

Supplemental Material to: Ruth Heyer, Marcella Dörr, Angelika Jellen-Ritter, Bettina Späth, Julia Babski, Katharina Jaschinski, et al. High throughput sequencing reveals a plethora of small RNAs including tRNA derived fragments in *Haloferax volcanii*. RNA Biology 2012; 9(7); DOI: 10.4161/rna.20826; <http://www.landesbioscience.com/journals/rnabiology/article/20826/>

Supplementary Tables

Supp.- Table 1. Expression profile of identified Hts sRNAs. The 145 Hts sRNAs identified in this study are listed (column Hts) (sequences for the Hts RNAs are listed in Supplementary Table 2) and the number of reads identified for each Hts sRNA at the different conditions is listed. For each of the six growth conditions a separate column is shown: column standard: standard growth conditions; high T: 48.5°C growth temperature (instead of the standard 45°C); low salt concentration in the medium (15% instead of the standard 18%). Columns expo: RNA from cells grown to exponential phase, column stat: RNA from cells grown to stationary phase.

Supp.- Table 2. Hts sRNA sequences. The sequences for the 145 Hts sRNAs identified in this study are listed as well as the respective gene number (HVO_XXXX).

Supp.-Table 3. Expression of identified tRNA derived fragments. The tRNA genes for which tRFs have been detected are shown. Column "start/ direction/ length" lists the start position of the respective tRNA gene on the *Haloferax* chromosome, the direction of the gene (F: forward, R: reverse) and the length of the encoded tRNA. Column "tRF" lists what type of tRF was found: 5': tRNA 5' fragment, 3' CCA: tRNA 3' fragment ending in CCA, 3' trailer: 3' trailer sequence. Column "reads at condition" lists the number of reads found at the listed condition.

Supp.-Table 4. Comparison of growth yields of mutants and parent strain H119 under ten different conditions. Three independent cultures were measured. The growth yields of the mutants are tabulated as fractions of that of the parent strain (%). The standard deviations are shown in parenthesis.

Supp.-Table 5. Results of the comparison of the transcriptomes of mutant *Δhts10* and parent strain H119. Tabulated are the gene or genes that differentially hybridised to the respective DNA microarray spots (HVO_XXXX number see www.halolex.mpg.de), the annotated function, the number of times the gene is represented on the microarray and the fold induction of repression. Average values of three independent biological replicates are shown, which included one dye swap.

Supp.-Table 6. tRNA genes encoded in the *Haloferax* genome. All tRNA genes encoded in the *Haloferax* genome are listed. If fragments were detected for a tRNA in the HTS approach the number of reads found at the respective conditions are listed. Column "strand/ start/ length" lists the start position of the respective tRNA gene on the *Haloferax* chromosome, the direction of the gene (chr (+) and chr (-) indicates the genome strand) and the length of the encoded tRNA. Column "tRF" lists what type of tRF was found: 5': tRNA 5' fragment, 3' CCA: tRNA 3' fragment ending in CCA, 3' trailer: 3' trailer sequence. Column "reads at condition" lists the number of reads found at the listed condition. Condition 1 and 2 standard growth conditions exponential and stationary phase, respectively, condition 3 and 4: high temperature, exponential and stationary phase, respectively, condition 5 and 6: low salt concentrations, exponential and stationary phase, respectively.

Supp.-Table 7. Primers used in this study. Sequences of primers used in this study are listed.

Supp.-Table 8. Target analysis for Hts sRNA 10 and up regulated mRNAs. Using the programme IntaRNA potential target regions in the up regulated mRNAs were identified. As input sequence for the ncRNA the Hts10 sequence (Supplementary Table 2) and the mRNA sequences with 100 nt up- and downstream sequence each were used. **A.** Table listing the respective mRNA analysed (the HVO_XXX number is shown, see Table 1), the binding energy between mRNA and Hts10 RNA and the positions involved in binding of the Hts10 sRNA as well as the mRNA. Below the table the interactions between Hts10 sRNA and the respective mRNA are shown. **B.** The potential targets can be clustered into four groups, where the respective mRNAs bind to similar or the same regions of the Hts10 sRNA. The mRNA clusters and their base pairing with the Hts10 RNA are shown. Nucleotides of the Hts RNA which bind to all target RNAs in one mRNA cluster are highlighted in yellow.

Supplementary Table 1

Hts	standard		high T		low salt	
	expo	stat	expo	stat	expo	stat
1	-	-	-	-	3,810	-
2	-	42	-	-	7,277	-
3	274	-	-	45	2,697	188
4	194	214	339	77	13,189	1,771
5	3,074	178	-	-	53	301
6	146	-	47	-	478	100
7	-	-	-	-	-	40
8	-	-	41	-	-	-
9	214	94	44	41	-	-
10	414	1,959	418	246	207	330
11	-	576	100	114	163	131
12	1,921	1,040	1,147	385	163	283
13	98	115	62	46	58	126
14	-	-	-	-	-	54
15	-	-	-	-	-	41
16	120	92	168	-	59	-
17	-	-	40	-	64	40
18	78	-	-	221	-	-
19	-	65	-	-	-	-
20	-	64	-	-	44	-
21	-	-	-	-	257	-
22	-	-	-	-	53	-
23	48	43	-	50	-	-
24	-	129	86	-	116	57
25	1,430	1,523	606	327	149	320
26	279	391	447	-	-	-
27	443	207	345	1769	223	131
28	-	49	-	-	-	-
29	45	61	98	-	-	49
30	-	479	136	-	101	450
31	101	60	68	59	52	-
32	-	53	-	-	-	-
33	53	155	58	-	41	-
34	129	140	-	-	-	-
35	67	125	231	-	-	-
36	-	65	-	-	-	804
37	125	393	56	70	-	-
38	137	221	141	168	89	101
39	88	790	143	254	236	1,369
40	-	41	-	-	-	-
41	450	211	-	69	-	-
42	-	-	-	-	54	-
43	-	639	100	317	1,516	4,634
44	-	-	-	-	-	109
45	105	112	-	-	-	48
46	-	101	-	-	-	-
47	-	42	-	-	-	-

48	-	-	52	-	-	-
49	-	-	-	-	55	-
50	373	-	42	-	-	-
51	1,678	1,592	593	904	4,888	204
52	-	-	41	-	-	132
53	-	-	-	-	53	59
54	-	84	-	-	-	-
55	58	-	-	-	-	-
56	-	-	-	-	51	-
57	-	-	-	-	368	-
58	65	-	-	-	63	-
59	271	513	139	252	49	43
60	-	-	-	-	53	-
61	-	134	95	46	51	-
62	-	118	70	-	-	90
63	53	182	58	-	41	-
64	-	-	-	-	-	40
65	-	58	-	-	-	-
66	88	150	-	-	-	-
67	-	-	62	42	132	88
68	-	47	-	-	-	-
69	-	-	-	-	170	-
70	183	423	171	248	229	364
71	2,639	1,333	770	1,969	622	1,046
72	158	199	-	45	44	-
73	96	49	93	53	50	111
74	-	-	-	-	-	60
75	-	-	-	-	158	851
76	40	-	-	-	69	56
77	95	162	155	-	-	42
78	-	324	65	64	146	-
79	140	369	59	50	-	51
80	144	322	91	-	51	-
81	-	-	-	-	58	-
82	-	88	-	64	132	560
83	-	75	83	-	-	-
84	-	297	71	67	104	123
85	395	57	100	93	54	81
86	-	-	-	-	60	-
87	-	48	-	-	-	-
88	-	-	44	-	-	-
89	-	-	-	-	-	52
90	-	-	-	63	-	-
91	263	474	442	85	44	41
92	-	-	-	-	177	-
93	43	-	-	-	-	-
94	-	220	72	-	433	94
95	-	-	53	-	-	-
96	56	43	229	41	-	206
97	-	108	-	-	-	-
98	-	143	91	100	82	440
99	366	957	1,533	178	56	198
100	48	-	-	-	84	52
101	61	1,852	220	143	-	813

