

Supplementary Materials

S1 TABLE | Designed primers for target proteins.

Protein ID	Primer ID	Sequence
Cel25	TA_Nested_225F	5'CCCGGACTAGAAAGGCAGAG
Cel25	TA_TECH_225F	5'GGTGATGATGATGACAAGATGAGTCAACAAATAATTGAAGAATTATTG
Cel25	TA_TECH_225R	5'GGAGATGGGAAGTCATTACTAGTTTCTAAAGGTTTTTCCTCG
Cel30	TA_TECH_230F	5'GGTGATGATGATGACAAGGACATGGTTGACTCCAAGAAAATAACG
Cel30	TA_TECH_230R	5'GGAGATGGGAAGTCATTAGGGTCCTCTGCCTCCACC
Cel40	TA_TECH_340F	5'GGTGATGATGATGACAAGATGGTTAGAAAGGAATTCCTGAG
Cel40	TA_Nested_340R	5'GCAACAGGTCGGATTGTTCG
Cel40	TA_TECH_340R	5'GGAGATGGGAAGTCATTATCATATATTTTCACTGCTATGTTTGTG
Cel45	TA_TECH_345F	5'GGTGATGATGATGACAAGATGACCAAAACCATAGCGGTAG
Cel45	TA_TECH_345R	5'GGAGATGGGAAGTCATTATCACTGTTTGCAATGTTTGG

S2 TABLE | CAZymes, identified in *T. adornatum* 1910b^T genome.

#Gene	dbCan 2.0 function prediction	Pfam domains organization	Probable function	Signal peptide	Transmem brane helices
<i>N186_RS00225</i>	GH3	GH3-GH3-Fn3	β-glucosidase	-	
<i>N186_RS00270</i>	GH113	ND	β-mannase	+	1
<i>N186_RS00340</i>	GH1	GH1	Putative β-glucosidase	-	
<i>N186_RS00420</i>	GT35	GT1+phosphorylase	Starch phosphorylase	-	
<i>N186_RS00845</i>	CE1	S33	Putative esterase	-	3
<i>N186_RS01315</i>	GT21	GT2	UDP-Glc: ceramide β-glucosyltransferase	-	4
<i>N186_RS01555</i>	GH57	GH57	Alpha-amylase	-	
<i>N186_RS01670</i>	GT2	GT2	Cellulose/polysaccharide-synthase	-	5
<i>N186_RS01830</i>	GT27	GT2	Polypeptide α-N-acetylgalactos-aminyltransferase	-	3
<i>N186_RS01850</i>	GH57	GH57	Alpha-amylase	-	
<i>N186_RS04390</i>	GT66	STT3	Oligosaccharyl transferase	-	14
<i>N186_RS04780</i>	GH109	GFO_IDH_MocA	α-N-acetylgalactosaminidase	-	
<i>N186_RS05430</i>	GT5	GT5	Glycogen synthase	-	
<i>N186_RS05435</i>	GH57	GH57-DuF1925-DuF1926	Alpha-amylase	-	
<i>N186_RS06215</i>	GH109	GFO_IDH_MocA	α-N-acetylgalactosaminidase	-	+
<i>N186_RS06465</i>	CE9	Amidohydro_1	N-acetylglucosamine-6-phosphate deacetylase	-	
<i>N186_RS06480</i>	GH109	GFO_IDH_MocA	α-N-acetylgalactosaminidase	-	+
<i>N186_RS06555</i>	GH1	GH1	Beta-galactosidase	-	
<i>N186_RS06910</i>	CE14	PIG-L	Diacetylchitobiose deacetylase	-	
<i>N186_RS07180</i>	AA4	FAD binding domain - FAD-oxidase	Vanillyl-alcohol oxidase	-	
<i>N186_RS07230</i>	GH130	GH130	β-1,4-mannosylglucose phosphorylase	-	
<i>N186_RS07265</i>	GH65	GH65	Kojibiose phosphorylase	-	1
<i>N186_RS07400</i>	GH38	GH38-Middledomain-	Alpha-mannosidase	-	

		GH38C		
<i>N186_RS07730</i>	GT2	GT2	-	4
<i>N186_RS07735</i>	GT2	GT2	-	3
<i>N186_RS07745</i>	GT2	GT2	-	3
<i>N186_RS07750</i>	GT2	GT2	Glycosyl transferases involved	-
<i>N186_RS07755</i>	GT4	GT1	in cell wall biosynthesis	-
<i>N186_RS07920</i>	GT2	Glyco_tranf_2_3		-
<i>N186_RS07935</i>	GT2	GT2		-
<i>N186_RS07940</i>	GT4	GT1		-
<i>N186_RS08040</i>	GH57	GH57-GlucodextranC	Alpha-amylase	-
<i>N186_RS08045</i>	GH13_20	Alpha-amylase	Alpha-amylase	-
<i>N186_RS08485</i>	GT4	GT1	Putative glycosyl transferase	-
<i>N186_RS08540</i>	GH4	GH4-GH4	Alpha-glucosidase	-
<i>N186_RS08615</i>	GH16	GH16	Putative endo-beta1-3 glucanase	-
<i>N186_RS08795</i>	CE7	Hydrolase_4	Cephalosporin-C deacetylase	-
<i>N186_RS09030</i>	GT2	Glyco_tranf_2_3	Putative glycosyl transferase	-
<i>N186_RS09365</i>	CE7	Hydrolase_4	Cephalosporin-C deacetylase	+

ND - not detected by the algorithm.

