

Table 2. List of predicted genes on fosmid HF10_25F10 (40220 bp).

N	Start	End	Strand	Description	Best BLASTP hit			
					GenBank gi	-log(e)	% Identity	Taxonomic affiliation
1	96	365	+	Hypothetical protein	67906766	44	98	uncultured bacterium MedeBAC46A06
2	460	2724	+	Hypothetical protein	67906767	>100	94	uncultured bacterium MedeBAC46A06
3	2732	4024	+	Histidinol dehydrogenase	67906768	>100	89	uncultured bacterium MedeBAC46A06
4	4069	4566	+	Sulfopyruvate decarboxylase subunit alpha	67906769	>100	55	uncultured bacterium MedeBAC46A06
5	4571	5125	+	Sulfopyruvate decarboxylase subunit ComD	67906770	>100	83	uncultured bacterium MedeBAC46A06
6	5139	5903	+	Gluconate 5-dehydrogenase	67906771	93	69	uncultured bacterium MedeBAC46A06
7	5900	6883	+	Sorbitol dehydrogenase	67906772	82	74	uncultured bacterium MedeBAC46A06
8	6976	7740	+	Deoxyribodipyrimidine photolyase	67906774	48	69	uncultured bacterium MedeBAC46A06
9	7733	8182	+	Unknown	68164595	0	28	uncultured bacterium BAC17H8
10	8269	9801	+	Propionyl-CoA carboxylase beta subunit	68164594	>100	87	uncultured bacterium BAC17H8
11	9844	11820	+	Propionyl-CoA carboxylase alpha subunit	67906776	>100	93	uncultured bacterium MedeBAC46A06
12	11817	12989	-	Amidohydrolase family protein	86138204	>100	95	<i>Roseobacter sp.</i> (Alpha Proteobacteria)
13	12986	14605	-	Oxidoreductase	67906777	>100	80	uncultured bacterium MedeBAC46A06
14	14726	15472	+	Membrane protein	68164591	>100	84	uncultured bacterium BAC17H8
15	15481	16095	+	3-Methyladenine DNA glycosylase	67906779	>100	80	uncultured bacterium MedeBAC46A06
16	16112	16504	-	Unknown	68164589	>100	66	uncultured bacterium BAC17H8
17	16416	16778	-	Alpha-amylase	41411249	>100	71	<i>Butyrivibrio fibrisolvens</i> (Clostridia)
18	16879	17697	-	Hypothetical protein	67906781	>100	79	uncultured bacterium MedeBAC46A06
19	18271	19047	+	Proteorhodopsin	68164586	98	70	uncultured bacterium BAC17H8
20	19146	20171	+	Geranylgeranyl pyrophosphate synthase CrtE	67906783	69	87	uncultured bacterium MedeBAC46A06
21	20182	21756	+	Phytoene dehydrogenase CrtI	67906784	>100	87	uncultured bacterium MedeBAC46A06
22	21775	22692	+	Phytoene synthase CrtB	67906785	>100	85	uncultured bacterium MedeBAC46A06
23	22643	23791	+	Lycopene cyclase CrtY	67906786	>100	93	uncultured bacterium MedeBAC46A06
24	23818	24648	+	15,15'-beta-carotene dioxygenase Blh	67906787	>100	89	uncultured bacterium MedeBAC46A06
25	24655	25740	+	Isopentenyl-diphosphate delta isomerase Idi	67906788	90	88	uncultured bacterium MedeBAC46A06
26	25747	26499	-	Hydroxyacylglutathione hydrolase	68164579	>100	91	uncultured bacterium BAC17H8
27	26504	26926	-	Lactoylglutathione lyase	68164578	16	45	uncultured bacterium BAC17H8
28	27059	28051	-	2-Dehydropantoate 2-reductase	67906791	>100	74	uncultured bacterium MedeBAC46A06
29	28089	29588	-	Acyl-CoA synthetase	67906792	>100	93	uncultured bacterium MedeBAC46A06
30	29986	30960	+	Conserved hypothetical protein	67906793	>100	77	uncultured bacterium MedeBAC46A06
31	31071	31601	+	Hypothetical protein	67906794	>100	68	uncultured bacterium MedeBAC46A06
32	31632	33167	+	Conserved hypothetical protein	67906795	65	92	uncultured bacterium MedeBAC46A06
33	33280	33483	+	Conserved hypothetical protein	67906797	>100	90	uncultured bacterium MedeBAC46A06
34	33571	34506	+	Ketopantoate reductase	67906799	82	90	uncultured bacterium MedeBAC46A06
35	34529	35332	+	Aldolase class II	68164572	>100	83	uncultured bacterium BAC17H8
36	35333	36496	-	Aminotransferase	67906801	0	33	uncultured bacterium MedeBAC46A06
37	36609	37511	-	Transcriptional regulator	67906803	91	93	uncultured bacterium MedeBAC46A06
38	37636	38025	+	Alpha subunit of protocatechuate 4,5-dioxygenase	68164568	>100	82	uncultured bacterium BAC17H8
39	38027	38866	+	Beta subunit of protocatechuate 4,5-dioxygenase	68164567	>100	74	uncultured bacterium BAC17H8
40	38901	39626	+	Acyl transferase	68164566	>100	86	uncultured bacterium BAC17H8
41	39910	40116	-	Hypothetical protein	18161831	45	57	<i>Pyrobaculum aerophilum</i> (Crenarchaeota)