACACTCTAAAC

mxb\_BT044881 (18) ATTAACCATTTTTT--TTTATCGCAAATC---ATGAATTATACGCTGAAC

101 150

mxa\_U66475 (101) CAACATTATGAGGAGAAGGTGCGTCCCTGTATAGACCTCATCGACTCCCT

mxb\_BT044881 (63) CAACATTATGAGGAGAAGGTGCGTCCTTGTATTGACCTCATCGACTCCCT

151 200

mxa\_U66475 (151) GCGCTCCCTTGGCGTAGAGAAGGACCTTGCGCTGCCAGCCATCGCGGTGA

mxb\_BT044881 (113) GCGCTCCCTTGGCGTAGAGAAGGACCTTGCGCTGCCAGCCATCGCGGTGA

201 250

mxa\_U66475 (201) TAGGGGACCAGAGTTCAGGGAAGAGCTCAGTGCTGGAGGCGCTATCTGGG

mxb\_BT044881 (163) TAGGGGACCAGAGTTCAGGGAAGAGCTCCGTGCTGGAGGCGCTATCTGGG

251 300

mxa\_U66475 (251) GTGGCTTTGCCAAGGGGGAGTGGTATTGTAACACGATGCCCTCTCGAGCT

mxb\_BT044881 (213) GTGGCTTTGCCAAGGGGGAGTGGTATTGTAACACGATGCCCTCTCGAGCT

301 350

mxa\_U66475 (301) GAAGATGAAGAGGAAGAAAGAAGGAGAGGAATGGCATGGAAAAATCAGCT

mxb\_BT044881 (263) GAAGATGAAGAGGAAGAAAGAAGGAGAGGAATGGCACGGAAAAATCCGCT

351 400

mxa\_U66475 (351) ACCAAGACCATGAGGAGGAGATTGAGGATCCCTCTGATGTGGAGAAGAAA

mxb\_BT044881 (313) ACCAAGACCGTGAGGAGGAGATTGAGGACCCCTCTGATGTGGAGAAGAAA

401 450

mxa\_U66475 (401) ATTCGTGAAGCCCAGGACGAAATGGCAGGTGTGGGGGTGGGTATCAGTGA

mxb\_BT044881 (363) ATTCGGAAAGCCCAGGATGAAATGGCAGGTGTGGGGGTGGGTATCAGTGA

451 500

mxa\_U66475 (451) TGACCTCATCAGCCTGGAGATTGGCTCCCCTGACGTCCCAGACCTCACAC

mxb\_BT044881 (413) TGACCTCATCAGCCTGGAGATTGGCTCCCCTGACGTCCCAGACCTCACAC

501 550

mxa\_U66475 (501) TCATCGACCTGCCAGGCATCGCCCGGGTAGCTGTCAAGGGTCAACCTGAG

mxb\_BT044881 (463) TCATCGACCTGCCAGGCATCGCCCGGGTAGCTGTCAAAGGTCAACCTGAG

551 600

mxa\_U66475 (551) AACATTGGTGAACAGATTAAGAGACTGATACGGAAGTTCATCACGAAGCA

mxb\_BT044881 (513) AACATTGGTGAACAGATTAAGAATCTGATACGCAAGTTCATCACAAAGCA

601 650

mxa\_U66475 (601) AGAAACAATCAATTTGGTGGTTGTGCCATGCAACGTTGACATTGCAACCA

mxb\_BT044881 (563) AGAAACAATCAACTTGGTGGTTGTGCCATGCAACGTTGACATTGCAACCA

651 700

mxa\_U66475 (651) CAGAGGCTTTGAAGATGGCACAAGAGGTGGACCCTGAAGGGGAAAGGACA

mxb\_BT044881 (613) CAGAGGCTTTGAAGATGGCACAAGAGGTGGACCCTCAAGGTGGAAGGACA

701 750

mxa\_U66475 (701) TTAGGCATCCTGACCAAGCCTGACCTGGTAGACAAAGGCACAGAAGAGAC

mxb\_BT044881 (663) TTAGGCATCCTGACCAAGCCTGACCTGGTAGACAAAGGCACAGAAGAGAT

751 800

mxa\_U66475 (751) GGTGGTGGACATAGTTCATAATGAGGTTATCCACCTGACTAAGGGCTACA

mxb\_BT044881 (713) GGTGGTGGACATAGTTCATAATGAGGTTATCCACCTGACTAAGGGCTACA