S3 TABLE | The genes with high ratio of cellulose/control riBAQ values.

riBAQ_cell_mean/ riBAQ_contr_mean	Gene ID	Function	Signal peptides (Phobius)	Signal peptides (TatP)	Signal peptides (SignalP)	Transmembrane helices (Phobius)	Transmembrane helices (TMHMM)
∞	<i>N186_RS00055</i>	AbrB/MazE/SpoVT_family_DNA-binding_domain-containing_protein_	NO	NO	NO	0	0
∞	<i>N186_RS00150</i>	ECF_transporter_S_component	NO	NO	NO	4	4
∞	<i>N186_RS00325</i>	ABC_transporter_permease_	YES	NO	NO	5	6
∞	<i>N186_RS01545</i>	hypothetical_protein	NO	NO	NO	11	11
∞	<i>N186_RS01575</i>	DUF429_domain-containing_protein_	NO	NO	NO	0	0
∞	<i>N186_RS01745</i>	ModE_family_transcriptional_regulator	NO	NO	NO	0	0
∞	<i>N186_RS01770</i>	hypothetical_protein	NO	NO	NO	4	4
∞	<i>N186_RS01865</i>	hypothetical_protein	NO	NO	NO	0	0
∞	<i>N186_RS02535</i>	hypothetical_protein	NO	NO	NO	0	0
∞	<i>N186_RS02740</i>	30S_ribosomal_protein_S30e	NO	NO	NO	0	0
∞	<i>N186_RS03045</i>	flap_endonuclease-1	NO	NO	NO	0	0
∞	<i>N186_RS03145</i>	Kae1-associated_kinase_Bud32_	NO	NO	NO	0	0
∞	<i>N186_RS03210</i>	hypothetical_protein	NO	NO	NO	0	0
∞	<i>N186_RS03455</i>	hypothetical_protein	NO	NO	NO	0	0
∞	<i>N186_RS03880</i>	hypothetical_protein	NO	NO	NO	0	0
∞	<i>N186_RS04130</i>	hypothetical_protein	NO	NO	NO	0	0
∞	<i>N186_RS04620</i>	hypothetical_protein	YES	NO	YES	0	1
∞	<i>N186_RS04695</i>	hypothetical_protein	YES	NO	YES	0	1
∞	<i>N186_RS04830</i>	hypothetical_protein	NO	NO	NO	0	0
∞	<i>N186_RS04845</i>	hypothetical_protein	NO	NO	NO	0	0
∞	<i>N186_RS05150</i>	hypothetical_protein	NO	NO	NO	1	0
∞	<i>N186_RS05800</i>	DUF91_domain-containing_protein_	NO	NO	NO	0	0
∞	<i>N186_RS05960</i>	hypothetical_protein	NO	NO	NO	1	1
∞	<i>N186_RS06210</i>	hypothetical_protein	NO	NO	NO	1	1
∞	<i>N186_RS06620</i>	hypothetical_protein	NO	NO	NO	3	3
∞	<i>N186_RS07105</i>	radical_SAM_protein_	NO	NO	NO	0	0
∞	<i>N186_RS07225</i>	NUDIX_domain-containing_protein_	NO	NO	NO	0	0
∞	<i>N186_RS07435</i>	hypothetical_protein	NO	NO	NO	0	0
∞	<i>N186_RS07490</i>	hypothetical_protein	NO	NO	NO	0	0
∞	<i>N186_RS07625</i>	hypothetical_protein	NO	NO	NO	5	3
∞	<i>N186_RS07905</i>	hypothetical_protein	NO	NO	NO	0	0
∞	<i>N186_RS08260</i>	ABC_transporter_permease_	NO	NO	NO	4	4
∞	<i>N186_RS08445</i>	hypothetical_protein	NO	NO	NO	0	0
∞	<i>N186_RS09020</i>	hypothetical_protein	NO	NO	NO	0	0
50,90718296	<i>N186_RS00335</i>	hypothetical_protein	NO	YES	NO	2	2
44,80889526	<i>N186_RS00340</i>	glycoside_hydrolase_family_1_protein	NO	NO	NO	0	0

