A

```
1     TATCAACGCAGAGTACATGGGACTTCTCGAAGCGCGCTTGCCGTTGCATCACCCTCCTTTGGGTTTTCCTCTAGT
76    TTCTGTCCTACCGTTTCCAGGATTCCAAAATGTTCGTCGGAGGCTTAGTTGGGCGTAACTTCACCAATGTCAGCC
1                                      M  F  V  G  G  L  V  G  R  N  F  T  N  V  S
151   ACGCAGTGTCTAGGCAGAGGCATTTCAGCATTTTATTAAAGAAACAAACCCCAGTTTTTGCTCAAGATGGACTTC
16    H  A  V  S  R  Q  R  H  F  S  I  L  L  K  K  Q  T  P  V  F  A  Q  D  G  L
226   AACAAAGAAACAAATCTGAGGGAGTTAAAGGTGCTGCCATTGGTATCGATCTTGGCACAACTAACTCCTGTGTTG
41    Q  Q  R  N  K  S  E  G  V  K  G  A  A  I  G  I  D  L  G  T  T  N  S  C  V
301   CTGTTATGGAAGGAAAGCAAGCAAAAGTTATTGAAAACGCAGAAGGATCCAGGACTACTCCCTCGGTTGTTGCAT
66    A  V  M  E  G  K  Q  A  K  V  I  E  N  A  E  G  S  R  T  T  P  S  V  V  A
376   TCAGCAAAGATGGAGAGCGCCTTGTGGGTATGCCGGCAAAACGCCAAGCTGTAACCAACTCAGCCAATACTTTTT
91    F  S  K  D  G  E  R  L  V  G  M  P  A  K  R  Q  A  V  T  N  S  A  N  T  F
451   ATGCAACCAAGCGCTTGATTGGCAGACGATTTGAGGATGCTGAAGTCAAAAAAGACATGAAAACAGTCTCATACA
116   Y  A  T  K  R  L  I  G  R  R  F  E  D  A  E  V  K  K  D  M  K  T  V  S  Y
526   AAATAGTGAAGGCATCTAATGGTGATGCTTGGGTACAAGCAACTGATGGTAAAATGTACTCACCCAGTCAAATAG
141   K  I  V  K  A  S  N  G  D  A  W  V  Q  A  T  D  G  K  M  Y  S  P  S  Q  I
601   GAGCATTCACATTAATGAAAATGAGGGAGACTGCTGAAAGTTACCTTAACACCCCTGTGAAGAATGCAGTTGTCA
166   G  A  F  T  L  M  K  M  R  E  T  A  E  S  Y  L  N  T  P  V  K  N  A  V  V
676   CAGTTCCTGCATACTTCAATGATTCTCAGAGACAGGCTACAAAAGATGCTGGCCAAATTGCTGGTTTAAATGTTT
191   T  V  P  A  Y  F  N  D  S  Q  R  Q  A  T  K  D  A  G  Q  I  A  G  L  N  V
751   TAAGAGTCATCAATGAACCAACCGCCGCTGCATTGGCTTACGGCATGGACAAGACTGAAGACAAAGTAATTGCTG
216   L  R  V  I  N  E  P  T  A  A  A  L  A  Y  G  M  D  K  T  E  D  K  V  I  A
826   TTTATGACCTCGGTGGTGGTACCTTTGATATTTCCATTTTGGAAATTCAGAAGGGAGTCTTTGAAGTCAAGTCAA
241   V  Y  D  L  G  G  G  T  F  D  I  S  I  L  E  I  Q  K  G  V  F  E  V  K  S
901   CTAATGGTGATACTTTCCTTGGTGGTGAAGACTTTGATAATACACTTGTGAATTTCTTAGTTGCTGAATTTAAGA
266   T  N  G  D  T  F  L  G  G  E  D  F  D  N  T  L  V  N  F  L  V  A  E  F  K
976   AAGAGCAAGGCCTTGACATCACCAAAGATCCTATGGCTATGCAGCGTCTTAAGGAGGCTGCTGAGAAAGCTAAAT
291   K  E  Q  G  L  D  I  T  K  D  P  M  A  M  Q  R  L  K  E  A  A  E  K  A  K
1051  GTGAACTTTCATCATCCATGCAGACAGACATTAATCTGCCTTATCTTACAATGGATGCTTCAGGACCTAAACACA
316   C  E  L  S  S  S  M  Q  T  D  I  N  L  P  Y  L  T  M  D  A  S  G  P  K  H
1126  TGAACCTGAAGCTGACTCGTTCCAAGTTTGAAACACTTGTAGATGGTCTTATCAAGAAAACTGTTGACCCTTGCA
341   M  N  L  K  L  T  R  S  K  F  E  T  L  V  D  G  L  I  K  K  T  V  D  P  C
1201  AGAAGGCTCTTCAGGATGGTGAGGTTGCCAAGTCTGATATCGGTGAAGTTCTTTTGGTTGGTGGTATGTCCCGAA
366   K  K  A  L  Q  D  G  E  V  A  K  S  D  I  G  E  V  L  L  V  G  G  M  S  R
