Table 3. Annotation of genes and protein coding regions in Hawaiian BAC clone HOT2C01

#	Nucleotide range	Dir.	Putative function	Closest BLASTP hit (E-value)	
1	85 - 756	-	Ribosomal protein S3	ZP_00012761.1 (5e-85)	alpha
2	760 - 1149	-	Ribosomal protein L22	ZP_00053920.1 (1e-27)	alpha
3	1425 - 2270	-	Ribosomal protein L2	NP_360640.1 (1e-89)	alpha
4	2275 - 2589	-	Ribosomal protein L23	NP_102122.1 (1e-23)	alpha
5	2570 - 3259	-	Ribosomal protein L4	NP_354922.1 (6e-32)	alpha
6	3195 - 3884	-	Ribosomal protein L3	ZP_00004268.1 (5e-46)	alpha
7	3888 - 4196	-	Ribosomal protein S10	ZP_00013720.1 (2e-42)	alpha
8	4206 - 6281	-	Predicted translation elongation factor G (EF-G)	ZP_00013722.1 (0.0)	alpha
9	6283 - 6753	-	Ribosomal protein S7	NP_223836.1 (4e-56)	epsilon
10	6754 - 7125	-	Ribosomal protein S12	NP_698242.1 (4e-56)	alpha
11	7266 - 11453	-	DNA-directed RNA polymerase beta' subunit (RpoC)	NP_354930.1 (0.0)	alpha
12	11462 - 15565	-	DNA-directed RNA polymerase beta subunit (RpoB)	ZP_00012785.1 (0.0)	alpha
13	15634 - 16014	-	Ribosomal protein L7/L12	ZP_00012786.1 (2e-34)	alpha
14	16038 - 16544	-	Ribosomal protein L10	ZP_00052577.1 (3e-38)	alpha
15	16548 - 17231	-	Ribosomal protein L1	ZP_00013730.1 (1e-59)	alpha
16	17231 - 17659	-	Ribosomal protein L11	NP_772055.1 (5e-44)	alpha
17	17659 - 18192	-	Predicted transcription antiterminator NusG	ZP_00013732.1 (7e-54)	alpha
18	18196 - 18429	-	Predicted preprotein translocase subunit SecE	ZP_00012792.1 (6e-07)	alpha
19	18400 - 18475	-	tRNA Trp (CCA anticodon)		
20	18480 - 19670	-	Predicted translation elongation factor Tu (EF-Tu)	ZP_00013734.1 (0.0)	alpha
21	19706 - 19779	-	tRNA Gly (TCC anticodon)		
22	19814 - 19898	-	tRNA Tyr (GTA anticodon)		
23	20049 - 20822	+	Predicted tRNA/rRNA methyltransferase	ZP_00053931.1 (4e-35)	alpha
24	20972 - 21047	+	tRNA Thr (TGT anticodon)		
25	21402 - 22022	-	Conserved hypothetical protein	NP_655509.1 (3e-15)	LGC
26	22073 - 23272	-	Predicted NAD-dependent formate dehydrogenase	AAG10470.1 (0.0)	gamma
27	23296 - 24042	-	Putative aldolase class II protein	Q9A8Z4 (9e-72)	alpha
28	24035 - 25528	-	Predicted glycerol kinase	Q9X1E4 (1e-142)	thermatogales
29	25609 - 26376	+	Predicted kinase	ZP_00056540.1 (9e-75)	alpha
30	26373 - 27233	-	Hypothetical protein	-	-
31	27237 - 28136	-	Putative SinH homolog	NP_754913.1 (1e-05)	gamma
32	28183 - 28270	-	tRNA Leu (TAA anticodon)		
33	28378 - 29070	-	Proteorhodopsin	AAO73933.1 (2e-81)	gamma
34	29195 - 29917	-	Predicted nucleotide-utilizing enzyme related to MoeA	ZP_00096270.1 (3e-55)	alpha
35	29924 - 30625	+	Predicted sugar fermentation stimulation protein	NP_354599.1 (5e-50)	alpha
36	30661 - 31392	+	Predicted methionine aminopeptidase	NP_421476.1 (2e-84)	alpha
37	31417 - 32709	+	Predicted adenylosuccinate lyase	NP_772330.1 (1e-146)	alpha
38	32960 - 33289	-	Conserved hypothetical protein	NP_101948.1 (4e-27)	alpha
39	33362 - 34081	+	Predicted phosphoribosylaminoimidazolesuccinocarboxamide synthase	NP_385878.1 (7e-60)	alpha
40	34331 - 35002	+	Predicted phosphoribosylformylglycinamidine (FGAM) synthase I	ZP_00054281.1 (2e-69)	alpha
41	35002 - 37200	+	Predicted phosphoribosylformylglycinamidine (FGAM) synthase II	ZP_00054280.1 (0.0)	alpha
42	37212 - 38021	-	Conserved hypothetical protein	ZP_00104055.1 (2e-29)	cyanobacteria
43	38027 - 38500	-	Hypothetical protein	-	-
44	38840 - 39313	+	Hypothetical protein	-	-
45	39861 - 40790	-	Hypothetical protein	-	-
46	40800 - 41108	-	Hypothetical protein	-	-
47	41138 - 41941	-	Hypothetical protein	-	-