## Supporting online material for:

## Molecular basis of canalization in an ascidian species complex adapted to different thermal conditions

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Supplementary Table S1. Complete list of gene models found in the transcriptome analysis. (see separate PDF file)

**Supplementary Table S2. The complete list of chaperone and other molecules found in the transcriptome analysis.** Raw counts ('B count' and 'A count') were normalized by the RPKM method <sup>46</sup>. Those genes validated by qPCR are highlighted in blue. We did not evaluate genes with less than 10 counts in either species, and others were not validated as we were not able to develop effective qPCR primers. Gene models derive from the KH gene model set <sup>15</sup>. Note some genes are represented by more than one gene model, reflecting splice variants and/or uncertainty in the modeling process.

		Gene					
		length	R	Δ	в	Δ	R/A
Gene name	KH Gene model	(ad)	count	count	normalised	normalised	ratio
dnaic4	KH.C4.524.v1.A.ND1-1	827	1	7	2.57	18.60	0.14
, methuselah	KH.C1.1280.v1.A.ND1-1	3642	1	4	0.58	2.41	0.24
dnajc12	KH.C2.472.v1.A.SL1-1	635	2	6	6.70	20.77	0.32
dnajb9	KH.C1.914.v1.A.ND1-1	<mark>1565</mark>	11	<mark>32</mark>	<mark>14.95</mark>	<mark>44.94</mark>	<mark>0.33</mark>
rbj	KH.C2.432.v1.A.ND1-1	1039	22	48	45.03	101.53	0.44
dnajc13	KH.C9.314.v1.A.SL1-1	7294	8	17	2.33	5.12	0.46
<mark>dnajc3</mark>	KH.C1.269.v1.A.SL1-1	<mark>1831</mark>	<mark>16</mark>	<mark>30</mark>	<mark>18.58</mark>	<mark>36.01</mark>	<mark>0.52</mark>
dnajc7	KH.C9.428.v1.A.ND2-1	882	10	18	24.11	44.85	0.54
dnajc7	KH.C9.428.v2.A.ND3-1	1950	25	44	27.26	49.59	0.55
<mark>hspa9b</mark>	KH.C3.429.v1.A.SL2-1	<mark>2290</mark>	<mark>237</mark>	<mark>401</mark>	<mark>220.09</mark>	<mark>384.85</mark>	<mark>0.57</mark>
hspa9b	KH.C3.429.v1.A.SL1-1	<mark>2278</mark>	<mark>237</mark>	<mark>401</mark>	221.25	386.87	<mark>0.57</mark>
hsp83	KH.C3.148.v2.C.ND2-1	<mark>1718</mark>	<mark>1383</mark>	<mark>2269</mark>	<mark>1711.94</mark>	2902.61	<mark>0.59</mark>
dnajc7	KH.C9.428.v3.A.SL1-1	2104	30	49	30.32	51.18	0.59
hsp83	KH.C3.148.v1.C.SL1-1	<mark>2169</mark>	<mark>1494</mark>	<mark>2417</mark>	<mark>1464.80</mark>	<mark>2449.03</mark>	<mark>0.60</mark>
hsp83	KH.C3.148.v1.C.SL3-1	<mark>2187</mark>	<mark>1494</mark>	<mark>2417</mark>	1452.75	2428.87	<mark>0.60</mark>
ubadc1	KH.L133.5.v1.A.SL3-1	1305	17	26	27.70	43.79	0.63
ubadc1	KH.L133.5.v1.A.SL1-1	1206	17	26	29.98	47.38	0.63
ubadc1	KH.L133.5.v1.A.ND2-1	1388	17	26	26.05	41.17	0.63
gng10	KH.C8.810.v1.A.SL1-1	1622	15	22	19.67	29.81	0.66
gng10	KH.C8.810.v1.A.ND2-1	1630	15	22	19.57	29.66	0.66
gng10	KH.C8.810.v1.A.SL3-1	1625	15	22	19.63	29.75	0.66
rbj	KH.C2.282.v1.A.ND1-1	1835	43	63	49.83	75.45	0.66
rbj	KH.C2.282.v2.A.ND1-1	1917	43	63	47.70	72.23	0.66
<mark>dnajc10</mark>	KH.C9.567.v2.A.SL1-1	<mark>2711</mark>	<mark>74</mark>	<mark>107</mark>	<mark>58.05</mark>	<mark>86.74</mark>	<mark>0.67</mark>
<mark>trap1</mark>	KH.C14.318.v1.A.ND1-1	<mark>2739</mark>	<mark>64</mark>	<mark>92</mark>	<mark>49.69</mark>	<mark>73.82</mark>	<mark>0.67</mark>
bat3	KH.L22.22.v1.B.SL1-1	3638	46	62	26.89	37.45	0.72
tcp1zeta	KH.S1665.1.v1.A.SL1-1	1796	87	117	103.02	143.17	0.72
dnajc8	KH.C14.114.v1.A.SL1-1	1260	6	8	10.13	13.95	0.73
dnajc5	KH.C2.944.v2.A.SL1-1	1682	120	158	151.72	206.45	0.73
dnajc5	KH.C2.944.v1.A.SL1-1	1596	120	158	159.90	217.57	0.73
tcp1theta	KH.L153.45.v1.A.SL1-1	<mark>2043</mark>	<mark>142</mark>	<mark>181</mark>	<mark>147.81</mark>	<mark>194.71</mark>	<mark>0.76</mark>