1276  TGCCAAAGGTTCAACAAACAGTACAAGAAATTTTTGGTAGGCAGCCTAGCAGGTCAGTGAACCCTGACGAGGCTG
391   M  P  K  V  Q  Q  T  V  Q  E  I  F  G  R  Q  P  S  R  S  V  N  P  D  E  A
1351  TGGCTGTGGGTGCTGCTGTGCAGGGAGGTGTTTTGGCGGGAGATGTCACCGATGTCTTGTTGTTGGATGTTACCC
416   V  A  V  G  A  A  V  Q  G  G  V  L  A  G  D  V  T  D  V  L  L  L  D  V  T
1426  CTCTTTCACTTGGAATTGAAACTTTGGGTGGAGTTTTCACTCGACTCATTTCAAGAAATACCACTATCCCCACCA
441   P  L  S  L  G  I  E  T  L  G  G  V  F  T  R  L  I  S  R  N  T  T  I  P  T
1501  AGAAAAGCCAGGTCTTTTCTACTGCTGCTGATGGTCAAACGCAAGTTGAAATCAAGGTTCATCAAGGTGAACGTG
466   K  K  S  Q  V  F  S  T  A  A  D  G  Q  T  Q  V  E  I  K  V  H  Q  G  E  R
1576  AGATGGCCTCTGACAACAAGTTACTTGGACAGTTCACTCTTGTTGGTATCCCTCCTGCACCCCGTGGCGTTCCTC
491   E  M  A  S  D  N  K  L  L  G  Q  F  T  L  V  G  I  P  P  A  P  R  G  V  P
1651  AGATTGAGGTCACCTTTGATATTGATGCCAACGGCATTGTCCATGTATCAGCACGCGACAAGGGAACTGGCAAGG
516   Q  I  E  V  T  F  D  I  D  A  N  G  I  V  H  V  S  A  R  D  K  G  T  G  K
1726  AGCAACAGATTGTTATTCAATCATCTGGTGGATTGAGCAAAGATGAAATTGAGAACATGGTACGCAATGCAGAAC
541   E  Q  Q  I  V  I  Q  S  S  G  G  L  S  K  D  E  I  E  N  M  V  R  N  A  E
1801  AGTATGCTGCTCAAGACAAGGTGAAGAAGGACCGTGTTGAAGCAGTCAACCAGGCTGAGGGTATTATTCATGACA
566   Q  Y  A  A  Q  D  K  V  K  K  D  R  V  E  A  V  N  Q  A  E  G  I  I  H  D
1876  CAGAATCCAAAATGGATGAGTTCAAGGACCAATTACCATCCGATGAGTGTGACAAGCTTCGCGAGCAAATTACAA
591   T  E  S  K  M  D  E  F  K  D  Q  L  P  S  D  E  C  D  K  L  R  E  Q  I  T
1951  GTGTTCGCGACCTTTTGGCTAATAAGGAAGACTCCGACCCTGAGGAAATCCGCAAAGCAACTGGCAACCTCCAGC
616   S  V  R  D  L  L  A  N  K  E  D  S  D  P  E  E  I  R  K  A  T  G  N  L  Q
2026  AGGCATCACTTAAGCTTTTTGAAATGGCATACAAGAAGATGGCCGCTGAGAGGGACAGTGGAAGCAAAAGTGAGG
641   Q  A  S  L  K  L  F  E  M  A  Y  K  K  M  A  A  E  R  D  S  G  S  K  S  E
2101  GTTCATCAGAAAGCTCATCAGAGAGCACAGAAAACCAAGCGAAGGATGATAAGGATAAGGATGAGAAGAAGAACT
666   G  S  S  E  S  S  S  E  S  T  E  N  Q  A  K  D  D  K  D  K  D  E  K  K  N
2176  AAGGAACATTTAGTTCTCTCCTCACCAGGTGTGTCCTTCATACCAAATGTCAAAAGTGGACTGAATAATTTCTTT
691   *
2251  TGACTTGGTTGGTGGGCAGTTTTAGTGATATTGTCTTTGTGTGAAAGTTTGCATTTTACTCAGACTGAGTGAATT
2326  GCTGGATATGTCATCAGGGTGATTTGAGAGGAATGTGGAGATTAGTAGCAATATTATTGCACAGGTTATCAAATG
2401  TGCTGTGCACTTTTTCTTGTGTCTGTACAAAGTATCTCTGTTCTCGTTCAAATAGCCCACCATATTATTTTTGAA
2476  GATGTGTTGGTGTGCCTAGTTCCAATAGTTACGCATTTGACGGTAAGAATGTGTGTAAGAGTCTGTGAATGTATG
2551  TGTGTGTGTGTCAGTTGAGGGGTGCCAATCAGCAGGAAAGTTGCTGTTTGCTAGATGCCAACAGTTTGAGGACAG
2626  TGATCTCTTGAACCAGTATCTTTAATTTTTAATGTGCTGACTTAGTTATTGCTTCTCACTGTATGAAATTTTGAG
2701  AAGCCCGGATTCTGTCTTAATCTTCTGAAAATTGTATATACAATGTTCACAGTTCTCTATAGACGAGGTGGCTGT