41,44190978	<i>N186_RS00330</i>	ABC_transporter_permease_	NO	NO	NO	6	6
36,10994726	<i>N186_RS00065</i>	hypothetical_protein	NO	NO	NO	1	0
25,16557729	<i>N186_RS09195</i>	hypothetical_protein	YES	NO	NO	0	1
18,64521484	<i>N186_RS00535</i>	ATP-cone_domain-containing_protein_	NO	NO	NO	0	0
17,73156259	<i>N186_RS08075</i>	hypothetical_protein	NO	NO	NO	1	1
14,76535538	<i>N186_RS07325</i>	hypothetical_protein	NO	NO	NO	1	1
13,59589106	<i>N186_RS09360</i>	hypothetical_protein	YES	NO	YES	0	1
13,19833686	<i>N186_RS03365</i>	radical_SAM_protein_	NO	NO	NO	0	0
13,1514073	<i>N186_RS06530</i>	hypothetical_protein	NO	NO	NO	8	7
12,02077174	<i>N186_RS05940</i>	hypothetical_protein	NO	NO	NO	0	0
11,70440609	<i>N186_RS01230</i>	ABC_transporter_ATP-binding_protein	NO	NO	NO	0	0
		carboxypeptidase_regulatory-					
11,30125896	<i>N186_RS00340</i>	like_domain-containing_protein	YES	NO	NO	1	2
10,50891896	<i>N186_RS03790</i>	hypothetical_protein	NO	YES	NO	0	0
10,28421264	<i>N186_RS03050</i>	hypothetical_protein	NO	NO	NO	0	0
9,255949394	<i>N186_RS04400</i>	50S_ribosomal_protein_L44e	NO	NO	NO	0	0
8,824295508	<i>N186_RS04590</i>	hypothetical_protein	NO	NO	NO	0	0
		hypA_hydrogenase_nickel_incorporatio					
8,76930959	<i>N186_RS07960</i>	n_protein_	NO	NO	NO	0	0
8,740729267	<i>N186_RS07610</i>	ATP-binding_protein	NO	NO	NO	0	0
7,925999569	<i>N186_RS02040</i>	50S_ribosomal_protein_L32e	NO	NO	NO	0	0
7,7182652	<i>N186_RS02905</i>	DUF87_domain-containing_protein_	NO	NO	NO	0	0
7,664465571	<i>N186_RS03100</i>	AbrB_family_transcriptional_regulator	NO	YES	NO	0	0
6,928690807	<i>N186_RS02215</i>	hypothetical_protein	NO	NO	NO	0	0
6,801554103	<i>N186_RS02075</i>	DUF99_domain-containing_protein_	NO	NO	NO	0	0
6,728909752	<i>N186_RS03885</i>	PIN_domain-containing_protein_	NO	NO	NO	0	0
		phosphoenolpyruvate--					
6,71403197	<i>N186_RS06460</i>	protein_phosphotransferase	NO	NO	NO	0	0
6,673026383	<i>N186_RS04655</i>	hypothetical_protein	NO	YES	NO	0	0
6,514179103	<i>N186_RS04310</i>	hypothetical_protein	NO	NO	NO	0	0
6,39210034	<i>N186_RS08505</i>	hypothetical_protein	YES	YES	NO	1	2
6,273899627	<i>N186_RS03950</i>	hypothetical_protein	NO	YES	NO	7	6
5,705866812	<i>N186_RS06650</i>	sugar_ABC_transporter_permease	NO	NO	NO	6	6
5,66924546	<i>N186_RS05325</i>	DUF126_domain-containing_protein_	NO	NO	NO	0	0
5,581344373	<i>N186_RS00730</i>	hypothetical_protein	NO	NO	NO	14	14
5,234149776	<i>N186_RS00050</i>	PIN_domain-containing_protein_	NO	NO	NO	0	0
5,070287082	<i>N186_RS07535</i>	hypothetical_protein	NO	NO	NO	0	0
5,003085771	<i>N186_RS00165</i>	hypothetical_protein	NO	NO	NO	5	5
4,992367763	<i>N186_RS03980</i>	hypothetical_protein	NO	YES	NO	0	0
		nucleotidyltransferase_domain-					
4,956264834	<i>N186_RS08700</i>	containing_protein_	NO	NO	NO	0	0
4,842324684	<i>N186_RS06020</i>	ECF_transporter_S_component	NO	NO	NO	5	5

4,826872668	<i>N186_RS06380</i>	hypothetical_protein	NO	NO	NO	14	14
4,813850867	<i>N186_RS00640</i>	aldehyde_ferredoxin_oxidoreductase_	NO	NO	NO	0	0
4,632599183	<i>N186_RS06365</i>	hypothetical_protein	NO	NO	NO	5	5
4,473133648	<i>N186_RS08245</i>	hypothetical_protein	NO	NO	NO	4	4
4,40893768	<i>N186_RS04580</i>	hypothetical_protein	NO	NO	NO	0	0
4,359956673	<i>N186_RS02420</i>	hypothetical_protein	NO	NO	NO	0	0
4,152293658	<i>N186_RS05330</i>	DUF521_domain-containing_protein_	NO	NO	NO	0	0
4,141215819	<i>N186_RS05460</i>	sugar_phosphate_isomerase/epimerase_	NO	NO	NO	0	0
4,11527964	<i>N186_RS06280</i>	hypothetical_protein	NO	NO	NO	2	2
4,060256849	<i>N186_RS05405</i>	hypothetical_protein	NO	NO	NO	0	0
4,050006725	<i>N186_RS07070</i>	ABC_transporter	NO	NO	NO	8	6
4,016790096	<i>N186_RS03095</i>	hypothetical_protein	NO	NO	NO	1	0
3,99130395	<i>N186_RS05750</i>	hypothetical_protein	NO	NO	NO	6	6
3,976466372	<i>N186_RS04185</i>	hypothetical_protein	NO	NO	NO	7	5
3,9277433	<i>N186_RS09025</i>	hypothetical_protein	YES	YES	NO	0	0
3,901796303	<i>N186_RS01080</i>	hypothetical_protein	NO	NO	NO	0	0
3,803695664	<i>N186_RS09160</i>	ATP-binding_protein	NO	NO	NO	0	0
3,766476248	<i>N186_RS00500</i>	hypothetical_protein	NO	NO	NO	0	0
3,699971272	<i>N186_RS00940</i>	hypothetical_protein	NO	NO	NO	0	0
3,656497266	<i>N186_RS03040</i>	thioredoxin_	NO	NO	NO	0	0
3,399808116	<i>N186_RS05775</i>	ferrous_iron_transport_protein_A_	NO	NO	NO	0	0
3,393979911	<i>N186_RS00980</i>	hypothetical_protein	NO	NO	NO	0	0
3,280690398	<i>N186_RS00395</i>	ZIP_family_metal_transporter	NO	NO	NO	5	5
3,182963414	<i>N186_RS00230</i>	hypothetical_protein	YES	NO	NO	0	1
2,988083312	<i>N186_RS06755</i>	hypothetical_protein	NO	NO	NO	0	0
2,980025618	<i>N186_RS02745</i>	hypothetical_protein	NO	NO	NO	0	0
2,965130739	<i>N186_RS09185</i>	DUF554_domain-containing_protein_	NO	NO	NO	6	5
2,931432391	<i>N186_RS02230</i>	50S_ribosomal_protein_L13	NO	NO	NO	0	0
2,930210825	<i>N186_RS00870</i>	QueT_transporter_family_protein	NO	NO	NO	8	8
2,928285052	<i>N186_RS05915</i>	hypothetical_protein	NO	NO	NO	5	5
2,902997747	<i>N186_RS00725</i>	hypothetical_protein	NO	NO	NO	5	5
2,893128599	<i>N186_RS07315</i>	hypothetical_protein	NO	NO	NO	6	6
2,833081547	<i>N186_RS05845</i>	hypothetical_protein	NO	NO	NO	0	0
2,820225251	<i>N186_RS06170</i>	hypothetical_protein	NO	NO	NO	0	0
2,810878891	<i>N186_RS01510</i>	hypothetical_protein	NO	NO	NO	0	0
2,801183439	<i>N186_RS00035</i>	hypothetical_protein	YES	NO	NO	0	0
2,737589876	<i>N186_RS01775</i>	ADP-ribose-binding_protein	NO	NO	NO	0	0
2,722919397	<i>N186_RS05115</i>	prenyltransferase_	NO	NO	NO	8	8
		energy-					
		coupling_factor_transporter_transmemb					
2,696439045	<i>N186_RS08740</i>	rane_protein_EcfT	NO	NO	NO	5	5
2,685166778	<i>N186_RS06355</i>	hypothetical_protein	NO	NO	NO	3	3
2,634314761	<i>N186_RS04380</i>	hypothetical_protein	NO	NO	NO	0	0