tcp1theta	KH.L153.45.v2.A.SL1-1	<mark>1894</mark>	<mark>142</mark>	<mark>181</mark>	<mark>159.44</mark>	210.03	<mark>0.76</mark>
tcp1theta	KH.L153.45.v1.A.ND2-1	<mark>2051</mark>	<mark>142</mark>	181	147.24	193.95	0.76
bag1	KH.C3.610.v2.A.ND1-2	2529	9	11	7.57	9.56	0.79
ubqln	KH.C4.426.v1.A.SL2-1	2283	93	110	86.63	105.89	0.82
ubqln	KH.C4.426.v1.A.SL1-1	2252	93	110	87.82	107.35	0.82
grpel	KH.C8.114.v1.A.SL1-1	897	39	46	92.46	112.70	0.82
timm44	KH.C8.96.v1.A.ND2-1	1479	29	34	41.70	50.52	0.83
timm44	KH.C8.96.v1.A.SL1-1	1468	29	34	42.01	50.90	0.83
hspa8	KH.L141.53.v1.A.ND1-1	<mark>2288</mark>	<b>3437</b>	<mark>4018</mark>	3194.57	3859.50	0.83
hspa8	KH.L141.53.v1.A.SL2-1	2254	3437	4017	3242.76	<b>3916.74</b>	0.83
hspa8	KH.L141.53.v1.A.SL3-1	<mark>2240</mark>	3437	4017	3263.02	<b>3941.22</b>	0.83
dnajc10	KH.C9.567.v1.A.ND2-1	707	18	21	<mark>54.14</mark>	65.28	0.83
hsp60	KH.C6.85.v1.A.SL1-1	<mark>2703</mark>	<mark>353</mark>	<mark>409</mark>	277.73	<mark>332.55</mark>	0.84
dnajb11	KH.C9.96.v1.A.SL2-1	1376	133	149	205.55	237.98	0.86
dnajb11	KH.C9.96.v1.A.SL1-1	1363	133	149	207.51	240.25	0.86
rbj	KH.C2.331.v1.A.SL1-1	1712	26	29	32.30	37.23	0.87
rbj	KH.C2.331.v1.A.SL2-1	1715	26	29	32.24	37.16	0.87
wbscr18	KH.C7.436.v2.A.SL2-1	928	63	70	144.37	165.78	0.87
wbscr18	KH.C7.436.v2.A.SL3-1	962	63	70	139.27	159.92	0.87
rbj	KH.C2.13.v1.A.SL1-1	1197	28	31	49.75	56.92	0.87
wbscr18	KH.C7.436.v1.A.ND1-1	1075	64	70	126.61	143.11	0.88
hsp90b1	KH.L61.14.v1.A.SL1-1	2970	116	120	83.06	88.80	0.94
dnajb12/14/dnajc18	KH.C1.303.v1.A.ND1-1	2490	102	99	87.11	87.38	1.00
dnaja1/4	KH.C3.139.v1.C.SL1-1	1948	616	594	672.48	670.15	1.00
dnaja1/4	KH.C3.139.v1.C.SL4-1	1951	616	594	671.45	669.12	1.00
hspa5/hsc70-3	KH.C9.680.v1.A.SL1-1	2382	124	119	110.71	109.79	1.01
, dnaja1/4	KH.C3.139.v2.C.SL2-1	1235	558	534	960.85	950.28	1.01
dnaja1/4	KH.C3.139.v3.C.ND3-1	1110	519	492	994.34	974.14	1.02
hyou	KH.C11.193.v1.A.SL1-1	3332	87	80	55.53	52.77	1.05
bag3	KH.C8.859.v1.A.nonSL1-1	957	176	157	391.10	360.55	1.08
dnaja3	KH.C14.339.v1.B.ND1-1	1924	22	19	24.32	21.70	1.12
dnajc7	KH.C9.410.v1.C.ND1-1	1508	290	248	408.96	361.43	1.13
dnajc7	KH.C9.410.v1.C.nonSL2-1	900	290	248	685.24	605.60	1.13
dnajc6	KH.C8.356.v2.A.SL1-1	4610	125	106	57.66	50.53	1.14
HSPH/hspa4	KH.C14.180.v1.A.SL1-1	3053	504	422	351.07	303.78	1.16
HSPH/ <i>hspa4</i>	KH.C14.180.v2.A.ND2-1	2884	503	421	370.90	320.82	1.16
dnajc2	KH.C1.289.v1.A.ND1-1	2065	159	128	163.74	136.23	1.20
sec63	KH.S437.4.v1.A.SL1-1	2415	167	132	147.06	120.13	1.22
dnajc6	KH.C8.356.v1.A.ND4-1	4225	122	96	61.41	49.94	1.23
dnajc6	KH.C8.356.v1.A.SL3-1	3796	122	96	68.35	55.58	1.23
dnajc6	KH.C8.356.v1.A.SL2-1	3859	122	96	67.23	54.67	1.23
dnajc11	KH.C4.798.v1.A.SL1-1	2190	21	16	20.39	16.06	1.27
Magmas	KH.C2.716.v2.A.ND2-1	1101	25	19	48.29	37.93	1.27
dnajb13	KH.L4.20.v1.C.SL2-1	862	4	3	9.87	7.65	1.29
hsc20	KH.C10.111.v1.A.SL1-1	1000	4	3	8.51	6.59	1.29
dnajb13	KH.L4.20.v1.A.ND1-1	1374	4	3	6.19	4.80	1.29
tcpbeta	KH.C14.531.v1.A.SL1-1	1798	132	94	156.13	114.90	1.36
tcpeta	KH.S1300.1.v1.A.nonSL1-1	1885	95	65	107.18	75.78	1.41
dnajc9	KH.C12.582.v1.C.SL1-1	1061	3	2	6.01	4.14	1.45
tcp1epsilon	KH.L95.8.v1.A.ND1-1	1802	229	150	270.25	182.94	1.48

tcp1epsilon	KH.L95.20.v1.A.ND1-1	1839	229	150	264.81	179.26	1.48
tcp1alpha	KH.C5.523.v1.A.SL1-1	2065	228	148	234.80	157.51	1.49
tcp1alpha	KH.L96.2.v1.A.ND2-1	1996	251	161	267.42	177.27	1.51
tcp1alpha	KH.L96.2.v1.A.SL1-1	1992	251	161	267.96	177.63	1.51
dnajc1	KH.L112.3.v1.A.ND1-1	1689	12	7	15.11	9.11	1.66
dnajc1	KH.L112.3.v1.A.SL2-1	1657	12	7	15.40	9.28	1.66
dnajb2/3/6/7/8	KH.C2.518.v1.A.SL1-1	1437	315	178	466.17	272.23	1.71
dnajb2/3/6/7/8	KH.C2.518.v1.A.SL2-1	1512	316	178	444.45	258.73	1.72
danjb1/4/5	KH.L170.59.v1.A.ND1-1	1595	1235	639	1646.63	880.48	1.87
bag3	KH.C8.85.v2.A.ND3-2	1043	256	121	521.97	254.96	2.05
bag3	KH.C8.85.v1.A.SL1-2	805	280	119	739.69	324.88	2.28
HSPB	KH.S455.4.v1.A.SL1-1	1100	72	29	139.20	57.94	2.40
dnajc16	KH.L20.7.v1.A.SL1-1	2554	11	4	9.16	3.44	2.66
<mark>hsp70</mark>	KH.L46.6.v1.A.ND1-1	<mark>1768</mark>	<mark>3433</mark>	<mark>1130</mark>	<mark>4129.34</mark>	<b>1404.67</b>	<mark>2.94</mark>
bag3	KH.C8.85.v5.A.ND2-1	1605	1600	478	2119.99	654.53	3.24
bag3	KH.C8.85.v4.A.SL1-1	1468	1627	478	2356.95	715.61	3.29
SIL (BAP)	KH.L124.16.v1.A.ND1-1	1828	31	7	36.06	8.42	4.29

Supplementary Table S3. qPCR analysis of prioritized chaperone genes including *dnajc3* and *dnajc10*. Two independent sets of primers designed on different exons were used for each gene, except where only one functional primer set could be established (hspa9b and hspa8). AA heat/ BB heat compares type A conspecific crosses with type B conspecific crosses after heat shock at 27°C for 1h. The data show significant differences in *dnajc3*, *tcp1theta*<sup>50</sup> and *trap1*, with marginal effect in dnajc10 and hsp83 but not in dnajc5, hsp60, hsp70, hspa8 and hsp9b. AA (heat/cont) shows comparison between heat shocked and control expression levels in type A conspecific crosses; BB (heat/cont) shows comparison between heat shocked and control expression levels in type B conspecific crosses. The data confirmed induction of transcription by heat shock of hsp60, hsp70, and hspa8 in at least one of these species. AB heat/ BA heat shows comparison of alternative hybrid crosses (AB; type A eggs and type B sperm. BA; type B eggs and type A sperm). Those not induced by heat, such as dnajc3, dnajc10, dnajc5, tcp1theta and trap1 (and marginally) dnajb9), show maternal inheritance of the expression level. A positive correlation to thermal tolerance was only observed for dnajc3 and dnajc10 (Fig. 2). P-value below the Bonferroni-corrected significance threshold of 0.0045 are shown in green, and P < P0.01 is considered as marginally significant and shown in blue.

		B/A 454	AA cont/	AA boot/	٨٨	DD	AR boot/
Target	Primers	ratio	BB cont	BB heat	(heat/cont)	(heat/cont)	BA heat
dnajb9	1+2	0.33	0.0103	0.2654	0.4767	0.4142	0.0061
dnajc10	1+2	0.67	0.0067	0.0067	0.1	0.1	<0.0001
dnajc3	1+2	0.51	2.00E-04	2.00E-04	0.1297	0.1297	<0.0001
dnajc5	1+2	0.73	0.0029	0.4388	0.2101	0.2562	0.0023
hsp60	1+2	0.83	1.00E-04	0.0116	0.1772	0.0016	0.2526
hsp70	1 + 2	2.94	0.4683	0.4683	<0.0001	<0.0001	0.0278
hsp83	1+2	0.59	0.0081	0.0081	0.013	0.013	0.8541
hspa8	1	0.83	0.0882	0.0882	0.0021	0.0021	0.8298
hspa9b	1	0.57	0.0366	0.0366	0.048	0.048	0.0066
TCP1theta	1 + 2	0.76	<0.0001	<0.0001	0.0331	0.0331	8.00E-04
trap1	1 + 2	0.67	1.00E-04	1.00E-04	0.6431	0.6431	1.00E-04