102	-	42	-	-	-	-
103	55	-	-	-	-	-
104	-	-	-	-	-	94
105	-	-	-	-	-	53
106	-	-	-	-	101	-
107	192	114	193	265	60	256
108	-	109	-	43	136	-
109	170	88	51	-	44	55
110	-	87	-	-	-	-
111	-	40	-	-	-	-
112	-	51	-	-	-	-
113	115	-	49	-	-	-
114	-	-	-	-	-	50
115	-	65	-	-	-	-
116	-	-	41	-	-	-
117	-	-	60	-	-	-
118	-	-	-	-	111	48
119	-	42	-	-	-	-
120	132	-	-	45	65	-
121	-	-	47	-	-	-
122	-	102	-	-	-	133
123	-	-	-	-	49	-
124	-	47	-	-	-	-
125	-	45	54	-	-	45
126	-	56	-	-	-	-
127	76	132	-	-	-	-
128	-	-	-	-	-	40
129	-	-	-	-	41	-
130	-	56	-	-	-	-
131	49	148	-	-	-	-
132	-	-	-	-	-	51
133	-	138	-	-	336	478
134	-	-	-	-	-	42
135	-	-	-	-	40	-
136	-	47	-	-	-	-
137	40	61	-	-	81	45
138	-	-	-	-	53	108
139	-	-	-	-	40	-
140	-	-	-	-	69	-
141	-	-	-	-	-	132
142	-	282	-	-	-	49
143	-	-	-	-	204	-
144	250	1,535	304	263	7,775	914
145	1,134	1,523	606	327	149	320

Supplementary Table 2

Hts sRNA	sequence
HVO_1885s 1	AAACCACCACCCCATCGTCGTTCTGGTTCCC
HVO_0404s 2	CCACCATCGTCGACCGACCCCGCCGCTGGGG
HVO_2522s 3	CCCGTTGTCAGAGACCCTCCCGTTCGCGTCGG
HVO_2019s 4	CCACCACCACTACCGGGGCCTCTGGCCACATT
HVO_2394s 5	GGGAACGCAGGCCACGCTTCGTGGTCGGTCCC
HVO_2488s 6	GCTGCTGTCACAGGCACATCCGGGGTGGCGAA
HVO_0799s 7	ACGTCGTTCCATCCCGCTTTTTTCGGTTTTTT
HVO_B0186s 8	GCGTTCCACGAGGAACGCGCAGTCGTATCGTG
HVO_1725s 9	GATACTCGTGAAGTAAAGAAATACTCGTAA
HVO_2213s 10	TCAGCGGGGACCAATCGAGGGCGGCATTTGCC
HVO_1038s 11	GTTTCGATTCACCTCCGCGGTCGCGTCAGGAC
HVO_2989s 12	GAGAAGTGACGCTGGAGAGATAATGATCCCTC
HVO_0906s 13	ATGTCGGATACCGATATCCTCGGACTCGTGCT
HVO_0104s 14	TGGTGGGGTGGGGAGGGTGGAGTGGAGTAAA
HVO_2619s 15	GAAGGGTGGGAGTAGAACAGCGGGCCGGGAGA
HVO_2293s 16 ¹	GTTAGTTATGAGGCCTCGGCACTCATAGGGCT
HVO_2354s HVO_17	CCGACTGCGCGTGCAGTCATCATCAACCTCGC
HVO_2821s 18	GCTGTCATCTGAGGCAGCACCTTTTTCCCGGT
HVO_2274s 19	GAGAATCATTATGGCACCGCCTTCAGGTTTCGC
HVO_1083s 20	AACCCGTGCCCCGAACCGCGCCGAGGCCGATAT
HVO_2583s 21	CACCCCATCCCCTCCCATGCCCTCTTACCAA
HVO_C0054s 22	TTTACTAGCGCCAATCTGTGGTCTTATTGCGC
HVO_A0232s 23	GTGTCGAGGTCCGGGTCCTTCTCCGGTCCC GC
HVO_A0064s 24	GTAGTAGAAATAATGAAAATATATCTTCTAGC
HVO_1456s 25	ATGTCCAAGAAGGCCAAACCCGTCCTGCTACT
HVO_1700s 26	GCCGGGGTGCCTCTGACAACCGGCTTATCGTT

¹ This sRNA has recently been identified as box C/D snoRNA (Joardar, Malliahgari, Skariah and Gupta (2011) RNA Biology 8: 782-791).

HVO_2520s 27	GTACCCGTGAATTCGGGATGGTTTCAGACGAA
HVO_2805s 28	TGAACGGGACCGATCAATTCATGTTCCGCCGTG
HVO_2804s 29	TCTCTCGCCGTTTTCACTCACGTTTTCCGGACC
HVO_2868s 30	TCAGCGGGGACCAATTCAGGGCGGCATGCCGT
HVO_1976s 31	GAAGCGGCAACCAAGCAACCGCCGCCCGTCCG
HVO_1345s 32	ATGGAACGGGAGGTGACGGGACGCCATCTCGA
HVO_1273s 33	ATGGACTCCACGTGTCCC GCCCCTCGCGCAT
HVO_0582s 34	GCGTAAGACGGTTGTCTTACAGCTCCCCGACG
HVO_0598s 35	TATACAGGGGAGGTTTTACCCAGTGTCCGTGG
HVO_0526s 36	ACTTGATCTTGGACTCATCGAATAGAACCTTT
HVO_0379s 37	ACAGAGGAGGCAGACATGACAGCTCAATCGTC
HVO_0400s 38	GCGAGCGACCGTAACACGGTCAATATGAATT
HVO_0049s 39	AACCATGGCGCCTCGCAGCACTTGCGCCACCT
HVO_0263s 40	GTTCACTAGACAAGGAAACTAGAATTGCGATT
HVO_0259s 41	ACGGAACCCTGAGAGACACCGTCGGCTGGAGA
HVO_0245s 42	CCTGCCCTCTCCCCGCCGTCTCGCGCCGCCCT
HVO_0197s 43	GCATGACCACTGAAGCGACAAAAGACCACCAC
HVO_0198s 44	CTCCTCCCCGTCCGGCTCGTAACGTAGTTTTTT
HVO_0099s1 45	ATTGGTCATGCACACCAACGCACTCGCCACGG
HVO_0099s2 46	ATGGATAGACAGCAGTTCCTCGCGTTGACGCT
HVO_2412s 47	ATTGTTGTAAACTCTAACGCCGATACGTCCGT
HVO_2501s 48	GACGCGGGAGCAGTCCGGTGGTGGGACTTTCC
HVO_2433s 49	CTAAAGGCGCGGGATTAACCCGTCAACCCCTC
HVO_2736s 50	ACAGCCTGTCCGGGGTTGATGAACCTCCTCGC
HVO_2071s 51	GTACCCCTGCCCATCCCCGCTAAAAAACAAA
HVO_2072s 52	CTCGTTCGGTCTTTTATTTTCTTTCAACAAA
HVO_2201s 53	CCAACTATCCGGTCCCGACCTCGACTTCCGCC
HVO_1425s 54	ATGGCAGGTGACTACTGGTGTGAGGAGTGCCA
HVO_1379s 55	GAGGCTTATGATGCCGCTTATCGCGTTCTAAC
HVO_1831s 56	TTTTCTCGCGACGCCACCCATCCCCGGCGAACC

