Heat Shock Protein Genes Undergo Dynamic Alteration in Their 3D Structure and Genomic Organization In Response To Thermal Stress

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Supplemental Figures
Supplemental Tables

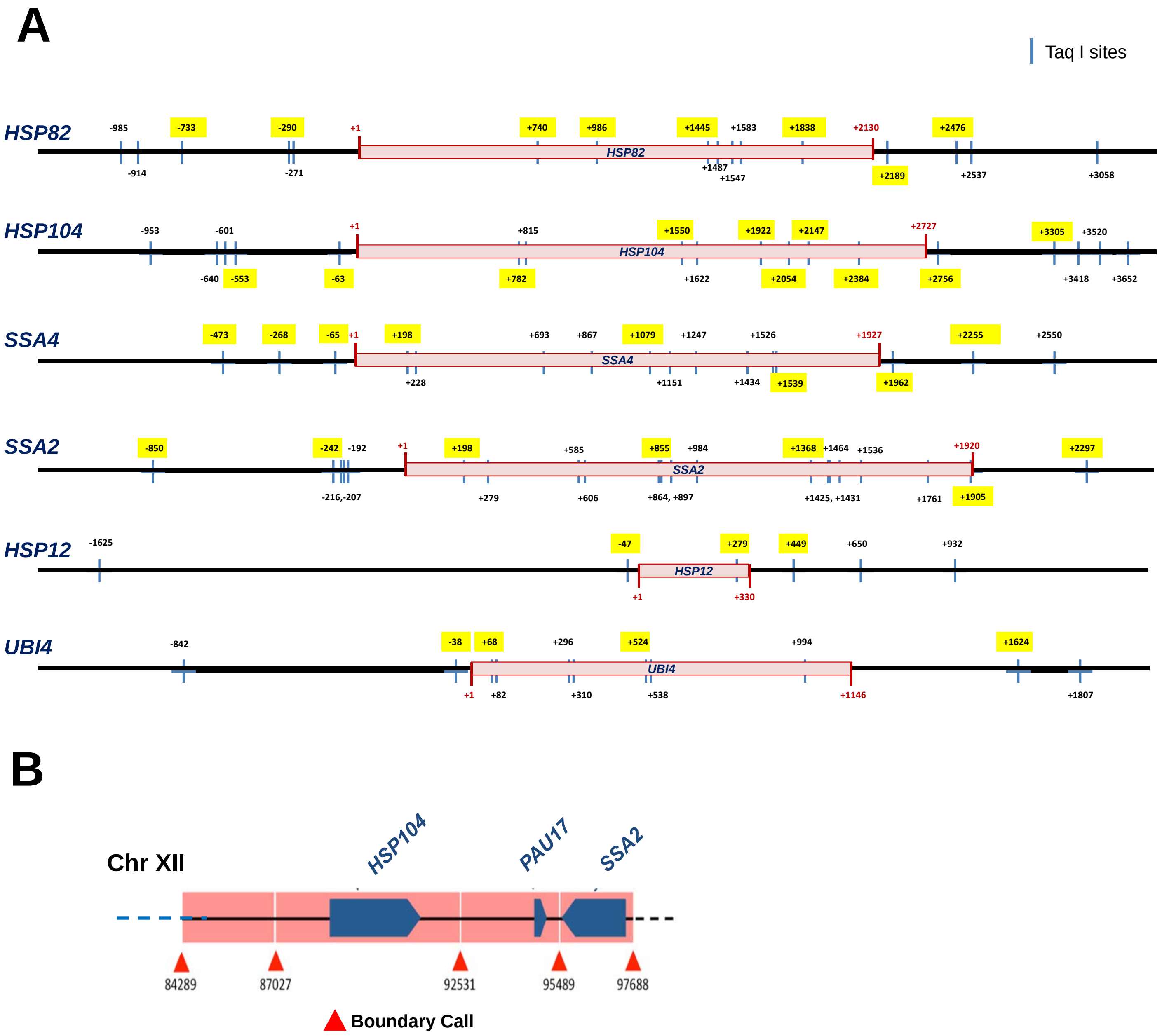
A
Taq I sites
HSP82
-985
-733
-290
+1
+740
+986
+1445
+1583
+1838
+2130
+2476
HSP82
-914
-271
+1487
+1547
+2189
+2537
+3058
HSP104
-953
-601
+1
+815
+1550
+1922
+2147
+2727
+3305
+3520
HSP104
-640
-553
-63
+782
+1622
+2054
+2384
+2756
+3418
+3652
SSA4
-473
-268
-65
+1
+198
+693
+867
+1079
+1247
+1526
+1927
+2255
+2550
SSA4
+228
+1151
+1434
+1539
+1962
SSA2
-850
-242
-192
+1
+198
+585
+855
+984
+1368
+1464
+1536
+1920
+2297
SSA2
-216,-207
+279
+606
+864, +897
+1425, +1431
+1761
+1905
HSP12
-1625
-47
+279
+449
+650
+932
HSP12
+1
+330
UBI4
-842
-38
+68
+296
+524
+994
+1624
UBI4
+1
+82
+310
+538
+1146
+1807
B
Chr XII
HSP104
PAU17
SSA2
84289
87027
92531
95489
97688
Boundary Call

