

## **Supplementary Information**

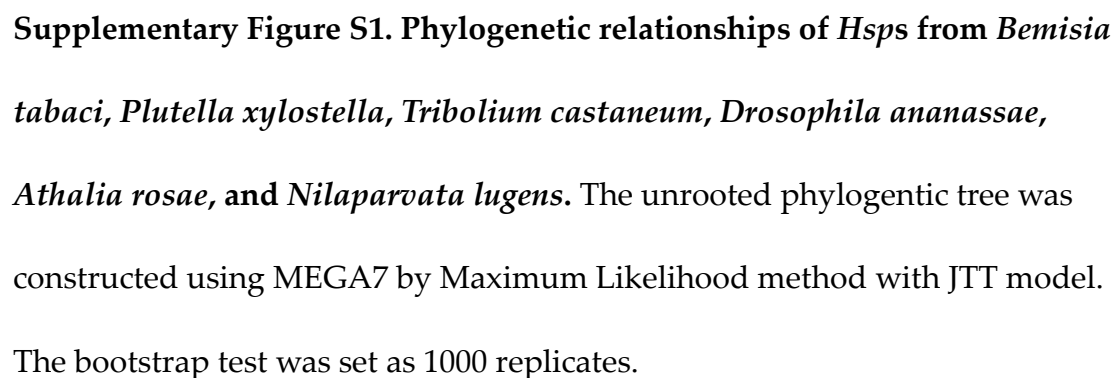
### **Genome-wide identification and analysis of Hsp gene superfamily in *Bemisia tabaci* and expression patterns analysis under heat shock**

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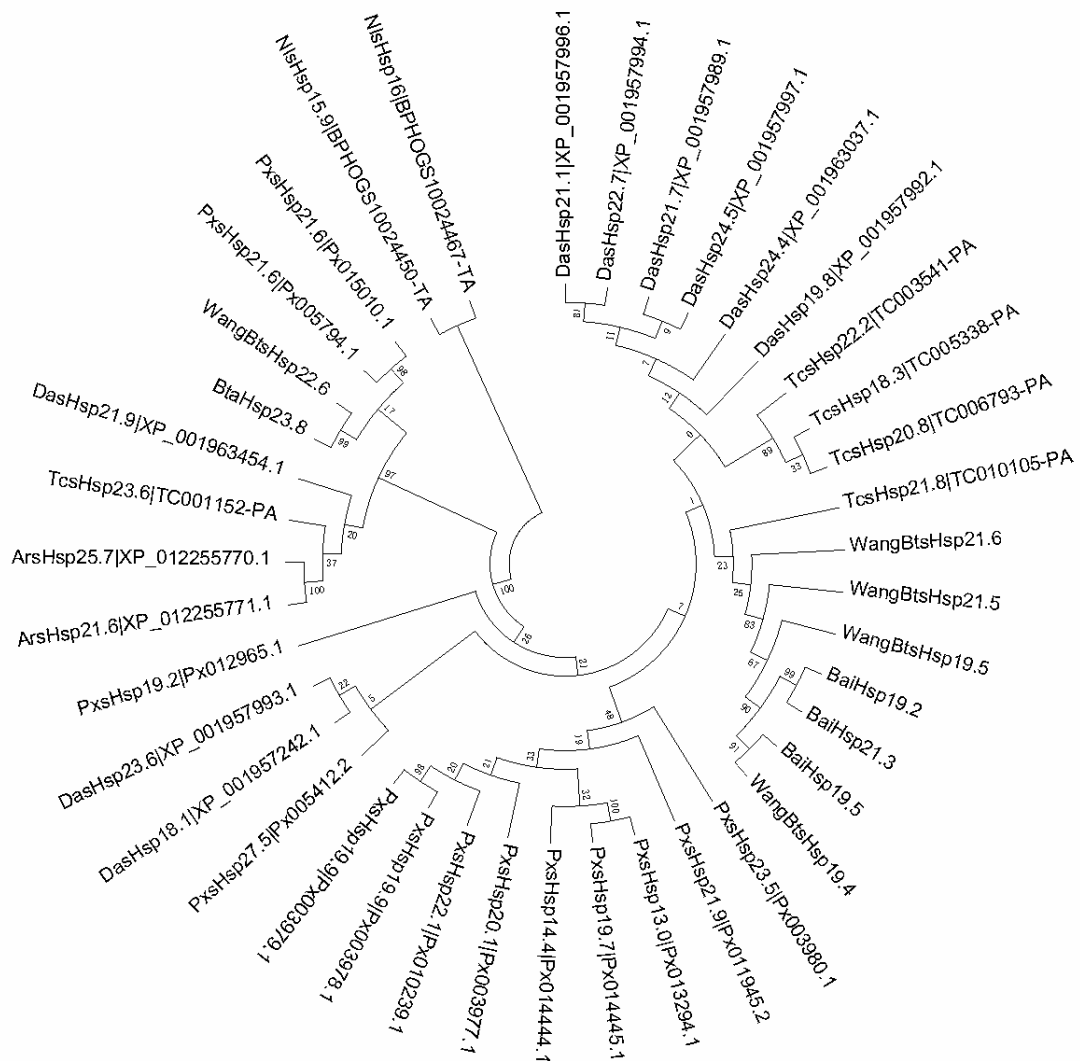
1 Key Lab of Integrated Crop Pest Management of Shandong Province, College of Plant Health and Medicine, Qingdao Agricultural University, Qingdao, 266109, China.

2 Department of Plant Protection, Institute of Vegetables and Flowers, Chinese Academy of Agricultural Sciences, Beijing, 100081, China.

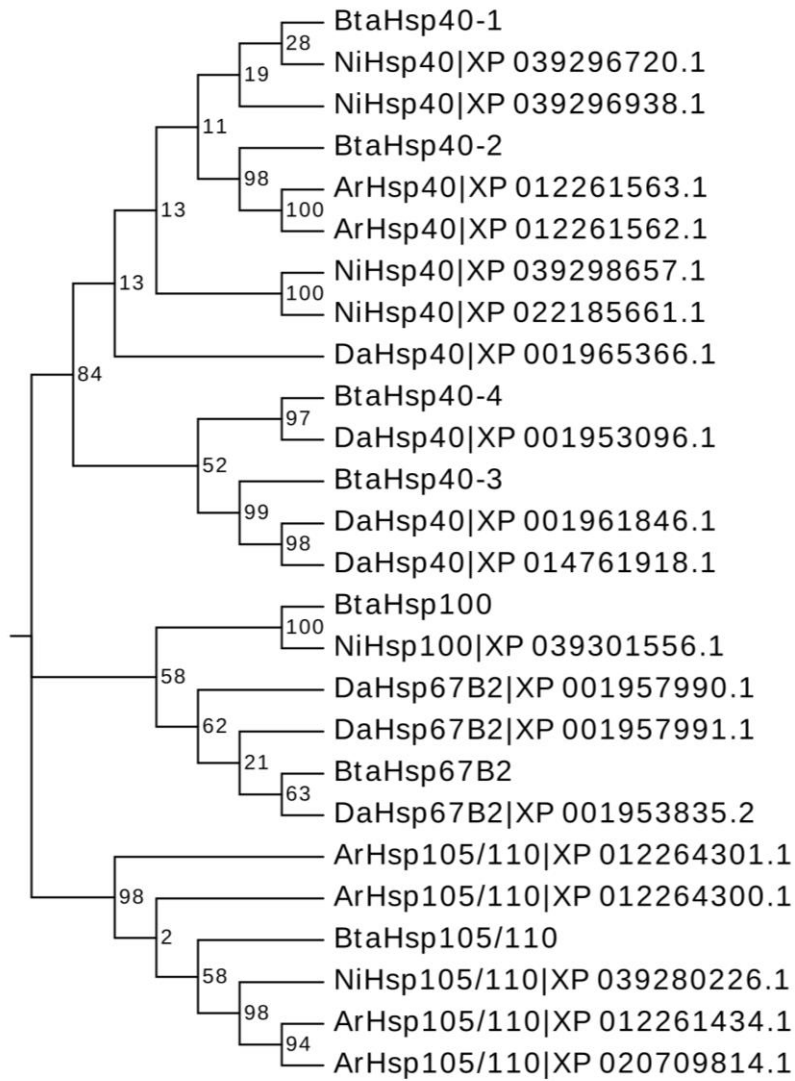
**Running title:** Identification and analysis of *Bemisia tabaci* HSP genes



**Supplementary Figure S1. Phylogenetic relationships of *Hsps* from *Bemisia tabaci*, *Plutella xylostella*, *Tribolium castaneum*, *Drosophila ananassae*, *Athalia rosae*, and *Nilaparvata lugens*.** The unrooted phylogentic tree was constructed using MEGA7 by Maximum Likelihood method with JTT model. The bootstrap test was set as 1000 replicates.