HVO_1072s 57	ACACCGACACGGCCGCGGCGTTCAGAGCCGCGT
HVO_1101s 58	GTGAACGACGCGACGCGGCCCTCGCAGGTCAC
HVO_1271s 59	ACAAGCCCGGTTTTCGGACGGCGTTACACAAGA
HVO_1244s 60	CACACCACCTCTCGCGCGGGATTTCGCGCACGC
HVO_2723s 61	ACCAGAAACCCGCGGGAAAATACGGGCGCGCC
HVO_2073s 62	ACTCGCAACGACAGGCCAGTAACATTCCACCT
HVO_1273s 63	ATGGACTCCACGTGTCCC GCCCCTCGCGCAT
HVO_2089s 64	ATATCGTCGCTTCTAATATATTCTCTCCATAT
HVO_2120s 65	ATCAGATAGAAATCCAAGTTCCCCATTATATT
HVO_1422s1 66	TCCATTGTGAGGCCGCGGTCCGGGTCGAGGAC
HVO_1422s2 67	CCGGCTGACGGTCCCTTTCACC
HVO_1907s 68	ACGTGTTCCGAATAAAGACACAATATACAATC
HVO_1950s 69	CCACCACCACAACCACCAGAGCGGCTCAACCC
HVO_0864s 70	TCGAACTTCTCCTGCGAATCCATATCCAACAA
HVO_0879s 71	ACCTGAGCGCCTCCGGCGTTCCGGCGGCATCG
HVO_2908s 72	GTGGACGCCGGAAGGGAACGAGGGTAGGGGTA
HVO_1834s 73	ACTCATACGGATCTGGTTTTAGATACCGTATA
HVO_1106s 74	CTCAATCCAGCCGTA CTCCAGTATTTAAAAAA
HVO_1148s 75	TCCACTCACTTCCTTTTCGGTCACTTCGTTCCC
HVO_C0073s 76	GCCGTCACCGGCCACTGTGAGCAACATATTTG
HVO_C0066s 77	ATATCACAGGACTGGTTGAGCTACGTTTCTAA
HVO_C0057s1 78	GTAGCCGCTTTTTAATTTTGAATTGGGTTGGA
HVO_C0057s2 79	GAGGACGCGGACTTGGCCCGCTGGCTTAGACC
HVO_C0036s 80	GCGCGTCTGCTGCCATCACAATCACCATTTCGC
HVO_C0020s 81	ATCGACCCTGAGTAAGCCTCTTTCAACTGTTC
HVO_C0001s 82	ATTCTCATCCGCTCCTCCTTTACACCTGAAGG
HVO_C0030s 83	TTGAGTTAGTTGGTCGCGGACACGCATCCCCG
HVO_B0156s 84	GATGGGCTTAGCGGTTCGAGAGCCCAGAATTGT
HVO_B0193s 85	GCGATGGGCCCCCGCCGA ACTGACGCCGGACTG
HVO_B0371s 86	GTCGTCGTCGTTGTGTACGACGCTTTCATTCT

HVO_B0329s 87	GGACTTCAACCATGAAAGTGGAGAAAGAAGGA
HVO_A0156s 88	GTATTATGTATATTTGTGATATCGCCACTCCT
HVO_B0155s 89	ATACAATCATCGCAAATGCTCTACACTATTT
HVO_A0212s 90	GAGTGCGGTTTTGAGACGAACCCTTGTAATAAAA
HVO_A0632s 91	GTTAGGTTAGAACGCAGGCGTTTCGAGCACCGA
HVO_A0633s 92	CCCTCCACCACTCGGAGTGACGATTTCTTTTCG
HVO_A0126s 93	ACGTACCCTTCGTCAGGTGTATGGAGTCCACT
HVO_A0018s 94	ATAGACCTGAAGGCGCTCAGCGCCCGACACCG
HVO_B0186s 95	GTCTAATCCAGGCGACCGCTCTCTATTTCGAGC
HVO_A0638s 96	GTAATACGGGCAACTATAATAGTTATATAGTA
HVO_A0596s 97	GACCCTCTGTATCTGGGGCGCGCTTGGTGGGG
HVO_A0257s 98	AGCTACATTCTCCACAACAAAAAAGACGAAT
HVO_A0240s 99	ACATTTCGAGTCTCCCGCTTCCCTTCCCTTTGC
HVO_A0143s 100	ATGTCGGGGCCATGCGTTCTAGTTTAGCAGAG
HVO_A0131s 101	ATGGATACCCCTCCAAGAGCCTTCATGCTTGG
HVO_B0327s 102	AATGGGAACCTCACACGGTCGTACTTCAACT
HVO_A0035s 103	ACGAACGGTTGCGGGATGTCTTCGGACCGTGA
HVO_A0024s 104	TATTGTTCAAGTAGAGGTAGCTTTTCGTAAGG
HVO_A0015s 105	AATATACCCCGACAGACCAGTACGAATTTGCT
HVO_A0547s 106	ACGCCACCGCATCCGGCGCGCTTCGACGAATG
HVO_1132s 107	ATCTCATTTTTTCGCCGGCTCGGAGGGCAAGG
HVO_1954s 108	GAACGCGACCGACACCACCTTCTCACTTTTAA
HVO_1675s 109	AAGGCCAGTCCAAGCCGATTATTCTTTTCGTC
HVO_1310s 110	GATGAGTTCATGCGTCGGCGCTGTGAACCCGG
HVO_2036s 111	AGCTAGATCTGCATACCGAATTTAACTTTTTTC
HVO_2006s 112	ACGCCGCGCGGGCCACAAGCCACCCCGCGCGG
HVO_C0036s 113	GCTAATTGTGATGGCAGCAGACGCGCATCCCG
HVO_2957s 114	TATCTCTCGGTGATGTTTGGGTTACCCGAAT
HVO_2806s 115	CTCAGTGGTAGAGCACACCGGCACAGGCCCTC
HVO_B0186s 116	GCGTTCCACGAGGAACGCGCAGTCGTATCGTG