2776  TGATATTTTTAGTTGACTATTGTTTTCAGATTGTTTCTAGAGCAGTATGCTTAAATAATTTGGACTGTCCTCGAA
2851  CTGTTTGTTAGTCATTGTCTAAACTTTATTAGTATGTTACCGTAGAGTCTAGTTTCATGTATCTTGTTTGCCAAG
2926  GAATCTGCAGTCATCTTTGTTTCCTATTTTGTTACAGTTATTGTTATAAAAGAATATGTCATCCCTACACCAGAA
3001  ATAAAATTAAGCATCATTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
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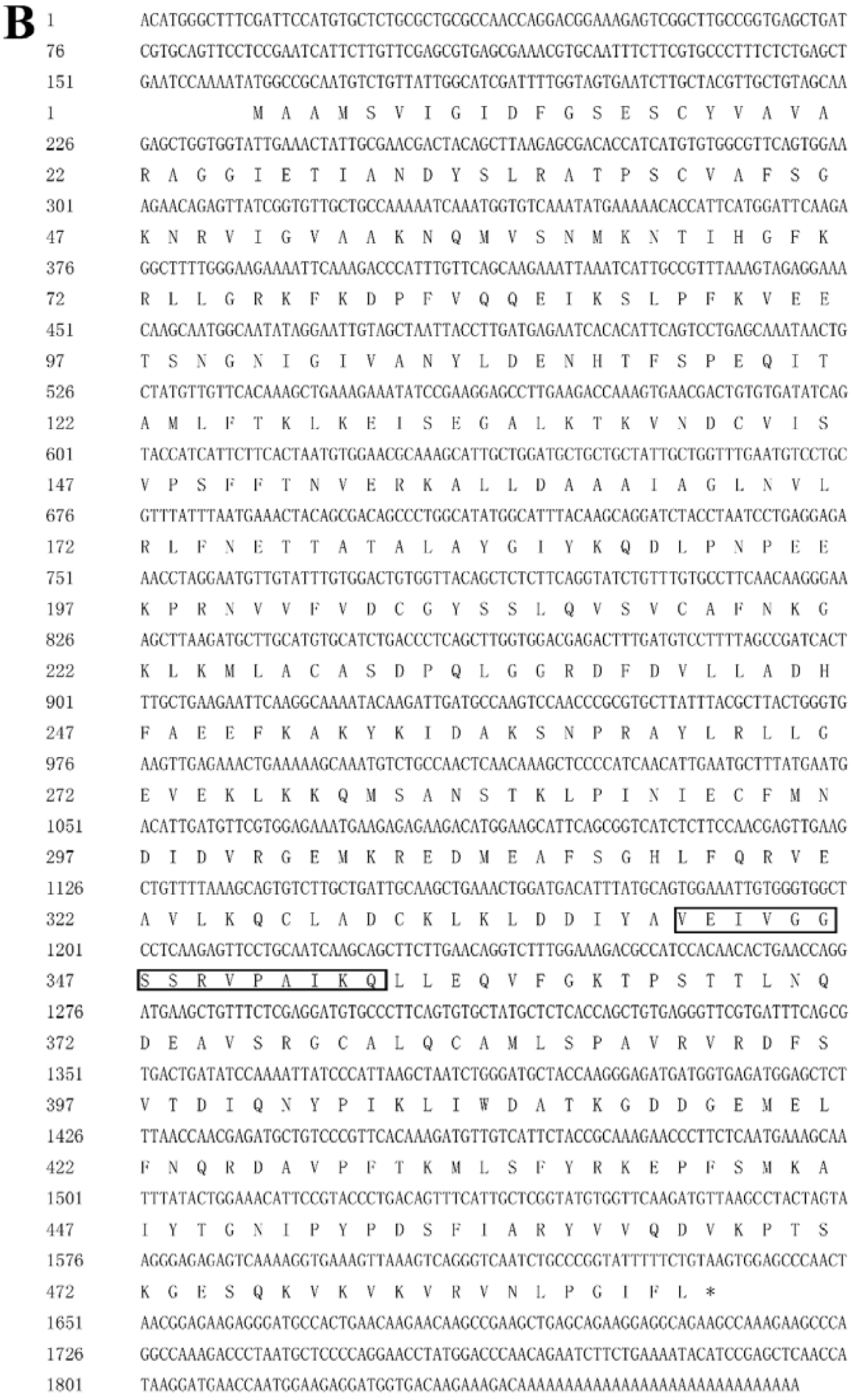
Appendix A Nucleotide sequence and deduced amino acids for *Fohsc704*. Signature sequences or motifs for *Fo*HSP704 were selected in the box. The putative polyadenylation signals (AATAAA) for *Fohsc704* were underlined.



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B 1     ACATGGGCTTTCGATTCCATGTGCTCTGCGCTGCGCCAACCAGGACGGAAAGAGTCGGCTTGCCGGTGAGCTGAT
  76    CGTGCAGTTCCTCCGAATCATTCTTGTTCGAGCGTGAGCGAAACGTGCAATTTCTTCGTGCCCTTTCTCTGAGCT
  151   GAATCCAAAATATGGCCGCAATGTCTGTTATTGGCATCGATTTTGGTAGTGAATCTTGCTACGTTGCTGTAGCAA
  1                 M  A  A  M  S  V  I  G  I  D  F  G  S  E  S  C  Y  V  A  V  A
  226   GAGCTGGTGGTATTGAAACTATTGCGAACGACTACAGCTTAAGAGCGACACCATCATGTGTGGCGTTCAGTGGAA
  22    R  A  G  G  I  E  T  I  A  N  D  Y  S  L  R  A  T  P  S  C  V  A  F  S  G
  301   AGAACAGAGTTATCGGTGTTGCTGCCAAAAATCAAATGGTGTCAAATATGAAAAACACCATTCATGGATTCAAGA
  47    K  N  R  V  I  G  V  A  A  K  N  Q  M  V  S  N  M  K  N  T  I  H  G  F  K
  376   GGCTTTTGGGAAGAAAATTCAAAGACCCATTTGTTCAGCAAGAAATTAAATCATTGCCGTTTAAAGTAGAGGAAA
  72    R  L  L  G  R  K  F  K  D  P  F  V  Q  Q  E  I  K  S  L  P  F  K  V  E  E
  451   CAAGCAATGGCAATATAGGAATTGTAGCTAATTACCTTGATGAGAATCACACATTCAGTCCTGAGCAAATAACTG
  97    T  S  N  G  N  I  G  I  V  A  N  Y  L  D  E  N  H  T  F  S  P  E  Q  I  T
  526   CTATGTTGTTCACAAAGCTGAAAGAAATATCCGAAGGAGCCTTGAAGACCAAAGTGAACGACTGTGTGATATCAG
  122   A  M  L  F  T  K  L  K  E  I  S  E  G  A  L  K  T  K  V  N  D  C  V  I  S
  601   TACCATCATTCTTCACTAATGTGGAACGCAAAGCATTGCTGGATGCTGCTGCTATTGCTGGTTTGAATGTCCTGC
  147   V  P  S  F  F  T  N  V  E  R  K  A  L  L  D  A  A  A  I  A  G  L  N  V  L
  676   GTTTATTTAATGAAACTACAGCGACAGCCCTGGCATATGGCATTTACAAGCAGGATCTACCTAATCCTGAGGAGA
  172   R  L  F  N  E  T  T  A  T  A  L  A  Y  G  I  Y  K  Q  D  L  P  N  P  E  E
  751   AACCTAGGAATGTTGTATTTGTGGACTGTGGTTACAGCTCTCTTCAGGTATCTGTTTGTGCCTTCAACAAGGGAA
  197   K  P  R  N  V  V  F  V  D  C  G  Y  S  S  L  Q  V  S  V  C  A  F  N  K  G
  826   AGCTTAAGATGCTTGCATGTGCATCTGACCCTCAGCTTGGTGGACGAGACTTTGATGTCCTTTTAGCCGATCACT
  222   K  L  K  M  L  A  C  A  S  D  P  Q  L  G  G  R  D  F  D  V  L  L  A  D  H
  901   TTGCTGAAGAATTCAAGGCAAAATACAAGATTGATGCCAAGTCCAACCCGCGTGCTTATTTACGCTTACTGGGTG
  247   F  A  E  E  F  K  A  K  Y  K  I  D  A  K  S  N  P  R  A  Y  L  R  L  L  G