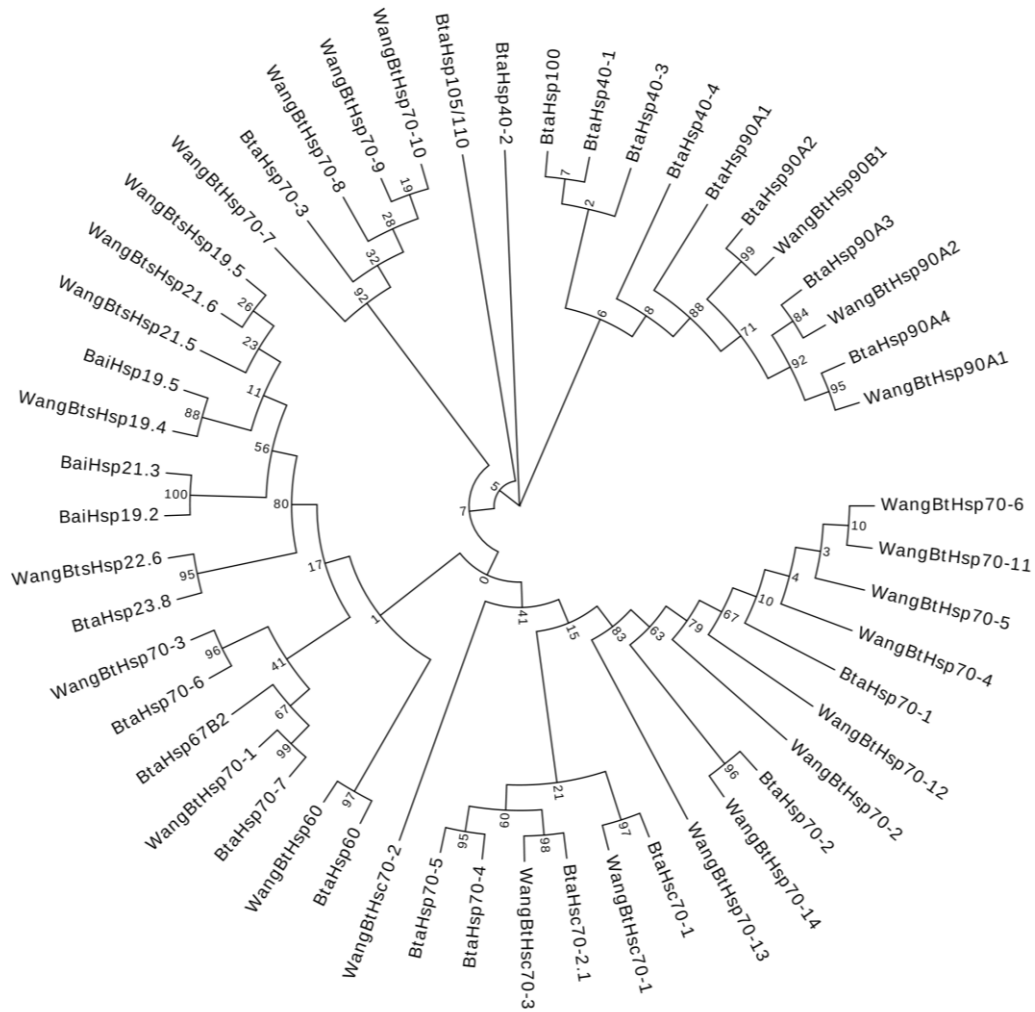


**Supplementary Figure S2. Phylogenetic relationships of sHsps from *Bemisia tabaci*, *Plutella xylostella*, *Tribolium castaneum*, *Drosophila ananassae*, *Athalia rosae*, and *Nilaparvata lugens*.** The unrooted phylogentic tree was constructed using MEGA7 by Maximum Likelihood method with JTT model. The bootstrap test was set as 1000 replicates.



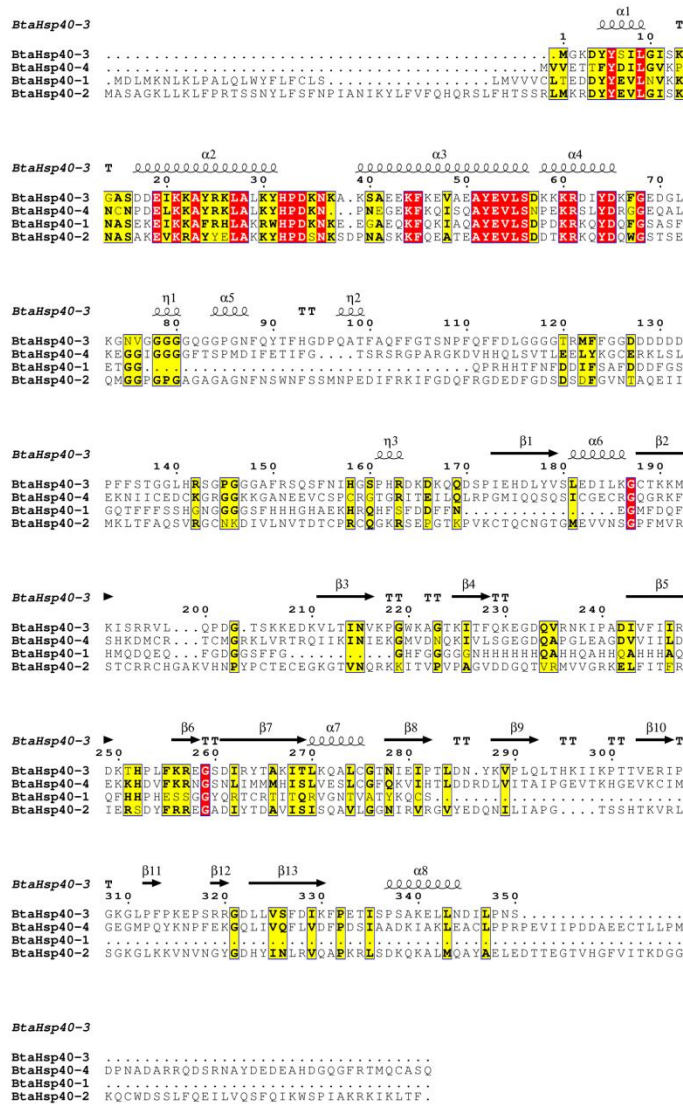
**Supplementary Figure S3. Phylogenetic relationships of *Hsp40*, *Hsp100*, *Hsp105/110*, *Hsp67B2* from *Bemisia tabaci*, *Drosophila ananassae*, *Athalia rosae*, and *Nilaparvata lugens*.** The unrooted phylogentic tree was constructed using MEGA7 by Maximum Likelihood method with JTT model. The bootstrap test was set as 1000 replicates.



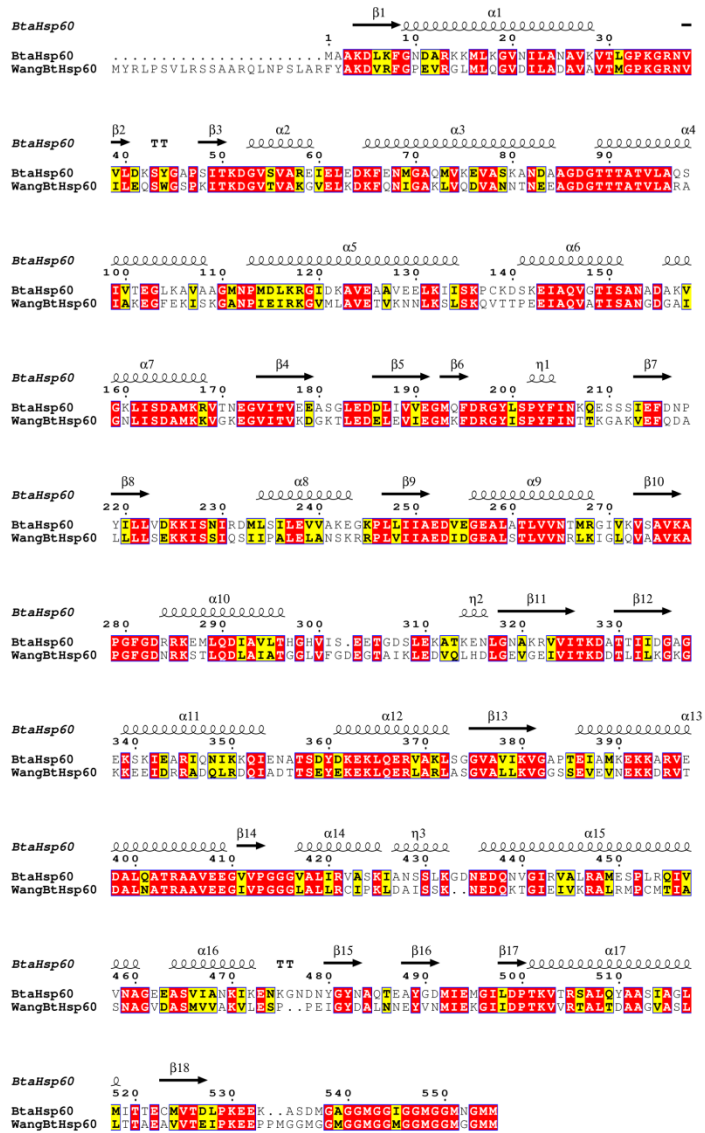


**Supplementary Figure S4. Phylogenetic relationships and gene structures analysis of the *Bemisia tabaci* HSP (BtaHSP) gene superfamily.** The unrooted phylogenetic tree was constructed using MEGA7 by Maximum Likelihood method with JTT model. The bootstrap test was set as 1000 replicates.





**Supplementary Figure S6. The secondary structures of *Bemisia tabaci* HSP40s.  $\alpha$ -helices and  $\beta$ -sheets were represented by yellow boxes and blue arrows shown above the sequence, respectively. The conserved domain of HSP40s were marked with a line under the sequences.**



Supplementary Figure S7. The secondary structures of *Bemisia tabaci*

HSP60s.  $\alpha$ -helices and  $\beta$ -sheets were represented by yellow boxes and blue

arrows shown above the sequence, respectively. The conserved domain of

Hsp60 proteins were marked with a line under the sequences.

BtaHsp70-7

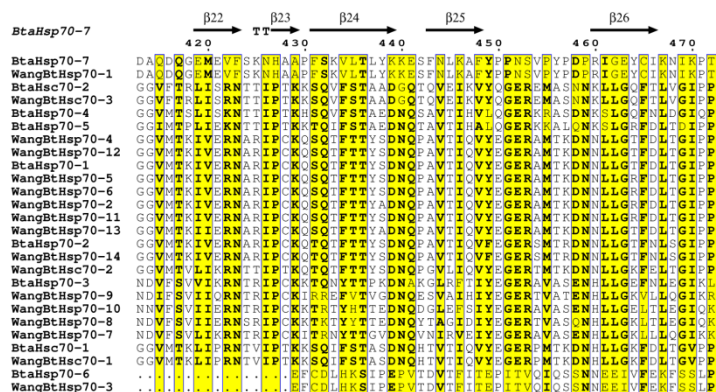
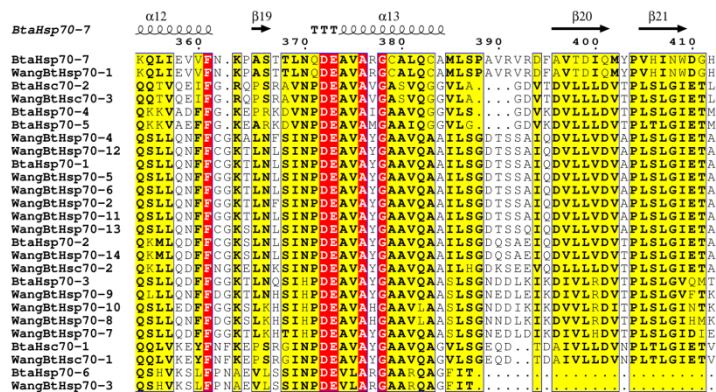
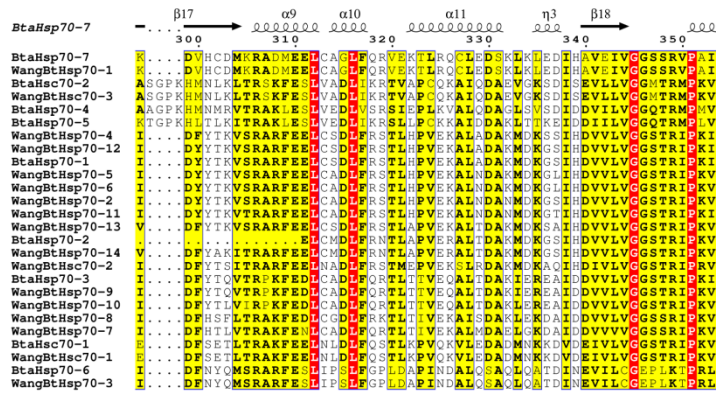
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WangBtHsp70-1	1	MAAMS	VI
BtaHsc70-2	1	MAAMS	VI
WangBtHsc70-3	1	MLYVARVVGKTLHCCLFNPSYITTSNFISIYLSKTPVIFNRIYEFQRRFRKSEQVKGT	VI
BtaHsp70-4	1	MTKRI	II
BtaHsp70-5	1	MIRRI	I
WangBtHsp70-4	1	MAKAP	AV
WangBtHsp70-12	1	MVKAP	AI
BtaHsp70-1	1	MVKAP	AI
WangBtHsp70-5	1	MPGKT	PAI
WangBtHsp70-6	1	MPGKT	PAI
WangBtHsp70-2	1	MPGKT	PAI
WangBtHsp70-11	1	MPGKT	PAI
WangBtHsp70-13	1	MKT	PAI
BtaHsp70-2	1	MGKQV	PAV
WangBtHsp70-14	1	MAKAP	AI
WangBtHsc70-2	1	MEKRA	I
BtaHsp70-3	1	MEKRA	I
WangBtHsp70-9	1	MEKRA	I
WangBtHsp70-10	1	MEKRA	I
WangBtHsp70-8	1	MEKRA	I
WangBtHsp70-7	1	MRLLFLSGAFCLLACVAFAKEKKDKEDFGT	VV
BtaHsc70-1	1	MRLLFLSGAFCLLACVAFAKEKKDKEDFGT	VV
WangBtHsc70-1	1	MRLLFLSGAFCLLACVAFAKEKKDKEDFGT	VV
BtaHsp70-6	1	MSRFT	TVF
WangBtHsp70-3	1	MSRFT	TVF