HVO_2787s 117	GTTGCTCGGGCGTGCGGGCGGCCGCAACGGAC
HVO_2757s 118	CATCGCTCCCGTGCTCGCCAGCCCGCATGTGT
HVO_2701s 119	GAGGCGTGGCGACTGTGAACCGCAATTCACCC
HVO_1833s 120	ATCGCGGTTGCTCCGCGCCCCACCCCTCTGT
HVO_2451s 121	CGACGGGTGCCGGGCAGGGATGCTGGTCGCGC
HVO_2399s 122	CGATTTGCTATCGCGATATTCGATTTATTTTC
HVO_0000s 123	GCATCATCTGGAATCGCCTTCTTCGGCGTGAT
HVO_0061s 124	ACAATTAGTGGCCACTATATGAAATAAACTCG
HVO_0276s 125	GCGTCCATAACTCAATTTTTAATTAGTATCGA
HVO_0809s 126	GTGACCGCGACGGGTCTCCCCGACAACATGCG
HVO_1183s 127	ATGACACGGAGTACCCACGCTCCTGATCGAGT
HVO_1779s 128	ACTCATTTGTTTCGCCAGACGAACGTTGTTCT
HVO_1876s 129	GCTTCGGAAGGCGGTTTCAAGCGAAGCGTAGC
HVO_1034s 130	AACTGACCGGGTGACGATGGCACGAGATACGA
HVO_0942s 131	ATGGCCGTTGATTCGACAGCAGAGGGAGCCGC
HVO_0988s 132	ATTCGGTTCAACTCCGTTTCGATTTCTTTTATT
HVO_0880s 133	CTCTAAACTTCGGTCACTTTCTCTCTTTCGT
HVO_0727s 134	TTCGAATTCGTCTACTAATCAAGAGGTGCGTC
HVO_0676s 135	CCGACGCGACCCCATTTTTGACAAACAAAAAA
HVO_0557s 136	AGCAGAATCTCCATCAAGTCAGCACGCCACTT
HVO_0457s 137	CCACCACAGACCCGACCGTATCAACTGTTCCG
HVO_0456s 138	ACACGACCTCCGACCACGCGAATTTTTATCAA
HVO_0238s 139	CACGCCCAACACCGATTTTTCTTTCAAAAAAA
HVO_0249s 140	CCTGACCTGACCTGACGACGCGACGGAGTCGC
HVO_0311s 141	ACTAACCCTCATCGTCGCTTCTTTTTTACAAA
HVO_0496s 142	TTCAGTACCAGACGAATCGATTTCTGAGCGTT
HVO_0480s 143	TACCCACCACTAAGTAACTCCTCTACGTTCTT
HVO_B0275s 144	GCTGTCTGGTCGGCGGACAGGTGACATATCTG
HVO_1456s 145	ATGTCCAAGAAGGCCAAACCCGTCTGCTACT

Supplementary Table 3.

tRNA	start/ direction length	tRF (5, 3' CCA, 3' trailer)	reads at condition
tRNA3-AlaCGC	329,507/ F 72 bp	3' trailer	1,136 - normal (stat)
tRNA48-AspGTC	311,755/ R 73 bp	3' trailer	1,555 - high T (expo)
tRNA1-GlnCTG	11,661/ F 73 bp	3' trailer 3' CCA	1,229 - high T (expo) 2,265 - high T (stat)
tRNA23-GlyGCC	2,420,668/ F 71 bp	3' trailer	2,277 - normal (expo) 1,615 - normal (stat)
tRNA50-HisGTG	259,298/ R 73 bp	3' trailer	1,550 - low salt (stat)
tRNA37-LysCTT	1,546,150/ R 74 bp	3' trailer	1,303 - low salt (expo) 1,061 - low salt (stat)
tRNA8-MetCAT	633,681/ F 75 bp	5'	1,591 - low salt (stat)
tRNA7-SerCGA	575,668/ F 85 bp	3' trailer	1,032 - low salt (stat)
tRNA42-ThrCGT	840,913/ R 73 bp	3' trailer	1,588 - normal (expo) 1,352 - high T (expo)
tRNA11-TrpCCA	1,165,740/ F 177 bp	3' trailer	1,149 - low salt (stat)
tRNA20-ValGAC	2,328,336/ F 75 bp	3' trailer	1,097 - high T (expo)

Supplementary Table 4.

condition ^{*1}	growth yields (and standard deviations) of parent strain (100%) and mutants						
	wild type	sRNA <i>gene</i> deletion mutants					
	H119	<i>Δhts4</i>		<i>Δhts10</i>		<i>Δhts21</i>	
acetate	100%	76%	(2%)	87%	(3%)	134%	(7%)
CAS	100%	95%	(1%)	95%	(2%)	103%	(2%)
xylose	100%	98%	(2%)	91%	(2%)	101%	(2%)
1.2 M NaCl	100%	95%	(2%)	113%	(1%)	92%	(9%)
2.1 M NaCl	100%	87%	(2%)	98%	(2%)	120%	(2%)
4 M NaCl	100%	84%	(3%)	89%	(3%)	127%	(2%)
salt stress ^{*2}	100%	94%	(2%)	101%	(3%)	264%	(24%)
cold stress ^{*2}	100%	97%	(2%)	112%	(2%)	103%	(23%)
EtOH stress ^{*2}	100%	79%	(1%)	94%	(2%)	120%	(6%)
oxidative stress ^{*2}	100%	80%	(2%)	92%	(1%)	95%	(1%)

^{*1} Standard conditions are 2.1 M NaCl, glucose as carbon source.

^{*2} Stress conditions were applied at mid-exponential growth.

Supplementary Table 5

A. up regulated

HVO number	gene name/function	no. of spots	regulation level (mean value)
HVO_0259	hypothetic protein	1	55.28
HVO_0255 - 0258	spermine/spermidine synthase family protein; conserved protein; XerC/D-like integrase	1	16.61
HVO_0160	CAAX amino terminal protease family, transmembrane	1	14.27
HVO_2079	conserved protein	1	12.82
HVO_0266 - 0271	all hypothetic proteins upstream of an ISH	5	11.15
HVO_B0128	glucose 1-dehydrogenase related protein	1	5.26
HVO_0260 - 0261	PhiH1 repressor-like; putative repressor phrH2	1	5.07
HVO_2447 - 2448	probable integral membrane protein; transcription initiation factor TFB	1	4.60
HVO_0299	membrane protein, putative	1	4.20
HVO_0226 - 0228	transcription initiation factor TFB; conserved prot.; cell division inhibitor	1	4.13
HVO_0273 - 0274	all hypothetic proteins	1	3.79
H11.1r	sRNA H11.1r	2	3.76
HVO_1717 - 1719	7-cyano-7-deazaguanine synthase; 7-carboxy-7-deaz. syn.; 6-carboxy-5,6,7,8-tetrahydropterin syn.	2	3.76
HVO_0219	conditioned medium-induced protein 4	1	3.46
HVO_0278 - 0279	conserved protein	1	3.40
HVO_1210 - 1212	flagellin A1; flagellin A2; KaiC-type circadian regulator CirA	2	3.32
HVO_B0314	ABC-type transport system permease protein (probable substrate glucose)	1	3.29
7HVO_A0603	spurious ('wrong') ORF (pHV4: 606371 - 606499 F)	1	3.13
HVO_B0318	ABC-type transport system periplasmic substrate-binding protein (probable substrate glucose)	1	3.06
HVO_2514	conditioned medium-induced protein 2	1	2.85
HVO_1683 - 1684	4-alpha-glucanotransferase; threonyl-tRNA synthetase	1	2.68
HVO_A0035	cell division protein FtsZ	1	2.60

HVO_A0062 - A0064	homologue to ISH4-type transposase; hypothetic protein; Orc1-type DNA replication protein	1	2.57
sRNA132	sRNA132	2	2.42
HVO_C0087 - C0089	all hypothetic proteins	1	2.19
HVO_0493 - 0496	all conserved proteins	1	2.16
HVO_C0034 - C0035	conserved protein; transfer complex protein, putative	1	2.15
HVO_B0217 - B0218	ABC-type transport system periplasmic substrate-binding protein	1	2.14
HVO_A0447	probable integral membrane protein	1	2.10
HVO_1895 - 1897	putative KEOPS component Kae1-Bud32; ribosomal protein S24.eR; cons. prot	1	2.02