  976   AAGTTGAGAAACTGAAAAAGCAAATGTCTGCCAACTCAACAAAGCTCCCCATCAACATTGAATGCTTTATGAATG
  272   E  V  E  K  L  K  K  Q  M  S  A  N  S  T  K  L  P  I  N  I  E  C  F  M  N
  1051  ACATTGATGTTCGTGGAGAAATGAAGAGAGAAGACATGGAAGCATTCAGCGGTCATCTCTTCCAACGAGTTGAAG
  297   D  I  D  V  R  G  E  M  K  R  E  D  M  E  A  F  S  G  H  L  F  Q  R  V  E
  1126  CTGTTTTAAAGCAGTGTCTTGCTGATTGCAAGCTGAAACTGGATGACATTTATGCAGTGGAAATTGTGGGTGGCT
  322   A  V  L  K  Q  C  L  A  D  C  K  L  K  L  D  D  I  Y  A  V  E  I  V  G  G
  1201  CCTCAAGAGTTCCTGCAATCAAGCAGCTTCTTGAACAGGTCTTTGGAAAGACGCCATCCACAACACTGAACCAGG
  347   S  S  R  V  P  A  I  K  Q  L  L  E  Q  V  F  G  K  T  P  S  T  T  L  N  Q
  1276  ATGAAGCTGTTTCTCGAGGATGTGCCCTTCAGTGTGCTATGCTCTCACCAGCTGTGAGGGTTCGTGATTTCAGCG
  372   D  E  A  V  S  R  G  C  A  L  Q  C  A  M  L  S  P  A  V  R  V  R  D  F  S
  1351  TGACTGATATCCAAAATTATCCCATTAAGCTAATCTGGGATGCTACCAAGGGAGATGATGGTGAGATGGAGCTCT
  397   V  T  D  I  Q  N  Y  P  I  K  L  I  W  D  A  T  K  G  D  D  G  E  M  E  L
  1426  TTAACCAACGAGATGCTGTCCCGTTCACAAAGATGTTGTCATTCTACCGCAAAGAACCCTTCTCAATGAAAGCAA
  422   F  N  Q  R  D  A  V  P  F  T  K  M  L  S  F  Y  R  K  E  P  F  S  M  K  A
  1501  TTTATACTGGAAACATTCCGTACCCTGACAGTTTCATTGCTCGGTATGTGGTTCAAGATGTTAAGCCTACTAGTA
  447   I  Y  T  G  N  I  P  Y  P  D  S  F  I  A  R  Y  V  V  Q  D  V  K  P  T  S
  1576  AGGGAGAGAGTCAAAAGGTGAAAGTTAAAGTCAGGGTCAATCTGCCCGGTATTTTTCTGTAAGTGGAGCCCAACT
  472   K  G  E  S  Q  K  V  K  V  K  V  R  V  N  L  P  G  I  F  L  *
  1651  AACGGAGAAGAGGGATGCCACTGAACAAGAACAAGCCGAAGCTGAGCAGAAGGAGGCAGAAGCCAAAGAAGCCCA
  1726  GGCCAAAGACCCTAATGCTCCCCAGGAACCTATGGACCCAACAGAATCTTCTGAAAATACATCCGAGCTCAACCA
  1801  TAAGGATGAACCAATGGAAGAGGATGGTGACAAGAAAGACAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
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Appendix B Nucleotide sequence and deduced amino acids for *Fohsc705*. Sequences or motifs for *Fo*HSP705 were selected in the box.

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FoHsc704  .MFVGGLVGR...NFTNVSHAVSRQRHFSILLK......KQTPVFAQDGIQQRNKSEGVKGAAIGIDLGT   60
ZnHsc70   MLLAGRIIGKKAFDCTSFTFNVVGKQEFSTLLK...KTASSTCVGQHNDVQRRHKSEGVKGAVIGIDLGT   67
ArHsc70   MLTAARLLSR...GCTGVVSDITRKQNFSTIIKNAAAPTMSMAQRQTDLHQYRYKSEGVKGAVIGIDLGT   67
LnHsc70   MLTAARLLNR...NYAGVACDIARKQQFSTILKNVAAPTVTGSHRLTDFQQYRHKSEGVKGAVIGIDLGT   67
EmHsc70   MLTAARLLTR...SCSNITCEITRKQQFSTILKNVAAPTFSVSQRFTDLHQYRHKSEGVKGAVIGIDLGT   67
EcHsc70   MLSAARIFTRKAYDCTKFGYDVANKRNFSCLIN...STTEKYGLHPKYDNQLRYKSEGVKGAVIGIDLGT   67

FoHsc704  TNSCVAVMEGKQAKVIENAEGSRTTPSVVAFSKDGERLVGMPAKRQAVTNSANTFYATKRLIGRRFEDAE  130
ZnHsc70   TNSCVAVMEGKQAKVIENAEGSRTTPSVVAFTKDGERLVGMPAKRQAVTNSANTFYATKRLIGRRFNDSE  137