BtaHsp70-7	β1	β2	β3	TT	β4	β5	β6	α1	η1
BtaHsp70-7	10	20	30	40	50	60	70	80	90
BtaHsp70-7	GIDFGNBS	SCVAVAR	AGGIEIT	ANDYSLR	ATPS	CVAFSEK	TRILGVA	AAKN	QLV
WangBtHsp70-1	GIDFGNBS	SCVAVAR	AGGIEIT	ANDYSLR	ATPS	CVAFSEK	TRILGVA	AAKN	QLV
BtaHsc70-2	.....	.....	ME	GKIPK	VIEN	SEGSRT	TPSV	VAFSK	DGE
WangBtHsc70-3	GIDLGT	TNSCVAVME	GKIPK	VIEN	SEGSRT	TPSV	VAFSK	DGE	ERIVG
BtaHsp70-4	GIDLGT	TNSCVAVME	GKIPK	VIEN	SEGSRT	TPSV	VAFSK	DGE	ERIVG
BtaHsp70-5	GIDLGT	TNSCVAVME	GKIPK	VIEN	SEGSRT	TPSV	VAFSK	DGE	ERIVG
WangBtHsp70-4	GIDLGT	TNSCVAVME	GKIPK	VIEN	SEGSRT	TPSV	VAFSK	DGE	ERIVG
WangBtHsp70-12	GIDLGT	TNSCVAVME	GKIPK	VIEN	SEGSRT	TPSV	VAFSK	DGE	ERIVG
BtaHsp70-1	GIDLGT	TNSCVAVME	GKIPK	VIEN	SEGSRT	TPSV	VAFSK	DGE	ERIVG
WangBtHsp70-5	GIDLGT	TNSCVAVME	GKIPK	VIEN	SEGSRT	TPSV	VAFSK	DGE	ERIVG
WangBtHsp70-6	GIDLGT	TNSCVAVME	GKIPK	VIEN	SEGSRT	TPSV	VAFSK	DGE	ERIVG
WangBtHsp70-2	GIDLGT	TNSCVAVME	GKIPK	VIEN	SEGSRT	TPSV	VAFSK	DGE	ERIVG
WangBtHsp70-11	GIDLGT	TNSCVAVME	GKIPK	VIEN	SEGSRT	TPSV	VAFSK	DGE	ERIVG
WangBtHsp70-13	GIDLGT	TNSCVAVME	GKIPK	VIEN	SEGSRT	TPSV	VAFSK	DGE	ERIVG
BtaHsp70-2	GIDLGT	TNSCVAVME	GKIPK	VIEN	SEGSRT	TPSV	VAFSK	DGE	ERIVG
WangBtHsp70-14	GIDLGT	TNSCVAVME	GKIPK	VIEN	SEGSRT	TPSV	VAFSK	DGE	ERIVG
WangBtHsc70-2	GIDLGT	TNSCVAVME	GKIPK	VIEN	SEGSRT	TPSV	VAFSK	DGE	ERIVG
BtaHsp70-3	GIDLGT	TNSCVAVME	GKIPK	VIEN	SEGSRT	TPSV	VAFSK	DGE	ERIVG
WangBtHsp70-9	GIDLGT	TNSCVAVME	GKIPK	VIEN	SEGSRT	TPSV	VAFSK	DGE	ERIVG
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WangBtHsp70-7	GIDLGT	TNSCVAVME	GKIPK	VIEN	SEGSRT	TPSV	VAFSK	DGE	ERIVG
BtaHsc70-1	GIDLGT	TNSCVAVME	GKIPK	VIEN	SEGSRT	TPSV	VAFSK	DGE	ERIVG
WangBtHsc70-1	GIDLGT	TNSCVAVME	GKIPK	VIEN	SEGSRT	TPSV	VAFSK	DGE	ERIVG
BtaHsp70-6	GIIVGNT	SASIA	CKED	GKVEV	LNA	AGER	TPA	VVA	TEK
WangBtHsp70-3	GIIVGNT	SASIA	CKED	GKVEV	LNA	AGER	TPA	VVA	TEK

BtaHsp70-7	β7	α2	TT	α3	β8	TT	β9	β10	α1
BtaHsp70-7	70	80	90	100	110	120	130	140	150
BtaHsp70-7	TVYGF	RR	LG	RYK	DP	IQ	KDL	QSL	TY
WangBtHsp70-1	TVYGF	RR	LG	RYK	DP	IQ	KDL	QSL	TY
BtaHsc70-2	TVYGF	RR	LG	RYK	DP	IQ	KDL	QSL	TY
WangBtHsc70-3	TVYGF	RR	LG	RYK	DP	IQ	KDL	QSL	TY
BtaHsp70-4	TVYGF	RR	LG	RYK	DP	IQ	KDL	QSL	TY
BtaHsp70-5	TVYGF	RR	LG	RYK	DP	IQ	KDL	QSL	TY
WangBtHsp70-4	TVYGF	RR	LG	RYK	DP	IQ	KDL	QSL	TY
WangBtHsp70-12	TVYGF	RR	LG	RYK	DP	IQ	KDL	QSL	TY
BtaHsp70-1	TVYGF	RR	LG	RYK	DP	IQ	KDL	QSL	TY
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WangBtHsp70-11	TVYGF	RR	LG	RYK	DP	IQ	KDL	QSL	TY
WangBtHsp70-13	TVYGF	RR	LG	RYK	DP	IQ	KDL	QSL	TY
BtaHsp70-2	TVYGF	RR	LG	RYK	DP	IQ	KDL	QSL	TY
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BtaHsp70-3	TVYGF	RR	LG	RYK	DP	IQ	KDL	QSL	TY
WangBtHsp70-9	TVYGF	RR	LG	RYK	DP	IQ	KDL	QSL	TY
WangBtHsp70-10	TVYGF	RR	LG	RYK	DP	IQ	KDL	QSL	TY
WangBtHsp70-8	TVYGF	RR	LG	RYK	DP	IQ	KDL	QSL	TY
WangBtHsp70-7	TVYGF	RR	LG	RYK	DP	IQ	KDL	QSL	TY
BtaHsc70-1	TVYGF	RR	LG	RYK	DP	IQ	KDL	QSL	TY
WangBtHsc70-1	TVYGF	RR	LG	RYK	DP	IQ	KDL	QSL	TY
BtaHsp70-6	TVYGF	RR	LG	RYK	DP	IQ	KDL	QSL	TY
WangBtHsp70-3	TVYGF	RR	LG	RYK	DP	IQ	KDL	QSL	TY





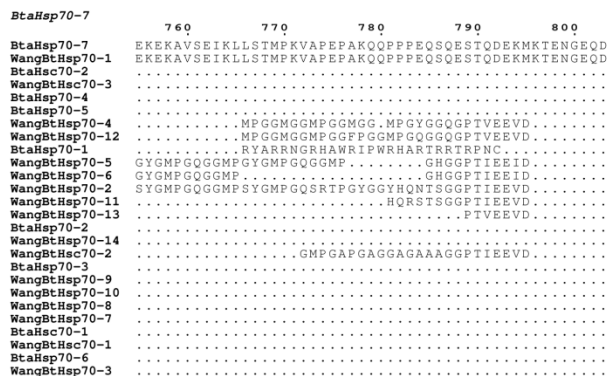
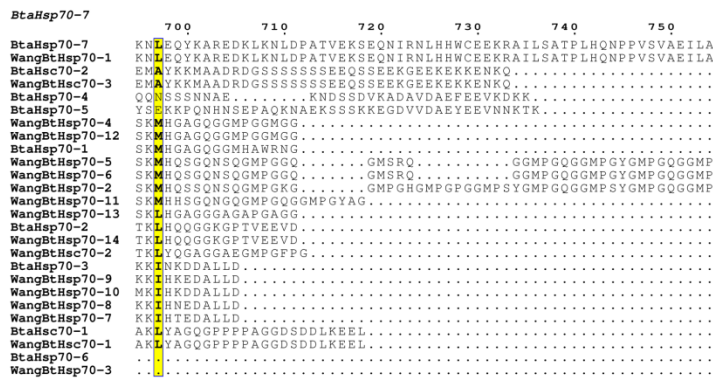
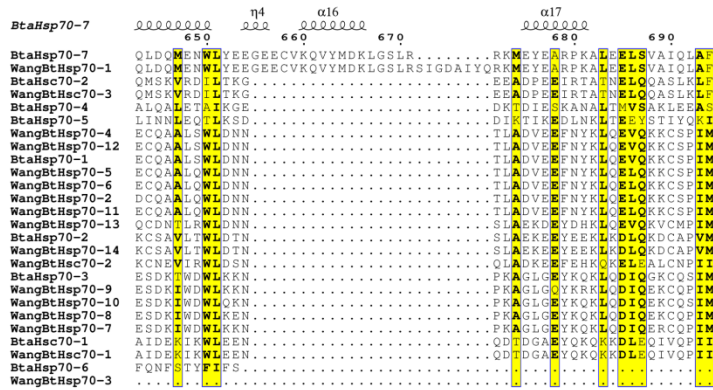


