Alignment of Sequence_1: [ToBRFV isolate Tom-BA21 comp + RP MinIon primrs.xdna]
with Sequence_2: [ToMMV isolate MX5 [NC_022230.1] .xdna]

Similarity : 5037/6398 (78,73 %)

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Seq_1  1     GTGTATTTTTTACAACATA---TACCAACAACAACAAACAACAAACAACAACATCACAAT  57
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Seq_2  1     --GTATTTATTATTACAACAATTACCAACAACAACAACAAACAACAACAACATTACATTT  58

Seq_1  58    TACTATTTACAACTACAATGGCATACACACAGACAGCTACCACATCCGCTTTGCTCGACA  117
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Seq_2  59    TACAATCTACAACTACAATGGCATACACACAAACAGCTACATCTTCCGCTTTGCTTGACA  118

Seq_1  118   CTGTCCGAGGTAACAATACCTTGGTCAACGATCTTGCGAAGCGGCGTCTTTATGACACAG  177
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Seq_2  119   CTGTCCGGGGTAACAACACCCTGGTCAATGATCTTGCAAAGCGTCGTCTTTATGACACAG  178

Seq_1  178   CGGTCGACGAGTTCAACGCTCGTGATCGCAGGCCCAAAGTAAATTTTTCCAAAGTAATAA  237
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Seq_2  179   CGGTCGATGAATTTAACGCTAGGGACCGCAGGCCCAAAGTCAACTTTTCTAAAGTAGTAA  238

Seq_1  238   GTGAGGAACAGACGCTTATTGCTACTAGGGCATATCCAGAATTCCAGATAACCTTCTATA  297
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Seq_2  239   GTGAGGAACAGACACTTATTGCTACCCGGGCATATCCTGAATTCCAGATCACGTTCTATA  298

Seq_1  298   ATACGCAGAACGCCGTGCATTCGCTTGCCGGTGGACTACGATCCTTAGAACTGGAATATC  357
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Seq_2  299   ACACTCAGAACGCAGTTCACTCGCTTGCGGGTGGTCTGCGATCATTAGAGCTGGAATATC  358

Seq_1  358   TAATGATGCAGATCCCGTACGGATCACTCACATATGATATAGGTGGGAATTTTGCATCTC  417
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Seq_2  359   TGATGATGCAAATCCCGTACGGCTCACTGACGTATGATATAGGAGGGAATTTTGCATCAC  418

Seq_1  418   ATCTGTTCAAAGGACGGGCATATGTTCACTGCTGTATGCCCAATCTTGATGTCCGCGACA  477
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Seq_2  419   ATCTGTTCAAAGGGCGAGCATACGTTCACTGCTGTATGCCGAATCTGGATGTCCGCGATA  478

Seq_1  478   TAATGCGGCACGAAGGCCAGAAAGACAGTATAGAATTATACCTTTCCAGGCTTGAGCGGG  537
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Seq_2  479   TTATGCGGCACGAAGGCCAAAAGGATAGCGTCGAGCTATACCTCGCTAGGCTAGAAAGGG  538

Seq_1  538   GCAACAAAGTTGTCCCAAATTTCCAAAAGGAAGCTTTTGACAGATACGCTGAAACGCCAG  597
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Seq_2  539   GCAACAAGTTTGTCCCGAACTTCCAAAAGGAAGCCTTTGACAGATACGCTGAAACGCCAG  598

Seq_1  598   ACGAAGTTGTCTGTCACAGTACCTTCCAAACGTGTACGCACCAGCAGGTGAAAAACACAG  657
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Seq_2  599   ATGAAGTAGTCTGTCACGATACCTTCCAAACCTGTAGGCACTCGCAAGAGATGTACACAG  658

Seq_1  658   GCAGGGTGTATGCTATTGCATTGCACAGTATATACGATATACCTGCTGATGAATTCGGAG  717
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Seq_1  718   CGGCACTTTTAAGGAAAAATGTCCATGTTTGTTACGCCGCCTTCCACTTTTCCGAGAATT  777
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Seq_2  719   CGGCATTACTTAGAAAGAATGTACATGTGTGCTATGCCGCTTTCCACTTCTCCGAGAATT  778

Seq_1  778   TACTTCTCGAAGATTCACACGTCAACCTTGACGAAATCAACGCGTGTTTTTCGCGTGATG  837
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Seq_2  779       TACTTCTCGAAGATTCGCACGTCAATCTCGATGAAATCAACGCATGTTTTCAGAGAGATG  838