801 850

mxa\_U66475 (801) TGATAGTCAAGTGCAGGGGCCAGAAGGAGATCATGGAGCGAGTCTCGCTG

mxb\_BT044881 (763) TGATAGTCAAGTGCAGGGGCCAGAAGGAGATCATGGAGCAAGTCTCACTG

851 900

mxa\_U66475 (851) TCCGAGGCCACAGAGAGGGAGAAGGCTTTCTTCAAAGAGCACGCTCATCT

mxb\_BT044881 (813) ACCGAGGCCACAGAGAGGGAGAAGGCCTTCTTCAAAGAGCACCTTCATCT

901 950

mxa\_U66475 (901) CAGCACACTATATGATGAGGGCCATGCCACCATCCCTAAACTGGCAGAGA

mxb\_BT044881 (863) CAGCACTCTTTATGATGAGGGGCATGCCACCATCCCTAAACTGGCAGAGA

951 1000

mxa\_U66475 (951) AATTAACTCTTGAACTAGTGCATCATATTGAGAAATCCCTACCTCGTCTA

mxb\_BT044881 (913) AATTAACTCTTGAACTAGTGCAACATATCGAGAAATCCATGCCTCGTCTA

1001 1050

mxa\_U66475 (1001) GAAGAGCAGATTGAGGCAAAGCTGGCAGAGACACATGCCGAGCTGGAAAG

mxb\_BT044881 (963) AAAGAGCAGATTGAGGAAAAGCTGGAGGAGAC**ACGCACCACTCTGGAGAA**

1051 1100

mxa\_U66475 (1051) ATATGGTACCGGGCCACCTGAGGACTCGGCAGAAAGGATGTACTTCCTGA

mxb\_BT044881 (1013) **AT**GTGGTACCGGACCCCCTGAAGACCCAAAAGAACGGCAGTATTTTCTGA

1101 1150

mxa\_U66475 (1101) TCGATAAAGTGACTGCATTCACCCATGATGCCATTAACCTGAGCACTGGG

mxb\_BT044881 (1063) TCGATAAAGTGACTTTGTTCACCCAGGATGTCATTAACCTGAGCACTGGG

1151 1200

mxa\_U66475 (1151) GAGGAG**CTGAAAAGCGGAGTTCGTCT**CAACGTCTTTTCCACACTCAGAAA

mxb\_BT044881 (1113) GAGGAGCTGAAAAGTGGAGACA---TCAACATCTTCTCCACACTCAGAAC

1201 1250

mxa\_U66475 (1201) AGAGTTTGGGAAATGGAAGTTACACCTGGATCACTCTGGAGAAAACTT**TA**

mxb\_BT044881 (1160) **AGAGTTCGGGAAATGGAAG**GCACAACTGGATCGCTCTGGAAAGAACTTTA

1251 1300

mxa\_U66475 (1251) **ACCAGAGGATCGAGGGAG**AAGTGGCTGATTATGAGAAGACGTACCGTGGA

mxb\_BT044881 (1210) ATAAGAAGATTGAAAAAGAAGTGGCTGATTATGAGAAGACGTACCGTGGA

1301 1350

mxa\_U66475 (1301) AGGGAGCTCCCAGGGTTCATCAACTACAAGACCTTTGAGGTGATGGTGAA

mxb\_BT044881 (1260) AGGGAGCTCCCAGGGTTCATCAACTACAAGACCTTTGAGGTGATGGTGAA

1351 1400

mxa\_U66475 (1351) AGACCAGATCAAACAACTGGAGGAACCAGCAGTCAAGAAACTGAAGGAGA

mxb\_BT044881 (1310) AGACCAGATCAAACAACTGGAGGAACCAGCAGTCAAGAAGCTGAAAGAGT

1401 1450

mxa\_U66475 (1401) TTTCAGATGCCGTTAGGAAGGTGTTCTTACTGCTGGCTCAGAGCAGCTTC

mxb\_BT044881 (1360) TATCAGATGTTGCTAGGAAGGCGTTCATACTGCTGGCTCAGAACAGCTTC

1451 1500

mxa\_U66475 (1451) ATTGGATTTCCTAACCTCCTGAAATCCGCGAAGACAAAGATTGAGGCCAT

mxb\_BT044881 (1410) ACAGGTTTCCCTATTCTCCTGAAAACAGCAAAGACTAAGATCGAGACAAT

