Table 2. Annotation of genes and protein coding regions in Antarctic fosmid ANT8C10

#	Nucleotide range	Dir.	Putative function	Closest BLASTP hit (E-value)	
1	956 - 1300	-	Hypothetical protein	-	-
2	1527 - 1913	+	Hypothetical protein	-	-
3	2062 - 3969	+	Putative ATP-dependent RNA helicase	ZP_00066212.1 (1e-118)	gamma
4	3958 - 4815	-	Predicted phosphatase	NP_713134.1 (7e-12)	spirochaetales
5	4864 - 5847	-	Predicted oxidoreductase	NP_641173.1 (2e-88)	gamma
6	5888 - 6367	-	Conserved hypothetical protein	ZP_00117528.1 (3e-13)	BCF
7	6643 - 7059	-	Hypothetical protein	-	-
8	7450 - 8619	+	Predicted Zn-dependent dipeptidase	ZP_00095596.1 (2e-82)	alpha
9	8622 - 9464	+	Conserved hypothetical protein	ZP_00008601.1 (5e-31)	alpha
10	9476 - 10324	+	Predicted sterol desaturase	NP_800607.1 (4e-52)	gamma
11	10352 - 11131	+	Conserved hypothetical protein	NP_490451.1 (2e-61)	cyanobacteria
12	11132 - 11533	+	Hypothetical protein	-	-
13	11514 - 12200	-	Predicted nitroreductase	NP_770830.1 (1e-67)	alpha
14	12265 - 13521	-	Predicted acyl-CoA transferases/carnitine dehydratase	CAB55821.1 (3e-57)	alpha
15	13672 - 14823	+	Predicted acyl-CoA dehydrogenases	ZP_00084445.1 (1e-151)	gamma
16	14826 - 16133	-	Predicted ATP-dependent exoDNAse (exonuclease V), alpha subunit	NP_809634.1 (1e-65)	BCF
17	16298 - 16936	+	Predicted methylase	NP_796491.1 (1e-38)	gamma
18	16933 - 17367	-	Conserved hypothetical protein	NP_417038.1 (8e-11)	gamma
19	17345 - 18547	+	Predicted beta-lactamase class C	NP_250918.1 (8e-76)	gamma
20	18627 - 19196	+	Hypothetical protein	-	-
21	19270 - 19905	+	Conserved hypothetical protein	NP_798383.1 (4e-17)	gamma
22	20023 - 20328	+	Conserved hypothetical protein	AAO52198.1 (6e-27)	eucarya
23	20398 - 20904	+	Conserved hypothetical protein	NP_353310.1 (1e-10)	alpha
24	20894 - 22267	+	Predicted NAD-dependent aldehyde dehydrogenase	NP_534637.1 (1e-143)	alpha
25	22257 - 23264	+	Putative saccharopine dehydrogenase	NP_105333.1 (1e-74)	alpha
26	24156 - 24605	-	Hypothetical protein	-	-
27	24731 - 25222	+	Conserved hypothetical protein	ZP_00055759.1 (8e-07)	alpha
28	25246 - 25932	+	Conserved hypothetical protein	NP_654746.1 (4e-23)	LGC
29	25935 - 26558	+	Predicted 1-acyl-sn-glycerol-3-phosphate acyltransferase	ZP_00064877.1 (7e-25)	gamma
30	26555 - 28387	-	Conserved hypothetical protein	NP_710310.1 (1e-119)	spirochaetales
31	28529 - 29224	+	Predicted enoyl-CoA hydratase/carnithine racemase	NP_250439.1 (2e-35)	gamma
32	29242 - 29748	+	Predicted acetyltransferase, GNAT superfamily	ZP_00100576.1 (4e-12)	LGC
33	30116 - 30808	-	Hypothetical protein	-	-
34	30900 - 31631	-	Hypothetical protein	-	-
35	31731 - 33521	-	Predicted TypA membrane GTPase	ZP_00065644.1 (0.0)	gamma
36	33562 - 34842	+	Predicted metal-dependent amidase/aminoacylase/carboxypeptidase	NP_639131.1 (1e-106)	gamma
37	34914 - 35879	+	Predicted dioxygenase related to 2-nitropropane dioxygenase	NP_421175.1 (1e-111)	alpha
38	36421 - 37350	+	Predicted oxidoreductase	|NP_250267.1 (7e-85)	gamma
39	37347 - 37715	-	Hypothetical protein	-	-