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$\beta 29$   $\beta 30$   
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 WangBtHsp70-1 Q Q Q P P E A N A N S Q D A Q P N G P A E D D D A E K K E K R K T V K S V D L P I E E F L P G F S S E V S S F F E A  
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 WangBtHsp70-11 . . . . . E N S T G R E R N I V I K N D K G L S R E I D R M V N E  
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 WangBtHsp70-3 . . . . . K L N G K V I T I S S K D S S L L L I D

$\alpha 14$   $\alpha 15$   
 600 610 620 630 640  
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 WangBtHsp70-1 E G Q M M A A D R Q E K D R V D A R N S L E E Y V Y L R K K L S E L S . . . . . A Y V V E K D R S S L V E  
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 WangBtHsp70-8 A R R K K E D D K K H L A R S R A R N Q L E D Y T Y K M Q E L K A A E S . . . . . E L S Q A D K S C L K D  
 WangBtHsp70-7 A K L F R K E D E K K H L A R S R A R N Q L E D Y T Y K M Q E L K A A E S . . . . . E L S Q A D K C O M K E  
 BtaHsc70-1 A K L F A D D K K L K E R V A R N L E S Y A Y S L R N Q L A D K E K L G S K V D G M I L F Q S D E E K T R M E E  
 WangBtHsc70-1 A K L F A D D K K L K E R V A R N L E S Y A Y S L R N Q L A D K E K L G S K L S . . . . . D E E K T R M E E  
 BtaHsp70-6 G K I N A E Q A I E I H L L N K S M E E L Q M Y T M D L V A G V F L F V P . . . . . Q I D G L S R K P R T S I A M  
 WangBtHsp70-3 V C I N A E Q A I E I H L L N K S M E E L Q M Y T M D L V A G V E A S . . . . . L . . . . L . .





## Supplementary Figure S8. The secondary structures of *Bemisia tabaci*

HSP70s.  $\alpha$ -helices and  $\beta$ -sheets were represented by yellow boxes and blue

arrows shown above the sequence, respectively. The conserved domain of

HSP70s were marked with a line under the sequences.

# BtaHsp90A4

1  
BtaHsp90A4 .....MSSWCTLGL  
WangBtHsp90A1 .....  
BtaHsp90A3 .....  
WangBtHsp90A2 .....  
BtaHsp90A2 MFRGSKLIALSLGLLIFALAGARAEDEITEKTIDIDLGASREGSRDTAEVQREERIL  
WangBtHsp90B1 MFRGSKLIALSLGLLIFALAGARAEDEITEKTIDIDLGASREGSRDTAEVQREERIL  
BtaHsp90A1 .....

BtaHsp90A4  
10 20 30 40 50 60  
α1 α2  
BtaHsp90A4 FRSRSEMPEDATMFOAEITFVFOAEIAQLMSLIVNTFYSNKEIFLRELISNSDALDKIRY  
WangBtHsp90A1 .....MPEDATMFOAEITFVFOAEIAQLMSLIVNTFYSNKEIFLRELISNSDALDKIRY  
BtaHsp90A3 .....MPEDATMFOAEITFVFOAEIAQLMSLIVNTFYSNKEIFLRELISNSDALDKIRY  
WangBtHsp90A2 .....MPEDVNMFOAEITFVFOAEIAQLMSLIVNTFYSNKEIFLRELISNSDALDKIRY  
BtaHsp90A2 IDGLNVAQLRELKKAQKQTFQAEVNRMMKLINSLYRNKEIFLRELISNSDALDKIRL  
WangBtHsp90B1 IDGLNVAQLRELKKAQKQTFQAEVNRMMKLINSLYRNKEIFLRELISNSDALDKIRL  
BtaHsp90A1 .....MDDDETRGFQSEVKKQLLSLMHSLSYSNKEIFLRELISNSDAADKLR

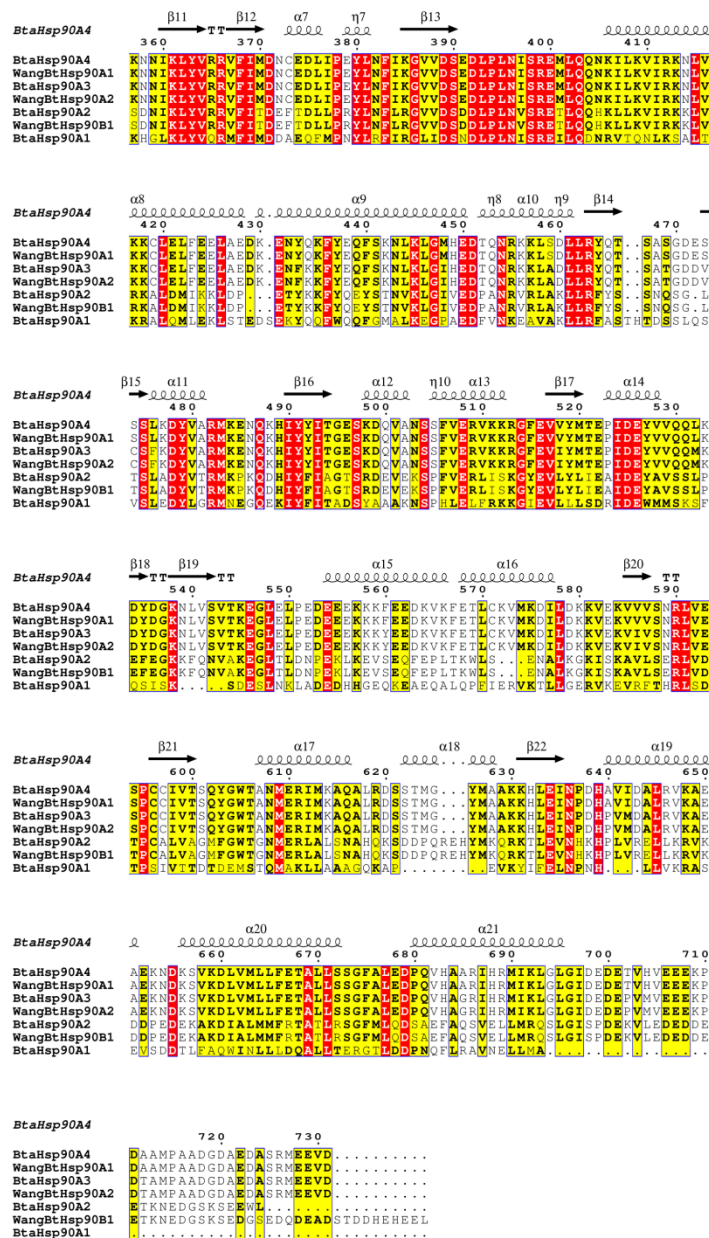
BtaHsp90A4  
70 80 90 100 110 120  
η1 β1 β2 α3 TT α4  
BtaHsp90A4 ES�TDPSRLESGRKELFKIIPNKNNDNTLTLLDSGIGMTKADLVNNGTIAKSGTKAFME  
WangBtHsp90A1 ES�TDPSRLESGRKELFKIIPNKNNDNTLTLLDSGIGMTKADLVNNGTIAKSGTKAFME  
BtaHsp90A3 .....MTELSPSLIRNGIGMTKADLVNNGTIAKSGTKAFME  
WangBtHsp90A2 ES�TDPSRLESGRKELFKIIPNKNDRTLTIIDTIGMTKADLVNNGTIAKSGTKAFME  
BtaHsp90A2 ES�TDPSRLESGRKELFKIIPNKNDRTLTIIDTIGMTKADLVNNGTIAKSGTKAFME  
WangBtHsp90B1 ES�TDPSRLESGRKELFKIIPNKNDRTLTIIDTIGMTKADLVNNGTIAKSGTKAFME  
BtaHsp90A1 RALSSEELVLEGEALRVRLSFDKDKRTLTLSDNIGMTKADLVNNGTIAKSGTKAFME

BtaHsp90A4  
130 140 150 160 170 180  
TT η2 β3 T...T β4 β5  
BtaHsp90A4 LAAG...ADISMIGQFGVGFYSAFVADTVVVSXHN...DDQYIWESAGGSFTIR  
WangBtHsp90A1 LAAG...ADISMIGQFGVGFYSAFVADTVVVSXHN...DDQYIWESAGGSFTIR  
BtaHsp90A3 LAAG...ADISMIGQFGVGFYSAFVADTVVVSXHN...DDQYIWESAGGSFTIR  
WangBtHsp90A2 LAAG...ADISMIGQFGVGFYSAFVADTVVVSXHN...DDQYIWESAGGSFTIR  
BtaHsp90A2 MNEKSEVKKQDNDNMIGQFGVGFYSAFVADTVVVSXHN...DDQYIWESAGGSFTIR  
WangBtHsp90B1 MNEKSEVKKQDNDNMIGQFGVGFYSAFVADTVVVSXHN...DDQYIWESAGGSFTIR  
BtaHsp90A1 LGSD...QSKESQIGQFGVGFYSAFVADTVVVSXHN...DDQYIWESAGGSFTIR

BtaHsp90A4  
190 200 210 220 230 240  
β6 TT η3 α5 β7 TT  
BtaHsp90A4 PDHSEPLGRGKRIIMHMKEDMTLEERKIKKIVKKSQFICYPDKLLVEKERDKELSED  
WangBtHsp90A1 PDHSEPLGRGKRIIMHMKEDMTLEERKIKKIVKKSQFICYPDKLLVEKERDKELSED  
BtaHsp90A3 SDHSEPLGRGKRIIMHMKEDMTLEERKIKKIVKKSQFICYPDKLLVEKERDKELSED  
WangBtHsp90A2 SDHSEPLGRGKRIIMHMKEDMTLEERKIKKIVKKSQFICYPDKLLVEKERDKELSED  
BtaHsp90A2 DPRCTTLKRGKRIISLQKDEAADVEIDLLKNLIRKKSQFINFPIYIWSSKIVTEVVPVD  
WangBtHsp90B1 DPRCTTLKRGKRIISLQKDEAADVEIDLLKNLIRKKSQFINFPIYIWSSKIVTEVVPVD  
BtaHsp90A1 TIIRKE...DRGTEHLLHKEGDEELNDWRLRSIISKYSQHSLEVDLECKN...