Figure S1. Distribution of Taq I sites within *Heat Shock Protein* genes

A. Taq I restriction maps of *HSP* genes surveyed in this work. Coordinates correspond to the location of Taq I sites (vertical blue lines) and are numbered relative to the ATG initiation codon (+1). Initiation and termination codons are indicated in red. Each map depicts the genomic locus encompassing the ORF (pink rectangle) -/+1 kb region. Taq I sites highlighted in yellow correspond to those tested by 3C.

B. Chromosomal interaction domain (CID) map of the indicated region within Chr. XII as defined by Micro-C analysis.

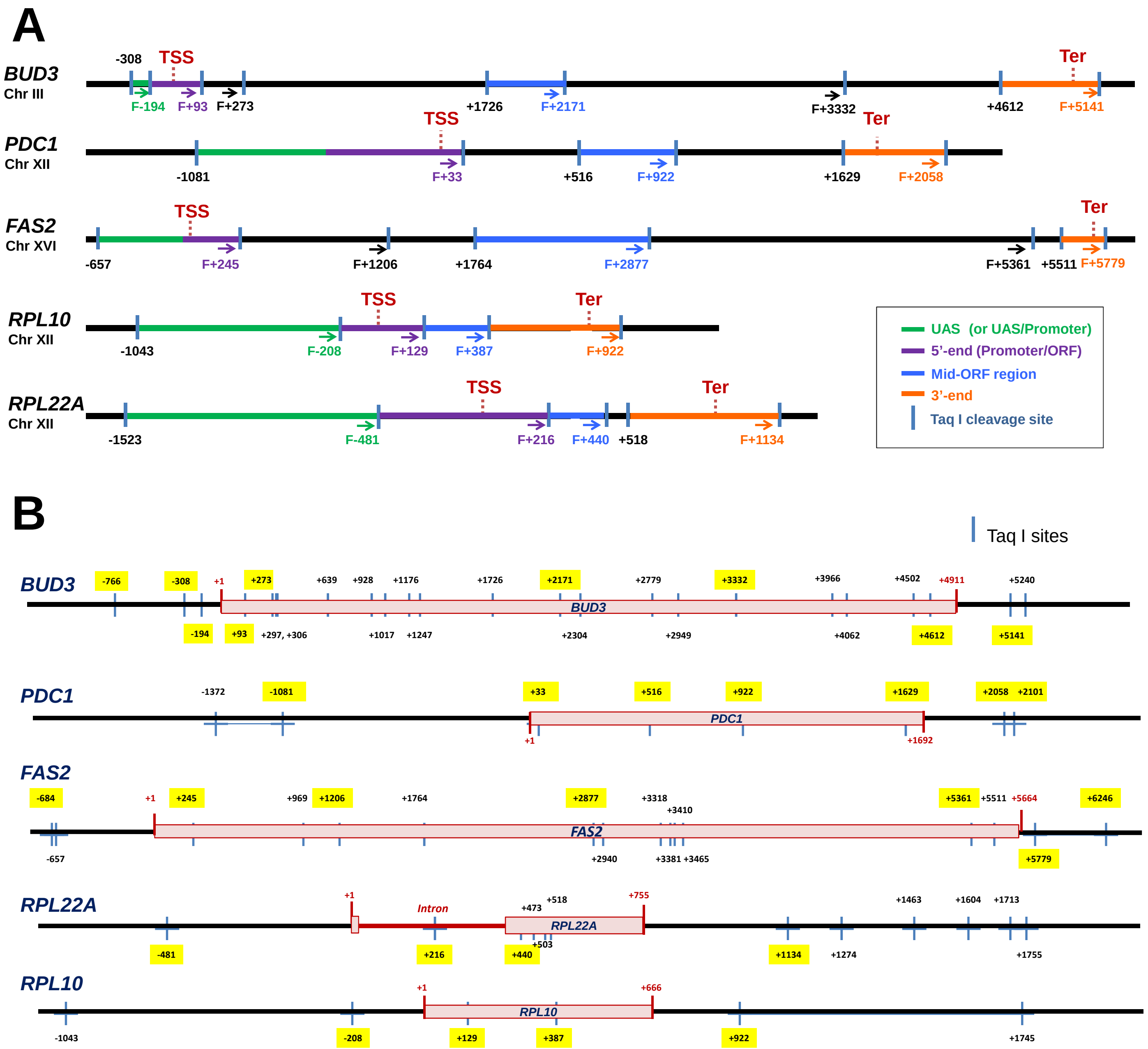
A
BUD3
Chr III
-308
TSS
F-194
F+93
F+273
+1726
F+2171
F+3332
+4612
Ter
F+5141
PDC1
Chr XII
TSS
-1081
F+33
+516
F+922
Ter
+1629
F+2058
FAS2
Chr XVI
TSS
-657
F+245
F+1206
+1764
F+2877
Ter
F+5361
+5511
F+5779
RPL10
Chr XII
TSS
Ter
-1043
F-208
F+129
F+387
F+922
RPL22A
Chr XII
TSS
Ter
-1523
F-481
F+216
F+440
+518
F+1134
UAS (or UAS/Promoter)
5'-end (Promoter/ORF)
Mid-ORF region
3'-end
Taq I cleavage site
B
Taq I sites
BUD3
-766
-308
+1
+273
+639
+928
+1176
+1726
+2171
+2779
+3332
+3966
+4502
+4911
+5240
BUD3
-194
+93
+297, +306
+1017
+1247
+2304
+2949
+4062
+4612
+5141
PDC1
-1372
-1081
+33
+516
+922
+1629
+2058
+2101
PDC1
+1
+1692
FAS2
-684
+1
+245
+969
+1206
+1764
+2877
+3318
+3410
+5361
+5511
+5664
+6246
FAS2
-657
+2940
+3381 +3465
+5779
RPL22A
+1
Intron
+473
+518
+755
+1463
+1604
+1713
RPL22A
+503
-481
+216
+440
+1134
+1274
+1755
RPL10
+1
+666
RPL10
-1043
-208
+129
+387
+922
+1745