dnajc31DNAJC3-F3AGCAGCAAAGAAGGTCATGC106DNAJC3-R3ATTTCCACGTTTAATGCGCC2DNAJC3-R4CAGCCTTGCCGGCCACTGTG114DNAJC10-R1CAGGATCCAGGAAGGCACGAA204dnajc101DNAJC10-F1CAGGATCCAGGAAGGCATTCCA2042DNAJC10-F2GCCCGTGTATGGCATTGCCAACA117DNAJC10-R2ACCCCAGCTTGGCTACAAATAC204bnsp831Hsp90-F5GGGTTCCTTCAATATCACTC127Hsp83-SRAACCTGGTCTTGATCACAACAC92Hsp83-SRAACCTGGACTTGATCATCAACAC92Hsp83-SRAACCTGGACTTGATCATCAACAC92Hsp60-3FAACTTGCAAGTGGTGTGCTG111Hsp60-3FCGCTGGCATGGAAGGACAAC98Hsp60-75CGCTGGCATGGAAGGACAAC98Hsp60-75CACTGGCCTTTCAAGGTAGT229Hsp70_R5CACTGGCATTGAAGGACAAC98Hsp70_R5CCACTGGCATGGAAGCACAC98Hsp70_R4ATCCTGGTTGATCCTCCGAC107trap R2GGTCGCGACGACATTGATCC201Hsp70_R5CAACTTGACAGAGACTGC107trap R2GGTCGCGACGACACTCAAGCTG113DNAJC5-R1ATGAACACGAGACTCCCCAAGT113DNAJC5-R2CCATTGGCGCATCACCTCC121DNAJC5-R2CGACAACTAGATTATCGGTAGA139TCP1theta_R1GACAAGTGTATACCGCTACT129Anajc51DNAJC5-R2CGACAGCGGAAGCAGA118DNAJC5-R2CCATTGGCAGATTAGCGTACT121DNAJC5-R2CGACACAGGCGGAAGCAGAC139TCP1thet	Target	Pr	imer sets	Sequence	Target length
Image: bit of the sector of	dnajc3	1	DNAJC3-F3	AGCAGCAAAGAAGGTCATGC	106
2   DNAJC3-F4   CAGCCTTGCCGGCCACTGTG   114     DNAJC3-R4   GGAATCCAGGAAGGCACGAA   204     Anajc10   1   DNAJC10-F1   CAGGATCCTGATGAAATAAC   204     DNAJC10-R1   GCGACAATACTTCCGCAACA   117     DNAJC10-F2   GCCCCTGTATGGCATCTCA   117     DNAJC10-R2   ACCCCAGCTTGGCTACAAAT   117     DNAJC10-R2   ACCCCAGCTTGGCACAAAT   117     DNAJC10-R2   ACCCCAGCTTGGCTACAAAT   117     DNAJC10-R2   ACCCCAGCTTGGCTACAAAAT   117     DNAJC10-R2   ACCCCAGCTTGGCTACAAAAT   117     DNAJC5-R2   GGGCCGATGATCACAAAC   92     Hsp83-6R   TATCGGATCTTGATCACACAC   92     Hsp80-3F   AACTTGCAAGTGGTGTTGCTG   111     Hsp60-3F   AACTTGCAGGTGATGCACAC   98     Hsp60-R5   GTCGTAGCATAGTAGACACAC   98     Hsp60-R5   CACTGGCCATGGAGAGACAC   98     Hsp70_R5   CCACTGGCATGCACAGT   237     Hsp70_R5   CCACTGGTTATCGAGAGTGC   107     trap   R2   GGTCGGCACACTTGATCC <t< td=""><td></td><td></td><td>DNAJC3-R3</td><td>ATTTCCACGTTTAATGCGCC</td><td></td></t<>			DNAJC3-R3	ATTTCCACGTTTAATGCGCC	
Image: DNAJC3-R4GGAATCCAGGAAGGCACGAAdnajc101DNAJC10-F1CAGGATCCTGATGAAATAAC204DNAJC10-R1GCGACAATACTTCCGCAACA117DNAJC10-R2GCCCGTGATGGCATTCTCA117DNAJC10-R2ACCCCAGCTGGCACAAAT127hsp831Hsp90-F5GGGTTCCTTCAATATCACTC127Hsp83-5RAACCTGGTCTTGATCATCAACAC92Hsp83-6FATGAGCTTGATCATCAACAC92Hsp83-6RTATCGGATCTTGTCAAGGC11Hsp60-75CGCTGGCATGGAGGTGTTGCG111Hsp60-75CGCTGGCATGGAAGGACAAC98Hsp60_75CGCTGGCATGGAAGGACAAC98Hsp60_75CCATGGCCTTTCAAGGTAGT229Hsp70_75CCATCGGCTTTCAAGGTAGT229Hsp70_75CCATCGGTTATCGAAGTCC237Hsp70_R5CCAGCCAAGTTCTAAGCAGAGC107trap1trap F2CGACCGACGACTTGATCC1trap F2CCATCTGGCGACGACTTGATCC237Hsp70_R5TCAACGCGGCACAACTGC107trap R2GGTCCCGACGACTTCATCC237dnajc51DNAJC5-F1AAGAACCTCAACCTCGACT2UNAJC5-R1GTCCTCAGGTTGTCTTCCC121DNAJC5-R2CCATTGGCGCATCACCTCC121DNAJC5-R2CCGACACTATGATTATGGA139TCP1theta_R1GACAAGTGTATACCGCTACT121DNAJC5-R2CCGACAGCGGGAAGCAA118DNAJC5-R2CGACAGCGGGAAGCAAGCAGCA101TCP1theta_R2CTTTCGCGAGACGCGGAAGCAA118DNAJS9-R3CCCATATTGTCATCTC121 <td></td> <td>2</td> <td>DNAJC3-F4</td> <td>CAGCCTTGCCGGCCACTGTG</td> <td>114</td>		2	DNAJC3-F4	CAGCCTTGCCGGCCACTGTG	114
dnajc101DNAJC10-F1CAGGATCCTGATGAAATAAC2042DNAJC10-F2GCCCCGTGTATGGCATCTCCA117DNAJC10-F2GCCCCGTGATGGCAACA117DNAJC10-R2ACCCCAGCTTGGCTACCAAAT117DNAJC10-R2ACCCCAGCTTGGCTACCAAAT127Hsp831Hsp90-F5GGGTTCCTTCAATATCACTC127Hsp83-5RAACCTGGTCTTGATTCAACAC922Hsp83-6RTATCGGATCTTGTCCAAGGC92Hsp83-6RTATCGGATCTTGTCCAAGGC111Hsp60-3FAACTTGCAAGTGGTGTGCTG111Hsp60-3FCACTGCACGCCATGGAAGGACAAC98Hsp60-F5CGCTGGCATGGAAGGACAAC98Hsp60-F5CCGTGGCTAGCCATAGTCACCTT229Hsp70_F5CACTGCCTTCAAGGTAGT229Hsp70_R5CCACTCGGTTATCGAAGTCC237Hsp70_R4ATCCTGGTTATCGAAGTCC237Hsp70_R4ATCCTGGTTGCTCCGGAC107trap R2GGTCGCGACGACTTTGATCC2102trap1_F5TGAACACGAGTTTCAAGGTG75trap1_R5TCTAAGCCGTCACCTCAAGG113DNAJC5-R1GTCCTCAGGTGATCACCTC121DNAJC5-R2CCCATTGGCGCACACTCCC121DNAJC5-R2CGACAACTAGTATACGGTAACC139TCP1theta_R1GACAAGTGTATACCGGTAGATGACG101TCP1theta_R2CTTTCCGAGATGAAGTGACGACA118DNAJB9-R3CCCATTCCAAGTGACGACCAA118DNAJB9-R4GATGTGAATGGGAACCTTCC90DNAJB9-R5TATAGCCGTGTACGACCTTCC122hspa9b1HSPA9B-R5T			DNAJC3-R4	GGAATCCAGGAAGGCACGAA	
Image   Image   DNAJC10-R1   GCGACAATACTTCCGGAACA     2   DNAJC10-F2   GCCCGTGTATGGCATTCTCA   117     DNAJC10-R2   ACCCCAGCTTGGCTACAAAT   117     hsp83   1   Hsp90-F5   GGGTTCTTGATACACTC   127     Hsp83-5R   AACCTGGTCTTGATTCAAC   92   1   Hsp83-6R   TATCGGATCTTGCCAAGGC   92     hsp60   1   Hsp60-3F   AACTTGCAAGTGGTGTTGCTG   111     Hsp60-3R   CTACTGCAGGTGGTGTGCGG   111   111     Hsp60-3R   CTACTGCAGGTGTGCAGGACAAC   98     Msp60   1   Hsp60-75   CGCTGGCATGGAAGGACAAC   98     Msp70_F5   CACTGGCCTTTCAAGGTAGT   229     Hsp70_F5   CCACTGGCATAGTCAGGTAGT   237     Hsp70_R4   ATCCTGGTTGATCCCGAC   107     trap R2   GGTCGCGACGAGTTTCAAGCTG   107     trap R2   GGTCGCACAGAGTTTCAAGCTG   113     DNAJC5-F1   AAGACACGAGTTTCAAGCTG   113     DNAJC5-R2   CGACACTAGGTGTTTCTCC   121     DNAJC5-R2   CGACAACTAGGTATACCGCATCA	dnajc10	1	DNAJC10-F1	CAGGATCCTGATGAAATAAC	204
2DNAJC10-F2GCCCGTGTATGGCATTCTCA117DNAJC10-R2ACCCCAGCTTGGCTACAAAT117hsp831Hsp90-F5GGGTTCTTGATTCAC127Hsp83-5RAACCTGGTCTTGATCACACAC92Hsp83-6FATGAGCTTGATCAACAACAC92Hsp83-6RTATCGGATCTTGTCCAAGGC111Hsp60-3FAACTTGCAAGTGGTGTTGCTG111Hsp60-3RCTACTGCAGCTCGTGTTGCG111Hsp60-3RCTACTGCAGCACTGTGATGCG98Hsp60-R5GTCGTAGCATAGCAAGTAC98Hsp70_R5CCACTGCCATAGTACACCTT229Hsp70_R5CCAGCCAAGTTCTTATCGAG237Hsp70_R4ATCCTGGTTGATCCTCCGAC237Hsp70_R4ATCCTGGTTGATCCTCCGAC107trap R2GGTCGCGACGACGTTGATCC237Hsp70_R4ATCCTGGTTGATCCTCCGAC107trap R2GGTCGCGACGACGTTGATCC237Hsp70_R4ATCCTGGTTGATCCTCCGAC107trap R2GGTCGCGCACGACGTTGATCC237Hsp70_R4ATCCTGGTTGATCCTCCAGC107trap R5TCTAACGCGTCACTCACCTCAAGT130DNAJC5-R1GTCCTCAGGTTGATCTCC121DNAJC5-R2CCAACTATGATTATGCAA139TCP1theta_R1GACAAGTGTATACCGCTACT124Lcp1theta1TCP1theta_R2CTTTCGCGAGTAACAGTGACGAC101TCP1theta_R2CTTTCGCGAGTGTATACCGCTACT121DNAJB9-R3GAGCCAGACGCGAAGCAAA118DNAJB9-R3CCCATATTGTCAAAGCC90DNAJB9-R4GATGTGAATGGGAACCTTCC122DNAJB9-R5 <td></td> <td></td> <td>DNAJC10-R1</td> <td>GCGACAATACTTCCGCAACA</td> <td></td>			DNAJC10-R1	GCGACAATACTTCCGCAACA	
Image   Image <th< td=""><td></td><td>2</td><td>DNAJC10-F2</td><td>GCCCGTGTATGGCATTCTCA</td><td>117</td></th<>		2	DNAJC10-F2	GCCCGTGTATGGCATTCTCA	117