ArHsc70   TFSCVAVMEGKQAKVIENAEGSRTTPSYVAFTKDGERLVGMPAKRQAVTNSANTFYATKRLIGRRFEDAE  137
LnHsc70   TFSCVAVMEGKQAKVIENAEGSRTTPSYVAFTKDDERLVGMPAKRQAVTNSANTFYATKRLIGRRFEDAE  137
EmHsc70   TFSCVAVMEGKQAKVIENAEGSRTTPSYVAFTKEGERLVGMPAKRQAVTNSSNTFYATKRLIGRKFEDPE  137
EcHsc70   TNSCVAVMEGKQAKVIENSEGSRTTPSVVAFSKDGERLVGMPAKRQAVTNSANTFYATKRLIGRRFDDPE  137

FoHsc704  VKKDMKTVSYKIVKASNGDAWVQATDGKMYSPSQIGAFTLMKMRETAESYLNTPVKNAVVTVPAYFNDSQ  200
ZnHsc70   VKKDMKTLSYKIVQASNGDAWVEGTDKKMYSPSQIGAFVLMKMKETAEAYLGTAIKNAVVTVPAYFNDSQ  207
ArHsc70   VKKDMKSVSYKIVRASNGDAWVQGGDGKMYSPSQIGAFVLMKMKETAEAYLNTPVKNAVVTVPAYFNDSQ  207
LnHsc70   VKKDMKSVTYKIVKASNGDAWVQGADGKMYSPSQIGAFVLMKMKETAAAYLNTPVKNAVITVPAYFNDSQ  207
EmHsc70   VKKDMKSVSYKIVRASNGDAWVQGGDGKMYSPSQIGAFVLMKMKETAESYLSTSVKNAVITVPAYFNDSQ  207
EcHsc70   VKKDMSNVSYKVVKATNGDAWVQGSDGKMYSPSQIGAFVLMKMRETAEAYLNTKVKNAVITVPAYFNDSQ  207

FoHsc704  RQATKDAGQIAGLNVLRVINEPTAAALAYGMDKTEDKVIAVYDLGGGTFDISILEIQKGVFEVKSTNGDT  270
ZnHsc70   RQATKDAGQIAGLNVLRVINEPTAAALAYGMDKTEDKVIAVYDLGGGTFDISVLEIQKGVFEVKSTNGDT  277
ArHsc70   RQATKDAGQIAGLNVLRVINEPTAAALAYGMDKTEDKIIAVYDLGGGTFDVSILEIQKGVFEVKSTNGDT  277
LnHsc70   RQATKDAGQIAGLNVLRVINEPTAAALAYGMDKQEDKIIAVYDLGGGTFDISILEIQKGVFEVKSTNGDT  277
EmHsc70   RQATKDAGQIAGLNVLRVINEPTAAALAYGMDKTEDKIIAVYDLGGGTFDISILEIQKGVFEVKSTNGDT  277
EcHsc70   RQATKDAGQIAGLNVLRVINEPTAAALAYGMDKTEDKIIAVYDLGGGTFDISILEIQKGVFEVKSTNGDT  277

FoHsc704  FLGGEDFDNTLVNFLVAEFKKEQGLDITKDPMAMQRLKEAAEKAKCELSSSMQTDINLPYLTMDASGPKH  340
ZnHsc70   FLGGEDFDNTLVNFLASEFKKEQGIDVAKDPMAMQRLKEAAEKAKIELSSSLQTDINLPYLTMDSSGPKH  347
ArHsc70   FLGGEDFDNALVNYLVAEFKKDQGLDVTKDAMAMQRLKEAAEKAKIELSSSSQTDVNLPYLTMDSSGPKH  347
LnHsc70   FLGGEDFDNTLVNYLVSEFKKEQGLDVTKDPMAMQRLKEAAEKAKIELSSSLQTDINLPYLTMDSSGPKH  347
EmHsc70   FLGGEDFDNALVNYLVLEFKKDVCIDVTKDTMAMQRLKEAAEKAKIELSSSLQTDINLPYLTMDSSGPKH  347
EcHsc70   FLGGEDFDNMLVNHLVSEFKKEQGTDISKDPMAMQRLKEAAEKAKIELSSSAQTDINLPYLTMDASGPKH  347

FoHsc704  MNLKLTRSKFETLVDGLIKKTVDPCKKALQDGEVAKSDIGEVLLVGGMSRMPKVQQTVQEIFGRQPSRSV  410
ZnHsc70   MNLKLTRSKFESLVGELIKKTISPCQKALSDAEVSKSDIGDVLLVGGMTRMPKVQSTVQEIFGRQPSRSV  417
ArHsc70   LNLKLSRSKFESLVGDLIKRTLQPCKKALSDAEVSKSDIGEVLLVGGMTRMPKVQQTVQEIFGKQPSKAV  417
LnHsc70   LNLKLSRSKFESLVNDLIKRTIQPCQKALSDAEVMKSDIGEVLLVGGMTRVPKVQQTVQEIFGRQPSKAV  417
EmHsc70   LNLKLSRSKFESLVGDLIKRTLQPCQKALSDAEVSKSDIGEVLLVGGMTRVPKVQQTVQEIFGRQPSKAV  417
EcHsc70   MNLKLSRSKFESLVGDLIKRTIQPCQKALKDAEVSKNEIGEILLVGGMTRMPKVQSTVQEIFGKQPSRAV  417

FoHsc704  NPDEAVAVGAAVQGGVLAGDVTDVLLLDVTPLSLGIETLGGVFTRLISRNTTIPTKKSQVFSTAADGQTQ  480
ZnHsc70   NPDEAVAVGAAIQGGVLAGDVTDVLLLDVTPLSLGIETLGGVFTRLITRNTTIPTKKSQVFSTAADGQTQ  487
ArHsc70   NPDEAVAVGAAVQGGVLAGDVTDVLLLDVTPLSLGIETLGGVFTRLISRNTTIPTKKSQVFSTAADGQTQ  487