BtaHsp90A4  
250 260 270 280 290  
TT η4 β8 η5 TT  
BtaHsp90A4 EEEEEKKKEDKE...EDKDTPKIEDAEDD...CKEKKKKKKTIKKEYTDEEENKTKPIWT  
WangBtHsp90A1 EEEEEKKKEDKE...EDKDTPKIEDAEDD...CKEKKKKKKTIKKEYTDEEENKTKPIWT  
BtaHsp90A3 EEEEEKKKEDKE...EDKDTPKIEDAEDD...CKEKKKKKKTIKKEYTDEEENKTKPIWT  
WangBtHsp90A2 EEEEEKKKEDKE...EDKDTPKIEDAEDD...CKEKKKKKKTIKKEYTDEEENKTKPIWT  
BtaHsp90A2 EEEEEKKKEDKE...EDKDTPKIEDAEDD...CKEKKKKKKTIKKEYTDEEENKTKPIWT  
WangBtHsp90B1 EEEEEKKKEDKE...EDKDTPKIEDAEDD...CKEKKKKKKTIKKEYTDEEENKTKPIWT  
BtaHsp90A1 EEEEEKKKEDKE...EDKDTPKIEDAEDD...CKEKKKKKKTIKKEYTDEEENKTKPIWT

BtaHsp90A4  
300 310 320 330 340 350  
η6 α6 β9 β10 TT  
BtaHsp90A4 RNFDDTTTEYGEFYKSLNDWSDHFAVRRHFSVEGQLEFKALLFVPRRAADPDLFENK.KK  
WangBtHsp90A1 RNFDDTTTEYGEFYKSLNDWSDHFAVRRHFSVEGQLEFKALLFVPRRAADPDLFENK.KK  
BtaHsp90A3 RNFDDTTTEYGEFYKSLNDWSDHFAVRRHFSVEGQLEFKALLFVPRRAADPDLFENK.KK  
WangBtHsp90A2 RNFDDTTTEYGEFYKSLNDWSDHFAVRRHFSVEGQLEFKALLFVPRRAADPDLFENK.KK  
BtaHsp90A2 RKNNEEDDAEYNEFYKSMRDNDPLAKTHFVAEGEVTFKSLFVPRRAADPDLFENK.KK  
WangBtHsp90B1 RKNNEEDDAEYNEFYKSMRDNDPLAKTHFVAEGEVTFKSLFVPRRAADPDLFENK.KK  
BtaHsp90A1 RKNNEEDDAEYNEFYKSMRDNDPLAKTHFVAEGEVTFKSLFVPRRAADPDLFENK.KK



**Supplementary Figure S9. The secondary structures of *Bemisia tabaci* HSP90s.**  $\alpha$ -helices and  $\beta$ -sheets were represented by yellow boxes and blue arrows shown above the sequence, respectively. The conserved domain of HSP90s were marked with a line under the sequences.

