Supplementary Table 1. Summary of similarities found in the Irish Sea metagenome to Glycoside Hydrolases present in a database constructed from twelve Pfam families.

Assembled contig ID	UniProt Accession number	% identity	alignment length	mismatches	gap openings	q. start	q. end	s. start	s. end	e-value	bit score
contig06721	Q11NQ3_CYTH3	75.29	170	42	0	684	175	56	225	2.00E-116	335
contig02397	Q11UC0_CYTH3	65.79	190	65	0	291	860	97	286	1.00E-100	318
contig05603	Q21NA7_SACD2	54.24	177	81	0	2	532	86	262	2.00E-95	265
contig26022	A7LS44_BACOV	54.14	133	61	0	455	853	778	910	2.00E-79	181
contig04690	Q11NQ3_CYTH3	76.98	126	29	0	73	450	33	158	2.00E-67	251
contig05277	Q11VQ4_CYTH3	50.26	193	96	0	2	580	938	1130	1.00E-64	243
contig03455	Q11PI8_CYTH3	41.06	263	155	0	113	901	1050	1312	1.00E-62	187
contig26107	Q11VQ4_CYTH3	68.06	144	46	0	443	12	673	816	2.00E-62	234
contig04179	A3HX16_9SPHI	55.56	153	68	0	4	462	105	257	2.00E-62	235
contig07415	Q11NQ3_CYTH3	77.14	70	16	0	599	390	236	305	1.00E-60	126
contig02925	Q11UC0_CYTH3	80.77	104	20	0	2	313	443	546	3.00E-60	227
contig01407	A6EHL7_9SPHI	49.39	164	83	0	1376	885	282	445	1.00E-58	224
contig04013	Q11PI8_CYTH3	68.75	112	35	0	337	2	340	451	2.00E-55	211
contig02917	Q308B9_9BACT	68.07	119	38	0	31	387	223	341	1.00E-54	209
contig12578	A7V9B3_BACUN	77.19	57	13	0	217	47	777	833	2.00E-53	118
contig05485	Q308B7_9BACT	70.73	82	24	0	502	257	227	308	1.00E-51	115
contig25936	B1ZP97_OPITP	56.67	60	26	0	387	208	131	190	2.00E-50	91.8
contig00226	Q11PI9_CYTH3	62.65	83	31	0	366	118	139	221	1.00E-49	95.9
contig04413	Q21NA7_SACD2	64.76	105	37	0	389	75	556	660	6.00E-47	184
contig26301	Q11PI9_CYTH3	57.8	109	46	0	339	13	839	947	2.00E-45	178
contig25564	Q11VQ4_CYTH3	51.16	129	63	0	395	9	902	1030	3.00E-44	174
contig08782	Q11PI8_CYTH3	72.04	93	26	0	285	7	467	559	3.00E-42	167

Supplementary Table 1. *Cont.*

Assembled contig ID	UniProt Accession number	% identity	alignment length	mismatches	gap openings	q. start	q. end	s. start	s. end	e-value	bit score
contig05185	Q9REW0_ERWCH	60.34	58	23	0	200	373	184	241	5.00E-42	95.5
contig05113	B3PD52_CELJU	51.72	116	56	0	83	430	325	440	7.00E-41	163
contig04687	C5BPZ6_9GAMM	68.18	88	28	0	3	266	82	169	6.00E-40	159
contig15223	Q11PI8_CYTH3	67.44	86	28	0	15	272	616	701	2.00E-39	157
contig04664	Q023N8_SOLUE	51.72	87	42	0	262	2	467	553	5.00E-37	126
contig08470	Q11VF9_CYTH3	68.18	66	21	0	801	998	54	119	6.00E-37	126
contig17088	Q06B38_9BACT	60.22	93	37	0	3	281	324	416	1.00E-36	149
contig01678	Q21HS9_SACD2	53.92	102	47	0	308	3	412	513	1.00E-36	149
contig18893	Q47XT7_COLP3	72.15	79	22	0	239	3	227	305	7.00E-36	145
contig08844	A4CKZ7_9FLAO	69.74	76	23	0	236	9	166	241	1.00E-34	141
contig24355	Q21GC6_SACD2	67.5	80	26	0	240	1	53	132	2.00E-34	141
contig14077	B3PEQ9_CELJU	69.62	79	24	0	2	238	197	275	2.00E-33	137
contig02702	Q12KZ3_SHEDO	73.24	71	19	0	215	3	112	182	5.00E-33	136
contig02598	B6CH67_9BILA	49.56	113	57	0	22	360	58	170	2.00E-32	134
contig25780	A7LS44_BACOV	45.71	105	57	0	2	316	556	660	3.00E-32	133
contig16934	Q21KX4_SACD2	68.29	82	26	0	2	247	1413	1494	1.00E-31	131
contig00765	Q21KX4_SACD2	51.35	111	54	0	384	52	1527	1637	1.00E-31	133
contig23140	Q2SFD8_HAHCH	64.56	79	28	0	239	3	160	238	2.00E-31	130
contig01065	Q11SW6_CYTH3	55.71	70	31	0	662	453	210	279	5.00E-31	96.4
contig00382	A7LS44_BACOV	46.15	91	49	0	373	101	807	897	5.00E-31	114
contig13597	C5BNN7_9GAMM	45.54	112	61	0	456	121	332	443	8.00E-30	126
contig06190	Q11PI8_CYTH3	67.53	77	25	0	95	325	23	99	9.00E-30	126
contig11004	Q11VL4_CYTH3	64.38	73	26	0	220	2	141	213	1.00E-28	121
contig20446	A5ZK01_9BACE	56.96	79	34	0	3	239	204	282	4.00E-28	120
contig22358	C5BPZ6_9GAMM	75.86	58	14	0	65	238	53	110	5.00E-28	119

Supplementary Table 1. *Cont.*

Assembled contig ID	**UniProt Accession number**	**% identity**	**alignment length**	**mismatches**	**gap openings**	**q. start**	**q. end**	**s. start**	**s. end**	**e-value**	**bit score**
contig02656	A9LDW9_9BACT	52.58	97	46	0	12	302	485	581	9.00E-28	119
contig10055	Q21PQ1_SACD2	56.25	80	35	0	1	240	117	196	3.00E-27	116
contig02758	Q21FN3_SACD2	47.22	72	38	0	217	432	35	106	9.00E-27	80.3
contig19798	Q21ID4_SACD2	69.49	59	18	0	179	3	93	151	1.00E-26	114
contig06707	Q11UJ1_CYTH3	70	60	18	0	3	182	350	409	1.00E-26	114
contig25876	B8D159_HALOH	53.42	73	34	0	219	1	198	270	3.00E-26	113
contig02648	Q21NF6_SACD2	74.14	58	15	0	176	3	134	191	4.00E-26	112
contig15633	Q21F54_SACD2	52.86	70	33	0	1	210	488	557	1.00E-25	111
contig04461	Q11VQ4_CYTH3	59.09	44	18	0	1	132	1024	1067	1.00E-25	73.5
contig20483	Q084Z3_SHEFN	56.96	79	34	0	239	3	74	152	4.00E-25	110
contig00162	Q11SW6_CYTH3	56.76	74	32	0	5	226	492	565	1.00E-24	109
contig04227	B1KJF6_SHEWM	69.09	55	17	0	3	167	30	84	1.00E-24	108
contig12437	Q5AU13_EMENI	38.74	111	68	0	3	335	393	503	7.00E-24	97.7
contig12453	Q21G01_SACD2	69.09	55	17	0	165	1	260	314	7.00E-24	105
contig26477	A6EIU7_9SPHI	60.32	63	25	0	341	153	188	250	9.00E-24	70.7
contig04615	Q11VQ4_CYTH3	65.08	63	22	0	2	190	714	776	2.00E-23	104
contig16578	Q47XT7_COLP3	76.92	52	12	0	239	84	1867	1918	5.00E-23	103
contig23608	Q11VQ4_CYTH3	51.85	54	26	0	70	231	1011	1064	6.00E-23	80.8
contig01684	Q11X01_CYTH3	57.33	75	32	0	853	629	601	675	7.00E-23	104
contig23338	Q11PI8_CYTH3	64.91	57	20	0	319	149	384	440	6.00E-22	100
contig04241	B0RNG4_XANCB	47.06	85	45	0	324	70	536	620	6.00E-22	100
contig17293	B7RVI9_9GAMM	58.46	65	27	0	215	21	253	317	1.00E-21	98.7
contig13913	C0INS7_9BACT	43.36	113	64	0	341	3	52	164	2.00E-21	98.2
contig03316	Q21N31_SACD2	54.69	64	29	0	195	4	462	525	2.00E-21	97.7
contig10093	B3PEQ9_CELJU	52.7	74	35	0	19	240	157	230	3.00E-21	97.3