B. down regulated

HVO number	gene name/function	no. of spots	regulation level (mean value)
HVO_2160	Muc19 precursor, putative	3	0.44
HVO_2401	glycine cleavage system P-protein	1	0.49

Supplementary Table 6

tRNA	strand/ start / length	tRF (5', 3' CCA, 3' trailer)	condition/ number of reads
tRNA3-AlaCGC	chr (+) 329,507 72 bp	3' trailer	2 / 1,136
tRNA10-AlaGGC	chr (+) 1,048,559 72 bp		
tRNA12-AlaTGC	chr (+) 1,599,762 72 bp		
tRNA28-AlaTGC	chr (-) 2,769,994 72 bp		
tRNA14-ArgCCG	chr (+) 1,692,867 73 bp		
tRNA40-ArgCCT	chr (-) 1,061,493 73 bp		
tRNA43-ArgGCG	chr (-) 452,351 73 bp		
tRNA39-ArgTCG	chr (-) 1,307,487 75 bp		
tRNA2-ArgTCT	chr (+) 121,223 74 bp		
tRNA4-AsnGTT	chr (+) 457,852 73 bp		
tRNA49-AspGTC	chr (-) 311,653 73 bp		
tRNA48-AspGTC	chr (-) 311,755 73 bp	3' trailer	3/ 1,555
tRNA13-CysGCA	chr (+) 1,603,383 77 bp		
tRNA1-GlnCTG	chr (+) 11,661 73 bp	3' trailer 3' CCA	3/ 1,229 4/ 2,265
tRNA9-GlnTTG	chr (+) 781,200 104 bp		
tRNA27-GluCTC	chr (+)		

	2,759,237 75 bp		
tRNA25-GluTTC	chr (+) 2,646,860 75 bp		
tRNA35-GlyCCC	chr (-) 1,733,316 71 bp		
tRNA22-GlyGCC	chr (+) 2,420,585 71 bp		
tRNA23-GlyGCC	chr (+) 2,420,668 71 bp	3' trailer	1 / 2,277, 2 / 1,615
tRNA41-GlyTCC	chr (-) 937,864 71 bp		
tRNA50-HisGTG	chr (-) 259,298 73 bp	3' trailer	8 / 1,550
tRNA18-IleGAT	chr (+) 2,217,987 74 bp		
tRNA26-LeuCAA	chr (+) 2,693,483 84 bp		
tRNA30-LeuCAG	chr (-) 2,617,832 85 bp		
tRNA31-LeuGAG	chr (-) 2,564,774 85 bp		
tRNA34-LeuTAA	chr (-) 2,082,040 85 bp		
tRNA38-LeuTAG	chr (-) 1,526,268 83 bp		
tRNA37-LysCTT	chr (-) 1,546,150 74 bp	3' trailer	7 / 1,303, 8 / 1,061
tRNA15-LysTTT	chr (+) 1,706,125 74 bp		
tRNA5-MetCAT	chr (+) 458,021 75 bp		
tRNA8-MetCAT	chr (+) 633,681 75 bp	5'	8 / 1,591
tRNA21-MetCAT	chr (+) 2,384,839 149 bp		
tRNA46-PheGAA	chr (-)		

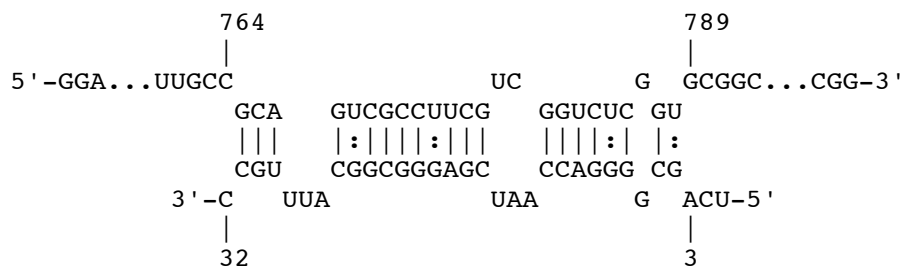
	439,239 74 bp		
tRNA45-PheGAA	chr (-) 441,236 74 bp		
tRNA17-ProCGG	chr (+) 1,836,712 73 bp		
tRNA32-ProGGG	chr (-) 2,358,758 71 bp		
tRNA51-ProTGG	chr (-) 252,026 73 bp		
tRNA7-SerCGA	chr (+) 575,668 85 bp	3'	8 / 1,032
tRNA29-SerGCT	chr (-) 2,620,287 85 bp		
tRNA47-SerGGA	chr (-) 408,343 81 bp		
tRNA24-SerTGA	chr (+) 2,626,534 84 bp		
tRNA42-ThrCGT	chr (-) 840,913 73 bp	3'	1/ 1,588, 3/ 1,352
tRNA16-ThrGGT	chr (+) 1,736,209 72 bp		
tRNA11-TrpCCA	chr (+) 1,165,740 177 bp	3'	8 / 1,149
tRNA6-TyrGTA	chr (+) 518,441 74 bp		
tRNA36-TyrGTA	chr (-) 1,590,379 74 bp		
tRNA33-ValCAC	chr (-) 2,264,001 75 bp		
tRNA19-ValGAC	chr (+) 2,328,216 75 bp		
tRNA20-ValGAC	chr (+) 2,328,336 75 bp	3'	3/ 1,097
tRNA44-ValTAC	chr (-) 443,018 74 bp		