## Supplementary data sheet 1

### 1. Sequence logos for the conserved motifs of sHSPs in *Bemisia tabaci*

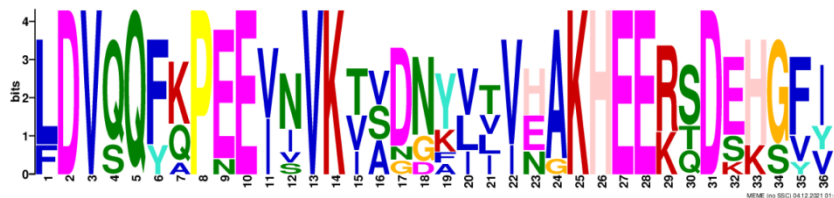
#### BtasHsp Motif

##### Motif 1

E-value 5.2e-138

Width 39

Sites 9

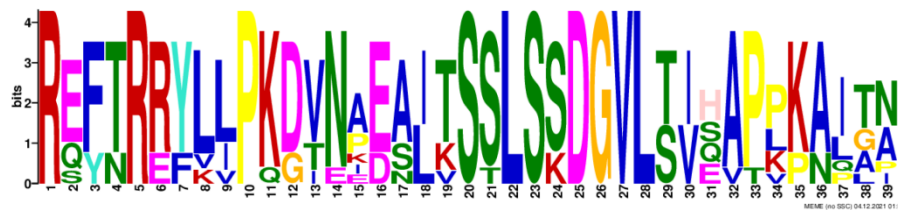


##### Motif 2

E-value 2.6e-133

Width 39

Sites 9



##### Motif 3

E-value 9.8e-077

Width 40

Sites 7



E-value 1.5e-041

Width 19

Sites 9



E-value 6.6e-035

Width 24

Sites 9



E-value 3.1e-010

Width 40

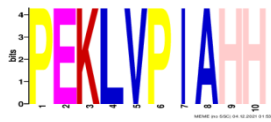
Sites 2



E-value 7.5e+000

Width 10

Sites 2



### Motif 8

E-value 1.0e+002

Width 10

Sites 2



### Motif 9

E-value 6.2e+003

Width 10

Sites 2



### Motif 10

E-value 5.7e+004

Width 14

Sites 2



### Motif 11

E-value 7.8e+005

Width 10

Sites 2



### Motif 12

E-value 8.2e+005

Width 10

Sites 2



## 2. Sequence logos for the conserved motifs of HSP40s in *Bemisia tabaci*

### BtaHsp40 Motif

#### Motif 1

E-value 1.7e-031

Width 34

Sites 4



## Motif 2

E-value 2.5e-019

Width 30

Sites 4



## Motif 3

E-value 4.3e-002

Width 34

Sites 3



## Motif 4

E-value 3.7e+001

Width 30

Sites 2

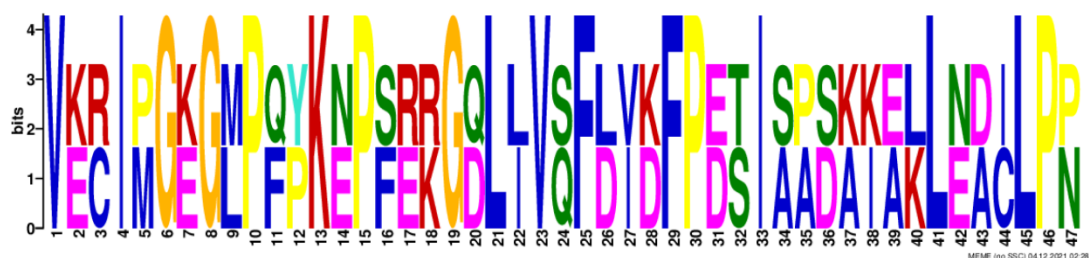




Sites 4



Sites 2



Sites 2



### Motif 8

E-value 2.7e+004

Width 31

Sites 2



### Motif 9

E-value 1.1e+004

Width 36

Sites 2



### Motif 10

E-value 1.2e+004

Width 30

Sites 2



## Motif 11

E-value 1.9e+004

Width 30

Sites 2



## Motif 12

E-value 1.0e+005

Width 30

Sites 2



## Motif 13

E-value 4.0e+005

Width 30

Sites 2



## Motif 14

E-value 9.3e+005

Width 30

Sites 2



## 3. Sequence logos for the conserved motifs of HSP60s in *Bemisia tabaci*

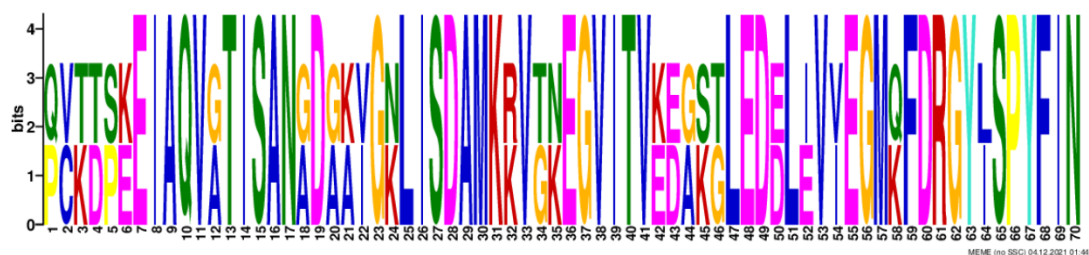
### BtaHsp60 Motif

#### Motif 1

E-value 4.2e-008

Width 70

Sites 2

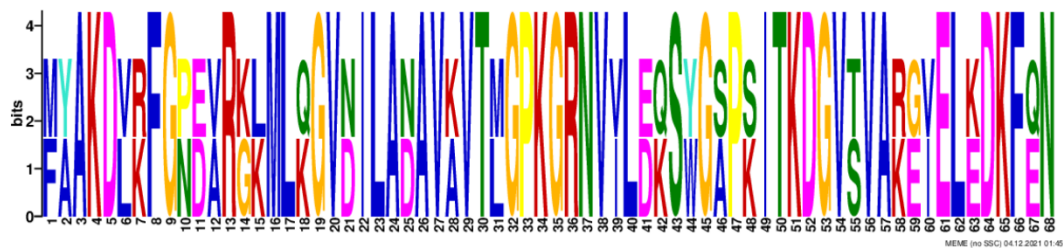


#### Motif 2

E-value 2.0e-006

Width 68

Sites 2

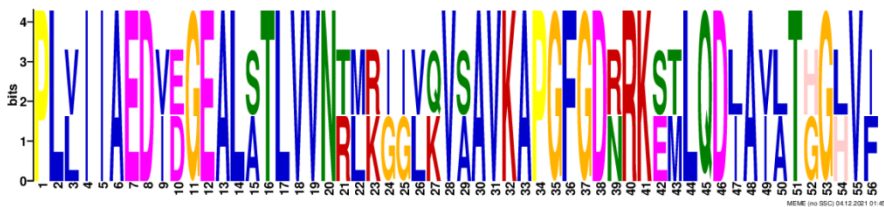


### Motif 3

E-value 1.6e-003

Width 56

Sites 2

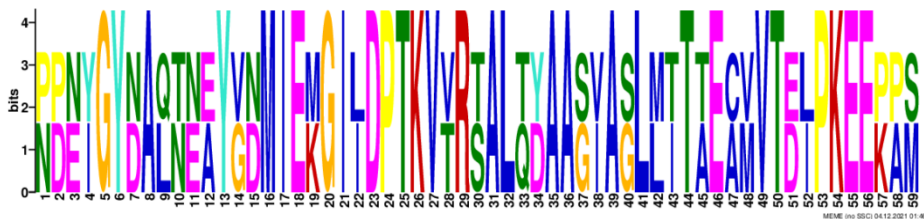


### Motif 4

E-value 3.5e-003

Width 59

Sites 2



### Motif 5

E-value 4.2e-002

Width 70

Sites 2



## Motif 6

E-value 2.0e+001

Width 31

Sites 2



## Motif 7

E-value 1.5e+002

Width 32

Sites 2



## Motif 8

E-value 4.6e+002

Width 30

Sites 2



## Motif 9

E-value 3.3e+003

Width 36

Sites 2



#### 4. Sequence logos for the conserved motifs of HSP70s in *Bemisia tabaci*

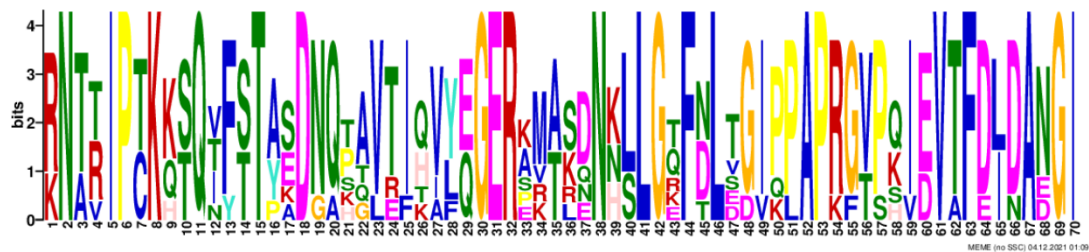
##### BtaHsp70 Motif

##### Motif 1

E-value 7.3e-179

Width 70

Sites 7

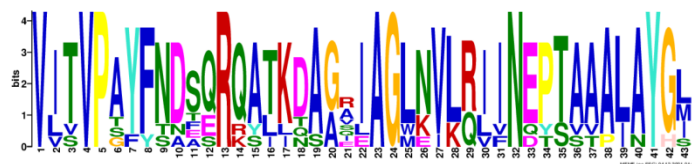


##### Motif 2

E-value 5.0e-147

Width 43

Sites 9

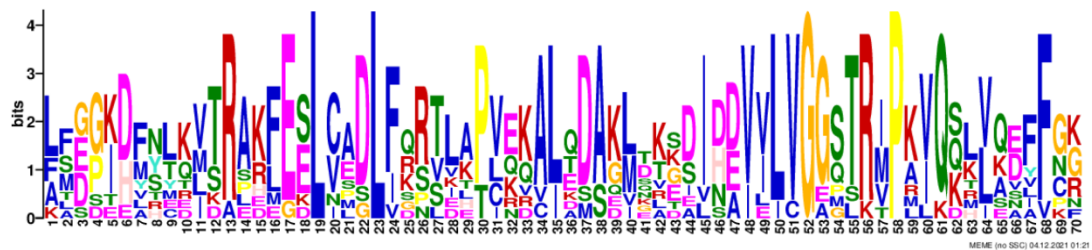


##### Motif 3

E-value 1.8e-149

Width 70

Sites 10

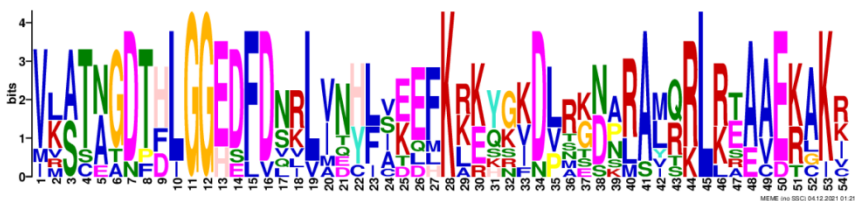


#### Motif 4

E-value 7.4e-122

Width 54

Sites 9



#### Motif 5

E-value 9.3e-088

Width 42

Sites 8



#### Motif 6

E-value 1.2e-064



Width 41

Sites 10



### Motif 7

E-value 4.4e-049

Width 30

Sites 8

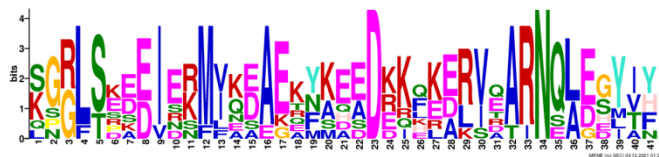


### Motif 8

E-value 1.5e-046

Width 41

Sites 8



### Motif 9

E-value 3.8e-046

Width 39

Sites 6



## Motif 10

E-value 4.4e-033

Width 30

Sites 6

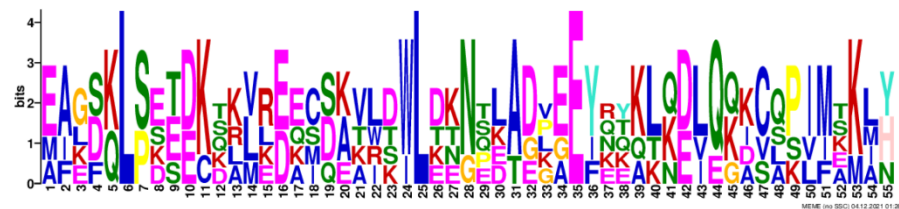


## Motif 11

E-value 1.4e-012

Width 55

Sites 5



## Motif 12

E-value 8.9e+001

Width 30

Sites 2

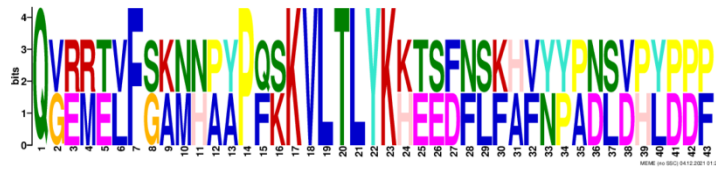


## Motif 13

E-value 1.3e+003

Width 43

Sites 2



### Motif 14

E-value 1.5e+004

Width 30

Sites 2



### Motif 15

E-value 4.4e+004

Width 30

Sites 2



### Motif 16

E-value 4.6e+004

Width 30

Sites 2



## Motif 17

E-value 4.9e+004

Width 38

Sites 2



## Motif 18

E-value 2.8e+004

Width 39

Sites 2



## Motif 19

E-value 4.1e+004

Width 30

Sites 2



## Motif 20

Sites 2

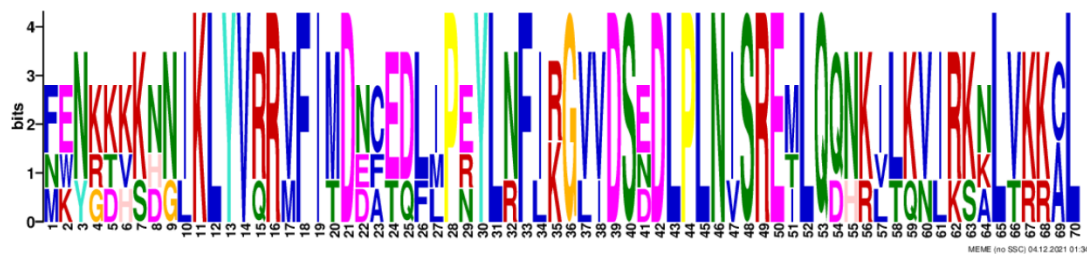


### 5. Sequence logos for the conserved motifs of HSP90s in *Bemisia tabaci*

### BtaHsp90 Motif

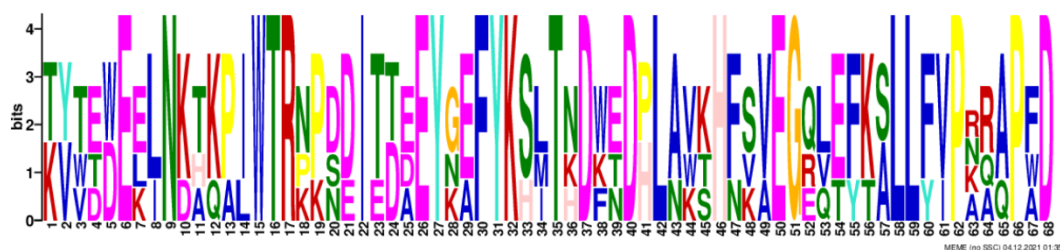
### Motif 1

Sites 4



## Motif 2

Sites 4



### Motif 3

E-value 4.1e-049

Width 61

Sites 4

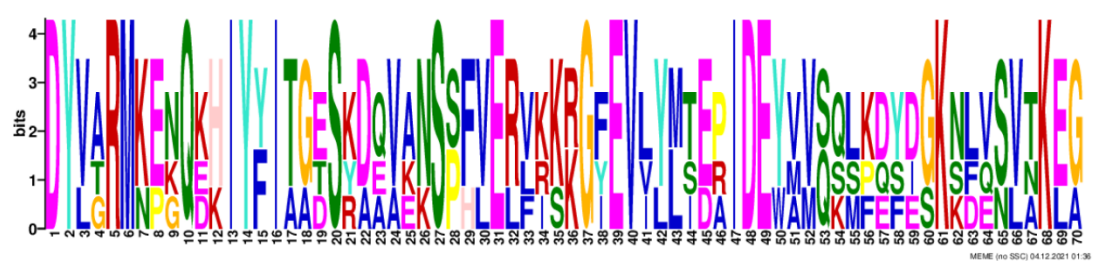


### Motif 4

E-value 1.6e-045

Width 70

Sites 4



### Motif 5

E-value 2.6e-029

Width 55

Sites 3



### Motif 6

E-value 3.8e-027

Width 31

Sites 4



### Motif 7

E-value 4.6e-023

Width 41

Sites 4

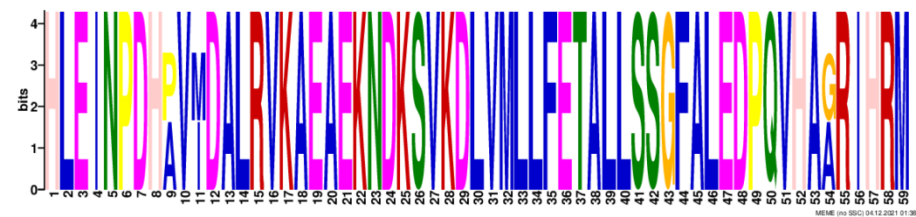


### Motif 8

E-value 1.1e-015

Width 59

Sites 2



### Motif 9

E-value 1.8e-018

Width 51

Sites 3

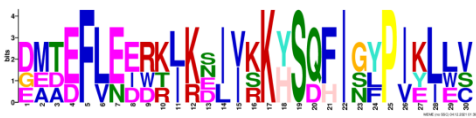


### Motif 10

E-value 2.4e-008

