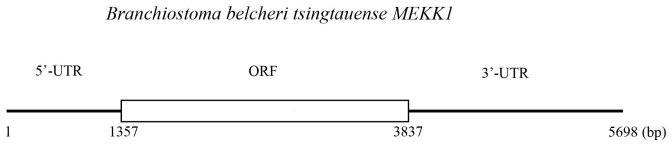
a



b

```
  1 ACGGGGGAGACGGAAGCGAGGCTGCTCAGATTCCAAACTTCGTGTAGTTTTTACGCCAAGTTACTCGTACAATTTGTGGATTTTGCAGCTAATTTCGCAGCCAATGTCTGTGACAGTGGT 120
121 CACAGAAGGCCAGTAAAGGTTATAATCTGATGGATCCATGTCCTGATCGGGCCCCGCGGGACAGTGTAGCGGCGCCCGCCAAGTGTGTTGACGGAAGCCGTGGCGCGCCAACCCCCCGC 240
241 CAGCAGAACCGCAAAGCATTCCCCCTGCCTCGTCCACGTTTATGGAGGCACGTCTGGGCGGCTCAGAAATACGGGAGAAGCTGCGTGGACGGCAACACGCTGTGGCCAAGAAGCAAAAGG 360
361 GACCAATGCTTGCCAAAACCCCAGTTTTTGCCCAAGGAGCCCAACTCCCCCAAGTAGTAGTGGTAGATCCAGAGTCAAACAACGTGGAGAACACAGAAAACTCACAGAACTCACAGAACA 480
481 CATCTTCGTTTGGAAGTGTGCAGAGTAAAATCCAGTTCTTCAACAAGAGAAACACTCCCTCCCCCACTCCCAGCAACGACCCAAGCGACGTCACAGATATCACGACCTCCAGTTCCAGCG 600
601 GCACCGACAGTCGCTCCCACCAAAGTCCGCCGGCGTAGGTCACTATCGCCAAGTTTCGGTGCCAACCGATCGCGAGGGAAAGGAGCGAAGGCACCAACCATGCACGAAGGTTAGGACGGACA 720
721 TGTGTAACTGTAACGAGGCACCCTTTCACCGCCCATCATGCCCTGCGAGGAGAGGACACAAACTGTTCCGCTCTAAATCGCACCAGAGTCAGGGCAATCGCGGCAAAAATACGCCGACTG 840
841 GAAGTCGGCCATCATCACCAGGGAGTGGACGAGGGACCCCAACGGGCACCACAGGTTCGGCAGACGAGATTGAGAAACTGCAGAAGAAAATCCGCAGAGTTCAGCGGATGAGGCTGTACC 960
961 TCCTGCAGCAGAGTGGACCCAACTCACTGTTGGTAGGCGGGGACTCCCCTGACGACAAGCACAGGGTGCTGATTGGTCAACAGAGCTGCAGCTGCGGGAAACACATGCCATGTGTGCACC 1080
1081 TGCTGTTCATCATGCTGCGGGTGTTCCAGGTGGCGGAAACCAACCCCCTGCTGCAGAGGAAGACGCTCAGGAACTACGAGGTGGAGAGTCTTTTCAGGAACTTTGAGGCCAGGAAAAGAA 1200
1201 ACCGTGTGTGGCGGAGACGGCCACCACAGGCTCCCAACAAGGCCGAGGATGTGGCTGAGTCTGATGGTGCTAAACAGGAGGAGGAGGCCTCTGGTGATGAGAAGAGGGTAAAACCGGAGG 1320
1321 ACGACACCTGTCCCATCTGTCTGTTAGAGATGGTGGATGGAGAGGAGTCTTACGTCGTGTGATGACGGCTGTAACAACCAGATGCACCACCAGTGTGTGGCTGTCTGGGCTGAGGCATGTA 1440
   1                                  M  E  R  V  L  R  R  V  M  T  A  V  T  T  R  C  T  T  S  V  W  L  S  G  L  R  H  V   28
1441 AGAGACAAGGAGACGCCTTCAGCTGTCCTCTCTGTCGTGCAGTCTGGACAGAGGAGGGCGAGGGGGTTCAGGATGAGGGTAGCCAGGCTCCGCCCAACTCCCGCGCCCCGTCCCCCTGTA 1560
  29  R  D  K  E  T  P  S  A  V  L  S  V  V  Q  S  G  Q  R  R  A  R  G  F  R  M  R  V  A  R  L  R  P  T  P  A  P  R  P  P  V   68
1561 CACCCACTCCCGGGGAGGGGGTCCACCTGCCCCACTCTGAACCCATCCCTCCTGAACATCGCGACATGGCCGCACCATGGATAGAGTTGTTTGGTTACAACCTTGTGAGCTGCCTGTTC 1680
  69  H  P  L  P  G  E  G  V  H  L  P  H  S  E  P  I  P  P  E  H  R  D  M  A  A  P  W  I  E  L  F  G  Y  N  L  V  S  C  L  F  108