2,569769831	<i>N186_RS06830</i>	hypothetical_protein	NO	NO	NO	0	0
2,54776169	<i>N186_RS07865</i>	hypothetical_protein	NO	NO	NO	0	0
2,523111874	<i>N186_RS02835</i>	hypothetical_protein	NO	NO	NO	0	0
2,522567586	<i>N186_RS08615</i>	hypothetical_protein	NO	NO	NO	0	0
2,469024407	<i>N186_RS05840</i>	DUF2208_domain-containing_protein_ CPBP_family_intramembrane_metallop rotease	YES	NO	NO	3	4
2,452516161	<i>N186_RS08455</i>	metal-dependent_hydrolase	NO	NO	NO	5	4
2,437141385	<i>N186_RS08650</i>	hypothetical_protein	NO	NO	NO	0	0
2,422009486	<i>N186_RS01215</i>	hypothetical_protein	NO	NO	NO	4	4
2,40147751	<i>N186_RS08895</i>	hypothetical_protein	NO	NO	NO	0	0
		energy- coupling_factor_transporter_transmemb rane_protein_EcfT					
2,392978405	<i>N186_RS08020</i>	hypothetical_protein	NO	NO	NO	6	5
2,321621631	<i>N186_RS01020</i>	hypothetical_protein	NO	NO	NO	4	4
2,308198158	<i>N186_RS07155</i>	hypothetical_protein	NO	NO	NO	0	0
2,288135134	<i>N186_RS03610</i>	hypothetical_protein	NO	NO	NO	5	5
2,275940129	<i>N186_RS00905</i>	hypothetical_protein	NO	NO	NO	0	0
2,271016817	<i>N186_RS08565</i>	hypothetical_protein	YES	NO	YES	0	1
2,246847777	<i>N186_RS07200</i>	DUF1667_domain-containing_protein_ non- canonical_purine_NTP_pyrophosphatas e_RdgB/HAM1_family	NO	NO	NO	0	0
2,238154319	<i>N186_RS05950</i>	serine/threonine_protein_phosphatase_ hypothetical_protein	NO	NO	NO	0	0
2,204579236	<i>N186_RS02590</i>	hypothetical_protein	NO	NO	NO	0	0
2,19030528	<i>N186_RS06855</i>	PIN_domain-containing_protein_ hypothetical_protein	NO	NO	NO	0	0
2,174533031	<i>N186_RS08545</i>	hypothetical_protein	NO	NO	NO	0	0
2,146392372	<i>N186_RS01500</i>	hypothetical_protein	NO	NO	NO	0	0
2,11864159	<i>N186_RS07985</i>	hypothetical_protein	YES	NO	NO	10	11
2,084776499	<i>N186_RS07720</i>	hypothetical_protein	NO	NO	NO	0	0
2,008578376	<i>N186_RS05475</i>	D-glycerate_dehydrogenase	NO	NO	NO	0	0

∞ - when the riBAQ value in control was zero.

S4 TABLE | Predicted glycosidases of *T. adornatum* 1910b^T.