Figure S2. Distribution of Taq I sites within constitutively expressed genes

A. Color-coded maps of constitutively expressed genes evaluated in this study. Abbreviations, symbols and color coding as in Fig. 1A.

B. Taq I restriction maps of constitutively transcribed genes surveyed in this work. Presentation as in Fig. S1A.

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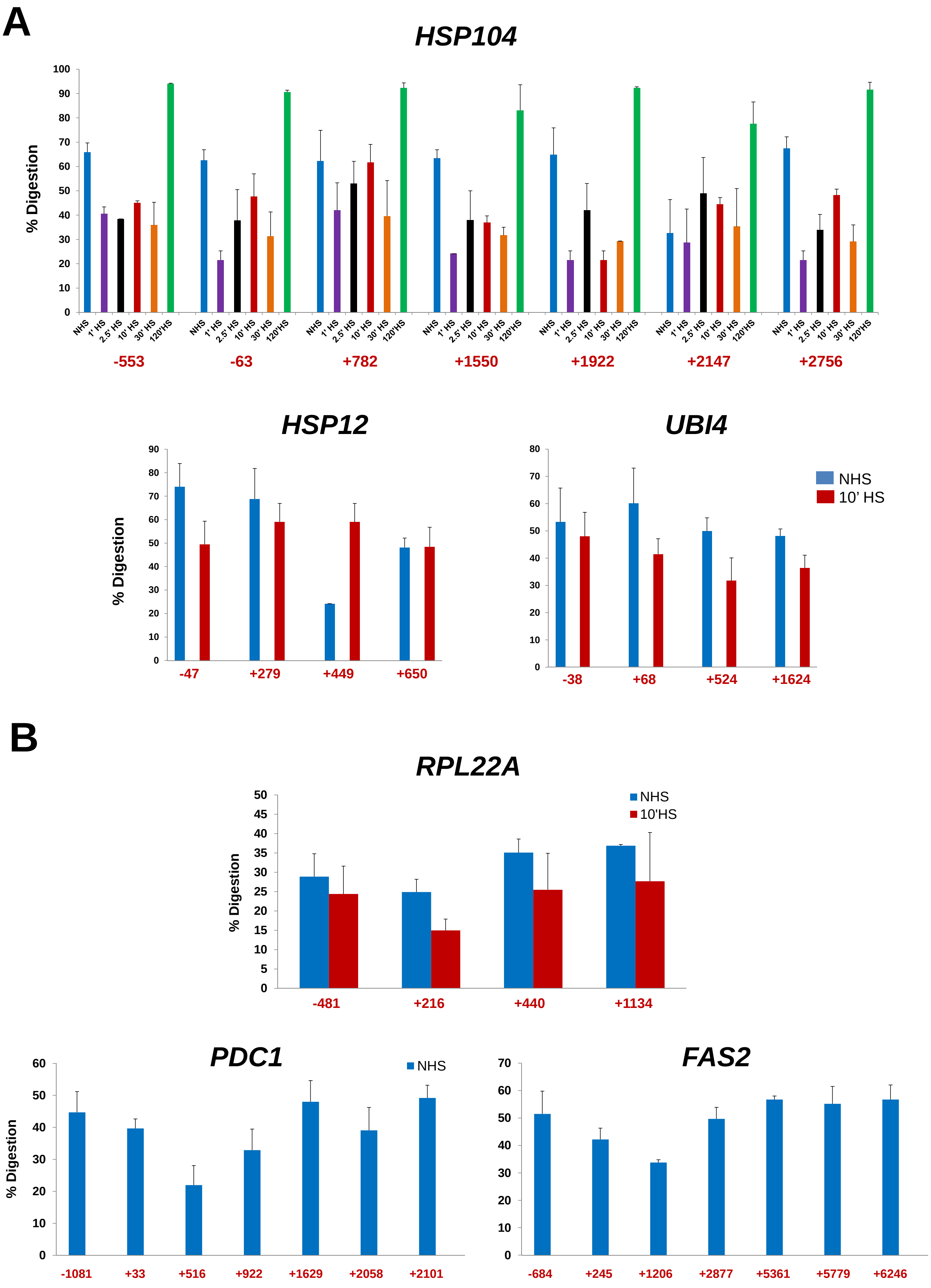

Figure S3. Efficiency of Taq I digestion of crosslinked chromatin

A. Efficiency of cleavage of Taq I sites within representative *HSP* genes. Templates used were crosslinked chromatin samples isolated from non-heat-shocked (NHS) cells or cells subjected to 30° to 39°C heat shock (HS) for the indicated times (strain BY4741). Quantification at each Taq I site, whose location relative to ATG codon is indicated, was done using qPCR. Depicted are means + SD from two independent biological samples.

B. Efficiency of cleavage of Taq I sites within representative constitutively expressed genes. Templates were isolated from either NHS or 10 min HS cells and processed as above.