Width 30

Sites 4



### Motif 11

E-value 3.6e-003

Width 30

Sites 2



### Motif 12

E-value 2.8e+004

Width 34

Sites 2



### Motif 13

E-value 3.4e+005

Width 30



Sites 2



## Motif 14

E-value 1.9e+005

Width 30

Sites 2



## Motif 15

E-value 3.1e+006

Width 30

Sites 2



## Motif 16

E-value 3.1e+006

Width 30

Sites 2



### Motif 17

E-value 3.1e+006

Width 30

Sites 2



### Motif 18

E-value 3.1e+006

Width 30

Sites 2



## 6. Sequence logos for the conserved motifs of HSP100s in *Bemisia tabaci*

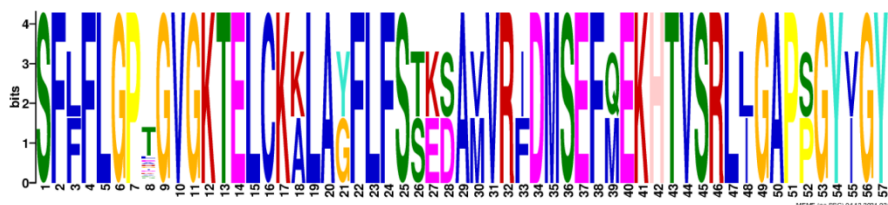
### BtaHsp100 Motif

#### Motif 1

E-value 1.2e-014

Width 57

Sites 2



#### Motif 2

E-value 1.7e-006

Width 57

Sites 2

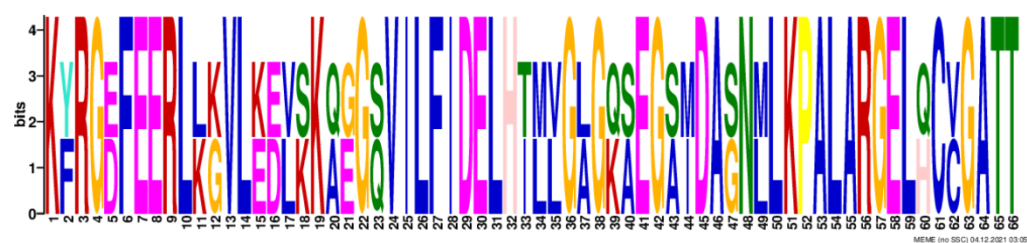


### Motif 3

E-value 1.3e-005

Width 66

Sites 2

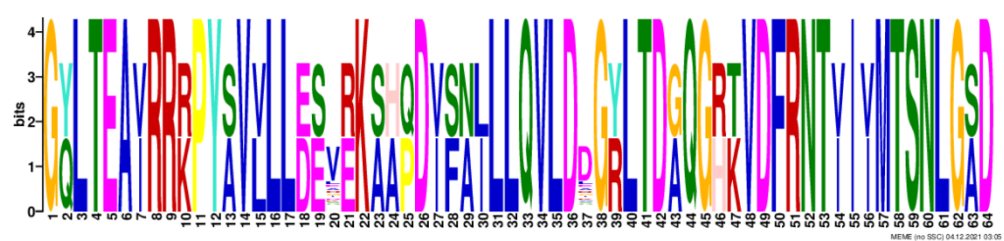


### Motif 4

E-value 3.4e-005

Width 64

Sites 2

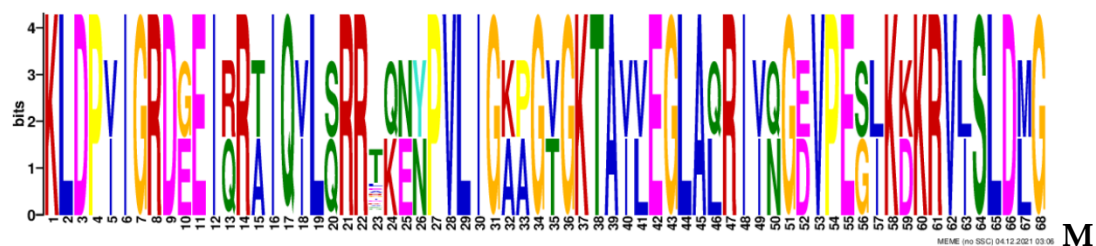


### Motif 5

E-value 5.4e-002

Width 68

Sites 2

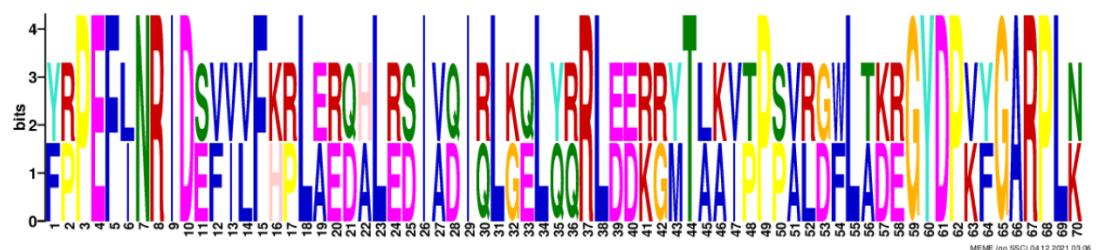


Motif 6

E-value 9.4e-002

Width 70

Sites 2

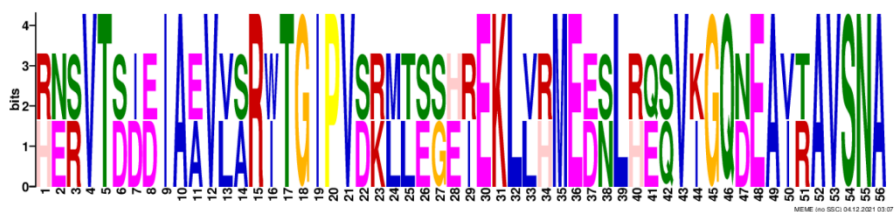


Motif 7

E-value 2.4e-001

Width 56

Sites 2

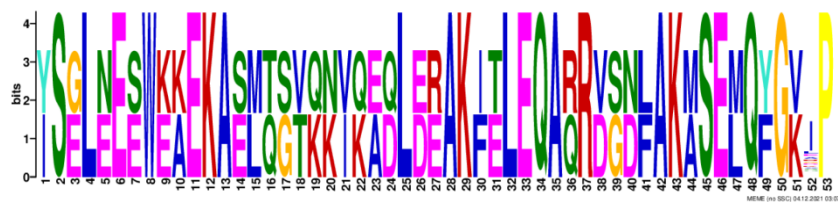


Motif 8

E-value 4.5e+001

Width 53

Sites 2

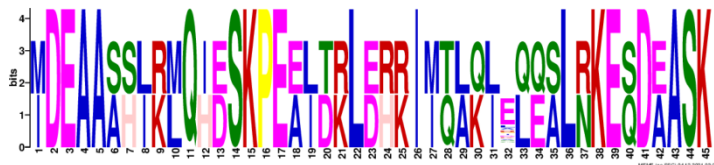


### Motif 9

E-value 4.6e+003

Width 45

Sites 2

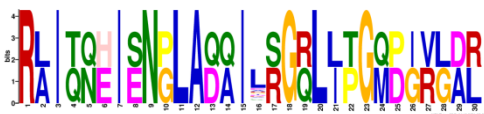


### Motif 10

E-value 3.3e+004

Width 30

Sites 2



### Motif 11

E-value 1.8e+004

Width 30

Sites 2



## Motif 12

E-value 5.6e+005

Width 30

Sites 2



## Motif 13

E-value 5.6e+005

Width 30

Sites 2



## Motif 14

E-value 5.6e+005

Width 30

Sites 2



## Supplementary data sheet 2

### Information of *Hsp* sequences in the six surveyed species

#### *Bemisia tabaci*

>BtaHsp70-1

MVKAPAIGIDLGTTYSCVGVWQQGKVEIIANDQGNRTTPSYVAFSDTERL  
IGDAAKNQVAMNPQNTIFDAKRLIGRRYDDPKIQDDMKHWPFKVINDC  
GKPKLQVEFKGETKTFAPEEVSSMVLTKMKETAEEAFLGGQVKDAVITVP  
AYFNDSQRQATKDAGAIAGLNVLRIINEPTAAALAYGLDKNLKGERNVL  
IFDLGGGTFDVSILTIDEGSLFEVRATAGDTHLGGEDFDNRLVNHLAEEFK  
RKYRKDLRGNNRALRRLRTAAERAKRTLSSSTEASIEIDALMDGIDYYTK  
VSRARFEELCSDLFRSTLHPVEKALADAKMDKGSIHVVLVGGSTRIPKIQ  
SLLQNFFCGKTLNLSINPDEAVAYGA AVQAAILSGDTSSAIQDVLLVDVA  
PLSLGIETAGGVMTKIVERNARIPCKQSQTFTTYSNQP AVTIQVYEGERA  
MTKDNLLGTFDLTGIPPAPRGV PKIDVTFDL DANGILNVS AKENSTGKS  
KNIVIKNDKGRLSREEIDRMVNEAEKYKEEDERQRAKIAARNQLESYVFN  
VKQAVDEAGDKLPESDKQLVRDECQAALSWLDNNTLADV EEFNYKLQE  
VQKKCSPIMSKMHGAGQGGMHAWRNGRYARRNGRHAWRIPWRHAR  
TRRTRPNC

>BtaHsp70-2

MNPKNTVFD AKRLIGRRFDDPKIQDDIKHWPFKVISDSGKPKIQVEFKGE  
QKIFAPEEISSMVLTKMKEVAEVYLGKGVSEAVITVPAYFNDSQRQATKD  
AGAIAGMNVLRIINEPTAAALAYGLDKNLKGERNVLIFDLGGGTFDVSIL

SIDEGSLFEVKSTAGDTHLGGEDFDNRLVTHFSEEFKRKYKKDLRGNARA  
LRLRTACERAKRTLSSSTEASLEIDALHEGELCMDLFRNTLAPVERALTD  
AKMDKGSIHVVLVGGSTRIPKVQKMLQDFFCGKSLNLSINPDEAVAYG  
AAVQAAILSGDQSAEIQDVLLVDVTPLSLGIETAGGVMTKIVERNARIPC  
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>WangBtHsp90B1

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>WangBtHsp70-1

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>WangBtHsc70-1

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>WangBtHsp70-2

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>WangBtHsp70-3

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>WangBtHsc70-2

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>WangBtHsp70-4

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>WangBtHsp70-5

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>WangBtHsp70-6

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>WangBtHsp70-7

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>WangBtHsp70-8

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>WangBtHsp70-9

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>WangBtHsp70-10

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FGGKSLKHSIHPDEAVAHGAAVLAASLSGNDDIKIKDVVLRDITPLSLGIN  
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>WangBtHsp70-11

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D

>WangBtHsp70-12

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GGQGPTVEEVD

>WangBtHsp70-13

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>WangBtHsc70-3

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>WangBtHsp70-14

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>WangBtHsp60

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GIETVGGVMTKLIPRNTVIPTKKSQVFSTASDNQHTVTIQVYEGERPMTK  
DNHLLGKFDLTGIPPAPRGVPQIEVTFEIDANGILQVSAEDKGTGNREKIV  
ITNDQNRLTPEDIDRTS