1501 1550

mxa\_U66475 (1501) TAAGCAGGTGAATGAGTCTACTGCTGAGTCCATGTTGAGGACTCAGTTCA

mxb\_BT044881 (1460) CAAGCAGGAGAAGGAGTCTACGGCTGAGTCCATGTTGAGGACTCAGTTCA

1551 1600

mxa\_U66475 (1551) AGATGGAGATGATAGTGTACACACAGGACAGCACCTACAGCCACAGTCTG

mxb\_BT044881 (1510) AGATGGAGCTGATAGTGTACACACAGGACATCACCTACAGCTCTAGCCTG

1601 1650

mxa\_U66475 (1601) AGTGAGAGGAAGAGGGAGGAGGAAGAC------GACCGACCCTTA-----

mxb\_BT044881 (1560) AGGAAGAGGAAGAGGGAGGAGGAAGAGTTGGAGGAGGGAGAGTTAGTTAA

1651 1700

mxa\_U66475 (1640) ----CCGACCATTA------------AGA---------------------

mxb\_BT044881 (1610) AAATCCTTCCCTTTCTTTTGGGAGTCAGAAAGTGTTATCTGTTTTCTCTG

1701 1750

mxa\_U66475 (1653) TAAGGAGTACAATCTTTAGCACAGACAACCATGCCACCCTACAGGAGATG

mxb\_BT044881 (1660) TAAGGAGTACTGTCAACGGCCATGACAACCATGCTGCCCTACGGGAGATG

1751 1800

mxa\_U66475 (1703) ATGCTGCACCTCAAGTCCTATTACAGGATATCCAGTCAACGTTTGGCTGA

mxb\_BT044881 (1710) ATGCTGCACCTCAAGTCCTATTATAATATTGCCAGTCAGCGTCTGGCTGA

1801 1850

mxa\_U66475 (1753) TCAGATTCCCATGGTGATCCGCTACCTGGTGCTGCAGGAGTTTGCTTCCC

mxb\_BT044881 (1760) TCAGATTCCCATGGTGATCCGCTACCTGGTTCTGCAGGAGTTTGCTTCCC

1851 1900

mxa\_U66475 (1803) AGCTGCAGAGGGAGATGCTTCAGACTCTGCAGGAGAAGGACAACATCGAG

mxb\_BT044881 (1810) AGCTGCAGAGGGAGATGCTTCAGACTCTGCAGGAGAAGGACAACATCGAG

1901 1950

mxa\_U66475 (1853) CAGCTGCTGAAGGAGGACTTCGACATCGGCAGCAAGAGGGCTGCACTGCA

mxb\_BT044881 (1860) CAGCTGCTGAAGGAGGACATCGACATCGGCAGCAAGAGGGCTTCACTGCA

1951 2000

mxa\_U66475 (1903) GAACAAGCTCAAACGTCTGATGAAGGCACGCAGCTACCTAGTTGAGTTCT

mxb\_BT044881 (1910) GAGCAAGCTCAAACGTCTGATGAAGGCACGCAGCTACCTAGTGGAGTTCT

2001 2050

mxa\_U66475 (1953) AGTATGGACAGCTGCTTGTTAACATTTAGGATGGTCTTGATTTTTTTTAA

mxb\_BT044881 (1960) AGTATGGACAGCTGCTTGTTAACATTTAGGATGGTCT------------A

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2051 2100

mxa\_U66475 (2003) ATGTAATGTATTTTTTGGGAGGATAACAGACATATACAACAAAATGTACA

mxb\_BT044881 (1998) ATTTCAGATAGCTTGGTCAATGGAAGTAGGCAT-TGGGGTTTGGGGTAGA

2101 2150

mxa\_U66475 (2053) ATGTGGACCCAGAGGATATCACTTGAAAGTGTTAATTAAAAAGCTTGTTT

mxb\_BT044881 (2047) TTCTGTTATC------TAACTTATAATAAAGTTACTATGCAATCAAAAAA

2151 2180

mxa\_U66475 (2103) CCAAAAAAAAAAAAAAAAAAAAAAAAAAA-

mxb\_BT044881 (2091) AAAAAAAAAAAAAAAAAAAAAAAAAAAAGA