Table S2 Annotation of the genes predicted in the fosmid/plasmid clones from the bovine rumen (R) metagenome library. (A) Fosmid r_01, (B) fosmid r_02, (C) fosmid r_03, (D) plasmid r_05, (E) plasmid r_06, (F) plasmid r_07, (G) plasmid r_08 and (H) plasmid r_09. Selected fosmids were sequenced by shotgun sequencing, and the sorted ORFs were annotated by homology using the BLAST alignment tool. The theoretical molecular weight (MW) and isoelectric point (p*I*) were calculated for each gene product using the ExPASy ProtParam online tool.

(A) Fosmid *r_01*

Gene name	Strand	Left End	Right End	Length (AA)	Gene product name	MW (Da)*	pI*	Organism (best hit)	Expected Value (E), Identities (I), Positives (P)	Top homolog
r_01-01	-	554	1651	365	Hypothetical protein	41519.62	6.55	*Coprococcus sp.*	E=4e-44; I=118/389 (30%); P=188/389 (48%)	CBK83438.1
r_01_02	-	1756	2556	266	Hypothetical protein	29042.66	4.26	*Eubacterium hallii*	E=2e-38; I=83/213 (38%); P=122/213 (57%)	ZP_03717785.1
r_01_03	+	2691	3578	295	Hhypothetical protein	32939.75	4.2	*Desulfovibrio piger*	E=4e-72; I=143/294 (48%); P=186/294 (63%)	ZP_03311848.1
r_01_04	-	3575	4423	282	Hypothetical protein	32109.03	5.88	*Eubacterium yurii*	E=0.007; I=17/43 (40%), P = 28/43 (66%)	ZP_07454699.1
r_01_05	-	4434	5318	294	Hypothetical protein	33207.73	5.4	*Eubacterium siraeum*	E=0.002; I=19/43 (44%); P=25/43 (58%)	CBK97501.1
r_01_06	-	5521	6924	467	Hhypothetical protein	50863.10	9.01	*Shuttleworthia satelles*	E=3e-103; I=201/463 (43%); P= 298/463 (64%)	ZP_04454784.1
r_01_07	+	7555	8472	305	Pprotein KINase family	34487.97	4.78	*Myxobacter sp.*	E=9e-13; I=71/240 (29%); P=110/240 (45%)	AAX82624.1
r_01_08	-	8835	9464	209	LuxR transcriptional regulator	23070.64	4.52	*Ruminococcus obeum*	E=1e-59; I=114/205(55%); P= 154/205 (75%)	ZP_01964629.1
r_01_09	-	9551	10687	378	Histidine kinase	41561.16	6.48	*Ruminococcus albus*	E=2e-47; I=96/225 (42%); P=145/225 (64%)	ZP_06717737.1
r_01_10	-	10700	11884	394	Hypothetical protein	43208.82	5.21	*Dorea longicatena*	E=2e-29; I=119/401 (29%); P=196/401 (48%)	ZP_01995410.1
r_01_11	-	11871	13019	382	ABC-2 type transporter	42561.68	4.75	*Ruminococcus albus* 7	E=3e-36; I=105/382 (28%); P=189/382 (50%)	ZP_07383825.1
r_01_12	-	13041	13982	313	ABC transporter related	34795.30	5.71	*Ruminococcus albus* 7	E=7e-115; I=205/310 (67%); P=245/310 (80%)	ZP_07383824.1
r_01_13	+	14147	16546	799	Sugar transporter	89500.04	4.02	*Bacillus mycoides*	E=2e-16; I=111/449 (24%); P=198/449 (44%)	ZP_04160063.1
r_01_14	-	16527	16970	147	Hypothetical protein	16164.02	9.36	*Nostoc punctiforme*	E=0.84; I=19/58 (32%; P=31/58 (53%)	YP_001867131.1
r_01_15	+	17233	17850	205	TetR transcriptional regulator	24154.64	5.82	*Clostridium hylemonae*	E=7e-46; I=91/204 (44%); P=137/204 (67%)	ZP_03777844.1
r_01_16	+	17850	18569	239	Hypothetical protein	27040.49	9.45	*Clostridium hylemonae*	E=7e-85; I=145/237 (61%); P=182/237 (76%)	ZP_03778041.1
r_01_17	-	18808	19617	269	Hypothetical protein	31513.88	8.71	*Butyrivibrio fibrisolvens*	E=0.038; I=29/106 (27%); P=53/106 (50%)	CBK73816.1
r_01_18	-	20087	20416	109	Hypothetical protein	12288.62	8.05	*Toxoplasma gondii*	E=3.7; I=22/66 (33%); P=36/66 (54%)	EEE34841.1
r_01_19	+	20677	21270	197	Hypothetical protein	20864.44	4.85	*Listeria welshimeri*	E=0.46; I=35/154 (22%); P=65/154 (42%)	YP_849623.1
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_01_22	-	26345	28159	604	Sugar transporter	65605.7	5.14	*Clostridium lentocvellum* DSM 5427	E=1e-86; I=172/299 (58%); P=220/299 (74%)	ZP_06885281.1
r_01_23	-	28175	29641	488	Hypothetical protein	54586.33	6.94	*Roseburia intestinales* L1-82	E=0.0; I=361/488 (73%); P=411/488 (84%)	ZP_04742652.2
r_01_24	-	29658	30224	188	Hypothetical protein	22227.74	5.83	*Roseburia inulinivorans*	E=1e-51; I=99/183 (54%); P=133/183 (72%)	ZP_03752806.1
r_01_25	+	30423	31670	415	Galactokinase	44143.84	4.93	*Clostridium sp.*	E=7e-139; I=240/405 (59%); P=307/405 (75%)	ZP_02073770.1
r_01_26	+	31682	33166	494	Galactose-1-phosphate uridylyltransferase	55737.38	5.4	*Clostridium sp.*	E=0.0; I=315/498 (63%); P=372/498 (74%)	ZP_02073769.1
r_01_27	+	33237	34520	427	Sugar transporter	45007.41	9.13	*Oribacterium sp*	E=3e-117; I=215/423 (50%); P=298/423 (70%)	ZP_06598814.1