Gene ID	riBAQ_cel/ riBAQ_contr	Function	Pfam
<i>N186_RS00340 (Cel40)</i>	61.7	glycoside hydrolase family 1 protein	GH1
<i>N186_RS06480</i>	6.97	α -N-acetylgalactosaminidase	GFO_IDH_MocA
<i>N186_RS04780</i>	6.7	α -N-acetylgalactosaminidase	GFO_IDH_MocA
<i>N186_RS08540</i>	6.2	alpha-glucosidase	GH4-GH4C
<i>N186_RS08045</i>	4.0	alpha-amylase	GH13
<i>N186_RS01850</i>	3.2	alpha-amylase	GH57
<i>N186_RS05435</i>	1.9	alpha-amylase	GH57-DuF1925-DuF1926
<i>N186_RS00225 (Cel25)</i>	1.0	beta-glucosidase	GH3-GH3-X
<i>N186_RS08040</i>	1.0	alpha-amylase	GH57-GlucodextranC
<i>N186_RS06215</i>	0.85	α -N-acetylgalactosaminidase	GFO_IDH_MocA
<i>N186_RS01555</i>	0.8	alpha-amylase	GH57
<i>N186_RS07400</i>	0.8	alpha-mannosidase	GH38-Middledomain-GH38C
<i>N186_RS07230</i>	0.8	β -1,4-mannosylglucose phosphorylase	GH130
<i>N186_RS06555</i>	0.1	beta-galactosidase	GH1
<i>N186_RS00270</i>	0	beta-mannanase	no hits
<i>N186_RS07265</i>	0	kojibiose phosphorylase	GH65
<i>N186_RS08615</i>	0	putative endo-beta1-3 glucanase	GH16

S5 TABLE | Representation of Cel20-45 homologs among four *Thermofilum* genomes.

Query Sequence Name	Gene Id	Gene Name	Genome Id	Genome Name	Query Start Coord	Query End Coord	Subject Start Coord	Subject End Coord	Bit Score	E-value	Identities	Subject Length	
N186_RS00225 N186_RS00225 glycosyl hydrolase 1714559:1716658 forward	2556034304	beta-glucosidase	2554235458	<i>Thermofilum adornatum</i> 1910b	1	699	1	699	1427	0.0	100	699	Cel25
N186_RS00225 N186_RS00225 glycosyl hydrolase 1714559:1716658 forward	2628708272	beta-glucosidase	2627853727	<i>Thermofilum adornatum</i> 1505	1	699	1	699	1427	0.0	100	699	
N186_RS00225 N186_RS00225 glycosyl hydrolase 1714559:1716658 forward	639774269	beta-glucosidase (EC:3.2.1.21)	639633064	<i>Thermofilum pendens</i> Hrk 5	13	697	8	699	790	0.0	57	701	
N186_RS00225 N186_RS00225 glycosyl hydrolase 1714559:1716658 forward	2641297020	beta-glucosidase	2639762927	<i>Thermofilum uzonense</i> 1807-2	6	695	5	696	967	0.0	67	702	
N186_RS00230 N186_RS00230 hypothetical protein 1713330:1714448	2556034305	hypothetical protein	2554235458	<i>Thermofilum adornatum</i> 1910b	1	372	1	372	749	0.0	100	372	Cel30
N186_RS00230 N186_RS00230 hypothetical protein 1713330:1714448	2628708274	hypothetical protein	2627853727	<i>Thermofilum adornatum</i> 1505	3	372	1	370	744	0.0	100	370	
N186_RS00340 N186_RS00340 glycoside hydrolase family 1 protein	2556034327	beta-galactosidase	2554235458	<i>Thermofilum adornatum</i> 1910b	1	518	1	518	1071	0.0	100	518	Cel40
N186_RS00340 N186_RS00340 glycoside hydrolase family 1 protein	2556035604	beta-galactosidase	2554235458	<i>Thermofilum adornatum</i> 1910b	23	506	1	490	427	4,00E-147	47	501	
N186_RS00340 N186_RS00340 glycoside hydrolase family 1 protein	2628708296	beta-galactosidase	2627853727	<i>Thermofilum adornatum</i> 1505	1	518	1	518	1071	0.0	100	518	
N186_RS00340 N186_RS00340 glycoside hydrolase family 1 protein	2628707601	beta-galactosidase	2627853727	<i>Thermofilum adornatum</i> 1505	6	506	2	508	457	2,00E-158	48	519	
N186_RS00340 N186_RS00340 glycoside hydrolase family 1 protein	639774448	glycoside hydrolase, family 1	639633064	<i>Thermofilum pendens</i> Hrk 5	1	510	1	510	713	0.0	65	513	
N186_RS00340 N186_RS00340 glycoside hydrolase family 1 protein	639773887	glycoside hydrolase, family 1	639633064	<i>Thermofilum pendens</i> Hrk 5	6	501	2	503	473	9,00E-165	49	517	
N186_RS00340 N186_RS00340 glycoside hydrolase family 1 protein	2641296933	beta-galactosidase	2639762927	<i>Thermofilum uzonense</i> 1807-2	6	516	2	517	480	1,00E-167	50	517	
N186_RS00345 N186_RS00345 hypothetical protein 1684981:1685214	2556034328	hypothetical protein	2554235458	<i>Thermofilum adornatum</i> 1910b	1	77	1	77	155	5,00E-53	100	77	Cel45
N186_RS00345 N186_RS00345 hypothetical protein 1684981:1685214	2628708297	hypothetical protein	2627853727	<i>Thermofilum adornatum</i> 1505	1	77	1	77	155	5,00E-53	100	77	

The analysis was done in the IMG using BLAST/Selected genomes option. BLASTp with 1e-50 cut-off. Cel25, Cel30, Cel40 & Cel 45 amino-acid sequences were used as the queries. The genomes of *T. pendens* strain Hrk 5^T, *T. uzonense* strain 1807-2^T, and *T. adornatum* strains 1505 and 1910b^T were used as the subjects.