SUPPLEMENTAL TABLES

Table S1. Forward (F) Primer Sequences Used in 3C Analysis

Name	Sequence (5’ ⟶ 3’)
HSP82 F-733	GATCTAACGGTTCACTGTGTAGGC
HSP82 F-290	CCTCTCTCAACACAGTAATCCATAAAC
HSP82 F+740	AATTAGTCGTCACCAAGGAAGTTG
HSP82 F+986	AGACCCATTGTACGTTAAGCATTTC
HSP82 F+1445	GCCAGAACACCAAAAGAACATCTAC
HSP82 F+1838	ACATGGAAAGAATCATGAAGGCTC
HSP82 F+2189	ATGAGGATGAAGAAACAGAGACTGC
HSP82 F+2476	AAAGGGTATGTTGAAACTCATCTGC
HSP104 F-553	ATGAGGTAGTAGAACAAGATGGCG
HSP104 F-63	AGGCATTGTAATCTTGCCTCAATTC
HSP104 F+782	GTAAGACCGCTATTATTGAAGGTG
HSP104 F+1550	CCCTTGATGCTGAACGTAGATATG
HSP104 F+1922	TTTAGCTAATCCAAGGCAACCAG
HSP104 F+2054	GAAGTATGCGGTCTCTAAGTTGTTG
HSP104 F+2147	ATGAAGTAGAAAAGGCACATCCTG
HSP104 F+2384	CATGACTTCCAATCTAGGTGCTG
HSP104 F+2756	AGGTGATGACGATAATGAGGACAG
HSP104 F+3305	GTGCCAATATAATGTTACAGCGAAC
SSA2 F-850	GTTCACTCCAAGATTTTCATTCAGC
SSA2 F-242	CACTGCATTCTTACTCTCTCTTGG
SSA2 F+198	AGGTAACAGAACCACTCCATCTTTC
SSA2 F+855	AAGGACTTGTCTACCAACCAAAGAG
SSA2 F+1368	TCTCTACTTATGCTGACAACCAACC