Supplementary Table 7

name	sequence	used for
hts4up	CAACGTTGTCCGACGGAGCGGCCAGTCGAGC	generation of the sRNA <i>hts4</i> gene fragment with 500 bp up- and downstream regions
hts4do	CTCGATGTTCTCCCGCTCGCACCGAACC	
hts5up	GTTGCGAGGTACCAGAAAGTGGGTTGGGGC	generation of the sRNA <i>hts5</i> gene fragment with 500 bp up- and downstream regions
hts5do	CGAGGCCTACGGGACCGTCGACGAG	
hts10up	GGCAAAGCTCGCCCGAACGACC	generation of the sRNA <i>hts10</i> gene fragment with 500 bp up- and downstream regions
hts10do	GACCGACTGGAGGAGGTGGACCAC	
hts21up	CAGGACGAGGCGCAGGTCGTCGAGGG	generation of the sRNA <i>hts21</i> gene fragment with 500 bp up- and downstream regions
hts21do	CAGGCGCGGTCCGCGCTGTTGGCGAAG	
hts4i1	GACCAGATAGCTATCTGTTAGGTGAGC	inverse PCR to delete the sRNA <i>hts4</i> gene
hts4i2	CAGCTGTTGGCCGTTGCGGCGGCC	
hts5i1	GTTTTAGGTATGCCTAAGAATCAC	inverse PCR to delete the sRNA <i>hts5</i> gene
hts5i2	CCTCGCGAGCGACCGCGCCGACACC	
hts10IP1	CAAAGCGAAGCGTCACCTGAACGGAGTGC	inverse PCR to delete the sRNA <i>hts10</i> gene
hts10IP2	TCGTATTCGCGCGCGCTCGAATCG	
hts21i1	GGACACGCCCCGCGGGTGCTCCCCGACG	inverse PCR to delete the sRNA <i>hts21</i> gene
hts21i2	GGTGAAACTGGCGCTCGGCGTCGTCCG	
hts4do	CTCGATGTTCTCCCGCTCGCACCGAACC	generation of a probe for southern of <i>hts4</i> gene deletion
hts4i2	CAGCTGTTGGCCGTTGCGGCGGCC	
hts5do	CGAGGCCTACGGGACCGTCGACGAG	generation of a probe for southern of <i>hts5</i> gene deletion
hts5i2	CCTCGCGAGCGACCGCGCCGACACC	
hts10up	GGCAAAGCTCGCCCGAACGACC	generation of a probe for southern of <i>hts10</i> gene deletion
hts10IP1	CAAAGCGAAGCGTCACCTGAACGGAGTGC	
hts21up	CAGGACGAGGCGCAGGTCGTCGAGGG	generation of a probe for southern of <i>hts21</i> gene deletion
hts21i1	GGACACGCCCCGCGGGTGCTCCCCGACG	
tRNA1-Gln(CTG)	TGGTAGTCCCACCAGGATTCGAACCTG	tRF northern tRNA1-Gln(CTG)
tRNA50-His(GTG)	CGCGGCGCTCACTGGTCGAAATGTAAAGAAGA	tRF northern tRNA50-His(GTG)
hts4#1	GGAGACCAGAATGTGGCCAGAGGCCCGGTAGTGGTGG	Hts northern Hts4
hts5#1	CTAACTGGGACCGACCACGAAGCGTGGCCTGCGTTCC	Hts northern Hts5
hts10#1	GCGGCCCGCGCGGCAAATGCCGCCCTAGATTGG	Hts northern Hts10
hts21	CCGCGTGTGAAGAGTGGCATGGGAGGGGATGGGGTG	Hts northern Hts21

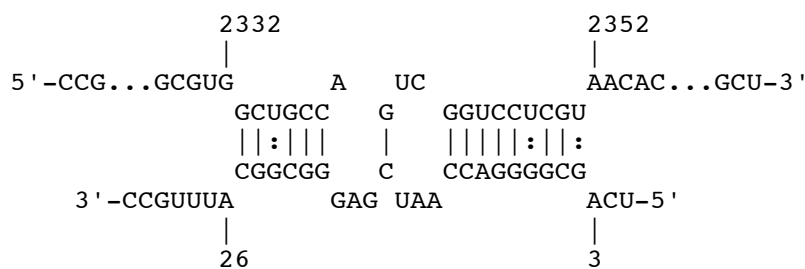
Energy: -19.7 kcal/mol Position - mRNA:
737 -- 753
Hybridization Energy: -33.7 kcal/mol Position - ncRNA:
4 -- 25
Unfolding Energy - mRNA: 7.8 kcal/mol Position Seed - mRNA:
747 -- 753
Unfolding Energy - ncRNA: 6.2 kcal/mol Position Seed - ncRNA:
4 -- 10

Predicted interaction between hts10 and 0268-0271_



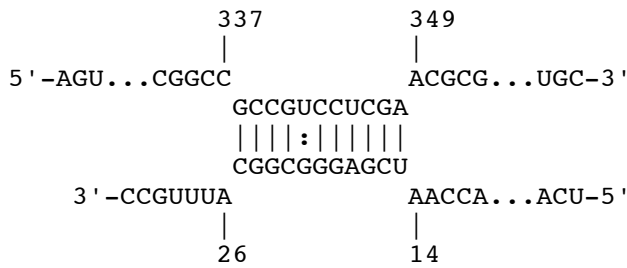
Energy: -18.6 kcal/mol Position - mRNA:
765 -- 788
Hybridization Energy: -33.4 kcal/mol Position - ncRNA:
4 -- 31
Unfolding Energy - mRNA: 8.6 kcal/mol Position Seed - mRNA:
771 -- 777
Unfolding Energy - ncRNA: 6.2 kcal/mol Position Seed - ncRNA:
16 -- 22

Predicted interaction between hts10 and 2079



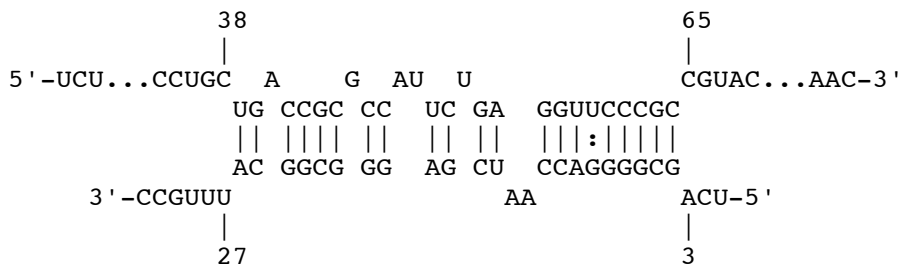
Energy: -16.8 kcal/mol Position - mRNA:
2333 -- 2351
Hybridization Energy: -29.3 kcal/mol Position - ncRNA:
4 -- 25
Unfolding Energy - mRNA: 6.3 kcal/mol Position Seed - mRNA:
2345 -- 2351
Unfolding Energy - ncRNA: 6.2 kcal/mol Position Seed - ncRNA:
4 -- 10

Predicted interaction between hts10 and 0299



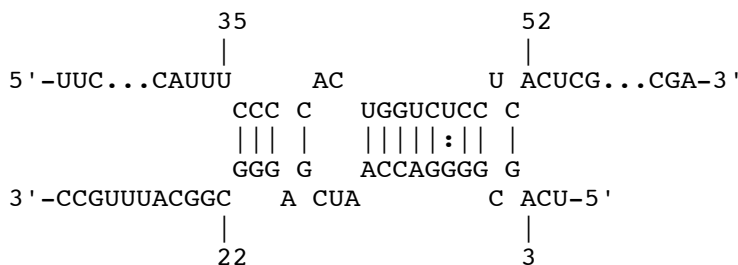
Energy: -16.7 kcal/mol Position - mRNA: 338 -- 348
 Hybridization Energy: -24.2 kcal/mol Position - ncRNA: 15 -- 25
 Unfolding Energy - mRNA: 3.1 kcal/mol Position Seed - mRNA: 342 -- 348
 Unfolding Energy - ncRNA: 4.4 kcal/mol Position Seed - ncRNA: 15 -- 21

Predicted interaction between hts10 and 0160



Energy: -15.4 kcal/mol Position - mRNA: -- 64
 Hybridization Energy: -28.1 kcal/mol Position - ncRNA: -- 26
 Unfolding Energy - mRNA: 6.5 kcal/mol Position Seed - mRNA: -- 64
 Unfolding Energy - ncRNA: 6.2 kcal/mol Position Seed - ncRNA: -- 10

Predicted interaction between hts10 and b0128

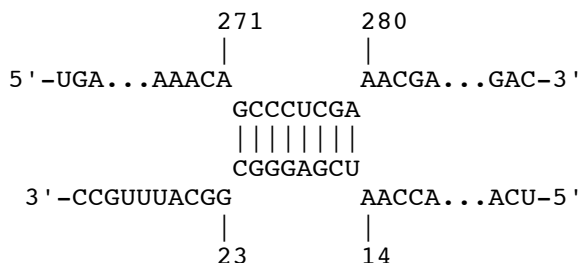


Energy: -14.1 kcal/mol Position - mRNA: -- 51
 Hybridization Energy: -18.3 kcal/mol Position - ncRNA: -- 21
 Unfolding Energy - mRNA: 1.3 kcal/mol Position Seed - mRNA: -- 49

