Table S3 Summary of the annotation features of the glycosyl- and feruloyl-like coding sequences (CDSs) predicted in the hydrolase-coding DNA fragments from the R library*.

Gene name	Strand	Left End	Right End	Length (AA)	Predicted product name	Family	MW (Da)	pI	Organism (best hit)	Expected Value (E). Identities (I). Positives (P)	Top homolog
r_01_20	-	21563	23923	786	beta-Galactosidase	GHF2	87991.29	5.17	*Roseburia inulinivorans*	E=0.0; I=441/777 (56%); P=541/777 (69%)	ZP_03752805.1
r_01_21	-	23943	26339	798	alpha-Galactosidase	GHF36	90107.58	5.71	*Roseburia inulinivorans*	E=0.0; I=482/807 (59%); P=603/807 (74%)	ZP_03752801.1
r_02-02	+	599	2191	530	alpha-L-Arabinofuranosidase	GHF51	59485.56	6.25	*Prevotella ruminicola*	E=0.0; I=458/530 (86%); P=490/530 (92%)	YP_003573794.1
r_02-15	-	13177	14682	501	alpha-Glucosidase	GHF13	56950.34	5.53	*Prevotella ruminicola*	E=0.0; I= 398/501 (79%); P= 436/501 (87%)	YP_003574036.1
r_03-04	+	7778	8731	317	Beta-Xylosidase	GHF43	35572.72	5.08	*Bacteroides intestinalis*	E=2e-102; I=184/316 (58%); P=228/316 (72%)	YP_001297392.1
r_03-05	+	8786	10405	539	alpha-L-Arabinofuranosidase	GHF43	59988.12	7.2	*Bacteroides xylanisolvens*	E=7e-170; I288/527 (54%=); P=378/527 (71%)	ZP_06769240.1
r_05-02	-	312	1949	546	Glycosyl hydrolase family 5	GHF5	61222.36	5.31	Unidentified microorganism	E=0.0; I=328/518 (63%); P=386/518 (74%)	CAJ19140.1
r_06-02	+	1560	3632	690	Endo-1,4-beta-xylanase	GHF5	78164.3	4.87	*Prevotella ruminicola*	E=5e-142; I=250/403 (62%); P=294/403 (72%)	YP_003575492.1
r_07-01	+	238	2718	827	alfa-L-Rhamnosidase	GHF78	94254.9	4.93	*Clostridium stercorarium*	E=7e-33; I=352/832 (42%); P=496/832 (59%)	CAB53341.1
r_07-02	+	3436	4176	260	beta-Galactosidase	GHF2	29543.47	8.69	*Roseburia intestinalis*	E=0.0; I=87/206 (42%); P=117/206 (56%)	CBL10828.1
r_08-01	+	258	3027	922	alfa-L-Rhamnosidase	GHF78	61801.6	5.62	*Enterococcus casseliflavus*	E=1e-112; I=208/487 (42%); P=300/487 (61%)	ZP_05654693.1
r_08-02	+	3033	4069	346	alpha/beta Hydrolase	FAE2	40359.5	4.95	*Lysinibacillus sphaericus*	E=7e-42; I=117/306 (38%); P=153/306 (50%)	YP_001698978.1
r_09-01	-	6	1148	381	Glycosyl hydrolase family 43	GHF43	44516.1	4.93	*Bryantella formatexigens*	E=3e-115; I=204/383 (53%); P=272/383 (71%)	ZP_05345324.1
r_09-02	-	1157	2649	496	Xylosidase/arabinosidase	GHF43	54939.62	4.96	*Bacteroides capillosus*	E=4e-120; I=233/502 (46%); P=303/502 (60%)	ZP_02035907.1
r_09-03	-	2691	3263	189	beta-Galactosidase	GHF1	22244.69	4.83	*Ruminococcus sp.*	E=2e-54; I=108/192 (56%); P=131/192 (68%)	CBL17177.1

*The theoretical molecular weight (MW) and isoelectric point (pI) were calculated for the gene product using ExPASy ProtParam online tool.

*Sequence analysis revealed no signal peptide, thereby assuming an intracellular location of the proteins under investigation