SSA2 F+1905	CTAAATTGTACCAAGCTGGTGGTG
SSA2 F+2297	AGTGACTTGAAGACTAGGAATATCG
SSA4 F-473	ACGTAAGATTCGTTGTATGTGCG
SSA4 F-268	ACACGAAAGATATCTCAACTCTAGCC
SSA4 F-65	AGTTCCTAGAACCTTATGGAAGCAC
SSA4 F+198	GCCTTCTTATGTGGCTTTTACTGAC
SSA4 F+1079	TGCTGATTTGTTTAGATCTACATTGG
SSA4 F+1539	ATCTACTGGGTAAATTTGAGTTGAGC
SSA4 F+1962	GAGGAATACAAGGAAAGGCAAAAG
SSA4 F+2255	ATAAGAAAGTCATCGCCAAACAAC
HSP12 F-47	ACGTATAAATAGGACGGTGAATTGC
HSP12 F+279	AAAAGGCAAGGATAACGCTGAAG
HSP12 F+449	TTTTCTTTATGATGTGTGATGTTCC
UBI4 F-38	ATTCGCCTGCTTATCTTTCTTCTTC
UBI4 F+68	ACTCTCCCTCCCACTTTACTTTAAC
UBI4 F+524	GTAAGCAGCTAGAAGATGGTAGAACC
UBI4 F+1624	TGATACGGATAGAATATTGTGACTACC
BUD3 F-766	ATGTGTCTCTCTGGTCTCAAATTC
BUD3 F-308	AGCAAGAAACACAACAGTATAAAGG
BUD3 F-194	GCTCTTTGTCATACGCATAGAATTG
BUD3 F+93	AAGACCTGTCGTCTCTTTACTCTG
BUD3 F+273	TCAGTATTCTATCACGGGTCAGATG
BUD3 F+2171	CGTCTTAACCAAACATGACGATAAAC
BUD3 F+3332	ACGATGAACACAGACAGAATGAAAG
BUD3 F+4612	ATGCTCAGAAAGTTCAAGAGTCTCC
BUD3 F+5141	TTTGGATCAATAGGGGTTCCATC
BUD3 F+5240	TGTTTAATCTCATTCTTGGAGACATC

BUD3 F+5980	CATAAAGTACACAGGTCATGGTTCG
PDC1 F-1081	CACCGCGTAAACTCTCTTAACATAC
PDC1 F+33	TAACCTCACGCAAAATAACACAGTC
PDC1 F+516	TGACTTCACTGTTTTCCACAGAATG
PDC1 F+922	AGTTAAGGAAGCCGTTGAATCTG
PDC1 F+1629	CTAAGGACTATGAAACCCACAGAGT
PDC1 F+2058	TAAGTCTGGGTCCGCTTCTTTAC
PDC1 F+2101	AATGGTTACTCAATTCAAAACTGCC
FAS2 F-684	GGCACCAAGAGTTATTGAAACTAGA
FAS2 F+245	CACTGAAAGGGTTGTTGAAATCG
FAS2 F+1206	AATGGACTTGGATAACGGTGAAAG
FAS2 F+2877	CAAAAATCACCTGTTATGGCTGAC
FAS2 F+5361	CATTGAAACTGCCAAGATGATTG
FAS2 F+5779	AACGTGTCGCTTCTATTTATCAGAC
FAS2 F+6246	AATACTCAGGGAAGAGAAAAATCG
RPL22A F-481	GACGATTCTGTGAAAACCTACTTCC
RPL22A F+216	GCGTCTATGTGTTTAGTTGCTTTTC
RPL22A F+440	TTAATAGCAGTAGGCAACTTTGTGG
RPL22A F+1134	TCTCAGTTTCCAATTAACATGAATCC
RPL10 F-208	ATTATAGTAGCGGTTATTTCCGTGG
RPL10 F+129	GATACCAAAAGAACAAGCCTTACC
RPL10 F+387	TTAAGAGTCAGAGTCCATCCTTTC
RPL10 F+922	TTTAAAGTTCAGCATGTTGGGTAG
ARS504F (internal control)	GTCAGACCTGTTCCTTTAAGAGG