Unfolding Energy - ncRNA: 3.0 kcal/mol
-- 12

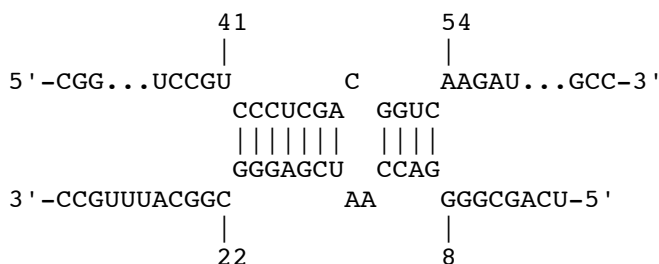
Position Seed - ncRNA: 6

Predicted interaction between hts10 and 0257_



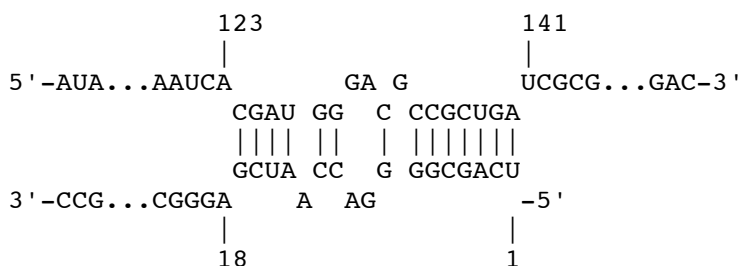
Energy: -12.8 kcal/mol Position - mRNA:
272 -- 279
Hybridization Energy: -15.8 kcal/mol Position - ncRNA:
15 -- 22
Unfolding Energy - mRNA: 2.1 kcal/mol Position Seed - mRNA:
273 -- 279
Unfolding Energy - ncRNA: 0.9 kcal/mol Position Seed - ncRNA:
15 -- 21

Predicted interaction between hts10 and 0259



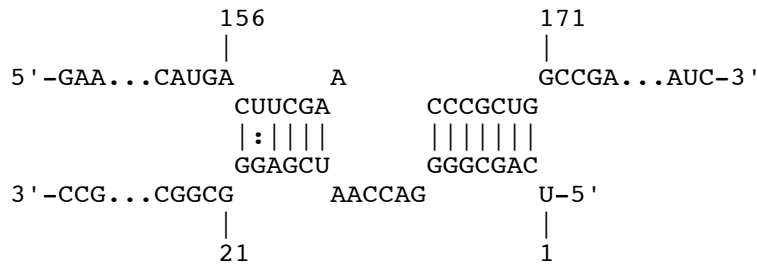
Energy: -12.5 kcal/mol Position - mRNA: 42
-- 53
Hybridization Energy: -18.7 kcal/mol Position - ncRNA: 9
-- 21
Unfolding Energy - mRNA: 3.3 kcal/mol Position Seed - mRNA: 42
-- 48
Unfolding Energy - ncRNA: 2.9 kcal/mol Position Seed - ncRNA: 15
-- 21

Predicted interaction between hts10 and 0267



Energy:	-10.6 kcal/mol	Position - mRNA:
124 -- 140		
Hybridization Energy:	-22.9 kcal/mol	Position - ncRNA:
1 -- 17		
Unfolding Energy - mRNA:	9.6 kcal/mol	Position Seed - mRNA:
134 -- 140		
Unfolding Energy - ncRNA:	2.6 kcal/mol	Position Seed - ncRNA:
1 -- 7		

Predicted interaction between hts10 and 0266



Energy:	-10.2 kcal/mol	Position - mRNA:
157 -- 170		
Hybridization Energy:	-21.3 kcal/mol	Position - ncRNA:
2 -- 20		
Unfolding Energy - mRNA:	8.1 kcal/mol	Position Seed - mRNA:
164 -- 170		
Unfolding Energy - ncRNA:	3.0 kcal/mol	Position Seed - ncRNA:
2 -- 8		

Predicted interaction between hts10 and 0260-0261

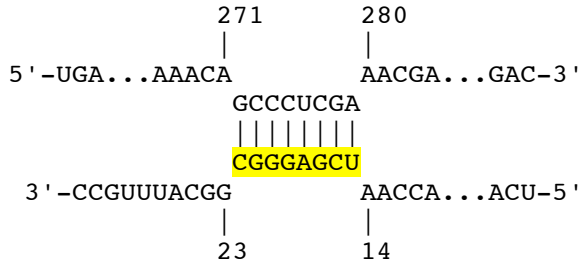


Energy:	-9.4 kcal/mol	Position - mRNA:
235 -- 245		
Hybridization Energy:	-19.3 kcal/mol	Position - ncRNA:
15 -- 25		
Unfolding Energy - mRNA:	5.5 kcal/mol	Position Seed - mRNA:
239 -- 245		
Unfolding Energy - ncRNA:	4.4 kcal/mol	Position Seed - ncRNA:
15 -- 21		

B.

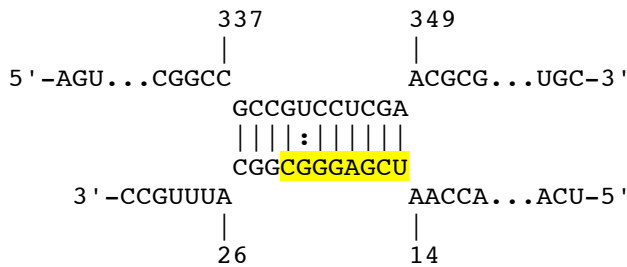
Cluster I: mRNAs 0257, 0299 and 0260-0261

Predicted interaction between hts10 and **0257_**



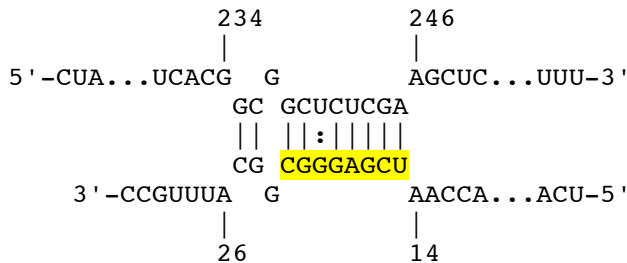
Energy: -12.8 kcal/mol Position - mRNA: 272 -- 279
Hybridization Energy: -15.8 kcal/mol Position - ncRNA: 15 -- 22
Unfolding Energy - mRNA: 2.1 kcal/mol Position Seed - mRNA: 273 -- 279
Unfolding Energy - ncRNA: 0.9 kcal/mol Position Seed - ncRNA: 15 -- 21

Predicted interaction between hts10 and **0299**



Energy: -16.7 kcal/mol Position - mRNA: 338 -- 348
Hybridization Energy: -24.2 kcal/mol Position - ncRNA: 15 -- 25
Unfolding Energy - mRNA: 3.1 kcal/mol Position Seed - mRNA: 342 -- 348
Unfolding Energy - ncRNA: 4.4 kcal/mol Position Seed - ncRNA: 15 -- 21