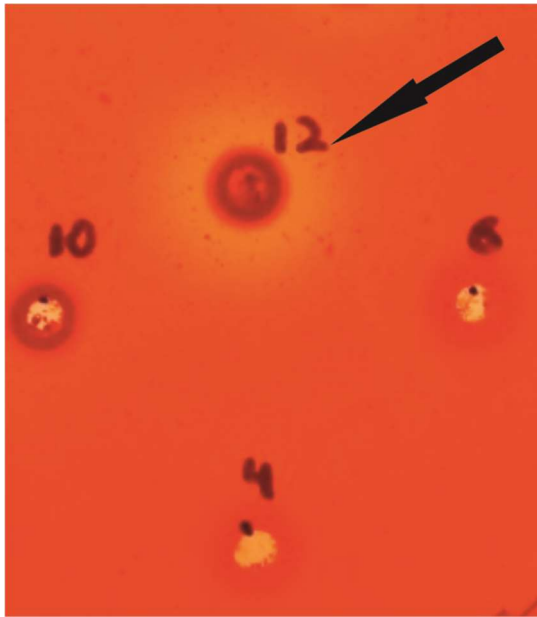
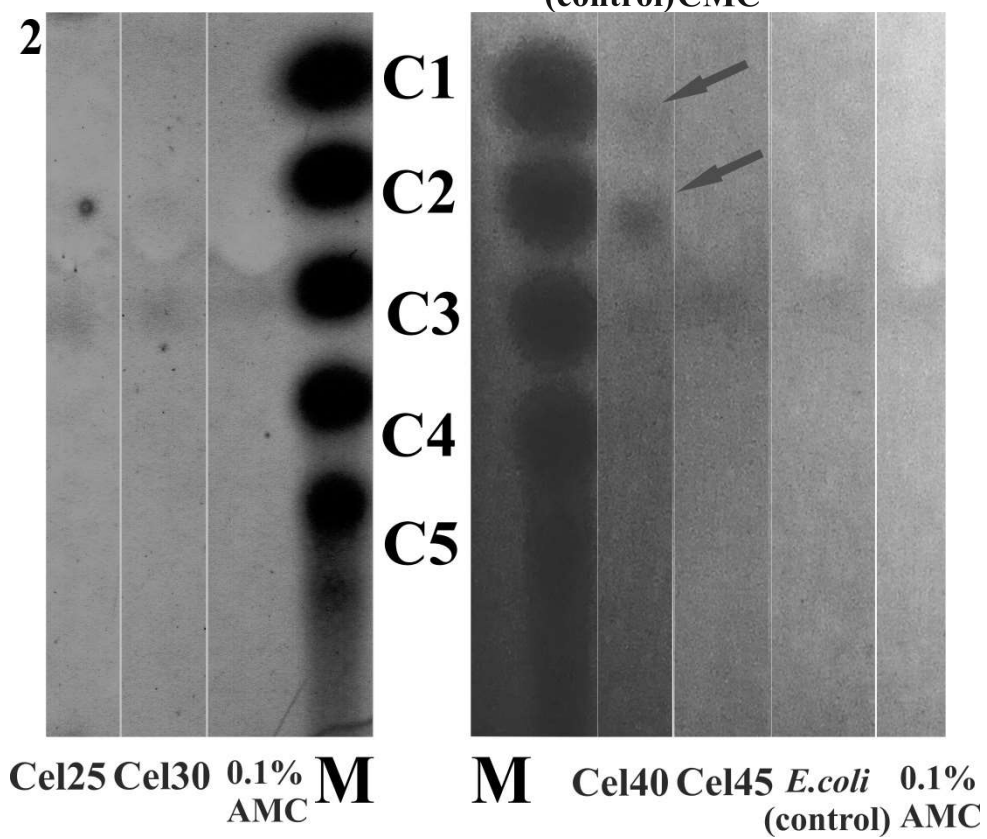
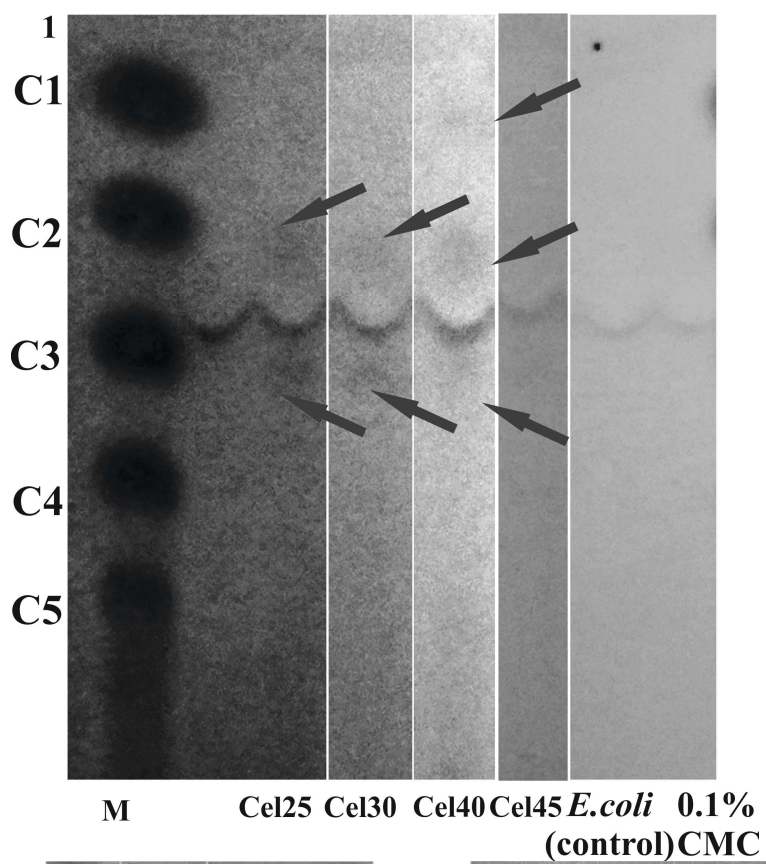