Table S2. Reverse (R) Primer Sequences Used in Determination of Percent Digestion

HSP82 R-733	CTCTTAGTAGCCATTCTTTGCCAC
HSP82 R-290	GAAGGACCTGGTTGGTATTAAGATG
HSP82 R+740	AATGCTTAACGTACAATGGGTCTTC
HSP82 R+986	ATGAAAACACGACGAACGTACAAC
HSP82 R+1445	ATTCATCAATTGGGTCGGTCAAG
HSP82 R+1838	AAGTCCTTGACAGTCTTGTCTTGAG
HSP82 R+2189	ACACACTAGACGCGTCGGAATAG
HSP82 R+2476	TTCTGCAAGGTCTTATAGTCACTCG
HSP104 R-553	TTTAAACCATGAAACTCTCGCCAC
HSP104 R-63	ATCGTTAGAGCCCTTTCTGTAAATTG
HSP104 R+782	TTCTTCGATTTCCTTCAAAACACC
HSP104 R+1550	CCACATTTTGGATCATGGAGTTG
HSP104 R+1922	ACCTTCATCGTACCCGACATAAC
HSP104 R+2054	CTACCGTCATCCAACATTTGTAGC
HSP104 R+2147	TCTTGGATCTTTGATCCTTGTTGAG
HSP104 R+2384	CACCCATATCATCGGAATAACC
HSP104 R+2756	TCTTTTGCTCGGGTGTCAAGTTC
HSP104 R+3305	GATTACATCGTTGGAAATCATCG
SSA2 R-850	GACCAAAATGAAAATAAGCAGCTC
SSA2 R-242	GATGGAATGTTCTAGAAAAAAACTTC
SSA2 R+198	GCTTCATATCACCTTGGACTTCTG
SSA2 R+855	TCTGGTGATGGAAGTGTAGAAATC
SSA2 R+1368	TTCAATTTGTGGGACACCTCTTG
SSA2 R+1905	AATACAGAGGAAAGCAAAAGTAAAAC
SSA2 R+2297	GACGCCCTTACGAATAGAACTTTAC
SSA4 R-473	TCTATAATACCCAATGGTGGGAGAG

SSA4 R-268	TGTTACTGTCGTCAAACTAAGGAG
SSA4 R-65	GTTGTACCTAAATCAATACCAACAGC
SSA4 R+198	TTTACGTCCGATCAGACGCTTAG
SSA4 R+1079	TAATACCACCTGCAGTTTCAATACC
SSA4 R+1539	CTAGCTGATTCTTAGCTTGAACACG
SSA4 R+1962	TTAAACTCTGGCTTATGACGATGAG
SSA4 R+2255	GTGTTAAACTCCGGTCAAAAGAAAC
HSP12 R-47	TTCAGAAGCTTTTTCACCGAATC
HSP12 R+279	AAACCATGTAACTACAAAGAGTTCCG
HSP12 R+449	AAGAAGCAACCGCCATGTTTAAG
UBI4 R-38	CAACTTCCAATGTTATGGTTTTACC
UBI4 R+68	GAATTTTCGACTTAACGTTGTCG
UBI4 R+524	TGAATTTTCGACTTAACGTTGTCG
UBI4 R+1624	ATCACCCAGTATCCCTGATTTCAC
BUD3 R-766	CAAGTCTGAAGTTGTACTGTGTTCG
BUD3 R-308	AAAACCCTAGGTCTTGGCAACTG
BUD3 R-194	CAGTAGAATGCGAGTACAGACAAAC
BUD3 R+93	TGATTGAGTGAACACATTATCCGTC
BUD3 R+273	AAGCATGATGTTCCTAATTTGTC
BUD3 R+2171	CTATTAACAGCCCTATGTTCGTCTG
BUD3 R+3332	GAGAGTTTCTGCGTCAATGTAGATG
BUD3 R+4612	CAAAGGAACAGTATTACGCTCTGG
BUD3 R+5141	TAAGAGGTGGTTTGGATGATGTCTC
BUD3 R+5240	CACTGCGTTCAAGAATACAATTACG
BUD3 R+5980	AATTTACTGAAGGTGTCAATCCAGG
PDC1 R-1081	TTTTTCAATTCTGGCCTTTAGGG
PDC1 R+33	CCCATCTCATACCTTCAACTTCG