Supplementary Table 1. *Cont.*

Assembled contig ID	UniProt Accession number	% identity	alignment length	mismatches	gap openings	q. start	q. end	s. start	s. end	e-value	bit score
contig14342	C1S930_9SPHI	44.32	88	49	0	599	336	481	568	3.00E-21	98.7
contig24475	B2UQH3_AKKM8	51.56	64	31	0	18	209	214	277	5.00E-21	96.4
contig02705	Q2SHX0_HAHCH	73.47	49	13	0	8	154	393	441	9.00E-21	95
contig19349	A0Y0X8_9GAMM	55.38	65	29	0	31	225	446	510	1.00E-20	95.5
contig01813	Q11PI8_CYTH3	39.58	96	58	0	846	559	2672	2767	1.00E-20	96.8
contig06502	A9EU19_SORC5	45.57	79	43	0	299	63	115	193	3.00E-20	94.5
contig22983	Q21ZF8_RHOFD	59.65	57	23	0	173	3	109	165	2.00E-19	90.4
contig10599	A0Y0X8_9GAMM	57.38	61	26	0	184	2	446	506	6.00E-19	89.5
contig17731	A7LS44_BACOV	48.61	72	37	0	227	12	545	616	3.00E-18	87.2
contig14052	Q11T98_CYTH3	62.96	27	10	0	250	330	93	119	4.00E-18	46.4
contig11080	C1S930_9SPHI	46.75	77	41	0	231	1	486	562	6.00E-18	86.3
contig00230	O66185_BACCI	57.41	54	23	0	10	171	275	328	8.00E-18	85.4
contig01917	Q21HS5_SACD2	50.82	61	30	0	192	10	348	408	4.00E-17	83.1
contig05872	Q11UJ1_CYTH3	74.42	43	11	0	131	3	352	394	4.00E-17	82.6
contig07156	Q11VQ4_CYTH3	45.95	74	40	0	783	562	1425	1498	5.00E-17	84.9
contig25655	Q8GRB4_9PSED	45	80	44	0	575	336	1	80	7.00E-17	84
contig05967	C0INS7_9BACT	66.2	71	24	0	222	10	500	570	7.00E-17	82.6
contig18210	Q21F54_SACD2	60.78	51	20	0	5	157	514	564	9.00E-17	81.7
contig01984	Q21KX4_SACD2	38.38	99	61	0	312	16	1512	1610	1.00E-16	82.6
contig24905	Q21KX4_SACD2	55.81	43	19	0	132	4	1661	1703	2.00E-16	63.8
contig05199	Q9BH59_MELIC	55.07	69	31	0	3	209	59	127	2.00E-16	80.8
contig06009	Q11PI9_CYTH3	43.66	71	40	0	396	184	2683	2753	6.00E-16	80.3
contig09168	Q11NQ3_CYTH3	49.15	59	30	0	191	15	636	694	7.00E-16	79
contig15044	Q2SFD8_HAHCH	60	50	20	0	169	20	437	486	8.00E-16	79
contig01223	Q11NQ3_CYTH3	63.64	44	16	0	96	227	571	614	9.00E-16	79

Supplementary Table 1. *Cont.*

Assembled contig ID	UniProt Accession number	% identity	alignment length	mismatches	gap openings	q. start	q. end	s. start	s. end	e-value	bit score
contig04098	Q308B9_9BACT	59.26	54	22	0	299	138	293	346	1.00E-15	79
contig04503	Q9X3P6_9FIRM	70.37	27	8	0	1	81	111	137	1.00E-15	53.3
contig06091	C4EIC3_STRRS	43.55	62	35	0	735	920	63	124	1.00E-15	80.8
contig00650	A9B2K3_HERA2	49.21	63	32	0	19	207	55	117	1.00E-15	78.5
contig05391	A7V9B3_BACUN	56	50	22	0	292	143	253	302	2.00E-15	78.5
contig14108	A4CA09_9GAMM	75	40	10	0	4	123	304	343	3.00E-15	77.1
contig11183	Q97G04_CLOAB	52.83	53	25	0	198	40	35	87	4.00E-15	78.5
contig14858	Q11PI8_CYTH3	87.88	33	4	0	95	193	936	968	7.00E-15	75.8
contig13599	B3C9G1_9BACE	43.55	62	35	0	1	186	450	511	9.00E-15	75.8
contig09264	B6EH15_ALISL	50	62	31	0	231	46	362	423	1.00E-14	75.3
contig07887	Q21KE5_SACD2	72.22	36	10	0	1	108	326	361	2.00E-14	74.4
contig01054	Q11PI8_CYTH3	50	58	29	0	636	809	2702	2759	3.00E-14	76.7
contig01703	Q21KX4_SACD2	86.67	30	4	0	129	40	1088	1117	3.00E-14	68.4
contig07593	B0ZSE6_9ACTO	75	32	8	0	97	2	492	523	3.00E-14	73.5
contig25464	A6MI38_9SPIT	45.9	61	33	0	201	19	167	227	5.00E-14	73
contig14490	Q18BV5_CLOD6	40.26	77	46	0	232	2	62	138	6.00E-14	73
contig07103	Q21HS9_SACD2	42.31	78	45	0	156	389	235	312	9.00E-14	73
contig10391	B6VYB2_9BACE	48.98	49	25	0	180	34	94	142	1.00E-13	72.1
contig10691	Q11UJ1_CYTH3	49.18	61	31	0	654	472	716	776	1.00E-13	73.5
contig02059	O24820_9BACT	53.57	56	26	0	341	508	5	60	1.00E-13	73
contig04779	Q11PI9_CYTH3	47.37	57	30	0	507	337	1355	1411	1.00E-13	73.5
contig11483	Q3R055_XYLFA	58.54	41	17	0	51	173	280	320	2.00E-13	71.2
contig01895	A4F259_9BACL	55.32	47	21	0	2	142	334	380	3.00E-13	70.3
contig09849	B6QSI9_PENMQ	36.89	103	65	0	601	293	241	343	5.00E-13	71.2
contig23872	B8D1V5_HALOH	43.9	41	23	0	123	1	870	910	6.00E-13	53.8

