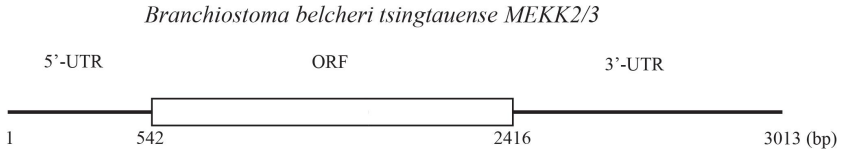
a



b

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 121 TGAGGGAGATGTTTGTCCACCCGTAGGATGCCCGGATGCGCGTTCGTGTCGCCGTTTCCCGCGGATCTACGGCAGTTTTGTTGGGTCTGGTGGTTCCTGTCCGAGGCACGGTACCTCCAT 240

 241 GTTTGTTTGCACTGATCTGCACCAGCCAGCCTTACTAGCGATTGTTCCCGGTCCGAGCTGCCATCCTGCCGCCCCGTGCATGTGTGGGACCTGTCCGGCCATCTATTTGTCCTGTCCGGC 360

 361 CGTCTGTGCGTGTCTGGGACCCGTCCTGTGCGCGTGTGTGGTCCGTGTACCTCACCAGAACCCTTCGCTGTGACCCAGGACCCAAACTCACTGTGGACATTACCTGCTATTTACTCTTCT 480

