

Table 1. List of predicted genes on fosmid HF10_19P19 (41802 bp).

N	Start	End	Strand	Description	Best BLASTP hit			
					GenBank gi	-log(e)	% Identity	Taxonomic affiliation
1	3	330	-	Flagellar motor protein MotB	91218602	56	100	<i>Psychroflexus torquis</i> (Bacteroidetes/Chlorobi)
2	386	1147	-	Flagellar motor protein MotA	68164501	>100	78	uncultured marine bacterium BAC17H8
3	1342	1914	+	Hypothetical protein	68164500	38	51	uncultured marine bacterium BAC17H8
4	1911	2093	-	Hypothetical protein	-----			
5	2411	3925	+	DNA-directed RNA polymerase specialized sigma subunit, sigma54	68164498	>100	49	uncultured marine bacterium BAC17H8
6	4042	4221	-	Hypothetical protein	-----			
7	4340	5686	-	Peptidase	68164492	54	34	uncultured marine bacterium BAC17H8
8	5696	6073	-	Hypothetical protein	68164491	10	32	uncultured marine bacterium BAC17H8
9	6272	6661	+	Membrane protein	87198088	12	33	<i>Novosphingobium aromaticivorans</i> (Alpha Proteobacteria)
10	6673	7110	+	Membrane protein	68164489	21	42	uncultured marine bacterium BAC17H8
11	7103	7441	+	Hypothetical protein	68164488	14	39	uncultured marine bacterium BAC17H8
12	7417	7746	-	Hypothetical protein	-----			
13	7763	8212	-	Hypothetical protein	68164493	5	28	uncultured marine bacterium BAC17H8
14	8533	8877	+	Hypothetical protein	-----			
15	8911	9558	-	Hypothetical protein	67906762	82	64	uncultured marine bacterium MedeBAC46A06
16	9716	10858	+	Aminotransferase	85704324	>100	60	<i>Roseovarius sp.</i> (Alpha Proteobacteria)
17	11065	11463	-	Phosphoribosyl-AMP cyclohydrolase	78700320	38	63	<i>Alkalimnicola ehrlichei</i> (Gamma Proteobacteria)
18	11598	11765	+	Hypothetical protein	-----			
19	11774	12367	-	Methyltransferase type 12	94310012	21	42	<i>Loktanella vestfoldensis</i> (Alpha Proteobacteria)
20	12364	13230	-	Sulfate/tungstate uptake family ABC transporter, substrate-binding protein	56678404	70	52	<i>Ralstonia metallidurans</i> (Beta Proteobacteria)
21	13372	13782	+	Transcriptional regulator, ModE family	87200527	6	36	<i>Silicibacter pomeroyi</i> (Alpha Proteobacteria)
22	13832	14119	+	Hypothetical protein	67906748	24	56	<i>Novosphingobium aromaticivorans</i> (Alpha Proteobacteria)
23	14138	14590	+	Hypothetical protein	67906749	22	45	uncultured marine bacterium MedeBAC46A06
24	14630	14875	+	Hypothetical protein	83950410	5	48	<i>Roseovarius nubinhibens</i> (Alpha Proteobacteria)
25	14875	15975	+	ATPase	67906750	>100	71	uncultured marine bacterium MedeBAC46A06
26	15972	16760	+	Hypothetical protein	67906751	61	49	uncultured marine bacterium MedeBAC46A06
27	16757	17272	+	Ribosomal protein L7/L12	67906752	47	57	uncultured marine bacterium MedeBAC46A06
28	17241	18248	+	Hypothetical protein	67906753	>100	57	uncultured marine bacterium MedeBAC46A06
29	18312	20321	-	Iron-sulfur cluster-binding protein	67906754	>100	59	uncultured marine bacterium MedeBAC46A06
30	20469	21077	+	Hypothetical protein	67906755	52	55	uncultured marine bacterium MedeBAC46A06
31	21105	21848	+	Hypothetical protein	67906756	36	40	uncultured marine bacterium MedeBAC46A06
32	22048	22671	+	Cytoplasmic chaperone TorD	67906757	64	61	uncultured marine bacterium MedeBAC46A06
33	22747	22941	+	Hypothetical protein	89092830	7	49	<i>Oceanospirillum sp.</i> (Gamma Proteobacteria)
34	22993	25884	+	Anaerobic dehydrogenase alpha subunit	67906758	>100	89	uncultured marine bacterium MedeBAC46A06
35	25897	26490	+	Anaerobic dehydrogenase, iron-sulfur subunit	83941749	>100	89	<i>Sulfitobacter sp.</i> (Alpha Proteobacteria)
36	26837	27919	+	Anaerobic dehydrogenase gamma subunit	67906759	>100	72	uncultured marine bacterium MedeBAC46A06
37	28072	29379	+	WD domain/cytochrome C family protein	67906760	>100	58	uncultured marine bacterium MedeBAC46A06
38	29398	29520	+	Hypothetical protein	-----			
39	29571	30272	+	Trypsin-like serine protease	67906761	58	54	uncultured marine bacterium MedeBAC46A06
40	30364	31260	+	Molybdenum cofactor biosynthesis protein A	67527057	>100	70	uncultured marine bacterium 66A03
41	31445	31984	+	Molybdopterin-guanine dinucleotide biosynthesis protein	71847033	43	56	<i>Dechloromonas aromatica</i> (Beta Proteobacteria)
42	31993	33225	+	Molybdopterin biosynthesis protein	67527055	90	44	uncultured marine bacterium 66A03
43	33225	33476	+	Molybdopterin-converting factor, small subunit	23016726	22	60	Magnetospirillum magnetotacticum MS-1
44	33481	33960	+	Molybdopterin-converting factor large subunit	27382584	42	52	<i>Bradyrhizobium japonicum</i> (Alpha Proteobacteria)
45	34208	35227	-	Isopentenyl diphosphate delta-isomerase Idi	68164580	86	54	uncultured marine bacterium BAC17H8
46	35224	36084	-	15,15'-beta-carotene dioxygenase Blh	67527050	50	40	uncultured marine bacterium 66A03
47	36127	37257	-	Lycopene cyclase CrtY	68164582	73	41	uncultured marine bacterium BAC17H8
48	37254	38237	-	Phytoene synthase CrtB	67527048	68	47	uncultured marine bacterium 66A03
49	38218	39765	-	Phytoene dehydrogenase CrtI	67906784	>100	71	uncultured marine bacterium MedeBAC46A06
50	39855	40871	-	Geranylgeranyl pyrophosphate synthetase CrtE	67527046	86	51	uncultured marine bacterium 66A03
51	40993	41766	-	Proteorhodopsin	67527045	97	67	uncultured marine bacterium 66A03