PDC1 R+516	AACAACAAGCATCAGCCAAGATAAC
PDC1 R+922	TTCTTGCTTCAATGGGGTAGAAG
PDC1 R+1629	TAAATCGCTTATTGCTTAGCGTTG
PDC1 R+2058	TGGCAGTTTTGAATTGAGTAACC
PDC1 R+2101	GGAGCAATCATTTTACATGGACC
FAS2 R-684	TTGAGCGTCTTCAACGTTCTTG
FAS2 R+245	CTTCAACTTGTGAGCAACCAAAAC
FAS2 R+1206	AGCTTCACTAACAACCTCTCTATCAA
FAS2 R+2877	TTGACAACCTTATGCTCCAAAGC
FAS2 R+5361	TTGACGCCTAAGGACTTGAAAAC
FAS2 R+5779	ATAGAAGAATTGAACGGTGTGTACG
FAS2 R+6246	AAAGCCAAAGGATGCTTCCCAC
RPL22A R-481	GACTTCGGCATTAACCTCTACAAAG
RPL22A R+216	CGATTTTCTTTCAATCCCGAAAC
RPL22A R+440	CACCGTTTTCAGTTGGAGAAGAG
RPL22A R+1134	AACGGTGACTTTTCATTGTCTTG
RPL10 R-208	CTAGAGAAACCAAACTGACCATC
RPL10 R+129	GATTCTCAAGACATGGAAAGGATG
RPL10 R+387	TTTGTTGACCTGGGAACTTGTATC
RPL10 R+922	GCTTCATCGTATTGAGGTTGTTTG
ARS504R (internal control)	CATACCCTCGGGTCAAACAC

Table S3. Primer Sequences Used in DNA Sequencing

Name	Sequence (5’ → 3’)
HSP82 F+740	AATTAGTCGTCACCAAGGAAGTTG

HSP82 F+2189	ATGAGGATGAAGAAACAGAGACTGC
HSP104 F-63	AGGCATTGTAATCTTGCCTCAATTC
HSP104 F+1550	CCCTTGATGCTGAACGTAGATATG
SSA2 F+855	AAGGACTTGTCTACCAACCAAAGAG

Table S4. Primer Sequences Used in ChIP Analysis

Name	Sequence (5’ → 3’)
BUD3 ORF F (+2055 to +2279)	CGTCTTAACCAAACATGACGATAAAC
BUD3 ORF R	CTATTAACAGCCCTATGTTCGTCTG
HSP82 UAS F (-393 to -155)	CCTCTCTCAACACAGTAATCCATAAAC
HSP82 UAS R	GAAGGACCTGGTTGGTATTAAGATG
HSP82 PROM F (-292 to -88)	GTTCGAACAATTCTGGTTCTTTC
HSP82 PROM R	TGAGGAGGTCACAGATGTTAA
HSP82 ORF F (+1392 to +1522)	GCCAGAACACCAAAAGAACATCTAC
HSP82 ORF R	ATTCATCAATTGGGTCGGTCAAG
HSP82 3’UTR F (+2036 to +2297)	ATGAGGATGAAGAAACAGAGACTGC
HSP82 3’UTR R	ACACACTAGACGCGTCGGAATAG

Table S5. Primer Sequences Used in RT-qPCR Analysis

Name	Sequence (5’ → 3’)
HSP82 3'UTR F+2134	AACATCATGGCCTTGAATAGGTTAT
HSP82 3'UTR R +2228	CATGCAGATGCCCTATTTACATACTT
HSP104 ORF F+1646	CAGCTGCAAGATTGACTGGTATCC
HSP104 ORF R+1799	CCTGATCTAGACAATCTAACGGC

SSA4 ORF F+816	GTCTTCGTCTGCTCAGACATC
SSA4 ORF R+946	CCACTGGCTCCAATGTAGATC
SSA2 ORF F+812	TGTCTTCCTCCGCTCAAACTTC
SSA2 ORF R+949	CCTTTTCAACTGGGTCCAAAG