Supplementary Table 1. *Cont.*

Assembled contig ID	**UniProt Accession number**	**% identity**	**alignment length**	**mismatches**	**gap openings**	**q. start**	**q. end**	**s. start**	**s. end**	**e-value**	**bit score**
contig03397	Q11PI9_CYTH3	35.71	84	54	0	614	363	2669	2752	6.00E-13	71.2
contig16794	C5BPZ6_9GAMM	65.71	35	12	0	105	1	189	223	8.00E-13	68.9
contig18313	B9MKT7_ANATD	50.98	51	25	0	8	160	102	152	9.00E-13	68.4
contig14908	C1Z0L6_PEDHE	62.79	43	16	0	215	343	6	48	1.00E-12	69.3
contig17865	Q11VF9_CYTH3	67.65	34	11	0	104	3	409	442	1.00E-12	62.5
contig08385	Q11PI9_CYTH3	52.17	69	33	0	209	3	580	648	2.00E-12	68.4
contig10324	Q5ZGC9_9CAUD	65.71	35	12	0	106	2	115	149	5.00E-12	66.1
contig16511	Q4UVY1_XANC8	50	38	19	0	171	58	79	116	5.00E-12	48.3
contig04307	A7V9A3_BACUN	73.08	26	7	0	2	79	537	562	7.00E-12	47.3
contig01403	B5JIL5_9BACT	54.55	44	20	0	2	133	321	364	8.00E-12	65.7
contig08855	B9K9B3_THENN	36	75	48	0	62	286	200	274	9.00E-12	66.1
contig13936	A9FK25_SORC5	52.27	44	21	0	2	133	18	61	1.00E-11	64.8
contig07270	C1UVR8_9DELT	67.65	34	11	0	6	107	46	79	1.00E-11	63.8
contig20317	Q092X1_STIAU	32.39	71	48	0	220	8	251	321	2.00E-11	64.3
contig13837	B8CL90_SHEPW	63.64	33	12	0	100	2	43	75	4.00E-11	63.4
contig08899	C1WMF5_9ACTO	47.17	53	28	0	224	382	67	119	4.00E-11	64.3
contig12904	A9EY77_9RHOB	56.1	41	18	0	124	2	275	315	5.00E-11	63.4
contig05947	Q2H8K5_CHAGB	27.48	131	95	0	1895	2287	558	688	5.00E-11	66.6
contig02283	Q9APG3_9PSED	45.28	53	29	0	6	164	376	428	6.00E-11	62.9
contig09275	Q47XT7_COLP3	47.06	51	27	0	160	8	160	210	6.00E-11	62.9
contig12768	Q11PI8_CYTH3	36.67	60	38	0	222	401	2693	2752	1.00E-10	62.9
contig15585	A5WEY2_PSYWF	72.73	33	9	0	162	64	82	114	1.00E-10	62
contig00744	A0Y0X8_9GAMM	78.57	28	6	0	3	86	683	710	2.00E-10	61.1
contig26451	B9XAL6_9BACT	43.14	51	29	0	154	2	552	602	3.00E-10	60.2
contig26454	C1W4K3_9MICO	52.94	34	16	0	28	129	316	349	3.00E-10	48.3

Supplementary Table 1. *Cont.*

Assembled contig ID	UniProt Accession number	% identity	alignment length	mismatches	gap openings	q. start	q. end	s. start	s. end	e-value	bit score
contig16506	GUN2_CLOJO	52.94	34	16	0	21	122	201	234	4.00E-10	54.2
contig20063	Q12KZ3_SHEDO	53.19	47	22	0	2	142	309	355	5.00E-10	59.7
contig10727	B1VW82_STRGG	53.85	39	18	0	1	117	72	110	6.00E-10	58.8
contig04801	Q21F54_SACD2	65.63	32	11	0	2	97	535	566	6.00E-10	58.8
contig14405	C5FQP0_MICCA	30.56	72	50	0	269	54	595	666	7.00E-10	59.7
contig11559	Q2SFD8_HAHCH	58.33	36	15	0	148	41	441	476	3.00E-09	57.4
contig25649	Q21KX4_SACD2	67.65	34	11	0	2	103	1448	1481	4.00E-09	56.5
contig09617	B7AFY4_9BACE	41.18	51	30	0	342	190	46	96	4.00E-09	58.3
contig15196	Q21KX4_SACD2	66.67	30	10	0	98	9	848	877	7.00E-09	56.1
contig09479	A5FL64_FLAJ1	30.67	75	52	0	16	240	378	452	7.00E-09	56.1
contig25208	Q11PI8_CYTH3	46.94	49	26	0	53	199	2682	2730	8.00E-09	55.6
contig05463	Q2SCY8_HAHCH	66.67	30	10	0	90	1	185	214	1.00E-08	55.6
contig14537	Q9X3P6_9FIRM	62.5	32	12	0	232	137	212	243	2.00E-08	54.7
contig25770	Q11PI9_CYTH3	56.41	39	17	0	118	2	8	46	2.00E-08	56.1
contig03641	B9AN63_9BACT	33.93	56	37	0	313	146	249	304	2.00E-08	56.1
contig19790	C5BTS3_9GAMM	51.22	41	20	0	124	2	277	317	3.00E-08	53.3
contig21717	A4BCU4_9GAMM	85.71	21	3	0	64	2	268	288	3.00E-08	52.8
contig09391	B7RVI9_9GAMM	55.88	34	15	0	10	111	264	297	3.00E-08	54.2
contig25883	Q47XT7_COLP3	64.71	34	12	0	110	9	160	193	4.00E-08	54.2
contig26116	Q11PI9_CYTH3	35.71	56	36	0	579	412	2686	2741	4.00E-08	56.5
contig12854	Q2SHX0_HAHCH	51.43	35	17	0	179	283	758	792	5.00E-08	54.2
contig15246	Q12KZ3_SHEDO	33.33	75	50	0	234	10	565	639	5.00E-08	53.3
contig13222	B7AFY4_9BACE	76.92	26	6	0	227	150	241	266	6.00E-08	52.8
contig16115	C1S6C0_9SPHI	42	50	29	0	31	180	503	552	6.00E-08	52.8
contig04127	Q21N15_SACD2	52.94	34	16	0	88	189	199	232	9.00E-08	52.4