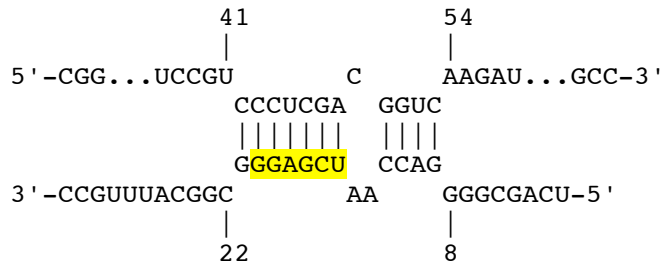
Predicted interaction between hts10 and **0260-0261**



Energy: -9.4 kcal/mol Position - mRNA: 235 -- 245
Hybridization Energy: -19.3 kcal/mol Position - ncRNA: 15 -- 25
Unfolding Energy - mRNA: 5.5 kcal/mol Position Seed - mRNA: 239 -- 245
Unfolding Energy - ncRNA: 4.4 kcal/mol Position Seed - ncRNA: 15 -- 21

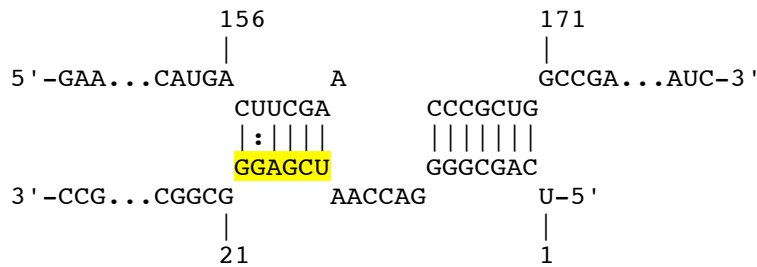
Cluster II: mRNAs 0259 and 0266

Predicted interaction between hts10 and **0259**



Energy:	-12.5 kcal/mol	Position - mRNA:	42 -- 53
Hybridization Energy:	-18.7 kcal/mol	Position - ncRNA:	9 -- 21
Unfolding Energy - mRNA:	3.3 kcal/mol	Position Seed - mRNA:	42 -- 48
Unfolding Energy - ncRNA:	2.9 kcal/mol	Position Seed - ncRNA:	15 -- 21

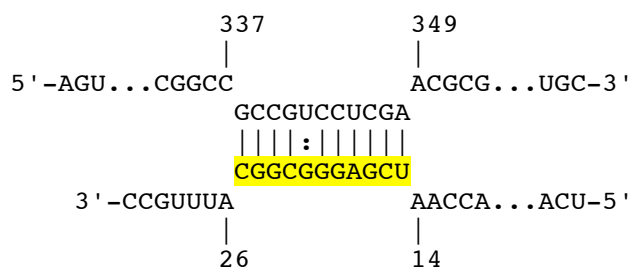
Predicted interaction between hts10 and **0266**



Energy:	-10.2 kcal/mol	Position - mRNA:	157 -- 170
Hybridization Energy:	-21.3 kcal/mol	Position - ncRNA:	2 -- 20
Unfolding Energy - mRNA:	8.1 kcal/mol	Position Seed - mRNA:	164 -- 170
Unfolding Energy - ncRNA:	3.0 kcal/mol	Position Seed - ncRNA:	2 -- 8

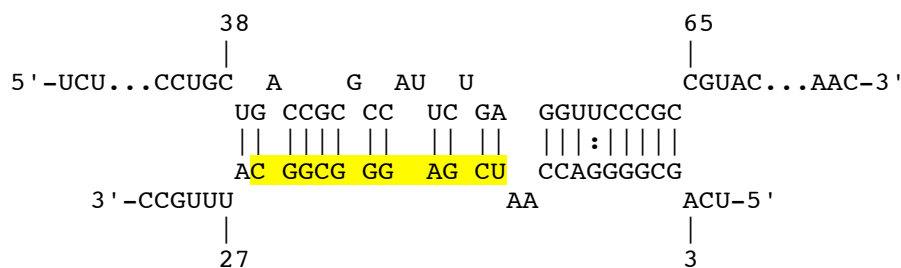
Cluster III: mRNAs 0299 and 0160

Predicted interaction between hts10 and **0299**



Energy:	-16.7 kcal/mol	Position - mRNA:	338 -- 348
Hybridization Energy:	-24.2 kcal/mol	Position - ncRNA:	15 -- 25
Unfolding Energy - mRNA:	3.1 kcal/mol	Position Seed - mRNA:	342 -- 348
Unfolding Energy - ncRNA:	4.4 kcal/mol	Position Seed - ncRNA:	15 -- 21

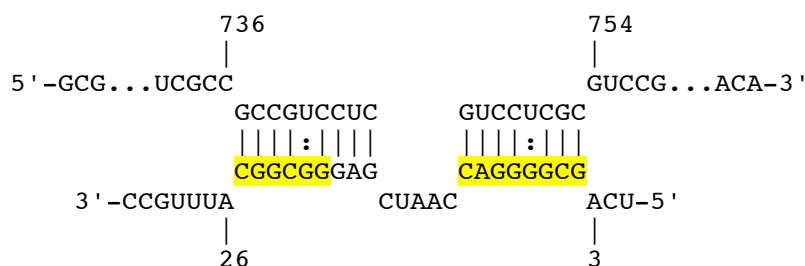
Predicted interaction between hts10 and **0160**



Energy:	-15.4 kcal/mol	Position - mRNA:	39 -- 64
Hybridization Energy:	-28.1 kcal/mol	Position - ncRNA:	4 -- 26
Unfolding Energy - mRNA:	6.5 kcal/mol	Position Seed - mRNA:	58 -- 64
Unfolding Energy - ncRNA:	6.2 kcal/mol	Position Seed - ncRNA:	4 -- 10

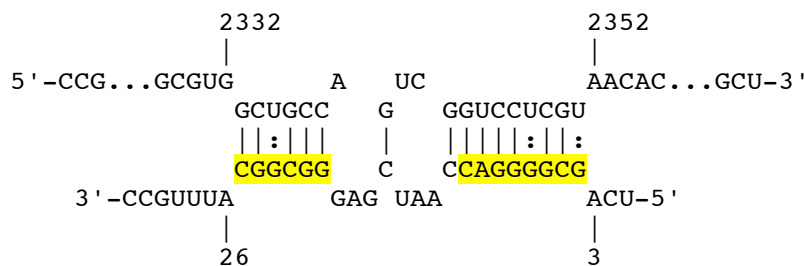
Cluster IV: mRNAs 0255-0256 and 2079

Predicted interaction between hts10 and **0255+0256**



Energy:	-19.7 kcal/mol	Position - mRNA:	737 -- 753
Hybridization Energy:	-33.7 kcal/mol	Position - ncRNA:	4 -- 25
Unfolding Energy - mRNA:	7.8 kcal/mol	Position Seed - mRNA:	747 -- 753
Unfolding Energy - ncRNA:	6.2 kcal/mol	Position Seed - ncRNA:	4 -- 10

Predicted interaction between hts10 and **2079**



Energy:	-16.8 kcal/mol	Position - mRNA:	2333 --
Hybridization Energy:	-29.3 kcal/mol	Position - ncRNA:	4 -- 25
Unfolding Energy - mRNA:	6.3 kcal/mol	Position Seed - mRNA:	2345 --
Unfolding Energy - ncRNA:	6.2 kcal/mol	Position Seed - ncRNA:	4 -- 10