hsp83   1   Hsp90-F5   GGGTTCCTTCAATATCACTC   127     Hsp83-5R   AACCTGGTCTTTGATTCAC   22     Hsp83-6R   ATGAGCTTGATCATCAACAC   92     Hsp83-6R   TATCGGATCTTGTCCAAGGC   92     hsp60   1   Hsp60-3F   AACTTGCAAGTGGTGTTGCTG   111     Hsp60-3R   CTACTGCAGCTGGTGTGCGG   111     Hsp60-7S   CGCTGGCATGGAAGGACAAC   98     Hsp70_R5   CCAGCGCATGGTAGCAATGTCACCTT   14     hsp70_R5   CCAGCCAAGTTCTTATCGAAG   229     Hsp70_R5   CCAGCCAAGTTCTTATCGAAG   237     Hsp70_R5   CCAGTCGGTGATCCTCCGAC   237     Hsp70_R5   CCAGCGAGAGAACTGC   107     trap   1   trap F2   GGTCGCGCACGACTTGATCC   237     trap1_R5   TCTAACGCGTCACTCGCACT   107   113     pNajC5-F1   AATGAACCTCAAGCTGAAGCTG   107     trap1_R5   TCTACGGGTGATCACCTCAAGCTG   121     pNAjC5-F1   AATGAACCTCAACCTCAAGCTG   121     pNAjC5-R2   CCCATTGGATCACCACTCC   121     <			DNAJC10-R2	ACCCCAGCTTGGCTACAAAT	
Image   Image <th< td=""><td>hsp83</td><td>1</td><td>Hsp90-F5</td><td>GGGTTCCTTCAATATCACTC</td><td>127</td></th<>	hsp83	1	Hsp90-F5	GGGTTCCTTCAATATCACTC	127
2Hsp83-6FATGAGCTTGATCATCAACAC92Hsp83-6RTATCGGATCTTGTCCAAGGCHsp83-6RTATCGGATCTTGTCCAAGGChsp601Hsp60-3FAACTTGCAAGTGGTGTTGCG111Hsp60-3RCTACTGCAGCTCGTGTTGCG982Hsp60_F5CGCTGGCATGGAAGGACAAC98Hsp60_R5GTCGTAGCCATAGTCACCTT229Hsp70_R5CCACTGGCTTTCAAGGTAGT229Hsp70_R4ATCCTGGTTGATCCTCCGAC237Hsp70_R4ATCCTGGTTGATCCTCCGAC107trap1trap F2CAACTTGAGCAGAGAACTGC107trap R2GGTCGCGACGACTTTGATCC107trap R2GGTCGCGACGACTTGATCC113DNAJC5-F1AATGAACCTCAACCTCAAGGTG75trap1_R5TCTAACGCGTCACTCACCTCC121DNAJC5-R1GTCCTCAGGTTGATCACCTCC121DNAJC5-R2CGACAACTATGATTTATGCA139tCp1theta1CP1theta_F1CGACAGGGGAGTAGACGACACT2DNAJC5-R2CGACAACTATGATTCATGCA139tCp1theta1CP1theta_F2GAGAGGGCAGTAGAGAGAA118dnajb91DNAJB9-F3GAGCCAGACGCGGAAGCAA118hspa9b1HSPA9B-F5TTATAGCCGTGTACACCTC90hspa9b1HSPA9B-F5TTATAGCCGTGTACGACCTT192			Hsp83-5R	AACCTGGTCTCTTGATTCAC	
Hsp83-6R   TATCGGATCTTGTCCAAGGC     hsp60   1   Hsp60-3F   AACTTGCAAGTGGTGTTGCG   111     Hsp60-3R   CTACTGCAGCTCGTGTTGCG   111     Hsp60_R5   GTCGTAGCATGGAAGGACAAC   98     Hsp60_R5   GTCGTAGCCATAGTCACCTT   229     hsp70   1   Hsp70_F5   CACTGGCTTTCAAGGTAGT   229     Hsp70_R5   CCAGCCAAGTTCTTATCGAAGTCC   237     Hsp70_R4   ATCCTGGTTGATCCTCCGAC   107     trap   1   trap F2   CAACTTGAGCAGAGAAACTGC   107     trap R2   GGTCGCGCACGACGACTTTGATCC   237   107   1113     dnajc5   1   trap F2   CAACTTGAGCAGAGAACTGC   107     trap R2   GGTCGCGCACGACGACTTGATCC   1107   1113     dnajc5   1   DNAJC5-F1   AATGAACGCGTCACTCGCATT   1121     dnajc5   1   DNAJC5-F2   CCCTTGGGCGCATCACCTCC   121     dnajc5   1   TCP1theta_F1   CGTAGATAACATTCGTGTGA   139     TCP1theta_R1   GACAAGTGTATACCGCTACT   113 <t< td=""><td></td><td>2</td><td>Hsp83-6F</td><td>ATGAGCTTGATCATCAACAC</td><td>92</td></t<>		2	Hsp83-6F	ATGAGCTTGATCATCAACAC	92
hsp60   1   Hsp60-3F   AACTTGCAAGTGGTGTTGCTG   111     Hsp60-3R   CTACTGCAGCTCGTGTTGCG   98     Hsp60_R5   GTCGTAGCCATAGTCACCTT   98     hsp70   1   Hsp70_F5   CACTGGCATGGAAGGACAAC   98     2   Hsp70_R5   CCAGCCAAGTTCTTATCGAAG   229     Hsp70_R5   CCAGCCAAGTTCTTATCGAAG   237     Hsp70_R4   ATCCTGGTTGATCCTCCGAC   237     trap   1   trap F2   CAACTTGAGCAGAGAGAACTGC   107     trap R2   GGTCGCGACGACTTTGATCC   237     dnajc5   1   trap1_F5   TGAACACGAGTTTCAAGCTG   107     trap R2   GGTCGCCGCACGACTTTGATCC   107   113     DNAJC5-F1   AATGAACCTCAACCTCAAGGT   113     DNAJC5-R2   CCCATTGGGCGCATCACCTCC   121     DNAJC5-R2   CGACAACTATGATTATATGCA   139     TCP1theta_R1   GACAAGTGTATACCGCTACT   121     DNAJC5-R2   CGTAGATAACATTCGTGTGA   139     TCP1theta_R1   GACAAGTGTATACCGCTACT   121     DNAJS9-R3   CCCA			Hsp83-6R	TATCGGATCTTGTCCAAGGC	
Hsp60-3R   CTACTGCAGCTCGTGTTGCG     2   Hsp60_F5   CGCTGGCATGGAAGGACAAC   98     Hsp60_R5   GTCGTAGCCATAGTCACCTT   229     hsp70   1   Hsp70_F5   CACTGGCCATAGTCACCTT   229     Hsp70_R5   CCAGCCAAGTTCTTATCGAAG   237     Hsp70_R4   ATCCTGGTTATCGAAGACCC   237     Hsp70_R4   ATCCTGGTTGATCCTCCGAC   107     trap   1   trap F2   CAACTTGAGCAGAGAACTGC   107     trap R2   GGTCGCGACGACTTTGATCC   20   107     trap R2   GGTCGCGACGACTTTGATCC   107     dnajc5   1   DNAJC5-F1   AATGAACCTCAAGCTGCATT   107     dnajc5   1   DNAJC5-R1   GTCCTCAGGTTGTCTCCC   113     DNAJC5-R2   CCCCTTGGCCATCACCTCC   121   104     tcp1theta   1   TCP1theta_F1   CGTAGATAACATTCGTGTGA   139     TCP1theta_R2   CTTTTCGCGAGTTCTATCTC   121   104   104     1   TCP1theta_R2   CTTTTCGCGAGTTCTATCTC   113     1   DNAJB9-F3	hsp60	1	Hsp60-3F	AACTTGCAAGTGGTGTTGCTG	111
2Hsp60_F5CGCTGGCATGGAAGGACAAC98Hsp60_R5GTCGTAGCCATAGTCACCTT229hsp701Hsp70_F5CACTGGCTTTCAAGGTAGT229Hsp70_R5CCAGCCAAGTTCTTATCGAG237Hsp70_R4ATCCTGGTTGATCCTCCGAC237trap1trap F2CAACTTGAGCAGAGAACTGC107trap R2GGTCGCGACGACGACTTGATCCA107trap R2GGTCGCGACGACTTGATCC23dnajc51DNAJC5-F1TGAACACGAGTTTCAAGCTG113DNAJC5-R1GTCCTCAGGTGTCTTCTCC121DNAJC5-R2CGACAACTATGATTATAGCA129tcp1theta1TCP1theta_F1CGTAGATAACATTCGTGTGA139TCP1theta_R1GACAAGTGTATACCGCTACT101TCPtheta_R2CTTTTCGCGAGTGATGATGACG101TCPtheta_R2CTTTTCGCGAGTGATCACCC118DNAJB9-R3GAGCCAGACGCGGAAGCAA118DNAJB9-R4GATGTGAATGGGAACCTTCC90DNAJB9-R5TTATAGCCGTGTACGACCTT192			Hsp60-3R	CTACTGCAGCTCGTGTTGCG	
ImageHsp60_R5GTCGTAGCCATAGTCACCTThsp701Hsp70_F5CACTGGCCTTTCAAGGTAGT229Hsp70_R5CCAGCCAAGTTCTTATCGAG2372Hsp70_R4ATCCTGGTTGATCCTCCGAC237trap1trap F2CAACTTGAGCAGAGAACTGC107trap R2GGTCGCGACGACTTTGATCC107trap1_R5TCTAACGCGTCACTCGCATT1dnajc51DNAJC5-F1AATGAACCTCAACCTCAAGG113DNAJC5-R1GTCCTCAGGTTGTCTTCTCC121DNAJC5-R2CGACAACTATGATTATGCA139tcp1theta1TCP1theta_F1CGTAGATAACATTCGTGTGA139TCP1theta_R1GACAAGTGTATACCGCTACT113dnajb91DNAJB9-F3GAGCCAGACGCGGAAGCAA118DNAJB9-R3CCCATATTGTCTTCTCC111111frap1TCP1theta_R1GAGCAGACGCGGAAGCAA118DNAJB9-R4GAGTGTGAATGGGAACCTTCC90114hspa9b1HSPA9B-F5TTATAGCCGTGTACGACCTT192		2	Hsp60_F5	CGCTGGCATGGAAGGACAAC	98
hsp701Hsp70_F5CACTGGCCTTTCAAGGTAGT229Hsp70_R5CCAGCCAAGTTCTTATCGAG237Hsp70_R4ATCCTGGTTGATCCTCCGAC237trap1trap F2CAACTTGAGCAGAGAACTGC107trap R2GGTCGCGACGACTTTGATCC22trap1_R5TCTAACGCGTCACTCGCATT75trap1_R5TCTAACGCGTCACTCGCATT113DNAJC5-R1GTCCTCAGGTTGTCTTCTCC121DNAJC5-R2CGACAACTATGATTATGCA139tcp1theta1TCP1theta_F1CGTAGATAACATTCGTGTGA139TCP1theta_R1GACAAGTGTATACCGCTACTC101tcp1theta1DNAJB9-F3GAGCCAGACGCGAAGCAA118dnajb91DNAJB9-F3GAGCCAGACGCGGAAGCAA118hspa9b1HSPA9B-F5TTATAGCCGTGTACGACCTT192hspa9b1HSPA9B-R5GGGCCGCTTGCATCCATGGT192			Hsp60_R5	GTCGTAGCCATAGTCACCTT	