Supplementary Table 1. *Cont.*

Assembled contig ID	UniProt Accession number	% identity	alignment length	mismatches	gap openings	q. start	q. end	s. start	s. end	e-value	bit score
contig14791	C0T375_9PSEU	43.48	46	26	0	216	79	32	77	1.00E-07	51.9
contig20202	Q5BDV7_EMENI	66.67	30	10	0	117	206	145	174	1.00E-07	51.9
contig01911	Q841J5_9ALTE	67.86	28	9	0	200	283	362	389	1.00E-07	52.4
contig22348	B7RVI9_9GAMM	46.81	47	25	0	142	2	1099	1145	1.00E-07	51.5
contig25525	Q21GU0_SACD2	39.71	68	41	0	259	56	38	105	1.00E-07	52.8
contig07601	Q308B8_9BACT	41.3	46	27	0	138	1	43	88	1.00E-07	51.9
contig16702	Q5ART1_EMENI	31.11	90	62	0	156	425	95	184	3.00E-07	51.9
contig18707	A5VF24_SPHWW	74.07	27	7	0	60	140	491	517	3.00E-07	50.1
contig18663	B9KKR0_RHOSK	56.45	62	27	0	5	190	352	413	4.00E-07	50.1
contig25920	Q2SJA2_HAHCH	51.43	35	17	0	134	30	717	751	4.00E-07	50.1
contig22036	O88021_STRCO	50	34	17	0	183	82	416	449	5.00E-07	49.6
contig23021	Q21GJ3_SACD2	51.52	33	16	0	3	101	84	116	5.00E-07	48.7
contig04598	Q11PI8_CYTH3	37.29	59	37	0	249	73	2717	2775	5.00E-07	52.4
contig10181	A2TX55_9FLAO	36.76	68	43	0	158	361	815	882	7.00E-07	50.1
contig11249	Q21GB9_SACD2	50	34	17	0	5	106	706	739	7.00E-07	48.3
contig07930	B5JIL5_9BACT	51.43	35	17	0	2	106	51	85	7.00E-07	50.1
contig20761	O69347_VIBSM	71.43	21	6	0	79	141	366	386	8.00E-07	48.7
contig25459	Q0FSH6_9RHOB	52.78	36	17	0	121	228	858	893	8.00E-07	49.2
contig20414	A7LS44_BACOV	50.82	61	30	0	1	183	927	987	9.00E-07	48.7
contig15701	Q21KX4_SACD2	56	25	11	0	128	54	711	735	1.00E-06	37.7
contig25008	A8XBB0_CAEBR	50	44	22	0	146	15	542	585	1.00E-06	48.7
contig00570	Q11PI8_CYTH3	45.95	37	20	0	330	220	2724	2760	1.00E-06	49.2
contig15304	A9FX20_SORC5	64.52	31	11	0	2	94	204	234	2.00E-06	47.3
contig21246	B1ZLP5_METPB	44.12	68	38	0	212	9	329	396	2.00E-06	47.8
contig23584	Q245S3_TETTH	45	40	22	0	124	5	1680	1719	2.00E-06	47.3

Supplementary Table 1. *Cont.*

Assembled contig ID	UniProt Accession number	% identity	alignment length	mismatches	gap openings	q. start	q. end	s. start	s. end	e-value	bit score
contig00357	Q3R055_XYLFA	55.56	27	12	0	19	99	188	214	2.00E-06	46.9
contig08179	C1UVR8_9DELT	63.33	30	11	0	188	277	31	60	2.00E-06	49.2
contig15332	Q2SCY8_HAHCH	71.43	21	6	0	196	134	264	284	3.00E-06	46.9
contig16110	B0CET5_ACAM1	69.23	26	8	0	173	96	629	654	3.00E-06	46.9
contig16669	Q21KX4_SACD2	69.23	26	8	0	27	104	1274	1299	3.00E-06	46.4
contig17172	A1ZFU5_9SPHI	38.6	57	35	0	173	3	229	285	3.00E-06	47.3
contig06033	Q55365_SYNY3	68	25	8	0	521	447	1017	1041	4.00E-06	48.3
contig04332	A9B399_HERA2	51.52	33	16	0	103	5	226	258	5.00E-06	45.5
contig01518	A7LS44_BACOV	37.7	61	38	0	65	247	810	870	6.00E-06	46.4
contig11361	Q21GB9_SACD2	40.82	49	29	0	198	52	677	725	7.00E-06	46
contig25454	B5HIM9_STRPR	48.72	39	20	0	40	156	19	57	7.00E-06	47.3
contig15581	Q245S3_TETTH	50	32	16	0	3	98	1683	1714	8.00E-06	45.1
contig02861	A7LS44_BACOV	64.29	28	10	0	131	48	683	710	1.00E-05	45.5
contig03003	A0Y0X8_9GAMM	84.21	19	3	0	3	59	691	709	1.00E-05	44.6

Supplementary Table 2. Summary of 211 sequences with Glycoside Hydrolase similarity used as a blast query against the NCBI-nr database.

Assembled contig ID	NCBI Accession number and Organism	% identity	alignment length	q. start	q. end	s. start	s. end	e-value	bit score
contig03003	gi|88859385 Pseudoalteromonas tunicata	71.43	21	3	65	858	878	0.038	41.2
contig06721	gi|110640093 Cytophaga hutchinsonii	70.94	234	684	1	56	289	4.00E-98	361
contig02397	gi|110638127 Cytophaga hutchinsonii	66	250	117	860	38	286	7.00E-101	354
contig05603	gb ABD79822.1 Saccharophagus degradans 2 40	54.24	177	2	532	86	262	1.00E-85	225
contig26022	gi|225012305 Flavobacteria bacterium MS024 2A	53.56	267	476	1273	486	752	3.00E-124	304
contig04690	gi|110640093 Cytophaga hutchinsonii	68.92	148	10	450	11	158	9.00E-55	216
contig05277	gi|86140693 Leeuwenhoekiella blandensis	73.97	242	918	1643	2	243	5.00E-104	382
contig03455	Cytophaga hutchinsonii	54.4	307	2	901	1016	1312	2.00E-73	280
contig26107	gi|110637645 Cytophaga hutchinsonii	68.06	144	443	12	673	816	9.00E-50	199
contig04179	gi|126646843 Algoriphagus sp PR1	55.56	153	4	462	105	257	1.00E-49	199
contig07415	gi|110640093 Cytophaga hutchinsonii	71.03	107	599	279	236	340	6.00E-56	153
contig02925	gi|110638127 Cytophaga hutchinsonii	80.77	104	2	313	443	546	6.00E-48	193
contig01407	gi|227539966 Sphingobacterium spiritivorum	64.6	161	1370	888	284	444	2.00E-59	234
contig04013	gi|110639808 Cytophaga hutchinsonii	68.75	112	337	2	340	451	7.00E-44	179
contig02917	gi|78926855 uncultured bacterium	68.07	119	31	387	223	341	3.00E-43	177
contig12578	gi|254788171 Teredinibacter turnerae T7901	54.55	99	555	259	629	727	1.00E-57	120
contig05485	gi|78926927 uncultured bacterium	60.24	166	502	8	227	392	6.00E-44	180
contig25936	gi|242260148 Clostridium cellulovorans 743B	52.51	179	588	52	85	250	8.00E-46	187
contig00226	gi|110639807 Cytophaga hutchinsonii	67.11	152	459	10	107	258	3.00E-44	181
contig04413	gi|124006662 Microscilla marina	73.88	134	751	350	10	143	2.00E-50	202
contig26301	gi|110639807 Cytophaga hutchinsonii	60.36	111	339	7	839	947	3.00E-36	154
contig25564	gi|110638770 Cytophaga hutchinsonii	59.69	129	395	9	314	442	2.00E-40	168
contig08782	gi|110639808 Cytophaga hutchinsonii	72.04	93	285	7	467	559	1.00E-32	142
contig05185	gi|242239319 Dickeya dadantii	56.91	123	8	373	119	241	6.00E-37	156
contig05113	gi|254787279 Teredinibacter turnerae T7901	57.14	133	74	451	501	633	2.00E-39	164