1681 TCCCGTGACTGGTCTGTACGTGAGGCGGGGTTGATGTGCCTGTCCCATGAGGTGGCACGGAGGTCGATACAGATGGAGGAGGAGGAGGACCCCGCCCAGTGGACGTCTGTCCTGAGGGTC 1800
 109  S  R  D  W  S  V  R  E  A  G  L  M  C  L  S  H  E  V  A  R  R  S  I  Q  M  E  E  E  E  D  P  A  Q  W  T  S  V  L  R  V  148
1801 TGCTGTAACATCCTCGCCATGCTGTGTAGAGACCCTGTCTATAATGTATACGTGGCATCACTGAGAAGTCTGCGGGACATGTCAGCGTACACGGTGTGTCGGACGGAGGACCAGGTGTCG 1920
 149  C  C  N  I  L  A  M  L  C  R  D  P  V  Y  N  V  Y  V  A  S  L  R  S  L  R  D  M  S  A  Y  T  V  C  R  T  E  D  Q  V  S  188
1921 TGTCTACAGGACATGCTGAGGCCTGTGGTCGACGTCATTCTCATCAAGTGCACTGACGGAGCCAAAAATAAAAGAAACCGTACCTGTCAGCTGTCCCTGTCCACTCTTCTGGAGCTGGCT 2040
 189  C  L  Q  D  M  L  R  P  V  V  D  V  I  L  I  K  C  T  D  G  A  K  N  K  R  N  R  T  C  Q  L  S  L  S  T  L  L  E  L  A  228
2041 AAGGGCCAGGAGGGCGGGCTAGCGACGGCCTCGGAGCTGCCTCGTGCGGAGTCCCTGGCCGTGGGCGACCTCCCGTTCCTACTGTCCTGTATCCTGGCCCCTCCCCCCGCAGACGCAGCC 2160
 229  K  G  Q  E  G  G  L  A  T  A  S  E  L  P  R  A  E  S  L  A  V  G  D  L  P  F  L  L  S  C  I  L  A  P  P  P  A  D  A  A  268
2161 TGGCAGTACTTCCTCGGGCGGCTCAACGTCATCGAGAGAATCATCGAAGACTTCCCCAACCACTTCGTCAGGCAGGGCAGCCAGTCCCCCCGCAGGAACGACCCTCCGTTCGACACCGAG 2280
 269  W  Q  Y  F  L  G  R  L  N  V  I  E  R  I  I  E  D  F  P  N  H  F  V  R  Q  G  S  Q  S  P  R  R  N  D  P  P  F  D  T  E  308
2281 CCCCTCGCCTCCGTTTTATCATACGTGTGTGAGTGTGTCAAGAGTCCGCACCCCAAGCTGGCCAAGCAGTCCAAGGATCTCTTCTTGAAGATCGCTCGCTGGGTGTCATCGGTGCCTACT 2400
 309  P  L  A  S  V  L  S  Y  V  C  E  C  V  K  S  P  H  P  K  L  A  K  Q  S  K  D  L  F  L  K  I  A  R  W  V  S  S  V  P  T  348
2401 GTCTTTAAGTTCATGTTTAATATCTTGAGTACGTACACTTCACGACGCCACGCTAGTCTGATGGAAAGCCTCCTGGCTCTTTCCACGGAGCTGGGCATCAGTAAGGACTGGCTGCTCGCC 2520
 349  V  F  K  F  M  F  N  I  L  S  T  Y  T  S  R  R  H  A  S  L  M  E  S  L  L  A  L  S  T  E  L  G  I  S  K  D  W  L  L  A  388
2521 TCGTACCCCATCAGCCCCTGCAAAGGTCCCAAGGAAGCCCCCACTGGTACGTCGGCTGACTCCACGCCATGCCTCACCCCACACTACAACACACCTTCCACATCGCCCGGCAGTACTGTG 2640
 389  S  Y  P  I  S  P  C  K  G  P  K  E  A  P  T  G  T  S  A  D  S  T  P  C  L  T  P  H  Y  N  T  P  S  T  S  P  G  S  T  V  428
2641 GAGATTCCTGCACCCACACAGGCAGGGCCCAGTACTGGTCCGGCTGGCGTGCTGACACCACCCCCTCCCCCGTACACTCAGCAAGGGAACCACAGCAGGGTACAGACAACAACACAGCA 2760
 429  E  I  P  A  P  T  Q  A  G  P  S  T  G  P  A  G  V  L  T  P  P  P  S  P  V  H  S  A  R  E  P  Q  Q  G  T  D  N  N  T  A  468