Image: https://image: https://image	hsp70	1	Hsp70_F5	CACTGGCCTTTCAAGGTAGT	229
2Hsp70-F3CCATTCGGTTATCGAAGTCC237Hsp70_R4ATCCTGGTTGATCCTCCGAC107trap1trap F2CAACTTGAGCAGAGAACTGC107trap R2GGTCGCGACGACTTTGATCC22trap1_F5TGAACACGAGTTTCAAGCTG75trap1_R5TCTAACGCGTCACTCGCATT113DNAJC5-F1AATGAACCTCAACCTCAAGG1130najc51DNAJC5-F2CCCTTGGGCGCATCACCTCC1212DNAJC5-R2CGACAACTATGATTATGCA121tcp1theta1TCP1theta_F1CGTAGATAACATTCGTGTGA1397CP1theta_R1GACAAGTGTATACCGCTACT1211TCP1theta_R2CTTTTCGCGAGTTCTATCTC1012TPC1theta_R2CTTTTCGCGAGTTCAACC1011DNAJB9-F3GAGCCAGACGGGAAGCAA1180najb91DNAJB9-F4CCGACTTCCAAAGTGACGAC901NAJB9-F5TTATAGCCGTGTACGACCTT192hspa9b1HSPA9B-F5GGGCCGCTTGCATCCATGGT192			Hsp70_R5	CCAGCCAAGTTCTTATCGAG	
Image		2	Hsp70-F3	CCATTCGGTTATCGAAGTCC	237
trap1trap F2CAACTTGAGCAGAGAACTGC107trap R2GGTCGCGACGACTTTGATCC107trap R2GGTCGCGACGACTTGATCC75trap1_F5TGAACACGAGTTTCAAGCTG75trap1_R5TCTAACGCGTCACTCGCATTdnajc51DNAJC5-F1AATGAACCTCAAGCGTACTCCC113DNAJC5-R1GTCCTCAGGTTGTCTTCTCC2DNAJC5-R2CGACAACTATGATTATGCAtcp1theta1TCP1theta_F14TCP1theta_F1CGTAGATAACATTCGTGTGA5TCP1theta_R1GACAAGTGTATACCGCTACT6TCP1theta_R2CTTTTCGCGAGTTCTATCTC6DNAJB9-F3GAGCCAGACGCGGAAGCAA6DNAJB9-R3CCCATATTGTCGTTCAAACC6DNAJB9-R4GATGTGAATGGGAACCTTCC6HSPA9B-R5GGGCCGCTTGCATCCATGGT			Hsp70_R4	ATCCTGGTTGATCCTCCGAC	
Image R2GGTCGCGACGACTTTGATCC2trap1_F5TGAACACGAGTTTCAAGCTG75imajc51DNAJC5-F1AATGAACCTCAACCTCAAGG113DNAJC5-R1GTCCTCAGGTTGTCTTCTCC2DNAJC5-F2CCCTTGGGCGCATCACCTCC121imajc52DNAJC5-F2CCCTTGGGCGCATCACCTCC121imajc51TCP1theta_F1CGTAGATAACATTCGTGTGA139imajc511TCP1theta_F1CGTAGATAACATTCGTGTGA139imajc511TCP1theta_R1GACAAGTGTATACCGCTACT101imajb91InnaJB9-F3GAGCCAGACGCGGAAGCAA118imajb91DNAJB9-F3CCCATATTGTCGTTCAAACC90imajb91HSPA9B-F5TTATAGCCGTGTACGACCTT192imajb91HSPA9B-F5GGGCCGCTTGCATCGACCTT192imajb91HSPA9B-F5GGGCCGCTTGCATCCATGGT192imajb91HSPA9B-F5GGGCCGCTTGCATCCATGGT192imajb91HSPA9B-F5GGGCCGCTTGCATCCATGGT192imajb91HSPA9B-F5GGGCCGCTTGCATCCATGGT192imajb91HSPA9B-F5GGGCCGCTTGCATCCATGGT192imajb91HSPA9B-F5GGGCCGCTTGCATCCATGGT192imajb11HSPA9B-F5GGGCCGCTTGCATCCATGGT192imajb21HSPA9B-F5GGGCCGCTTGCATCCATGGT192imajb21HSPA9B-F5GGGCCGCTTGCATCCATGGT192imajb21HSPA9B-F5GGGCCGCTTGCATCCATGGT	trap	1	trap F2	CAACTTGAGCAGAGAACTGC	107
2trap1_F5TGAACACGAGTTTCAAGCTG75trap1_R5TCTAACGCGTCACTCGCATTdnajc51DNAJC5-F1AATGAACCTCAACCTCAAGG113DNAJC5-R1GTCCTCAGGTTGTCTTCTCC2DNAJC5-R2CCCTTGGGCGCATCACCTCC121DNAJC5-R2CGACAACTATGATTTATGCA139tcp1theta1TCP1theta_F1CGTAGATAACATTCGTGTGA139TCP1theta_R1GACAAGTGTATACCGCTACT101TCP1theta_R2CTTTTCGCGAGTTCTATCTC101dnajb91DNAJB9-F3GAGCCAGACGCGGAAGCAA118DNAJB9-R3CCCATATTGTCGTTCAAACC90hspa9b1HSPA9B-F5TTATAGCCGTGTACGACCTT192hSPA9B-R5GGGCCGCTTGCATCCATGGT192			trap R2	GGTCGCGACGACTTTGATCC	
Image		2	trap1_F5	TGAACACGAGTTTCAAGCTG	75
dnajc51DNAJC5-F1AATGAACCTCAACCTCAAGG113DNAJC5-R1GTCCTCAGGTTGTCTTCTCC22DNAJC5-F2CCCTTGGGCGCATCACCTCC121DNAJC5-R2CGACAACTATGATTTATGCA139tcp1theta1TCP1theta_F1CGTAGATAACATTCGTGTGA1397CP1theta_R1GACAAGTGTATACCGCTACT1012TPC1theta_F2GGAGAGGGCAGTAGATGACG1017CP1theta_R2CTTTTCGCGAGTTCTATCTC118dnajb91DNAJB9-F3GAGCCAGACGCGGAAGCAA118DNAJB9-R3CCCATATTGTCGTTCAAACC902DNAJB9-F4CCGACTTCCAAAGTGACGAC90hspa9b1HSPA9B-F5TTATAGCCGTGTACGACCTT192HSPA9B-R5GGGCCGCTTGCATCCATGGT192			trap1_R5	TCTAACGCGTCACTCGCATT	
Image: bit is bit bit is bit bit bit is bit	dnajc5	1	DNAJC5-F1	AATGAACCTCAACCTCAAGG	113
2DNAJC5-F2CCCTTGGGCGCATCACCTCC121DNAJC5-R2CGACAACTATGATTTATGCA139tcp1theta1TCP1theta_F1CGTAGATAACATTCGTGTGA139TCP1theta_R1GACAAGTGTATACCGCTACT2TPC1theta_F2GGAGAGGGCAGTAGATGACG101TCPtheta_R2CTTTTCGCGAGTTCTATCTC1181000000000000000000000000000000000000	-		DNAJC5-R1	GTCCTCAGGTTGTCTTCTCC	
Image: marked base base base base base base base base		2	DNAJC5-F2	CCCTTGGGCGCATCACCTCC	121
tcp1theta1TCP1theta_F1CGTAGATAACATTCGTGTGA139TCP1theta_R1GACAAGTGTATACCGCTACT1392TPC1theta_R2GGAGAGGGCAGTAGATGACG101TCPtheta_R2CTTTTCGCGAGTTCTATCTC101dnajb91DNAJB9-F3GAGCCAGACGCGGAAGCAA118DNAJB9-R3CCCATATTGTCGTTCAAACC902DNAJB9-F4CCGACTTCCAAAGTGACGAC90bNAJB9-R4GATGTGAATGGGAACCTTCC192hspa9b1HSPA9B-F5TTATAGCCGTGTACGACCATGGT192			DNAJC5-R2	CGACAACTATGATTTATGCA	
TCP1theta_R1GACAAGTGTATACCGCTACT2TPC1theta_F2GGAGAGGGCAGTAGATGACG101TCPtheta_R2CTTTTCGCGAGTTCTATCTCdnajb91DNAJB9-F3GAGCCAGACGCGGAAGCAA118DNAJB9-R3CCCATATTGTCGTTCAAACC2DNAJB9-F4CCGACTTCCAAAGTGACGAC90DNAJB9-R4GATGTGAATGGGAACCTTCC90192192hspa9b1HSPA9B-F5TTATAGCCGTGTACGACCATGGT192	tcp1theta	1	TCP1theta_F1	CGTAGATAACATTCGTGTGA	139
2TPC1theta_F2GGAGAGGGCAGTAGATGACG101TCPtheta_R2CTTTTCGCGAGTTCTATCTCdnajb91DNAJB9-F3GAGCCAGACGCGGAAGCAA118DNAJB9-R3CCCATATTGTCGTTCAAACC22DNAJB9-F4CCGACTTCCAAAGTGACGAC90DNAJB9-R4GATGTGAATGGGAACCTTCC90hspa9b1HSPA9B-F5TTATAGCCGTGTACGACCTT192HSPA9B-R5GGGCCGCTTGCATCCATGGT192	-		TCP1theta_R1	GACAAGTGTATACCGCTACT	
Image: marked base with the stress of the		2	TPC1theta_F2	GGAGAGGGCAGTAGATGACG	101
dnajb91DNAJB9-F3GAGCCAGACGCGGAAGCAA118DNAJB9-R3CCCATATTGTCGTTCAAACC1182DNAJB9-F4CCGACTTCCAAAGTGACGAC90DNAJB9-R4GATGTGAATGGGAACCTTCC90hspa9b1HSPA9B-F5TTATAGCCGTGTACGACCTT192HSPA9B-R5GGGCCGCTTGCATCCATGGT192			TCPtheta R2	CTTTTCGCGAGTTCTATCTC	
DNAJB9-R3 CCCATATTGTCGTTCAAACC   2 DNAJB9-F4 CCGACTTCCAAAGTGACGAC 90   DNAJB9-R4 GATGTGAATGGGAACCTTCC 90   hspa9b 1 HSPA9B-F5 TTATAGCCGTGTACGACCTT 192   HSPA9B-R5 GGGCCGCTTGCATCCATGGT 192	dnaib9	1	DNAJB9-F3	GAGCCAGACGCGGAAGCAA	118
2 DNAJB9-F4 CCGACTTCCAAAGTGACGAC 90   DNAJB9-R4 GATGTGAATGGGAACCTTCC 90   hspa9b 1 HSPA9B-F5 TTATAGCCGTGTACGACCTT 192   HSPA9B-R5 GGGCCGCTTGCATCCATGGT 192	<b>j</b>		DNAJB9-R3	CCCATATTGTCGTTCAAACC	
Image: bit		2	DNAJB9-F4	CCGACTTCCAAAGTGACGAC	90
hspa9b 1 HSPA9B-F5 TTATAGCCGTGTACGACCTT 192 HSPA9B-R5 GGGCCGCTTGCATCCATGGT		_	DNAJB9-R4	GATGTGAATGGGAACCTTCC	
HSPA9B-R5 GGGCCGCTTGCATCCATGGT	hspa9h	1	HSPA9B-F5	TTATAGCCGTGTACGACCTT	192
		.	HSPA9B-R5	GGGCCGCTTGCATCCATGGT	102
hspa8 1 HSPA2/8-4F CTTCGTGACGCTAAGATGGG 91	hspa8	1	HSPA2/8-4F	CTTCGTGACGCTAAGATGGG	.91
HSPA2/8-4R GGAATACGAGTGGAGCCACC			HSPA2/8-4R	GGAATACGAGTGGAGCCACC	01