Supplementary Table 2. *Cont.*

Assembled contig ID	NCBI Accession number and Organism	% identity	alignment length	q. start	q. end	s. start	s. end	e-value	bit score
contig04687	gi|254787186 protein Teredinibacter turnerae	68.18	88	3	266	82	169	9.00E-31	136
contig15223	gi|110639808 Cytophaga hutchinsonii	67.44	86	15	272	616	701	3.00E-30	134
contig04664	gi|90019972 Saccharophagus degradans 2 40	64.39	132	397	2	498	629	1.00E-48	195
contig08470	gi|110637740 Cytophaga hutchinsonii	54.4	125	627	998	1	119	1.00E-31	141
contig17088	gi|115334997 uncultured bacterium	46.99	166	3	491	324	486	2.00E-40	168
contig01678	gi|90022135 Saccharophagus degradans 2 40	53.92	102	308	3	412	513	4.00E-28	127
contig18893	gi|71281571 Colwellia psychrerythraea 34H	72.15	79	239	3	227	305	3.00E-27	124
contig08844	gi|260062808 Robiginitalea biformata	69.74	76	236	9	166	241	3.00E-26	121
contig24355	gi|90022638 Saccharophagus degradans	67.5	80	240	1	53	132	4.00E-26	120
contig14077	gi|192361876 Cellvibrio japonicus	69.62	79	2	238	197	275	3.00E-25	117
contig02702	gi|91793955 Shewanella denitrificans	73.24	71	215	3	112	182	7.00E-25	116
contig02598	gi|242239319 Dickeya dadantii	51.61	124	1	372	70	193	2.00E-31	138
contig25780	gi|255607952 Ricinus communis	66.67	105	2	316	210	314	2.00E-33	145
contig16934	gi|90021040 Saccharophagus degradans 2 40	68.29	82	2	247	1413	1494	1.00E-23	112
contig00765	gi|88803060 Polaribacter irgensii	61.63	172	510	1	262	433	9.00E-56	219
contig23140	gi|83646626 Hahella chejuensis	64.56	79	239	3	160	238	2.00E-23	112
contig01065	gi|110638631 Cytophaga hutchinsonii	45.32	267	773	6	177	438	6.00E-57	224
contig00382	gi|86143269 Leeuwenhoekiella blandensis	68.99	129	400	14	620	748	3.00E-48	194
contig13597	gi|254784817 Teredinibacter turnerae T7901	45.54	112	456	121	332	443	1.00E-26	108
contig06190	gi|110639808 Cytophaga hutchinsonii	70	80	95	325	20	99	2.00E-22	108
contig11004	gi|110637685 Cytophaga hutchinsonii	64.38	73	220	2	141	213	4.00E-21	104
contig20446	gi|237719706 Bacteroides sp	56.96	79	3	239	201	279	8.00E-21	103
contig22358	gi|254787186 Teredinibacter turnerae T7901	75.86	58	65	238	53	110	6.00E-25	102
contig02656	gi|78926900 uncultured bacterium	53.06	98	9	302	469	559	4.00E-23	110
contig10055	gi|90019713 Saccharophagus degradans 2 40	56.25	80	1	240	117	196	5.00E-20	100
contig02758	gi|90022881 Saccharophagus degradans 2 40	47.22	72	217	432	35	106	2.00E-19	69.7

Supplementary Table 2. *Cont.*

Assembled contig ID	NCBI Accession number and Organism	% identity	alignment length	q. start	q. end	s. start	s. end	e-value	bit score
contig19798	gi|90021930 Saccharophagus degradans 2 40	69.49	59	179	3	93	151	2.00E-19	98.6
contig06707	gi|110638056 Cytophaga hutchinsonii	70	60	3	182	350	409	2.00E-19	98.6
contig25876	gi|242259850 Clostridium cellulovorans	57.5	80	222	1	249	327	5.00E-20	100
contig02648	gi|90020158 Saccharophagus degradans 2 40	74.14	58	176	3	134	191	6.00E-19	97.1
contig15633	gi|90023060 Saccharophagus degradans 2 40	52.86	70	1	210	488	557	1.00E-18	96.3
contig04461	gi|110638770 Cytophaga hutchinsonii	45.53	123	1	363	436	555	2.00E-21	106
contig20483	gi|212634478 Shewanella piezotolerans	56.96	79	239	3	69	147	3.00E-18	94.7
contig00162	gi|110638631 Cytophaga hutchinsonii	56.76	74	5	226	492	565	5.00E-18	94
contig04227	gi|170728697 Shewanella woodyi	69.09	55	3	167	30	84	9.00E-18	93.2
contig12437	gi|110637223 Cytophaga hutchinsonii	76.32	114	3	344	264	377	4.00E-88	200
contig12453	gi|90022763 Saccharophagus degradans 2 40	69.09	55	165	1	260	314	4.00E-17	90.9
contig26477	gi|261404702 Geobacillus sp	65.26	95	437	153	161	251	7.00E-30	111
contig04615	gi|110637645 Cytophaga hutchinsonii	65.08	63	2	190	714	776	1.00E-16	89.7
contig16578	gi|71281571 Colwellia psychrerythraea	76.92	52	239	84	1867	1918	2.00E-16	89
contig23608	gi|110638770 Cytophaga hutchinsonii	57.69	78	1	231	399	476	2.00E-21	105
contig01684	gi|110637198 Cytophaga hutchinsonii	44.59	148	886	452	592	736	1.00E-26	124
contig23338	gi|110639808 Cytophaga hutchinsonii	46.02	113	319	2	384	496	3.00E-19	98.2
contig04241	gi|159897669 Herpetosiphon aurantiacus	50.93	108	318	1	111	218	3.00E-24	114
contig17293	gi|83645744 Hahella chejuensis	60	65	215	21	576	640	3.00E-16	88.2
contig13913	gi|192361876 Cellvibrio japonicus	45.13	113	341	3	85	197	2.00E-20	102
contig03316	gi|90020283 Saccharophagus degradans 2 40	54.69	64	195	4	462	525	4.00E-15	84.3
contig10093	gi|192361876 Cellvibrio japonicus	52.7	74	19	240	157	230	5.00E-15	84
contig14342	gi|110637461 Cytophaga hutchinsonii	46.15	91	599	330	868	958	6.00E-19	97.8
contig24475	gi|153808937 Bacteroides caccae	50.68	73	21	239	201	273	5.00E-16	87.4
contig02705	gi|83645744 Hahella chejuensis	73.47	49	8	154	393	441	2.00E-14	82
contig19349	gi|119469861 Alteromonadales bacterium	53.95	76	1	225	435	510	2.00E-16	88.6

Supplementary Table 2. *Cont.*

Assembled contig ID	NCBI Accession number and Organism	% identity	alignment length	q. start	q. end	s. start	s. end	e-value	bit score
contig01813	gi|110639806 Cytophaga hutchinsonii	39.17	120	846	505	2319	2437	8.00E-19	98.6
contig06502	gi|254787279 Teredinibacter turnerae	49.54	109	323	3	311	414	5.00E-26	120
contig22983	gi|90022638 Saccharophagus degradans 2 40	59.65	57	173	3	102	158	1.00E-14	82.8
contig10599	gi|119469861 Alteromonadales bacterium	55.13	78	232	2	429	506	2.00E-15	85.1
contig17731	gi|110640149 Cytophaga hutchinsonii	56	75	227	3	231	305	4.00E-16	87.8
contig14052	gi|162449739 Sorangium cellulosum	54.24	59	154	330	151	208	1.00E-16	68.9
contig11080	gi|110637461 Cytophaga hutchinsonii	43.59	78	231	1	873	950	2.00E-13	79
contig00230	gi|3090434 Bacillus circulans	57.14	56	10	174	275	330	4.00E-12	74.3
contig01917	gi|90022139 Saccharophagus degradans 2 40	50.82	61	192	10	348	408	2.00E-11	72
contig05872	gi|110638056 Cytophaga hutchinsonii	74.42	43	131	3	352	394	3.00E-11	71.6
contig07156	gi|256424202 Chitinophaga pinensis	42.67	225	783	121	19	243	2.00E-37	160
contig25655	gi|90019761Saccharophagus degradans 2 40	51.22	82	334	89	696	776	3.00E-27	79.7
contig05967	gi|56675038 uncultured bacterium	70.42	71	222	10	497	564	9.00E-12	73.2
contig18210	gi|90023060 Saccharophagus degradans 2 40	60.78	51	5	157	514	564	5.00E-11	70.9
contig01984	gi|254785013 Teredinibacter turnerae T7901	58.74	143	432	4	279	420	8.00E-40	166
contig24905	gi|91792085 Shewanella denitrificans OS217	63.49	63	192	4	483	544	3.00E-16	88.2
contig05199	gi|17826951 Pseudomonas sp ND137	61.43	70	3	209	181	250	5.00E-12	73.9
contig06009	gi|110639300 Cytophaga hutchinsonii	43.3	97	411	133	467	561	2.00E-18	95.5
contig09168	gi|110638770 Cytophaga hutchinsonii	55.74	61	191	9	453	513	1.00E-12	75.9
contig15044	gi|83646626 Hahella chejuensis	60	50	169	20	437	486	2.00E-10	68.6
contig01223	gi|110638770 Cytophaga hutchinsonii	59.15	71	6	218	355	425	2.00E-19	99
contig04098	gi|78926855 uncultured bacterium	52.94	102	299	3	293	394	2.00E-22	108
contig04503	gi|254443020 Verrucomicrobiae bacterium	72.06	68	1	201	92	159	5.00E-24	114
contig06091	gi|68525474 Flavobacterium sp MSY2	67.63	173	1	519	199	371	1.00E-65	254
contig00650	gi|256393254 protein Catenulispora acidiphila	56.92	65	19	213	705	769	1.00E-13	79.3
contig05391	gi|254788171 protein Teredinibacter turnerae	55	80	289	53	225	304	7.00E-18	93.6