>TcHsp70|TC000487-PA

MLAAARVLSRKAVECSKFSDVVGKRNFSYLTNNTSSYTLHPKYDIQTRF  
KSEGVKGAVIGIDLGT TNSCVAVMEGKQAKVIENSEGSRTTPSVVAFTKD  
GERLVGMPAKRQAVTNSANTFYATKRLIGRRFDDSEVKKDMNNVSYKIV  
KASNGDAWVQGS DGKMYSQIGAFILTKMKETA EAYLNTKVKNVITV

PAYFNDSQRQATKDAGQIAGLNVLRVINEPTAAALAYGMDKTEDKIIAV  
YDLGGGTFDISILEIQKGVFEVKSTNGDTFLGGEDFDNVLVNHLVSEFKKE  
QGIDVTKDPMAMQRLKEAAEKAKIELSSSMQTDINLPYLTMDASGPKH  
MNLKLSRSKFESLVGELVKRTVQPCQKALKDAEVAKNEIGEVLVGGMT  
RMPKVQSTVQDIFGKQPSRAVNPDEAVAVGAAVQGGVLAGDVTDVLLL  
DVTPLSLGIETLGGVFTRLISRNTTIPTKKSQVFSTAADGQTQVEIKVHQGE  
REMAADNKLLGQFSLVGIPPAPRGVPQIEVTFDIDANGIVHVSARDKGTG  
KEQQIVIQSSGGLSKEEENMVRRAEEYAKEDKIKKERVEAINQAEGIVHD  
TETKMEEYKDQLPKEECDKLKEEIAKVREMLAKKDEADPEEIRKVTGTLQ  
QSSLKLFEMAYKKMAADREGSGGSSSGSSEQQSEEPKEKKEDKN

>TcHsp70|TC000188-PA

MGKVPGIGIDLGTITYSCVGVWQHKGKVEIANDQGNRTTPSYVAFTDTERL  
IGDAAKSQVAMNPKNTVFDKRLIGRKFDDTKIQEDMKHWPFTVINDG  
GKPKIQVEYKGEIKKFAPEEISSMVLTKMKEIADTYLGAKVNDVITVPAY  
FNDSQRQATKDAGAIAGLNVLRINEPTAAALAYGLDKNLKGEKNVLIF  
DLGGGTFDVSILSIDEGLFEVKSTAGDTHLGGEDFDNRLVNHFIQEFKRK  
HHKDLSSNTRAVRRLRTACERAKRTLSSSAEASIEIDALHEGIDFYSKVSR  
ARFEEMCMDYFRSTLQPVERALADAKLDKGAIHDIVLVGGSTRIPKIQKM  
LQDFFCGKPLNLSINPDEAVAYGAAVQAAILTGDTSSQIQDVLLVDVAPL  
SLGIETAGGVMTKIVERNSRIPCKQQQTFTTYSNQNNAVTIQVFEGERAM  
TKDNNLLGTFNLTGIPPAPRGVPKIEVTFDLDANGILNVSAKDTSTGKSER  
ITITNDKGRLSKADIDKMLAEAEKYKAEDDKQKERIAARNQLEGYIFSVK

QAGEDAPADKLTEDDKKIIREKCSAALSWLDSNQLAEKEEFEDKCLKELQ  
KDCSPIMMKLHQGAQGGAAPGAKGPTVEEVD

>TcHsp70|TC005884-PA

MSELVVGIDLGTTNSCIAVERNGKIEVIPNREGNRTTLSYVYYGEDSILVG  
KTAKYMASANPSNGIYEIKRLIGCLHDDPDIESERKSLNYELVRGTNGEILI  
QVEQNSEKFHTLP EEVCARILHRLKIDAEMYLGQKVSKAVVTVPAYFNN  
NQRAATRDAARIAGFEVLKLVNEPSAAALAYVRENRIKNGRVILIYDLGG  
GTFDVSIVRTENGTIKVLSDGDTHLGGQDFLNRLVDHVVDYVQTKHGI  
KVRENRKRLMMNILNSCEKTKKILTSANRTVIPLEFSGHFDQLEVTREQFEE  
LNRDLFAKTVKILDNCIRNRRMSKEEIDEVLLVGGSSRIPRIETLLKAYFDK  
PIQRNINADEAIAIGAALAEAHHFAQTHHNSLLIDVLPLSIGTVFDEETIFFN  
FARNTPLPANSKHVHVFKNRKQKNCILSVYEGGHLDCNKNVLLGAHEI  
KWTATTKKNRNVEITMQINNYGIIWVTARGESIKTFSIALNKGRLLEDDEIR  
KLSRGLQVS

>TcsHsp21.8|TC010105-PA

MSVVP LLFRDWWDDDDFHFSRPSRLLDQQFGLGLRRDDLNTFSSMPRS  
SLFRNYVRPWRSTAIQRQDSGSTIQQDKDKFQVILDVQQFAPNEITVKTS  
NSIIVEGKHEEKQDEHGFISRHFVRRYLLPQDHDINDVVSSLSSDGILTVSA  
PKKSLQQPAGERVVPITQTGPAKATVTPVAESQPKVEQPN

>TcsHsp23.6|TC001152-PA

MSEGIRRDIPKLGDFSVIDTEFSSIRERFDAEMRKMEEEEMSKFRSELMNRE  
SNNFFRSTTRS YEYETVSGGNKSKSSSTTTQSSHNSGLDVAQRPSEVRTWY

DDLNSPLIQQDGNDKCLKLRFDVSQYAPEEIVVKTVDNKLLVHAKHEEK  
TESKSVYREYNREFLLPKGTNPEQIKSSLSKDGVLTV EAPLPAITAGETLIPI  
QH

>TcsHsp22.2|TC003541-PA

MALLSFVTDPLDYFRPSLLLDQQFGMGLDDDDFLQPCLPRKVRRMMLTS  
PYARPWRSQASKKDKGSTLSVDKDKFQVSLDVQQFTPEEITVKASDDTITI  
EGKHEEKEDEHGFISRHFIRKYKLPEGHDISQVTSKLSTDGVLTTAPKSEE  
KIKERNIPISFTGQPSQIEATPTIEVGADDKKPEEKKEARKRK

>TcsHsp18.3|TC005338-PA

MALWLYTDPDFDYRPAHRFLERWFDPEDLFPRDFRLLQDHGSSDINFDK  
DKFQANIDVQQFRPEEITVKVSDDTVTVEGKHEEKRDEHGYISRHFVRKY  
VLPKGHDVNRVESKLSSDGVLTTAPKVG DGKEQEKSIPVVQTGQPTPAV  
QQKQEEKK

>TcsHsp20.8|TC006793-PA

MSLLLFSDPFEYSRPSRILDQHFGLGLDPEDLLSPLIPREMRHLMRCPAGY  
LRPW RSAASQRDTGSTVTFDKDKFQANLDVQQFKPEEISVKVNDNTITIE  
GKHEEKEDEHGFISRHFVRRYVLPKDCDVSKVESRLSTDGVLSITAPKICA  
SKETERSIPVVQTGQPSKA VENKEEKKKEK

## Supplementary Tables

**Table 1. Gene-specific primers for q-RT-PCR used in this study.**

Gene name	Forward primer (5'-3')	Reverse primer (5'-3')
<i>BtaHsp70-1</i>	GTCTATGAAGGTGAGCGAGCA ATGA	CGTTGAGGATACCGTTGGCATC A
<i>BtaHsp70-2</i>	GGAGACCAGAGTGCGGAAAT	AGCGTTCCTCTCGACGATCT
<i>BtaHsp70-3</i>	TGAAGGTGAGCGTGCAGTAG	CGTGACATCAACTGAAGGTAC AA
<i>BtaHsc70-1</i>	ACAGCAAGCCTCACATCGAA	GGTTGAAACTACAGGTTTGCC A
<i>BtaHsc70-2</i>	CCCTCTGTCGTAGCATTCTCTA	TTCTTCACTTCAGCATCGTCAA
<i>BtaHsp70-4</i>	TGTGGTCACTGTGCCCCGCTTA	CGTTCCGCCTCCGAGATCGTAA
<i>BtaHsp70-5</i>	AGTCGGTGGTCAAACACGCAT G	TCGCCACCTAATACGCCTCCTT
<i>BtaHsp70-6</i>	ACTGAACGGAAAGATCAATG CAG	GGTTTCCGACTAAGGCCATCA
<i>BtaHsp105/110</i>	GCGAGTGGTTGGATGAAGAA GG	CAATGCCTCTGGTGTGGTCTCA
<i>BtaHsp70-7</i>	GGATCTTTAAGGCGGAAGATG G	TGAACGCAAGTTGGATGGCT
<i>BtaHsp67B2</i>	TCCGTCCCAATGAGTGCTTGT	GCTTGAGTGACTTCGCCTAAGG

<i>BtaHsp60</i>	ACAGGCAACAAGAGCAGCAG TA	TGGCACGAAGAGCAACACGA AT
<i>BtaHsp90A1</i>	CGCTCTCCTCGCCAGAATTGT	CCAACACCGAACTGACCGATG A
<i>BtaHsp90A2</i>	CCTCTTGCCACGCTACCTGAA C	CTTGGCGAGCCTCACTCTGTTG
<i>BtaHsp90A3</i>	ATTGGAATGACCAAGGCTGAC C	AGCGACGAGGAAGGCTGAG
<i>BtaHsp90A4</i>	AGCTCATGGTGCACCTTTAGG	GACATCAACTGGGCGATTTC
<i>BtaHsp100</i>	AGCCGACGGTAGAAGACACC AT	TGCCGCCGCTTCATCAATCAA
<i>BtaHsp23.8</i>	TGTGTTGCAGCTCGACCAA	TGACGTCGAACCTCAGCTTG
<i>BtaHsp40-1</i>	GGTCGTTCTTCGGCGGACATT	TGGTGGAATTGCTGAGCGTGAT
<i>BtaHsp40-2</i>	AAGCGAAGTGAACCAGGAAC CA	GCGACCGACTACCATCCTAAC G
<i>BtaHsp40-3</i>	CGCCCTGAAATACCACCCTGA C	TCCTCCTCCACCTCCGACATTG
<i>BtaHsp40-4</i>	CGAAGGAATGCCTCAGTACA AGAA	TTATCCGCTGCTATCGAATCTG G
<i>dsgfp</i>	TAATACGACTCACTATAGGGA GAC CACTGACCCTGAAGTTCATCT	TAATACGACTCACTATAGGGA GAC CACGTCTTGTAGTTGCCGTCGT

	GC	C
<i>dsBtaHsp90A</i>	TAATACGACTCACTATAGGGT	TAATACGACTCACTATAGGGA
3	GGACAACCTGCGAAGACCTCAT	GACCAGGTTCTTACCGTCGTAG
	C	T

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