LnHsc70   NPDEAVAVGAAVQGGVLAGDVTDVLLLDVTPLSLGIETLGGVFTRLISRNTTIPTKKGQVFSTAADGQTQ  487
EmHsc70   NPDEAVAVGAAVQGGVLAGDVTDVLLLDVTPLSLGIETLGGVFTRLISRNTTIPTKKSQVFSTAADGQTQ  487
EcHsc70   NPDEAVAVGAAVQGGVLAGDVTDVLLLDVTPLSLGIETLGGVFTRLITRNTTIPTKKSQVFSTAADGQTQ  487

FoHsc704  VEIKVHQGEREMASDNKLLGQFTLVGIPPAPRGVPQIEVTFDIDANGIVHVSARDKGTGKEQQIVIQSSG  550
ZnHsc70   VEIRVHQGEREMASDNKLLGQFTLVGIPPAPRGVPQIEVTFDIDANGIVHVSARDKGTGKEQQIVIQSSG  557
ArHsc70   VEIKVHQGEREMAGDNKLLGQFTLVGIPPAPRGVPQIEVTFDIDANGIVHVSARDKGTGKEQQIVIQSSG  557
LnHsc70   VEIKVHQGEREMASDNKLLGQFSLIGIPPAPRGVPQIEVTFDIDANGIVHVSARDKGTGKEQQIVIQSSG  557
EmHsc70   VEIKVHQGEREMASDNKLLGQFTLIGIPPAPRGVPQIEVTFDIDANGIVHVSARDKGTGKEQQIVIQSSG  557
EcHsc70   VEIKVHQGEREMAADNKLLGQFSLVGIPPAPRGVPQIEVTFDIDANGIVHVSARDKGTGKEQQIVIQSSG  557

FoHsc704  GLSKDEIENMVRNAEQYAAQDKVKKDRVEAVNQAEGIIHDTESKMDEFKDQLPSDECDKLREQITSVRDL  620
ZnHsc70   GLSKDEIENMVRKAETYAAQDKVKKERVEAVNQAEGIIHDTESKMNEFKDQLPKEECDKLQEQIAQVREV  627
ArHsc70   GLSKDEIENMVKKAEQYAKEDRVKKDRVEAVNQAEGIMHDTESKMEEFKSQLPAEECEKLKEQVAKVRET  627
LnHsc70   GLSKDEIENMVKNAEQYAKADRIKKERVEAINQAEGIIHDTESKLEEFKAQLPQEECDKLKELVGKLRET  627
EmHsc70   GLSKDEIENMVKNAEQYAKQDKIKKDRVEAVNQAEGIIHDTEAKLEEFKAQLPQDECDKLRELVAKVRET  627
EcHsc70   GLSKDEIENMIRRAEEYAKEDKVRKERVEAINQAEGIVHDTETKMEEYKDQLPKEECDKLKEEIAKVREI  627

FoHsc704  LANKEDSLPEEIRKATGNLQQASLKLFEMAYKKMAAERDSGSKSEGSSESSSESTENQAKDDKDKDEKKN  690
ZnHsc70   VSKKDETSPEEIRKLTDALQQASLKLFEMAYKKMAAERESSS......GSSSDSSGQTSEEKQEKKEEKN  691
ArHsc70   LANKDDTDPEEIKKQTNELQQASLKLFEMAYKKMAAERESSS......GSSDQSS.QQEGEEEKKKEEKN  690
LnHsc70   LAKKDDVEPEEIKKQTNELQQASLKLFEMAYKKMAAERE..........SQNQSQ.QEPEG..EKKEEKN  684
EmHsc70   LAKKDDTAPEEIKSQTNELQQASLKLFEMAYKKMAAEREGQ........SQSQSQ.QQQEDGPEKKEEKN  688
EcHsc70   LAKKDTADPEEIRQVTSTLQQSSLKLFEMAYKKMAAERESGS......GSSSGEQ.QQEEP.PKEQKEKN  689
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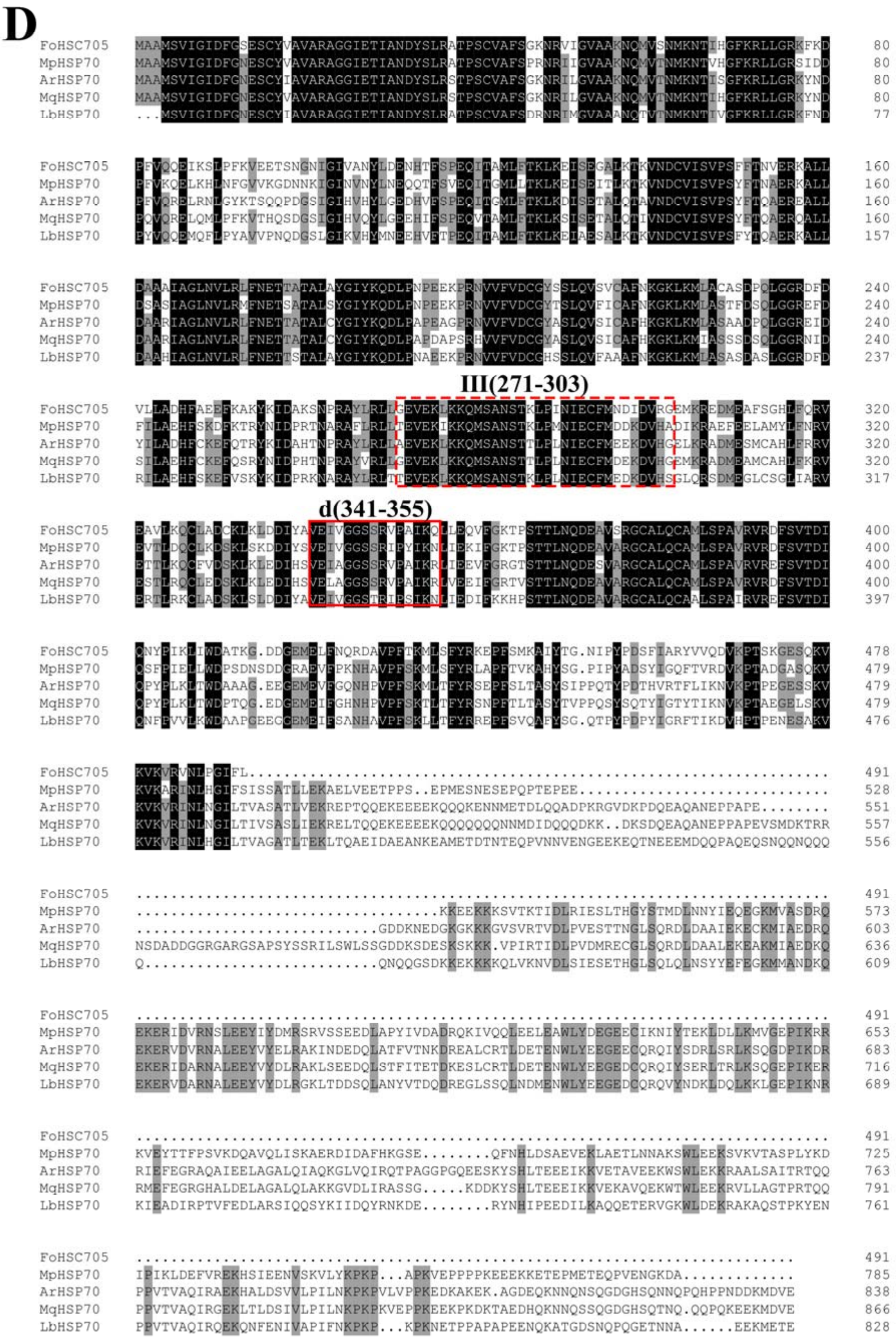
Appendix C Multiple alignment of deduced amino acids of five HSPs in *Frankliniella occidentalis* and the counterparts from other species. Note: The sequence of *Fo*HSC704 was compared with those of *Zootermopsis nevadensis* (KDR08641.1), *Athalia rosae* (XP_012264348.1), *Lasius niger* (KMQ94354.1), *Eufriesea mexicana* (OAD62568.1), and *Epicauta chinensis* (AHK26790.1). 4354.1), *Eufriesea mexicana* (OAD62568.1), and *Epicauta chinensis* (AHK26790.1). The a, b and c sequences in red solid boxes are highly variable regions. Ⅰ represents a putative ATP/GTP-binding site and Ⅱ represents EF-hand (EFh) domain. Identical amino acids were shown in black boxes and similar amino acids were highlighted in gray. Gaps have been introduced to permit alignment.