2761 CAGAGTCACAACAGAGACACGGGTGGGGAGGGGGGCGATGATGATGATGATGAAGTGCGGAGAGAAAATCGTGAGATTATGAACGGCGGGCATCACCACAACCAGTGTCACAACGCCGAC 2880
 469  Q  S  H  N  R  D  T  G  G  E  G  G  D  D  D  D  D  E  V  R  R  E  N  R  E  I  M  N  G  G  H  H  H  N  Q  C  H  N  A  D  508
2881 CAACCAACCGTGGTCGCTTCAGGACAAAACGGACTGAGAGTGTCCTTCGAAAGCGAGGTCGCGCTAGGCTTCTCCGCCAGCAGTACGAAGGTCCTTGAAGGAGGGCCTGTAGTCTTCTCA 3000
 509  Q  P  T  V  V  A  S  G  Q  N  G  L  R  V  S  F  E  S  E  V  A  L  G  F  S  A  S  S  T  K  V  L  E  G  G  P  V  V  F  S  548
3001 ACATCGTGTAAAGAACAAGTGGAGGTGGAGGAAGCCCAGGCGTTGGCTGTTGCCATGGAGATGTCCACCCTTCCCCAGCAGGCCCTTCCCAGAGTTCCAGGGCTGACCAGGAGGACTGAG 3120
 549  T  S  C  K  E  Q  V  E  V  E  E  A  Q  A  L  A  V  A  M  E  M  S  T  L  P  Q  Q  A  L  P  R  V  P  G  L  T  R  R  T  E  588
3121 GAGAAGGAACTGATCATCCATGTGCAGCCCAAGCACCTGAAGGGTGAGAAGCAGGGTGGTGCATACAGGATGGACCAGCAGTGGCTGAAGGGGACCATGATCGGTACAGGGGCCTTCTCT 3240
 589  E  K  E  L  I  I  H  V  Q  P  K  H  L  K  G  E  K  Q  G  G  A  Y  R  M  D  Q  Q  W  L  K  G  T  M  I  G  T  G  A  F  S  628
3241 ACATGTTACCAGGCACGGGACGTCCAGACAGGCACACTCATGGCATGTAAACAGGTGTCGTTCTGTCGTAACTCTCCGACGGAACAGGAGAAGGTTGCGGAGGAGATCCGTGGAGAGATC 3360
 629  T  C  Y  Q  A  R  D  V  Q  T  G  T  L  M  A  C  K  Q  V  S  F  C  R  N  S  P  T  E  Q  E  K  V  A  E  E  I  R  G  E  I  668
3361 CAGCTGATGGCCCGGCTGGATCACCCCAACATCGTACGAGTCCTGGGCGCTACGCAGGAGGGAACGCACTTCAACATCTTCCAGGAGTGGATGCCAGGGGGCTCTGTTGCCGGACTGCTG 3480
 669  Q  L  M  A  R  L  D  H  P  N  I  V  R  V  L  G  A  T  Q  E  G  T  H  F  N  I  F  Q  E  W  M  P  G  G  S  V  A  G  L  L  708
3481 GACCAGTATGGTGCCTTCTCTGACACGGTCATCAAGAACTTCACCCGGCAGATCCTCTTGGGCGTGTCTTATCTCCATGACAACTGCATCATCCACAGAGACATCAAGGGAGCTAACCTG 3600
 709  D  Q  Y  G  A  F  S  D  T  V  I  K  N  F  T  R  Q  I  L  L  G  V  S  Y  L  H  D  N  C  I  I  H  R  D  I  K  G  A  N  L  748
3601 CTAGTTGACAGTACAGGGACCAGACTGAGGATTGCTGACTTTGGGACAGCAGCACGGCTGGCCACCAAGCTGACAGGAGCAGGGGAGTTCCAGGGACAGCTGCTGGGCACCATAGCCTTC 3720
 749  L  V  D  S  T  G  T  R  L  R  I  A  D  F  G  T  A  A  R  L  A  T  K  L  T  G  A  G  E  F  Q  G  Q  L  L  G  T  I  A  F  788
3721 ATGGCACCAGAAGTCCTACGAGGGGAGCAGTACGGGCGCTCCTGTGATGTCTGGAGTATCGGCTGTACGGTCATCGAGATGGGCACAGCCTCCCGCCGTGGAACGCTAATGCAGTAGACA 3840
 789  M  A  P  E  V  L  R  G  E  Q  Y  G  R  S  C  D  V  W  S  I  G  C  T  V  I  E  M  G  T  A  S  R  R  G  T  L  M  Q  *      826