Supplementary Table S4. List of primer sequences used for qPCR analysis.

Supplementary Table S5. ER chaperones identified from genomes of various organisms with special focus on marine invertebrates. All except *M. brevicollis* are animals, and most have planktonic larvae. Accession numbers are given where these exist. In other cases gene models or equivalent identifiers are listed, which can be accessed via the database shown.

Species	Database/ Source	dnajc3 orthologue	dnajc10 orthologue	dnajb9 orthologue
<i>H. sapiens</i> (human)	NCBI	EAX08959	AAI17300	Q9UBS3
<i>C. intestinalis</i> (sea squirt)	Aniseed	KH.C1.269.	KH.C9.567.	KH.C9.914.
<i>B. floridae</i> (amphioxus)	JGI	jgi Brafl1 122581  jgi Brafl1 119688	jgi Brafl1 125408 est Ext_fgenesh2_pg.C _1820034	jgi Brafl1 203558 e_gw.1 0.429.1
S. purpuratus (sea urchin)	Spbase	SPU_005174	SPU_017259	Not found
<i>S. kowalevskii</i> (acorn worm)	NCBI; http://blast. hgsc.bcm.t mc.edu/	Contig96435*	XP_002740489.1	XP_002730538.1
<i>C. teleta</i> (annelid)	JGI	jgi Capca1 228061  estExt_fgenesh1_p g.C_660051	jgi Capca1 228052 e stExt_fgenesh1_pg. C_660035	jgi Capca1 19566 estExt _fgenesh1_pm.C_50000 3 (DNAJB1/4/5 and DNAJB9 orthologue) jgi Capca1 225634
L. gigantea (limpet)	JGI	jgi Lotgi1 151060 fg enesh2_kg.C_sca_ 80000004	jgi Lotgi1 171701  jgi Lotgi1 237821	jgi Lotgi1 235906  jgi Lotgi1 168037
C. gigas (oyster)	NCBI	EKC24329	EKC28571	EKC30878.1
<i>C. elegans</i> (nematode)	wormbase	dnj7	dnj27	Not found
<i>D. melanogaster</i> (fruitfly)	flybase	P58IPK	Not found	Not found
<i>A. digitifera</i> (coral)	http://marin egenomics. oist.jp/geno mes/gallery	aug_v2a.19366.t1*	aug_v2a.21205.t1	aug_v2a.18536.t1
<i>N. vectensis</i> (sea anemone)	JGI	jgi Nemve1 174406  estExt_gwp.C_304 0037	jgi Nemve1 163820  estExt_gwp.C_4400 26	jgi Nemve1 106836 e_g w.84.88.1
T. adhaerens	JGI	jgi Triad1 32828 e_	Not found	jgi Triad1 56372 fgenesh