Supplementary Table 2. *Cont.*

Assembled contig ID	NCBI Accession number and Organism	% identity	alignment length	q. start	q. end	s. start	s. end	e-value	bit score
contig14108	gi|8885938 Pseudoalteromonas tunicata	64.71	51	4	156	304	349	3.00E-10	68.2
contig11183	gi|125973914 Clostridium thermocellum	45.56	90	255	1	11	100	2.00E-13	80.5
contig14858	gi|110639808 Cytophaga hutchinsonii	74.24	66	2	193	903	968	4.00E-21	104
contig13599	gi|189464233 Bacteroides intestinalis	63.29	79	1	237	77	155	6.00E-24	113
contig09264	gi|110637461 Cytophaga hutchinsonii	48.72	78	231	1	732	809	1.00E-12	75.9
contig07887	gi|90021219 Saccharophagus degradans 2 40	72.22	36	1	108	326	361	3.00E-09	64.7
contig01054	gi|110638938 2552 Cytophaga hutchinsonii	28.72	282	66	887	476	732	4.00E-20	103
contig01703	gi|88799706 oxidoreductase Reinekea sp	90	30	129	40	455	484	2.00E-09	60.8
contig07593	gi|166835917 Streptomyces sp s6 204	75	32	97	2	492	523	5.00E-09	63.9
contig25464	gi|254787942 Teredinibacter turnerae	68.66	67	204	4	182	248	2.00E-19	98.6
contig14490	gi|110639833 Cytophaga hutchinsonii	83.33	78	235	2	57	134	2.00E-30	135
contig07103	gi|90022135 Saccharophagus degradans 2 40	39.26	135	3	389	179	312	2.00E-16	89
contig10391	gi|254786327 Teredinibacter turnerae T7901	74.68	79	240	4	352	426	2.00E-27	125
contig10691	gi|110638056 Cytophaga hutchinsonii	35.38	130	654	277	716	845	2.00E-12	76.6
contig02059	gi|237718505 Bacteroides sp	46.73	107	212	520	13	119	1.00E-21	106
contig04779	gi|110639807 Cytophaga hutchinsonii	37.6	125	609	241	1324	1445	3.00E-15	85.9
contig11483	gi|15837868|ref|NP_298556.1|	58.54	41	51	173	280	320	2.00E-08	62
contig01895	gi|283846038 Bacillus cellulosilyticus	56	50	2	151	330	379	9.00E-09	63.2
contig09849	gi|124003516 dehydrogenase Microscilla marina	59.15	213	622	2	239	451	1.00E-63	246
contig23872	gi|163786454 Flavobacteriales bacterium	84.48	58	174	1	160	217	4.00E-23	110
contig03397	gi|149277963 Pedobacter sp BAL39	41.51	106	677	363	1072	1176	4.00E-14	82.4
contig16794	gi|254787186 Teredinibacter turnerae T7901	65.71	35	105	1	189	223	8.00E-08	60.1
contig18313	gi|254445795 Verrucomicrobiae bacterium	62.75	51	5	157	66	116	8.00E-13	76.6
contig14908	gi|227539966 Sphingobacterium spiritivorum	71.11	45	209	343	5	49	3.00E-12	74.7
contig17865	gi|110637740 Cytophaga hutchinsonii	55.56	81	227	3	362	442	5.00E-16	87.4
contig08385	gi|110639807 Cytophaga hutchinsonii	46.92	130	380	3	519	648	3.00E-23	111

Supplementary Table 2. *Cont.*

Assembled contig ID	NCBI Accession number and Organism	% identity	alignment length	q. start	q. end	s. start	s. end	e-value	bit score
contig10324	gi|53793624 Flavobacterium phage.11b	65.71	35	106	2	115	149	4.00E-07	57.8
contig16511	gi|21231824 Xanthomonas campestris	50	38	171	58	79	116	4.00E-07	42.7
contig04307	gi|254788171 Teredinibacter turnerae T7901	87.5	24	8	79	512	535	3.00E-07	43.9
contig01403	gi|254788056 Teredinibacter turnerae T7901	59.38	64	5	196	339	402	3.00E-15	84.7
contig08855	gi|254786327 Teredinibacter turnerae T7901	74.42	86	56	313	494	579	5.00E-31	137
contig13936	gi|162449739 Sorangium cellulosum	59.09	44	2	133	134	175	2.00E-07	58.5
contig07270	gi|262197465 Haliangium ochraceum	67.65	34	6	107	67	100	2.00E-06	55.8
contig20317	gi|83643752 Hahella chejuensis KCTC 2396	40.79	76	229	2	401	472	7.00E-10	67
contig13837	gi|212634478 Shewanella piezotolerans WP3	63.64	33	100	2	43	75	2.00E-06	55.5
contig08899	gi|256421052 Chitinophaga pinensis DSM 2588	47.54	61	206	382	29	89	9.00E-07	56.6
contig12904	gi|269218354 Actinomyces sp	46.84	79	238	2	234	310	7.00E-12	73.6
contig05947	gi|126648235 Algoriphagus sp	72.54	244	2	733	272	514	8.00E-91	339
contig02283	gi|261416250 Fibrobacter succinogenes	39.22	51	6	158	428	478	4.00E-08	45.1
contig09275	gi|119502900 marine gamma proteobacterium	53.95	76	229	2	390	465	2.00E-11	72
contig12768	gi|110639806 Cytophaga hutchinsonii	36.67	60	222	401	2340	2399	3.00E-06	55.1
contig15585	gi|148653080 Psychrobacter sp	72.73	33	162	64	82	114	4.00E-06	54.3
contig00744	gi|88859385 Pseudoalteromonas tunicata	72.73	33	3	98	680	712	2.00E-06	55.5
contig26451	gi|223934655 bacterium Ellin514	43.14	51	154	2	552	602	1.00E-05	52.8
contig26454	gi|282869827 Streptomyces sp	43.04	79	25	207	295	373	3.00E-08	61.6
contig16506	gi|585231 Clostridium josui	52.94	34	21	122	201	234	2.00E-05	47.8
contig20063	gi|192360365 Cellvibrio japonicus	45.45	55	2	160	376	430	2.00E-05	52.4
contig10727	gi|260913278 Pasteurella dagmatis	72.97	37	4	114	18	54	4.00E-08	61.2
contig04801	gi|90023060 Saccharophagus degradans 2 40	65.63	32	2	97	535	566	3.00E-05	51.6
contig14405	gi|202953357 Debaryomyces hansenii	32.95	88	269	9	229	316	2.00E-10	68.6
contig11559	gi|253573954 Paenibacillus sp	50.75	67	226	41	231	297	5.00E-07	57.4
contig25649	gi|90021040 Saccharophagus degradans 2 40	67.65	34	2	103	1448	1481	5.00E-09	49.7