D
FoHSC705 MAAMSVIGIDFGSESCYVAVARAGGIETIANDYSLRATPSCVAFSGKNRVIGVAAKNQMVSNMKNTIHGFKRLLGRKFKD 80
MpHSP70 MAAMSVIGIDFGNESCYVAVARAGGIETIANDYSLRATPSCVAFSPRNRIIGVAAKNQMVTNMKNTVHGFKRLLGRSIDD 80
ArHSP70 MAAMSVIGIDFGNESCYIAVARAGGIETIANDYSLRSTPSCVAFSGKNRILGVAAKNQMVTNMKNTISGFKRLLGRKYND 80
MqHSP70 MAAMSVIGIDFGNESCYVAVARAGGIETIANDYSLRSTPSCVAFSGKNRILGVAAKNQMVTNMKNTIHGFKRLLGRKYND 80
LbHSP70 ...MSVIGIDFGNESCYIAVARAGGIETIANDYSLRATPSCVAFSDRNRIMGVAAANQTVTNMKNTIVGFKRLLGRKFND 77
FoHSC705 PFVQQEIKSLPFKVEETSNGNIGIVANYLDENHTFSPEQITAMLFTKLKEISEGALKTKVNDCVISVPSFFTNVERKALL 160
MpHSP70 PFVKQELKHLNFGVVKGDNNKIGINVNYLNEQQTFSVEQITGMLLTKLKEISEITLKTKVNDCVISVPSYFTNAERKALL 160
ArHSP70 PFVQRELRNLGYKTSQQPDGSIGIHVHYLGEDHVFSPEQITGMLFTKLKDISETALQTAVNDCVISVPSYFTQAEREALL 160
MqHSP70 PQVQRELQMLPFKVTHQSDGSIGIHVQYLGEEHIFSPEQVTAMLFTKLKSISETALQTIVNDCVISVPSYFTQAERQALL 160
LbHSP70 PYVQQEMQFLPYAVVPNQDGSLGIKVHYMNEEHVFTPEQITAMLFTKLKEIAESALKTKVNDCVISVPSFYTQAERKALL 157
FoHSC705 DAAAIAGLNVLRLFNETTATALAYGIYKQDLPNPEEKPRNVVFVDCGYSSLQVSVCAFNKGKLKMLACASDPQLGGRDFD 240
MpHSP70 DSASIAGLNVLRMFNETSATALSYGIYKQDLPNPEEKPRNVVFVDCGYTSLQVFICAFNKGKLKMLASTFDSQLGGREFD 240
ArHSP70 DAARIAGLNVLRLFNETTATALCYGIYKQDLPAPEAGPRNVVFVDCGYASLQVSICAFHKGKLKMLASAADPQLGGREID 240
MqHSP70 DAARIAGLNVLRLFNETTATALCYGIYKQDLPAPDAPSRHVVFVDCGYASLQVSICAFHKGKLKMIASSSDSQLGGRNID 240
LbHSP70 DAAHIAGLNVLRLFNETTSTALAYGIYKQDLPNAEEKPRNVVFVDCGHSSLQVFAAAFNKGKLKMLASASDASLGGRDFD 237
III(271-303)
FoHSC705 VLLADHFAEEFKAKYKIDAKSNPRAYLRLLGEVEKLKKQMSANSTKLPINIECFMNDIDVRGEMKREDMEAFSGHLFQRV 320
MpHSP70 FILAEHFSKDFKTRYNIDPRTNARAFLRLLTEVEKIKKQMSANSTKLPMNIECFMDDKDVHADIKRAEFEELAMYLFNRV 320
ArHSP70 YILADHFCKEFQTRYKIDAHTNPRAYLRLLAEVEKLKKQMSANSTTLPLNIECFMEEKDVHGELKRADMESMCAHLFRRV 320
MqHSP70 SILAEHFCKEFQSRYNIDPHTNPRAYVRLLGEVEKLKKQMSANSTTLPLNIECFMDEKDVHGEMKRADMEAMCAHLFKRV 320
LbHSP70 RILAEHFSKEFVSKYKIDPRKNARAYLRLTTEVEKLKKQMSANSTKLPLNIECFMEDKDVHSGLQRSDMEGLCSGLIARV 317
d(341-355)
FoHSC705 EAVLKQCLADCKLKLDDIYAVEIVGGSSRVPAIKQLLEQVFGKTPSTTLNQDEAVSRGCALQCAMLSPAVRVRDFSVTDI 400
MpHSP70 EVTLDQCLKDSKLSKDDIYSVEIVGGSSRIPYIKNLIEKIFGKTPSTTLNQDEAVARGCALQCAMLSPAVRVRDFSVTDI 400
ArHSP70 ETTLKQCFVDSKLKLEDIHSVEIAGGSSRVPAIKRLIEEVFGRGTSTTLNQDESVARGCALQCAMLSPAVRVREFSVTDI 400
MqHSP70 ESTLRQCLEDSKLKLEDIHSVELAGGSSRVPAIKRLVEEIFGRTVSTTLNQDEAVARGCALQCAMLSPAVRVRDFSVTDI 400
LbHSP70 ERTLRKCLADSKLSLDDIYAVEIVGGSTRIPSIKNLIEDIFKKHPSTTLNQDEAVARGCALQCAALSPAIRVREFSVTDI 397
FoHSC705 QNYPIKLIWDATKG.DDGEMELFNQRDAVPFTKMLSFYRKEPFSMKAIYTG.NIPYPDSFIARYVVQDVKPTSKGESQKV 478
MpHSP70 QSFPIELLWDPSDNSDDGRAEVFPKNHAVPFSKMLSFYRLAPFTVKAHYSG.PIPYADSYIGQFTVRDVKPTADGASQKV 479
ArHSP70 QPYPLKLTWDAAAG.EEGEMEVFGQNHPVPFSKMLTFYRSEPFSLTASYSIPPQTYPDTHVRTFLIKNVKPTPEGESSKV 479