(placozoan)		gw1.26.21.1	Triad1 60480?	TA2_pg.C_scaffold_500
				0266
M. leidyi	http://resea	ML06971a	ML01344a	ML07989a
(ctenophore)	rch.nhgri.ni			ML37595a
	h.gov/mne			ML01344a
	miopsis/			
Α.	NCBI	XP_003390240.1	Not found	Not found
queenslandica		XP_003391066.1		
(sponge)		XP_003389230.1		
M. brevicollis	JGI	jgi Monbr1 6406	jgi Monbr1 21911	Not found
(choanoflagell-		jgi Monbr1 15161		jgi Monbr1 22976?
ate)		jgi Monbr1 18047		
		jgi Monbr1 18048		
		jgi Monbr1 20049		

\*Only whole genome contig and/or incomplete gene prediction available. Orthology of hit verified by reciprocal BLAST.



**Supplementary Fig. 1. Comparison of expression levels of** *dnajc3.* **a**, **b**, show results from primer set 1, whereas **c**, **d** show primer set 2. **a**, **c**, Quantification of *dnajc3* expression levels by qPCR in control (C) or heat shocked (H: 27°C for 1h at neurula stage as in Fig. 1a) embryos. Heat shock did not significantly affect the expression of *dnajc3*, however expression in type A (AA) was significantly higher than in type B (BB) (P = 0.002). Reciprocal hybridization (AB/BA) showed strong correlation to the maternal genotype (P < 0.0001). Significances are shown by asterisks: \*\*P < 0.01; \*\*\*P < 0.001. **b**, **d**, Correlation between the amount of *dnajc3* transcripts and Normal proportion after heat shock in individual crosses. Analysis of Variance (ANOVA) rejected the null hypothesis and supported linear correlation of the amount of *dnajc3* transcripts and normal proportion (P < 0.04 for primer sets 1 and P < 0.002 for primer sets 2).



**Supplementary Fig. 2. Comparison of expression levels of** *dnajc10***. a, b,** show results from primer set 1, whereas **c**, **d** show primer set 2. **a, c,** Quantification of *dnajc10* expression levels by qPCR in control (C) or heat shocked (H: 27°C for 1h at neurula stage as in Fig. 1a) embryos. Heat shock did not significantly affect the expression of *dnajc10*, and expression in type A (AA) under control condition was significantly higher than in type B (BB) (P = 0.0067). Reciprocal hybridization (AB/BA) suggested this was linked to the maternal genotype ( $P \ll 0.0001$ ). Significances are shown by asterisks: \*\* P < 0.01; \*\*\* P < 0.001. **b, d,** Correlation between the amount of *dnajc10* transcripts and normal proportion after heat shock in individual crosses. Analysis of Variance (ANOVA) supports linear correlation of the amount of *dnajc10* transcripts and normal proportion after shock in individual crosses. Analysis of Variance (ANOVA) supports linear correlation of the amount of *dnajc10* transcripts and normal proportion after heat shock in individual crosses. Analysis of Variance (ANOVA) supports linear correlation of the amount of *dnajc10* transcripts and normal proportion after heat shock in individual crosses. Analysis of Variance (ANOVA) supports linear correlation of the amount of *dnajc10* transcripts and normal proportion after heat shock in individual crosses.