 481 GTCAGGTCTGTACAGGTCTGAAGATTGATGAGTGACACGACAGACAGACGTCACCATTACCATGGATGAAAAAGAGGCTTTGAACTCCATTAAGAATGACCTGGCTGCAGGCATGAAGCA 600
   1                                                       M  D  E  K  E  A  L  N  S  I  K  N  D  L  A  A  G  M  K  Q  20
 601 GTCGGCGTGGCACAAGTCACATTCCAGCTCCAAATCCTCCTCCCAGACAGACGTCAGGGTCAAATTCGAGTTCCAGGGGGAGAAAAGAATTATCCAGGTCCCCCGACCAGTCAACTTCCA 720
  21  S  A  W  H  K  S  H  S  S  S  K  S  S  S  Q  T  D  V  R  V  K  F  E  F  Q  G  E  K  R  I  I  Q  V  P  R  P  V  N  F  Q  60
 721 GGACTTGCAGAGTAAAGTCAAGACAGCATACGGGCAGCTACTCACCATGTTCTACACTAACACTGAGATTTCCATTCCGATCCTGAACCAGTCGGATCTGGAGAAGGCCATCATCCTGCT 840
  61  D  L  Q  S  K  V  K  T  A  Y  G  Q  L  T  M  F  Y  T  N  T  E  I  S  I  P  I  L  N  Q  S  D  L  E  K  A  I  I  L  L  100
 841 GGACCACAACCCACACATGAAGAGCCTGCGCATCTACCTATGCAAGGAGAACCCCACGCCACCTGGGTCACCCCAGGGACCACCCCACGGGCCACTACGGGACCTCTTCCACCCACCTAC 960
 101  D  H  N  P  H  M  K  S  L  R  I  Y  L  C  K  E  N  P  T  P  P  G  S  P  Q  G  P  P  H  G  P  L  R  D  L  F  H  P  P  T  140
 961 CAGTACCACAGGCACGAAGCCGGTGCCCATCTCCAGGTCCAAGTCCACCACAGATGCCAGTAAGAAGAAGACGGACCGGCAGTCTCCTCCGCCGGGCTACATTCCCGACTCCGAAGTGCG 1080
 141  S  T  T  G  T  K  P  V  P  I  S  R  S  K  S  T  T  D  A  S  K  K  K  T  D  R  Q  S  P  P  P  G  Y  I  P  D  S  E  V  R  180
1081 ACACAGTAGCTCCTACACTTCCATTGAAGGGGAGGGCACCTTCATACCCGAGTCAAGTCTCGACTCTGAGTCGGTCGACCCTCTGGAATACAGCAGTCCAGAAAACTCTGGCAGCTCCGC 1200
 181  H  S  S  S  Y  T  S  I  E  G  E  G  T  F  I  P  E  S  S  L  D  S  E  S  V  D  P  L  E  Y  S  S  P  E  N  S  G  S  S  A  220
1201 TTCACTCGACAGACTAAGTAGTGACAGCTACTATAACAGACTACGGATGAGTCGGACCAAGAGTTCCTCAGCATTCTCAGACGAGTTCCTCGGAGAACACGAGCTGGCCCACGTGGAGAG 1320
 221  S  L  D  R  L  S  S  D  S  Y  Y  N  R  L  R  M  S  R  T  K  S  S  S  A  F  S  D  E  F  L  G  E  H  E  L  A  H  V  E  R  260
1321 AGCTGGGAAAGGCGGGACGTACCCCAGAAGATCCACCATAATGACCAACCCACACCACGACTACAGCGATGGGCGTAAAACATTCCCCAGAACAAGAAGACCGCAGCCCAGCCCCACCTT 1440
 261  A  G  K  G  G  T  Y  P  R  R  S  T  I  M  T  N  P  H  H  D  Y  S  D  G  R  K  T  F  P  R  T  R  R  P  Q  P  S  P  T  L  300
1441 GAGAAGACCTGTGGGCACGTTCAGTCCGCGGTCGGGCAGCGAACGGTCGCTTAGCAACAGCAGCAGCAGCAGTGGGCTGGTGACGGACTCAGAGAGACGAGACAGCGACTATGACTTAGC 1560
 301  R  R  P  V  G  T  F  S  P  R  S  G  S  E  R  S  L  S  N  S  S  S  S  S  G  L  V  T  D  S  E  R  R  D  S  D  Y  D  L  A  340
1561 CGTCCTCAGTCTGCAGGACCTCAACCCGGCCAGATGTAAGTCATCCCCCCGAGCGCCGACCAACTGGCGACAAGGCAAGTTGCTGGGCCAGGGCGCCTTCGGGCAGGTCTATCTCTGCTA 1680
 341  V  L  S  L  Q  D  L  N  P  A  R  C  K  S  S  P  R  A  P  T  N  W  R  Q  G  K  L  L  G  Q  G  A  F  G  Q  V  Y  L  C  Y  380
1681 CGATGCCGACACCGGCCGAGAGCTCGCGCTCAAACAGGTCCACCTCGACCCCAAAAATGTGGAAGCCTCAAAGCAGGAAGTCAAAGCTCTGGAGTGTGAGATCCAGCTGTTGAAGAACCT 1800
 381  D  A  D  T  G  R  E  L  A  L  K  Q  V  H  L  D  P  K  N  V  E  A  S  K  Q  E  V  K  A  L  E  C  E  I  Q  L  L  K  N  L  420
1801 TCAGCACGAGAGGATAGTTCAGTATTACGGCTGCATCCAGGATGAGAACAGGCTCTGCATCTTCATGGAGTACATGCCAGGGGGTTCTGTTAAAGACCAGATCCGACAGTACGGAGCTCT 1920
 421  Q  H  E  R  I  V  Q  Y  Y  G  C  I  Q  D  E  N  R  L  C  I  F  M  E  Y  M  P  G  G  S  V  K  D  Q  I  R  Q  Y  G  A  L  460
1921 TACTGAGAATGTGACACGGAAATACACGCGGCAGATTCTGGAGGGAATTCTCTATCTGCATAGCAACATGATCGTCCACAGCGACATTAAAGGTGCAAATATATTGAGGGACTCCTCAGG 2040
 461  T  E  N  V  T  R  K  Y  T  R  Q  I  L  E  G  I  L  Y  L  H  S  N  M  I  V  H  S  D  I  K  G  A  N  I  L  R  D  S  S  G  500
2041 AAATGTGAAGCTGGGAGATTTCGGGGCGTCAAAGCGGATCCAGACAATCTGCAGCGCCACCGGAATGCGCACAGTCACGGGGACACCATATTGGATGAGTCCAGAGGTCATCAACGGTGA 2160
 501  N  V  K  L  G  D  F  G  A  S  K  R  I  Q  T  I  C  S  A  T  G  M  R  T  V  T  G  T  P  Y  W  M  S  P  E  V  I  N  G  E  540
2161 AGGTTATGGCAGAAAAGCTGATATATGGAGTATAGGTTGTACAGTTGTGGAGATGTTAACAGAGAAGCCCCCTTGGTTCGACTATGAGCCCATGGCAGCCATCTTTAAGATTGCCACGCA 2280
 541  G  Y  G  R  K  A  D  I  W  S  I  G  C  T  V  V  E  M  L  T  E  K  P  P  W  F  D  Y  E  P  M  A  A  I  F  K  I  A  T  Q  580
2281 GCCCACCATTCCCAAGCTTCCTGCCGGCGTGTCGGACTGCGCACACGACTTTCTCAGGATCATTTTCCAGAAAGACCACAGACAAAGGGCATCGGCCCAGGAACTCCTAGAGCACTCCTT 2400
 581  P  T  I  P  K  L  P  A  G  V  S  D  C  A  H  D  F  L  R  I  I  F  Q  K  D  H  R  Q  R  A  S  A  Q  E  L  L  E  H  S  F  620
2401 TGTCTTCAACTACTGACCTGTGTGATGTCACGTGATGTGACTGTCGTAATGATCCAATGTGACTGGCCTTTGCTACCCATGTGACTGGTCATGTGCTGCCCATGTGGCTGTCAGGTGCTG 2520
 621  V  F  N  Y  *                                                                                                          624
2521 CCCATGTGATTATCATATGATACCCACATGGGCTGAGGTGTGTTCCACAGAAGCTACCATTGCTACTGTCTGTGTGGTGTTGGGTGTGAGATGGCTCTTTGTGGAACAGACCTCGGACTC 2640

2641 AGCTGGACACACAAGAATAGAGCAGCCAGTGTACAAGATGAGACCAAATTGTTGCGATAGGTTTTCTAGATCAGGGGCCATGCACTTCTAACAGCAAATTAGTATTTGTTCTGTGCTCAG 2760

2761 TTGGTCCCTAAGAAGTGAATTCCCAGTACATGATTCTTTGGACTACCTGTATATTTATTGGAGCATTTGATTGCCATACAGAGGTTTTTAATCAAAGCAAATATGTTGGTTTTATGAGAG 2880

2881 TAAATTATTGATAATACTTCCATCTTGTGGCCCTTGAAAACAGTTTGTAAATGTTGTGAGAGGAAGGAAGAGGTCACCCTCATTCTGTCTGATTTGGCACAAGGAGAATCAACCAAGTAT 3000

3001 GAAAAAAAAAAAA 3013
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Figure S3 The detailed information of the *AmphiMEKK2/3*.

(a) The schematic diagram of the full-length cDNA of *AmphiMEKK2/3*. Lines represent UTRs, and boxes represent ORFs. (b) The detailed cDNA and protein sequence of *AmphiMEKK2/3*. The red-colored sequences represent protein-coding regions.