Seq_1  838       GAGACAAGCTGACTTTTTCTTTCGCATCTGAGAGCACTTTAAATTATTGTCATAGTTATT  897
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Seq_2  839       GCGATAGGTTAACTTTTTCCTTTGCTTCTGAGAGTACTCTTAATTATACGCATAGTTTTC  898

Seq_1  898       CTAATATTTTAAAATACGTGTGCAAAACTTACTTCCCGGCATCTAATAGAGAGGTCTACA  957
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Seq_2  899       CTAATATTTTAAAGTATGTGTGCAAAACTTACTTCCCAGCCTCTAATAGAGAGGTTTACA  958

Seq_1  958       TGAAGGAGTTTTTGGTCACCAGGGTTAACACCTGGTTTTGTAAGTTTTCTAGGATAGATA  1017
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Seq_2  959       TGAAGGAGTTTTTAGTAACTAGAGTAAATACCTGGTTTTGTAAATTCTCTAGAATAGATA  1018

Seq_1  1018      CTTTTTTATTATACAAGGGGGTAGCCCACAAAGGTGTAAATAGTGAGCAATTTTACAACG  1077
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Seq_2  1019      CTTTCCTATTGTACAAAGGTGTAGCGCACAAAGGTGTAGATAGTGAGCAATTTTACAAGG  1078

Seq_1  1078      CAATGGAAGATGCATGGCACTACAAAAAGACTCTTGCAATGTGTAACAGCGAGAGGATTC  1137
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Seq_1  1138      TTCTTGAAGATTCCTCATCGGTCAATTACTGGTTCCCAAAAATGAGAGATATGGTCATAG  1197
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Seq_2  1139      TTTTAGAAGATTCCTCATCCGTCAACTACTGGTTTCCAAAAATGCGGGATATGGTGATCG  1198

Seq_1  1198      TTCCTCTATTCGACATATCTCTCGACACCAGTAAAAGGACCCGCAAAGAAGTCTTAGTGT  1257
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Seq_2  1199      TTCCGCTTTTTGACATTTGTCTTGAAACCAGTAAAAGGTCACGCAAAGAGGTCTTAGTGT  1258

Seq_1  1258      CAAAGGATTTTGTATTCACAGTTTTAAATCACATTCGCACTTATCAAGCCAAGGCACTTA  1317
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Seq_2  1259      CCAAGGATTTTGTTTACACAGTGTTAAATCATATCCGTACATACCAGGCAAAAGCCCTGA  1318

Seq_1  1318      CATACTCCAATGTTTTATCCTTTGTCGAATCAATTCGTTCAAGGGTAATTATCAACGGAG  1377
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Seq_2  1319      CATACGCTAATGTTTTATCCTTCGTCGAATCAATTCGTTCGAGGGTGATCATTAATGGAG  1378

Seq_1  1378      TGACTGCCAGGTCTGAGTGGGATGTTGACAAATCTCTTTTGCAATCCTTGTCCATGACAT  1437
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Seq_2  1379      TCACCGCTAGGTCTGAGTGGGATGTTGATAAATCGTTATTACAATCCTTATCTATGACGT  1438

Seq_1  1438      TTTTCTTGCATACTAAGCTTGCCGTTTTAAAAGACGAATTGTTAATCAGCAAGTTTAGTT  1497
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Seq_2  1499      TTGGTCCCAAACCAGTGTCTCAATTTGTGTGGGAGGAGATATCATTAGCGTTTGGCAATG  1558

Seq_1  1558      CATTTCCATCGATCAAGGAGAGACTGCTAAATCGGAAACTAATTAAAGTGTCGGGAGACG  1617
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Seq_2  1559      CCTTTCCAACAATTAAGGAAAGATTGATCAACCGTAAACTGATCCAAATCACGGAGAATG  1618

Seq_1  1618      CATTAGAAATCAGGGTGCCTGATTTATATGTGACTTTCCACGATAGATTAGTGACTGAGT  1677
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Seq_2  1619  CGTTAGAAATTAGGGTGCCTGATTTATACGTAACTTTCCATGATAGGTTGGTTTCCGAGT  1678

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Seq_2  1679  ACAAGCTCTCAGTCGAGATGCCGGCGCTTGATATCAGGAAGAAAATGGAAGAGACCGAAG  1738

Seq_1  1738  TTATGTACAATGCATTGTCTGAGCTATCTGTGCTCAAGGAGTCGGACAAGTTCGACGTTG  1797
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Seq_2  1799  ATGTTTTTTCCCAGATGTGCCAATCTTTAGAAGTAGATCCTATGACTGCAGCGAAGGTTA  1858