FIGURE S1 | Endoglucanase activity of *T. adornatum* 1910b^T recombinant cellulase Cel45. 10 - crude extract of sonicated *E. coli* BL21 DE3 cells with empty vector (control); 4 - culture broth of *E. coli* cells, containing empty vector (control); 12 – crude extract of sonicated *E. coli* cells, containing recombinant cellulase Cel45; 6 – culture broth of *E. coli* from the same experiment. Substrate, CMC; incubation, 16 h at 80°C. Staining by Congo Red. A halo of CMC hydrolysis is pointed by an arrow.



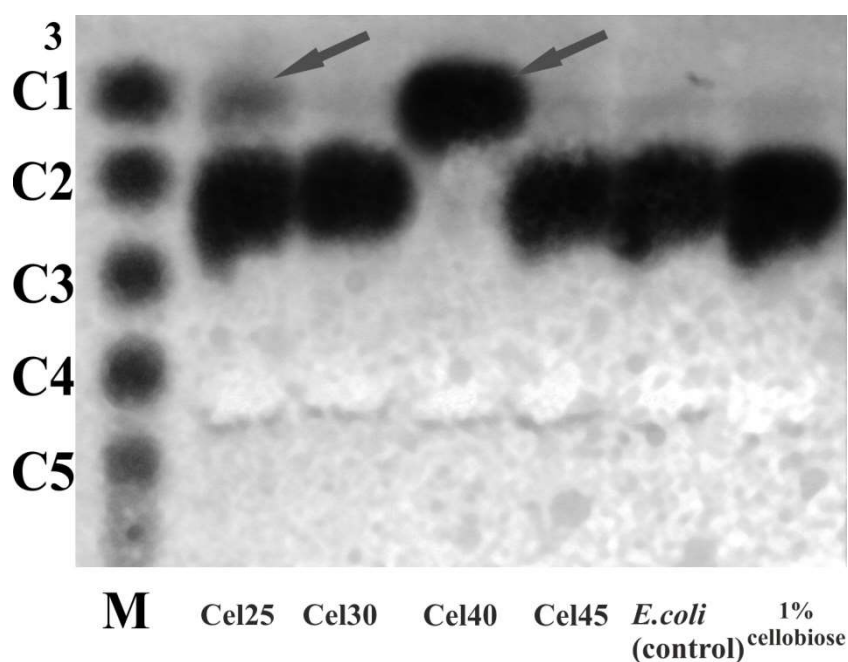


FIGURE S2 | Degradation of CMC, AMC and cellobiose by the recombinant glycosidases of *T. adornatum* 1910b^T. Formation of glucose and cellooligosaccharides from CMC (1), AMC (2) and cellobiose (3). C - number of glucose units (C1 – glucose; C2 – cellobiose; C3 – cellotriose; C4 – cellotetraose; C5 – cellopentaose); M - a mixture of mentioned above C1-C5 sugars. Arrows indicate the hydrolysis products. Cel25, Cel30, Cel40, Cel45, studied recombinant cellulases of *T. adornatum*.