Supplementary Table 2. *Cont.*

Assembled contig ID	**NCBI Accession number and Organism**	**% identity**	**alignment length**	**q. start**	**q. end**	**s. start**	**s. end**	**e-value**	**bit score**
contig09617	gi|110637643 Cytophaga hutchinsonii	65.41	133	390	1	27	159	8.00E-45	183
contig15196	gi|90021040 Saccharophagus degradans 2 40	49.33	75	230	9	968	1032	1.00E-10	69.7
contig09479	gi|163753699 Kordia algicida	51.25	80	1	240	254	333	9.00E-18	93.2
contig25208	gi|110639806 Cytophaga hutchinsonii	46.94	49	53	199	2329	2377	2.00E-04	48.9
contig05463	gi|83645744 Hahella chejuensis	51.47	68	195	4	701	768	2.00E-12	75.1
contig14537	gi|150002649 Bacteroides vulgatus	48.08	52	156	1	219	270	5.00E-15	57.4
contig25770	gi|124002135 Microscilla marina	65.47	139	363	776	1	137	3.00E-44	182
contig03641	gi|254785542 Teredinibacter turnerae T7901	72.79	136	544	137	204	339	5.00E-53	210
contig19790	gi|188990414 Xanthomonas campestris	47.37	57	166	2	82	138	2.00E-06	55.5
contig21717	gi|88798396 glucanase Reinekea sp	85.71	21	64	2	268	288	0.001	46.6
contig09391	gi|110637461 Cytophaga hutchinsonii	48.61	72	13	228	844	915	4.00E-16	87.8
contig25883	gi|119502900 marine gamma proteobacterium	45.07	71	221	9	576	644	3.00E-12	61.6
contig26116	gi|124009083 Microscilla marina	33.12	157	780	334	1498	1648	2.00E-17	95.1
contig12854	gi|55376769 protein Haloarcula marismortui	45.3	117	68	418	546	658	2.00E-22	108
contig15246	gi|91793955 Shewanella denitrificans OS217	47.37	76	234	10	565	639	2.00E-13	78.6
contig13222	gi|110637643 Cytophaga hutchinsonii ATCC	67.09	79	227	3	240	316	8.00E-21	103
contig16115	gi|269963230 Vibrio harveyi	47.76	67	1	198	233	299	5.00E-08	60.8
contig04127	gi|256396581 Catenulispora acidiphila DSM 44928	48.1	79	1	237	217	293	1.00E-15	86.3
contig14791	gi|19262983 Pseudomonas sp	45.61	57	201	31	27	82	3.00E-06	55.1
contig20202	gi|259488404 Aspergillus nidulans	62.16	37	117	227	103	136	0.001	46.6
contig01911	gi|119502900 marine gamma proteobacterium	53.62	69	80	286	591	659	2.00E-12	71.2
contig22348	gi|90021040 Saccharophagus degradans 2 40	59.57	47	142	2	1484	1530	2.00E-08	62
contig25525	gi|120436187 Gramella forsetii KT0803	49.21	126	379	2	2267	2392	1.00E-26	122
contig07601	gi|283844144 Bacillus cellulosilyticus	38.04	92	249	7	1	89	9.00E-07	56.6
contig16702	gi|53803512 Methylococcus capsulatus	36.77	155	30	488	104	254	2.00E-17	92.8
contig18707	gi|239820612 Variovorax paradoxus	71.88	32	57	152	39	70	2.00E-05	52.4

Supplementary Table 2. *Cont.*

Assembled contig ID	NCBI Accession number and Organism	% identity	alignment length	q. start	q. end	s. start	s. end	e-value	bit score
contig18663	gi|83950901 Roseovarius nubinhibens	59.72	72	2	217	318	389	7.00E-12	73.6
contig25920	gi|115372711 Stigmatella aurantiaca	44.29	70	203	3	2165	2234	3.00E-07	58.2
contig22036	gi|220928668 Clostridium cellulolyticum	54.17	48	177	34	1047	1094	7.00E-10	67
contig23021	gi|90022139 Saccharophagus degradans 2 40	54.55	33	3	101	379	411	0.001	46.6
contig04598	gi|228473605 Capnocytophaga gingivalis	30.57	193	555	40	35	220	5.00E-12	77
contig10181	gi|120436187 Gramella forsetii KT0803	44.17	120	2	361	2209	2328	7.00E-22	106
contig11249	gi|90022645 Saccharophagus degradans 2 40	50	34	5	106	706	739	0.014	42.7
contig07930	gi|198274843 Bacteroides plebeius	75	120	2	361	41	158	6.00E-51	203
contig20761	gi|254784408 Teredinibacter turnerae T7901	63.33	30	52	141	297	326	0.002	45.8
contig25459	gi|189347360 Chlorobium limicola DSM 245	46.99	83	1	228	1854	1936	4.00E-11	71.2
contig20414	gi|156740923 Roseiflexus castenholzii DSM	65.57	61	1	183	708	768	1.00E-08	63.2
contig15701	gi|90021040 Saccharophagus degradans 2 40	51.72	58	212	54	678	735	2.00E-08	62
contig25008	gi|153872900 cyclase Beggiatoa sp	44.16	77	230	3	152	221	9.00E-07	56.6
contig00570	gi|146301709 Flavobacterium johnsoniae	38.67	75	318	94	3526	3587	2.00E-06	55.5
contig15304	gi|260454326 Streptomyces flavogriseus	67.86	28	2	85	277	304	0.005	44.3
contig21246	gi|71736991 putative Pseudomonas syringae	46.75	77	233	3	4944	5002	2.00E-10	68.6
contig23584	gi|269124685 Thermomonospora curvata	63.41	41	124	2	412	452	3.00E-06	54.7
contig00357	gi|182681111 Xylella fastidiosa	55.56	27	19	99	188	214	0.029	41.6
contig08179	gi|83646812 Hahella chejuensis	62.5	32	179	274	390	421	8.00E-11	49.3
contig15332	gi|146301068 Flavobacterium johnsoniae	50	54	196	35	749	802	8.00E-05	50.1
contig16110	gi|255258429 Sideroxydans lithotrophicus ES.1	69.23	39	173	57	734	772	1.00E-08	62.8
contig16669	gi|90021040 like Saccharophagus degradans 2 40	69.23	26	27	104	1274	1299	0.04	41.2
contig17172	gi|90023532 Saccharophagus degradans 2 40	44.26	61	185	3	90	150	3.00E-04	48.1
contig06033	gi|110637740 Cytophaga hutchinsonii |	37.65	170	521	12	468	631	1.00E-24	116
contig04332	gi|159897943 Herpetosiphon aurantiacus	51.52	33	103	5	226	258	0.067	40.4
contig01518	gi|71282619 Colwellia psychrerythraea 34H	64.1	78	2	235	508	585	2.00E-19	98.6

Supplementary Table 2. *Cont.*

Assembled contig ID	**NCBI Accession number and Organism**	**% identity**	**alignment length**	**q. start**	**q. end**	**s. start**	**s. end**	**e-value**	**bit score**
contig11361	gi|253573954 Paenibacillus sp	40.63	64	198	7	208	268	6.00E-05	50.4
contig25454	gi|254786337 Teredinibacter turnerae T7901	28.88	187	1	549	239	383	4.00E-11	71.6
contig15581	gi|186686820 Nostoc punctiforme	70	40	3	122	958	997	8.00E-08	60.1
contig02861	gi|110639943 Cytophaga hutchinsonii	76.67	30	282	193	350	379	8.00E-11	46.2

Supplementary Table 3. Summary of multiple assembled contigs providing similarities with the same protein in the constructed Glycoside Hydrolase database.

