

NAME	SITES (5'→3')	START
Hsp17.9A-CI	CTCGAGTTTG TTC TG GACGATTC GGGTCGTGCT	270
Hsp17.4-CI	TACTG GAA GT TTT TGC TTC CG GATAGTTC TCGTTTG TTC GTT AA T	348
	GAAGTGGTC TTC TG GATTG TTC TAGGCCTGCTT	302
	AGAGAGC TTG TT GATCTTTC GA	520
Hsp18.0-CI	AAGCAGGCCTA GAA CA ATC CAG AA GACCACTTC	234
Hsp17.7-CI	AGCTAGAGTA GAA AG TTC CC GAA TTACTAAAA	507
	CCACAGGGCCA AA AG TTC TG GAA GGCACTC GATGATTC	250
Hsp16.9C-CI	AT GAA TACT TC TAG G CAAATTAAGGTGAG	273
	TGGAGCGACG GAA GC GAA GCAGATCGAGTGTGCTG	210
	AG GAAAG TC CAG AGATTC AG G CAGATTAG	157
Hsp16.9A-CI	TCGAGACGCC TC AA GAA CGTCCATTGCGCAGCTCC	175
	GAAGCAAAGCCTT TTC TAG GAA GGGAGCAGATCAA	240
Hsp16.9B-CI	GAGATGCT TTC AA G ACCAAGTTCTGAAGAA	152
Hsp16.6-CVIII	TC CAG AA CAAGCAG GAA ACCTCATCACTCACC	217
	ACTCC TC GACCC TTC AC G ACGCATCCAA	188
Hsp17.9B-CIX	ACGCTGGAG GAA GAAGAAG GAA TGGCGCC GAT CGCC	310
Hsp23.6-III	AATTAT GAA TCACC GAA TGTACTCAGAAAAA	583
Hsp17.8-CXI	GAA AACGCGAG AA ACTAC CAGAA AAATCGCGTGTTTC	214
	ACACGCG TTC TC GATCATTC TCGCGCGCCACC	97
Hsp23.2-ER	GATCC TTC TCTTTTCT TTC CGG TC TGTACAAT	510
	CTC GATCC TTC GG GAA ACCTCTCCCGCCG	214
Hsp22.3-CVI	AGTG GAA ATCT TC CAG AA AAAGGAAAAAAG	194
Hsp18.8-CV	TTTAGATTT ACA TTC GT GAA ATAAACCAA	356

Manual analysis of promoters of sHsp genes.

In addition to MEME based analysis, sHsp genes were analyzed manually. The HSEs which were not identified in promoters by MEME analysis are displayed in the figure. Consensus nucleotides of HSEs are shown in pink font.