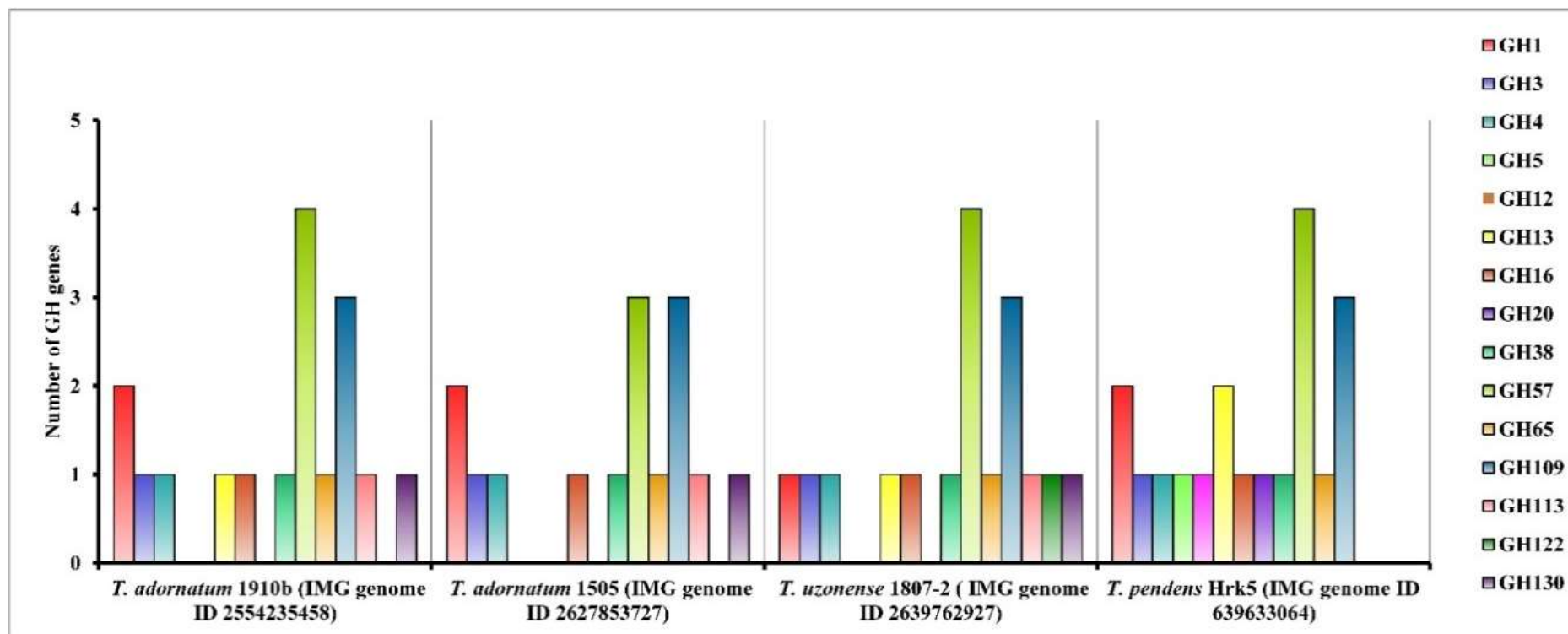


FIGURE S3 | Distribution of glycosidases families' genes among the genomes of cultivated *Thermofilum*.

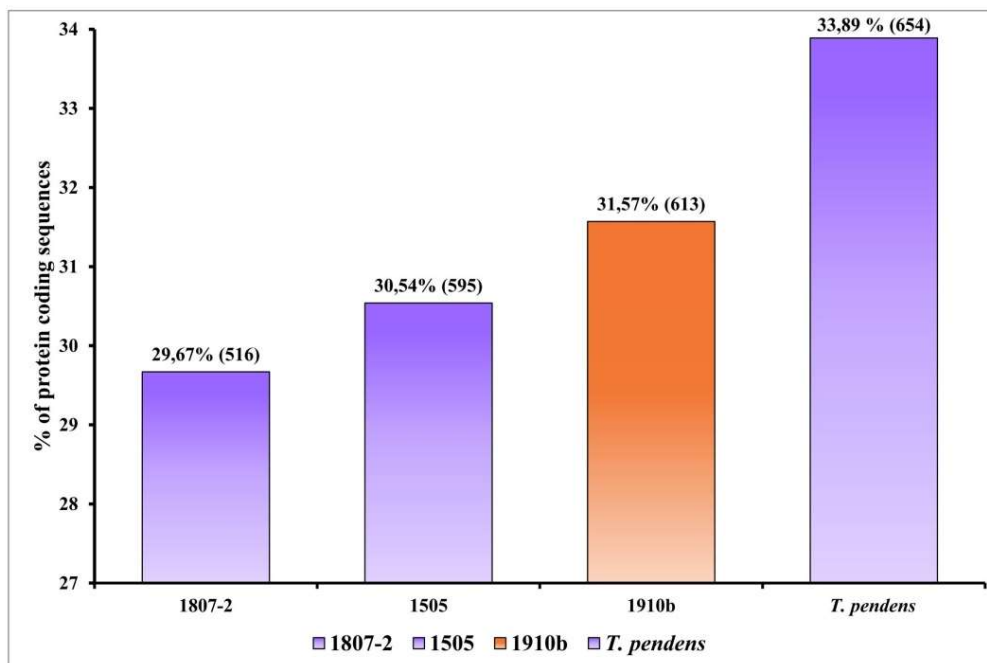


FIGURE S4 | Number of protein-coding genes without function prediction.

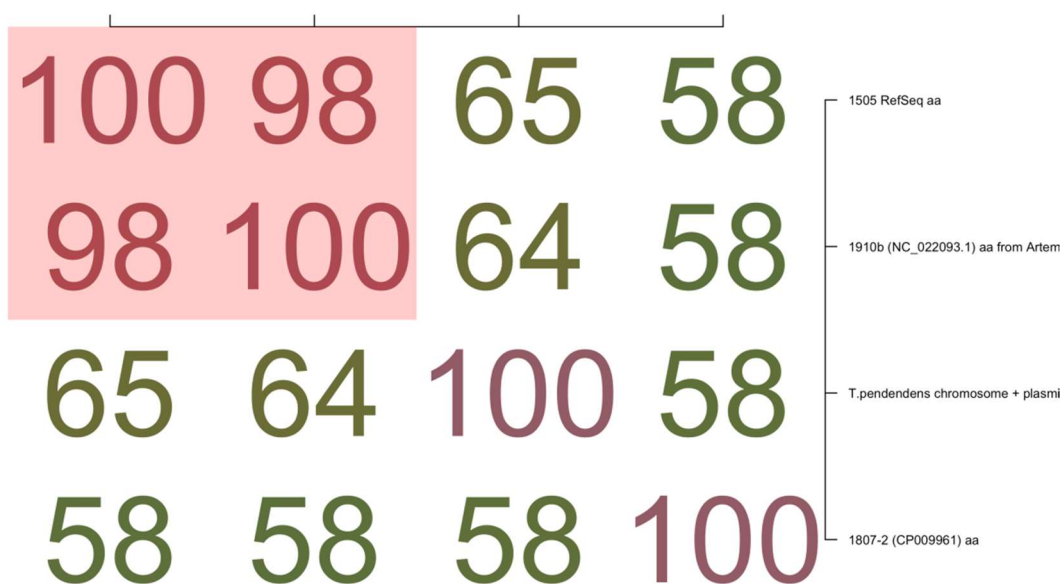


FIGURE S5 | Four *Thermophilum* strains Average Aminoacid Identity Matrix.