3841 ACCATCTGGCTCTCATCTTCAGGATTGCGAGTTCCAGCGAGCCTCCCCCGCTGCCACAGAACTTCTCGCCCGGTCTGCGGGACCTGGTCCTGCGGTGTCTGGAACAGACCGGATCGGACC 3960
3961 GCCCGTCCACGAGGGAACTGCTACAGCACGCTGTCTTCACCGCACCCTGAGCACCATGGGAATCTACGTGGACTGGTACAACTGTGGAAATCATGTGGATTGACTTCTCAATTCTGTGAT 4080
4081 GTGATTTTGAAAAATCTGTGGAAAGAGAAAGTCATGACATGACAGGCCAGTTGAGATGGAAGTTCTTAAATTGGTCCGTGGACTCCATGTTGAAAAAATGGTTTCAGCCATCTTTTCTGG 4200
4201 CTTGTCACTGAGAAGTACAGGTTTGAAGAGACCTAGAACTAAAACAAGAGCTAAAAAGCAATACTCAACTTGGAGTGTAGTACTTACAACTGGAATGTAAGACTAACGAACGCCAAGTTA 4320
4321 GAGTGAGCACCATGGCTTAGAGGAGCACCATGGCTAGGTAGGAACCAGAAGGTTCAGGGCTCGAGTCCTAACATAGATAACCTCTTTGATATGAGGACTTGTTTCACTTGTTGAAACAAT 4440
4441 CTGGGAATGGCTGTCAATGTAGATTATTTTACATGCAATGTAAACTACTACTTTTAGTGTGTTTTCACTCTATACTCTGAGAAAACAATTGTAAAGTCCAGCATGTCTTACCAAACACGT 4560
4561 TTGGACTATCAGCTACTGTGTAAGCTACTGTGTGAACAGGTTGAGCCTGTTGTTTTATTTTAAACAGAGGCCTGTTATTCTGCACAGATTTGACAGGACTCTCAGCCAATCAGCTGGTTC 4680
4681 CATTTCTCAGACGATAATTTTGATTGGTCACATACAAGGCTGCGTCCTATTGGTCAGCCCCCTTGCCACTACATCTCAAACCTTGCCATAAACCATTGGGTCTTGAATGGCCGATATCTG 4800
4801 TCACCAGAAACTACAATGACACAAATACAGGTAGCTACTTTGTAATGGTCGTTGAACCAGAGCCGTAAGTACTGTACAGCCAGTATTACAACCAGGCCGCTTTTAGAAAGTATCTTTAAA 4920
4921 CATACACAACAGTTGTATGATTATTACACTGATGTTGCCTTCAGTTTTAATCTTCTGATCTAAGGTAACCACATTACCTTTGGACTTACAAATTTTGACAACTTTGAAAAAATTTGTACC 5040
5041 ATGTGGAAAGCTGGACTTTCTGTTGTGAACTATGGTAACTAACACATACCTGTTGTTTAATCTGTAATATGCTGTGCAGAGTTTTAAGTATTGTACTGGTGATGGCATATTAATTGCAGT 5160
5161 ATTTGAGACTAAGGAAGTAGAGCTTTCTTTTAATGGGAATCTTCCACCATTATTAAGAATAAGTGGTCTTAATTTGTAAGGATTACAGTGTTAAAGAAAATGTTTTTCTTAAAGAATTGT 5280
5281 GGAATACATGTACGTCAAGAATTGTATACTTCTTCCAATCTGGCAGCCATGATGTATATTCTTAGTCCCTTGGATCAGTATGTTCTGTTTCTGTATAGAGTCAACCTAGTAAGCTTTTCT 5400
5401 GCAGACTATATAGCATTATATAGATAAGAGTTTGAGTTGTTTTGAGGGAACCAAACTTTTCTAGTTCACAAAGCCTCTCTGTTAGTTGCATTTTAAGTTGACTGTCAAGGAGTTTGTTTT 5520
5521 GTTCTGATGATAACCAGAAAGGAAATTAGGAGACAGTATGTGGGTTGTGTGTAACTGCAGAGCAGTCAGTGAGGAGAAACTGTTGAACAGTTGAGCTACAGGAATGGCTCTGTGACAAGT 5640
5641 GGTGATGTCTACTCTGTCAGGATACAGAATAAAACTTCTTAATAACAAAAAAAAAAAA 5698
```

Figure S2 The detailed information of the *AmphiMEKK1*.

(a) The schematic diagram of the full-length cDNA of *AmphiMEKK1*. Lines represent UTRs, and boxes represent ORFs. (b) The detailed cDNA and protein sequence of *AmphiMEKK1*.The red-colored sequences represent protein-coding regions.