MqHSP70 QPYPLKLTWDPTQG.EDGEMEIFGHNHPVPFSKTLTFYRSNPFTLTASYTVPPQSYSQTYIGTYTIKNVKPTAEGELSKV 479
LbHSP70 QNFPVVLKWDAAPGEEGGEMEIFSANHAVPFSKLLTFYRREPFSVQAFYSG.QTPYPDPYIGRFTIKDVHPTPENESAKV 476
FoHSC705 KVKVRVNLPGIFL.. 491
MpHSP70 KVKARINLHGIFSISSATLLEKAELVEETPPS..EPMESNESEPQPTEPEE.............................. 528
ArHSP70 KVKVRINLNGILTVASATLVEKREPTQQEKEEEEKQQQKENNMETDLQQADPKRGVDKPDQEAQANEPPAPE........ 551
MqHSP70 KVKVRINLNGILTIVSASLIEKRELTQQEKEEEEKQQQQQQNNMDIDQQQDKK..DKSDQEAQANEPPAPEVSMDKTRR 557
LbHSP70 KVKVRINLHGILTVAGATLTEKLTQAEIDAEANKEAMETDTNTEQPVNNVENGEEKEQTNEEEMDQQPAQEQSNQQNQQQ 556
FoHSC705 491
MpHSP70 ...................................KKEEKKKSVTKTIDLRIESLTHGYSTMDLNNYIEQEGKMVASDRQ 573
ArHSP70 ............................GDDKNEDGKGKKKGVSVRTVDLPVESTTNGLSQRDLDAAIEKECKMIAEDRQ 603
MqHSP70 NSDADDGGRGARGSAPSYSSRILSWLSSGDDKSDESKSKKK.VPIRTIDLPVDMRECGLSQRDLDAALEKEAKMIAEDKQ 636
LbHSP70 Q...........................QNQQGSDKKEKKKKQLVKNVDLSIESETHGLSQLQLNSYYEFEGKMMANDKQ 609
FoHSC705 491
MpHSP70 EKERIDVRNSLEEYIYDMRSRVSSEEDLAPYIVDADRQKIVQQLEELEAWLYDEGEECIKNIYTEKLDLLKMVGEPIKRR 653
ArHSP70 EKERVDVRNALEEYVYELRAKINDEDQLATFVTNKDREALCRTLDETENWLYEEGEECQRQIYSDRLSRLKSQGDPIKDR 683
MqHSP70 EKERIDARNALEEYVYDLRAKLSEEDQLSTFITETDKESLCRTLDETENWLYEEGEDCQRQIYSERLTRLKSQGEPIKER 716
LbHSP70 EKERVDARNALEEYVYDLRGKLTDDSQLANYVTDQDREGLSSQLNDMENWLYEEGEDCQRQVYNDKLDQLKKLGEPIKNR 689
FoHSC705 491
MpHSP70 KVEYTTFPSVKDQAVQLISKAERDIDAFHKGSE........QFNHLDSAEVEKLAETLNNAKSWLEEKSVKVTASPLYKD 725
ArHSP70 RIEFEGRAQAIEELAGALQIAQKGLVQIRQTPAGGPGQEESKYSHLTEEEIKKVETAVEEKWSWLEKKRAALSAITRTQQ 763
MqHSP70 RMEFEGRGHALDELAGALQLAKKGVDLIRASSG.....KDDKYSHLTEEEIKKVEKAVQEKWTWLEEKRVLLAGTPRTQQ 791
LbHSP70 KIEADIRPTVFEDLARSIQQSYKIIDQYRNKDE........RYNHIPEEDILKAQQETERVGKWLDEKRAKAQSTPKYEN 761
FoHSC705 491
MpHSP70 IPIKLDEFVREKHSIEENVSKVLYKPKP...APKVEPPPPKEEEKKETEPMETEQPVENGKDA............. 785
ArHSP70 PPVTVAQIRAEKHALDSVVLPILNKPKPVLVPPKEDKAKEK.AGDEQKNNQNSQGDGHSQNNQPQHPPNDDKMDVE 838
MqHSP70 PPVTVAQIRGEKLTLDSIVLPILNKPKPKVEPPKEEKPKDKTAEDHQKNNQSSQGDGHSQTNQ.QQPQKEEKMDVE 866
LbHSP70 PPVTVAQIRQEKQNFENIVAPIFNKPKP...KPKNETPPAPAPEENQKATGDSNQPQGETNNA......EEKMETE 828

Appendix D Multiple alignment of deduced amino acids of five HSPs in *Frankliniella occidentalis* and the counterparts from other species. Note: *Fo*HSP705 was compared with those of *Myzus persicae* (XP_022174838.1), *Athalia rosae* (XP_020709814.1), *Melipona quadrifasciata* (KOX73871.1), and *Liposcelis bostrychophila* (AKP54258.1). The d sequence in red solid box is a typical feature of the HSP70 family and Ⅲ represents Thymopoietin domain. Identical amino acids were shown in black boxes and similar amino acids were highlighted in gray. Gaps have been introduced to permit alignment.