Supplementary Fig. 3. Comparison of expression levels of *hspa83*. a, b, show results from primer set 1, whereas c, d show primer set 2. a, c, Quantification of *hspa83* expression levels by qPCR in control (C) or heat shocked (H: 27°C for 1h at neurula stage as in Fig. 1a) embryos. Heat shock did not significantly affect the expression of *hspa83* (P = 0.013), but expression in type A (AA) was significantly higher than in type B (BB) (P = 0.0081). However, reciprocal hybridization (AB/BA) did not suggest this was linked to the maternal genotype (P > 0.85). Significances are shown by asterisks: \*\* P < 0.01. b, d, Correlation between the amount of *hspa83* transcripts and normal proportion after heat shock in individual crosses. Analysis of Variance (ANOVA) did not support linear correlation of the amount of *hsp83* transcripts and Normal proportion (P < 0.008 for primer set 1; for primer set 2 P > 0.25).



**Supplementary Fig. 4. Comparison of expression levels of** *hsp60.* **a**, **b**, show results from primer set 1, whereas **c**, **d** show primer set 2. **a**, **c**, Quantification of *hsp60* expression levels by qPCR in control (C) or heat shocked (H: 27°C for 1h at neurula stage as in Fig. 1a) embryos. Heat shock significantly affected the expression of *hsp60* only in type B (BB). Comparisons of expression in type A (AA) and in type B (BB) showed significant differences under control condition (P = 0.001). However, reciprocal hybridization (AB/BA) did not suggest this was linked to the maternal genotype (P = 0.2526). Significances are shown by asterisks: \*\* P < 0.01; \*\*\*P < 0.001. **b**, **d**, Correlation between the amount of *hsp60* transcripts and Normal proportion after heat shock in individual crosses. Analysis of Variance (ANOVA) did not support linear correlation of the amount of *hsp60* transcripts and normal proportion (P > 0.42 for both primer sets 1 and 2).



**Supplementary Fig. 5. Comparison of expression levels of** *hsp70.* **a, b,** show results from primer set 1, whereas **c, d** show primer set 2. **a, c,** Quantification of *hsp70* expression levels by qPCR in control (C) or heat shocked (H: 27°C for 1h at neurula stage as in Fig. 1a) embryos. Heat shock significantly affected the expression of *hsp70* in both types A and B (P << 0.0001). Reciprocal hybridization (AB/BA) did not show its link to the maternal genotype (P > 0.02), but the level of expression was negatively correlated to thermal tolerance of these hybrid types. Significances are shown by asterisks: \*\*\*P < 0.001. **b, d,** Correlation between the amount of *hsp70* transcripts and normal proportion after heat shock in individual crosses. Analysis of Variance (ANOVA) did not support linear correlation of the amount of *hsp70* transcripts and Normal proportion (P = 0.08933 for primer set 1 and P = 0.103 for primer set 2).



**Supplementary Fig. 6. Comparison of expression levels of** *trap1.* **a, b,** show results from primer set 1, whereas **c, d** show primer set 2. **a, c,** Quantification of *trap1* expression levels by qPCR in control (C) or heat shocked (H: 27°C for 1h at neurula stage as in Fig. 1a) embryos. Heat shock did not significantly affect the expression of *trap1* (P = 0.6431), but expression in type A (AA) was significantly higher than in type B (BB) (P << 0.0001). Reciprocal hybridization (AB/BA) also showed this was linked to the maternal genotype (P << 0.0001). Significances are shown by asterisks: \*\*\*P < 0.001. **b, d,** Correlation between the amount of *trap1* transcripts and normal proportion after heat shock in individual crosses. Analysis of Variance (ANOVA) did not supports linear correlation of the amount of *trap1* transcripts and Normal proportion (P = 0.09315 for primer set 1 and P = 0.046 for primer set 2).



**Supplementary Fig. 7. Comparison of expression levels of** *tcp1theta.* **a**, **b**, show results from primer set 1, whereas **c**, **d** show primer set 2. **a**, **c**, Quantification of *trap1* expression levels by qPCR in control (C) or heat shocked (H: 27°C for 1h at neurula stage as in Fig. 1a) embryos. Heat shock did not significantly affect the expression of *TCP1theta* (P = 0.0331), but expression in type A (AA) was significantly higher than in type B (BB) (P << 0.0001). Reciprocal hybridization (AB/BA) also suggested this was linked to the maternal genotype (P = 0.0008). Significances are shown by asterisks: \*\*\*P < 0.001. **b**, **d**, Correlation between the amount of *trap1* transcripts and Normal proportion after heat shock in individual crosses. Analysis of Variance (ANOVA) did not supports linear correlation of the amount of *tcp1theta* transcripts and normal proportion (P=0.286 for primer set 1 and P=0.6196 for primer set 2).



**Supplementary Fig. 8. Comparison of expression levels of** *dnajc5.* **a**, **b**, show results from primer set 1, whereas **c**, **d** show primer set 2. **a**, **c**, Quantification of *dnajc5* expression levels by qPCR in control (C) or heat shocked (H: 27°C for 1h at neurula stage as in Fig. 1a) embryos. Heat shock did not significantly affect the expression of *dnajc5* (P > 0.2), and type A (AA) was significantly higher than in type B (BB) in the expression levels only under control condition (P = 0.0029). Reciprocal hybridization (AB/BA) did not show this was linked to the maternal genotype (P = 0.0023). Significances are shown by asterisks: \*\*P < 0.01. **b**, **d**, Correlation between the amount of *dnajc5* transcripts and Normal proportion after heat shock in individual crosses. Analysis of Variance (ANOVA) did not supports linear correlation of the amount of *dnajc5* transcripts and normal proportion (P = 0.1197 for primer set 1 and P = 0.03274 for primer set 2).



**Supplementary Fig. 9. Comparison of expression levels of** *dnajb9.* **a**, **b**, show results from primer set 1, whereas **c**, **d** show primer set 2. **a**, **c**, Quantification of *dnajb9* expression levels by qPCR in control (C) or heat shocked (H: 27°C for 1h at neurula stage as in Fig. 1a) embryos. Heat shock did not significantly affect the expression of *dnajb9* (P < 0.4), and expression in type A (AA) did not show significant difference from expression in type B (BB). However, reciprocal hybridization (AB/BA) suggests this was linked to the maternal genotype (P = 0.0061). **b**, **d**, Correlation between the amount of *dnajb9* transcripts and Normal proportion after heat shock in individual crosses. Analysis of Variance (ANOVA) did not support linear correlation of the amount of *dnajb9* transcripts and normal proportion (P = 0.554 for primer set 1, and P = 0.335 for primer set 2).



**Supplementary Fig. 10.** Comparison of expression levels of *hspa9b* and *hspa8.* a, b, show results from *hspa9b*, whereas c, d show *hspa8.* a, c, Quantification of each gene expression levels by qPCR in control (C) or heat shocked (H: 27°C for 1h at neurula stage as in Fig. 1a) embryos. Expression in type A (AA) did not show significant difference from expression in type B (BB) in both genes (for *hspa9b* P = 0.0366, for *hspa8* P = 0.0882). Heat shock significantly affected the expression of *hspa8* (P = 0.0021) but not in *hspa9b* (P = 0.048). Reciprocal hybridization (AB/BA) marginally supported this was linked to the maternal genotype in *hspa9b* (P = 0.0066) but not for *hspa8* (P = 0.8298). Significances are shown by asterisks: \*\*P < 0.01. b, d, Correlation between the amount of each gene transcripts and Normal proportion after heat shock in individual crosses. Analysis of Variance (ANOVA) did not support linear correlation of the amount of transcripts and normal proportion in neither of these genes (P=0.1575 for *hspa9b* and P=0.2384 for *hspa8*).



**Supplementary Fig. 11. Maximum Likelihood analysis of** *dnajc3* **and** *dnajc10* **genes.** Species used for the tree are as follows: *Drosophila melanogaster*, *Caenorhabditis elegans*, *Homo sapiens*, *Ciona intestinalis*, *Branchiostoma floridae* (amphioxus), *Strongylocentrotus purpuratus* (sea urchin), *Saccoglossus kowalevskii* (acorn worm), *Lottia gigantea* (mollusc), *Crassostrea gigas* (mollusc), *Capitella teleta* (annelid), *Nematostella vectensis* (anemone), *Mnemiopsis leidyi* (ctenophore), *Amphimedon queenslandica* (sponge), *Monosiga brevicolis* (choanoflagellate). Accession numbers are given in the figure for outgroup sequences and sequences from model species, for other sequence sources please refer to Supplementary Table S7.