454 Sequencing contig	UniProt Accession number	Organism known to encode the protein	UniProt description
contig03455 **contig04013** **contig08782** **contig15223** **contig06190** **contig23338** **contig01813** **contig14858** **contig01054** **contig12768** **contig25208** **contig04598** **contig00570**	Q11PI8_CYTH3	Cytophaga hutchinsonii (strain ATCC 33406 / NCIMB 9469)	Beta-glycosidase related protein GH8
contig12578 **contig05391**	A7V9B3_BACUN	Bacteroides uniformis ATCC 8492	Uncharacterised protein GH9
contig14077 **contig10093**	B3PEQ9_CELJU	Cellvibrio japonicus (strain Ueda107	Endo-1,4-beta-D-glucanase (Cel9B) GH9
contig01403 **contig07930**	B5JIL5_9BACT	Verrucomicrobiae bacterium DG1235	Cellulase GH5
contig09617 **contig13222**	B7AFY4_9BACE	Bacteroides eggerthii DSM 20697	Uncharacterised protein of GH8
contig13913 **contig05967**	C0INS7_9BACT	uncultured bacterium BLR10	Cellulase GH 9

Supplementary Table 3. *Cont.*

454 Sequencing contig	**UniProt Accession number**	**Organism known to encode the protein**	**UniProt description**
contig14342 **contig11080**	C1S930_9SPHI	Chitinophaga pinensis DSM 2588	Chitinase GH18
contig07270 **contig08179**	C1UVR8_9DELT	Haliangium ochraceum DSM 14365	Cellulase
contig01065 **contig00162**	Q11SW6_CYTH3	Cytophaga hutchinsonii (strain ATCC 33406 / NCIMB 9469)	Endoglucanase realted protein GH9
contig02397 **contig02925**	Q11UC0_CYTH3	Cytophaga hutchinsonii (strain ATCC 33406 / NCIMB 9469)	Endoglucanase related protein GH 5
contig08470 **contig17865**	Q11VF9_CYTH3	Cytophaga hutchinsonii (strain ATCC 33406 / NCIMB 9469)	Endoglucanase related protein GH 9
contig11249 **contig11361**	Q21GB9_SACD2	Saccharophagus degradans (strain 2-40 / ATCC 43961 / DSM 17024)	Endoglucanase GH5
contig01678 **contig07103**	Q21HS9_SACD2	Saccharophagus degradans (strain 2-40 / ATCC 43961 / DSM 17024)	Endoglucanase like protein GH5
contig05603 **contig04413**	Q21NA7_SACD2	Saccharophagus degradans (strain 2-40 / ATCC 43961 / DSM 17024)	b-glycosidase GH 9
contig23584 **contig15581**	Q245S3_TETTH	Tetrahymena thermophila SB210	Cellulase GH5
contig05463 **contig15332**	Q2SCY8_HAHCH	Hahella chejuensis (strain KCTC 2396)	Beta-glucanase/Beta-glucan synthetase GH16

Supplementary Table 3. *Cont.*

454 Sequencing contig	**UniProt Accession number**	**Organism known to encode the protein**	**UniProt description**
contig02705 **contig12854**	Q2SHX0_HAHCH	Hahella chejuensis (strain KCTC 2396)	Beta-glucanase/Beta-glucan synthetase GH16
contig02917 **contig04098**	Q308B9_9BACT	Uncultured bacterium	Endo-1,4-beta-D-glucanase GH9
contig11483 **contig00357**	Q3R055_XYLFA	Xylella fastidiosa Ann-1	Cellulase GH6
contig04503 **contig14537**	Q9X3P6_9FIRM	Caldicellulosiruptor sp. Tok7B.1	CelB GH5
contig17293 **contig09391** **contig22348** **contig03216**	B7RVI9_9GAMM	marine gamma proteobacterium HTCC2148	Uncharacterised protein GH16
contig04687 **contig22358** **contig16794**	C5BPZ6_9GAMM	Teredinibacter turnerae T7901	GH16 protein
contig06707 **contig05872** **contig10691**	Q11UJ1_CYTH3	Cytophaga hutchinsonii (strain ATCC 33406 / NCIMB 9469)	Endoglucanase GH9
contig02702 **contig20063** **contig15246**	Q12KZ3_SHEDO	Shewanella denitrificans (strain OS217 / ATCC BAA-1090 / DSM 15013)	GH16

Supplementary Table 3. *Cont.*

454 Sequencing contig	UniProt Accession number	Organism known to encode the protein	UniProt description
contig15633 **contig18210** **contig04801**	Q21F54_SACD2	Saccharophagus degradans (strain 2-40 / ATCC 43961 / DSM 17024)	Putative retaining b-glycosidase GH5
contig23140 **contig15044** **contig11559**	Q2SFD8_HAHCH	Hahella chejuensis (strain KCTC 2396)	Endoglucanase GH5
contig19349 **contig10599** **contig00744** **contig03003**	A0Y0X8_9GAMM	Alteromonadales bacterium TW-7	GH16
contig18893 **contig16578** **contig09275** **contig25883**	Q47XT7_COLP3	Colwellia psychrerythraea (strain 34H / ATCC BAA-681)	GH16
contig06721 **contig04690** **contig07415** **contig09168** **contig01223**	Q11NQ3_CYTH3	Cytophaga hutchinsonii (strain ATCC 33406 / NCIMB 9469)	GH8
contig26022 **contig25780** **contig00382** **contig17731** **contig20414** **contig01518** **contig02861**	A7LS44_BACOV	Bacteroides ovatus ATCC 8483	GH16

Supplementary Table 3. *Cont.*

454 Sequencing contig	**UniProt Accession number**	**Organism known to encode the protein**	**UniProt description**
contig05277 **contig26107** **contig25564** **contig04461** **contig04615** **contig23608** **contig07156** **contig20679** **contig06547**	Q11VQ4_CYTH3	Cytophaga hutchinsonii (strain ATCC 33406 / NCIMB 9469)	GH8
contig00226 **contig26301** **contig06009** **contig04779** **contig03397** **contig08385** **contig25770** **contig26116**	Q11PI9_CYTH3	Cytophaga hutchinsonii (strain ATCC 33406 / NCIMB 9469)	Beta-glycosidase related protein GH8
contig16934 **contig00765** **contig01984** **contig24905** **contig01703** **contig25649** **contig15196** **contig15701** **contig16669**	Q21KX4_SACD2	Saccharophagus degradans (strain 2-40 / ATCC 43961 / DSM 17024)	Retaining b-glycosidase GH16