Additional File 7

MEME alignment of upstream regions of putative targets of HspR as identified by Sco-Chip²-v2

NAME	STRAND OF MOTIF DETECTION	START POSITION IN GENOME OF SITE DETECTED	P-VALUE	<u>SITES</u>
tRNA_GLU	+	6049648	2.53e-15	CTCAAGGCGGTAGCGCCGGTTCGAATCCGGTCGGGGGTAC TCGAAGTCCA
tRNA_GLU	+	6049438	2.53e-15	CTCAAGGCGGTAGCGCCGGTTCGAATCCGGTCGGGGGTAC GAACTGGTCT
tRNA_GLU	+	6049303	2.53e-15	CTCAAGGCGGTAGCGCCGGTTCGAATCCGGTCGGGGGTAC AGATCCTTCC
SC03671	-	4050797	2.61e-11	TCATGCACACTTGAGCCTGTTCCACTCAAGTCAGCTGGAG GTTATTCACC
$tRNA\_GLN$	+	6049192	2.65e-10	CTGGTTCAGTTAGTCTAGGTTCGAGTCCTGGTAGGCCAGC TCGCAGAGCT
tRNA_GLU	+	6049530	7.19e-10	CTGGTTCAGTTAGTCTAGGTTCGAGTCCTGGTAGACCAGC TCGGATCTGC
SC05285	-	5756784	9.53e-10	GGCAGTCAAGTTGAGTTACATCGACTCAATGAAAGGGAGC CCGGGATTGT
SC03671	-	4050745	7.44e-09	CGGATAAGAGTTGAGTCCGCTCGACTCACCTCTGTTGACC CATCGCCGGG
SC03661	+	4040399	2.21e-08	GTACACAAAGTTGAGTCAGGGCCACTCAAGGAGTCGGGCG CACTTCTCCG
rRNA_100034	+	3300027	2.21e-08	TTCATCGGGA GAGTGCTTCGTCGAATTCGTTGATTCGGA G AAGCTGGTAG

For the target regions identified by Sco-Chip²-v2 there were clear peaks of enrichment that indicated binding of HspR to the following targets: SCO5285 (Ion) (highest peak in Figure 3C), SCO3671 (Ional) (highest peak in Figure 3A), SCO3661 (highest peak in Ional) (Figure 3B), Ional100034 (Figure 3D), Ional100034 (Figure 3D), Ional100034 (Figure 3D), Ional36 (Ional37), Ional37 (Ional38), Ional38 (Ional38), Ional39 (Ional39), Ional300 (Ional39), Ional39 (Ional39), Ional300 (Ional39), Ional300 (Ional39), Ional300 (Ional39), Ional300 (Ional39), Ional300 (Ional30), Ional30), Ional300 (Ional30), Ional30), Ional31), Ional30), Ional31), Ional31), Ional31), Ional31), Ional31), Ional31), Ional31), Ional31), Ional31), Ional32), Ional31), Ional32), Ional32), Ional33), Ional33), Ional33), Ional34), Ional32), Ional33), Ional34), Ional36), Ional36), Ional36), Ional37), Ional37), Ional38), Ional38), Ional38), Ional38), Ional38), Ional38), Ional38), Ional38), Ional39), Ional38), Ional38),