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Seq_1  1918  CAAATGTCGCATTGGCACTTAAAGATTCAGAAAAAGCCTCTGAGGGTGCACTAGTGGTTA  1977
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Seq_2  1919  CCAATATTGCACTGGCACTTCAAGACTCTGAAAAAGCTTCGGAAGGCGCGTTGGTAGTTA  1978

Seq_1  1978  CTTCTAGAGATGTTGAAGAACCATCCATGAAGGGTTCAATGGCAAGAGGAGAGTTACAAT  2037
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Seq_2  1979  CCTCGCGTGATGTGGAGGAACCCTCTATGAAAGGTTCAATGGCCCGTGGTGAGTTACAAT  2038

Seq_1  2038  TGGCCGGTCT-GTCTGGAGACCAACCAGAGTCTTCCTATACTCGGAACGAGGAAATAGAG  2096
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Seq_2  2039  TGGCCGGATTAG-CAGGTGACATTCCAGAATCTTCGTTTACAAGGAGCGAGGAGATTGAG  2097

Seq_1  2097  TCATTAGAGCAATTCCACATGGCAACGGCTAGTTCGTTAATTCGGAAACAGATGAGTTCG  2156
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Seq_2  2098  TCTTTAGAGCAGTTTCATATGGCAACAGCCAGTTCTCTGATTCAAAAGCAGATGTGTTCG  2157

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Seq_1  2217  GCATCACTCTCTGCTGCGGTGTCGAACCTAGTCAAGATCCTAAAGGATACAGCTGCTATA  2276
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Seq_2  2218  GCCTCGCTCTCTGCTGCTGTTTCGAACTTGGTGAAGATCCTCAAAGATACTGCTGCTATT  2277

Seq_1  2277  GACCTCGAAACCCGTCAGAAGTTTGGAGTCTTAGATGTTGCGACCAAAAGATGGTTAATT  2336
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Seq_2  2278  GACCTTGAAACTCGTCAGAAGTTCGGAGTTCTGGACGTTACCTCAAAGAAATGGCTGATT  2337

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Seq_2  2458  GCCGTAAGTTCTGAATCAGTAGTATACTCTGATATGGCCAAGCTCAAAACTTTGAGGAAG  2517
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Seq_1  2517  TTATTAAGAGATGGTGAGCCTCATGTCAGCAGTGCTAAAGTCGTCCTAGTTGACGGTGTC  2576
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Seq_2  2518  TTGCTCTTGGATGGCGAACCACCGGTTAGCTCTGCTAAGGTTGTACTGGTAGACGGCGTT  2577

Seq_1  2577  CCGGGTTGTGGAAAGACAAAAGAGATTCTCTCGAAAGTAAATTTTGAGGAAGATCTAATC  2636
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Seq_1  2697  ATTCAAGCCACAAGAGATAATGTTCGTACTGTTGATTCATTTATAATGAATTACGGTAAA  2756
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Seq_2  3058  GTATCTCAAGAGATGGTTAGTGGGGCTGCCACAATCAATCCAGTATCCAAACCACTCAGT  3117

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Seq_1  3357  ATTAGGGATTTAGAAAAACTTAGTTCTTACTTGTTAGATATGTATAAAGTAGATGCAGGG  3416
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Seq_1  3537  AGCACCATGTTAAATAACTATGATGCTGTTACCATGAGGTTGACTGACATTTCTCTTAAT  3596
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Seq_1  3956  TGCCGTTGATCAGTACAGGCATATGATTAAAGCGCAACCTAAGCAGAAGCTGGATACATC  4015
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Seq_1  4076  AATCTTCGGTCCTTTGTTCAGTGAGCTCACAAGGCAAATGCTCGAAAGCATAGACTCAAG  4135
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Seq_2  4077  AATTTTTGGACCGCTCTTCAGCGAACTGACAAGGCAACTACTGGACAGTGTTGACTCAAG  4136

Seq_1  4136  TAAGTTTTTGTTCTTTACAAGGAAGACGCCAGCTCAAATTGAGGATTTCTTCGGAGATCT  4195
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Seq_2  4137  CAGATTTTTGTTCTTCACGAGGAAGACACCAGCTCAAATCGAAGATTTCTTCGGAGATCT  4196
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Seq_2  4197  AGATAGTCATGTCCCCATGGATGTGTTGGAGTTGGATATTTCCAAATACGACAAATCTCA  4256

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RP2 : [1999 : 2019]
RP3 : [2965 : 2984]
RP4 : [3990 : 4009]
RP5 : [5182 : 5201]
RP6 : [6373 : 6392]