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

Table S2 (B) Fosmid *r_02*

Gene name	Strand	Left End	Right End	Length (AA)	Gene product name	MW (Da)	pI	Organism (best hit)	Expected Value (E). Identities (I). Positives (P)	Top homolog
r_02-01	+	31	516	161	Serine phosphatase	17971.32	4.54	*Prevotella ruminicola*	E=3e-47; I=90/152 (59%); P=113/152 (74%)	YP_003576084.1
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_02-03	+	2199	4211	670	Transketolase	73006.93	5.31	*Prevotella ruminicola*	E=0.0; I=634/664 (95%); P=649/664 (97%)	YP_003573769.1
r_02-04	-	4259	4618	119	Hypothetical protein	12711.51	4.71	*Anaerococcus vaginalis*	E=0.052; I=23/79 (29%); P=37/79 (46%)	ZP_05471839.1
r_02-05	-	4703	5143	146	Hypothetical protein	*16867.94*	*9.07*	*Prevotella sp*	E=0.002; I= 33/130 (25%); P= 61/130 (46%)	ZP_06406453.1
r_02-06	-	5167	5550	127	Hypothetical protein	15298.50	4.37	*Bacteroides plebeius*	E=7e-47; I=84/124 (67%); P=103/124 (83%)	ZP_03208046.1
r_02-07	-	5570	6103	177	tRNA modification GTPase	20051.82	4.49	*Prevotella ruminicola*	E= 5e-48; I= 94/173 (54%); P= 132/173 (76%)	YP_003575005.1
r_02-08	-	6100	6813	237	Purine nucleoside phosphorylase	25718.42	5.45	*Epulopiscium sp.*	E=4e-89; I=157/232 (67%); P=186/232 (80%)	ZP_02693126.1
r_02-09	+	6998	7273	91	DNA-binding protein HU	10088.72	9.65	*Prevotella melaninogenica*	E=4e-31; I=67/91 (73%); P=76/91 (83%)	YP_003574043.1
r_02-10	+	7627	9087	486	Ribonuclease G	55414.48	9.28	*Prevotella ruminicola*	E=0.0; I=432/480 (90%); P=458/480 (95%)	YP_003574042.1
r_02-11	+	9203	10285	360	Glycosyltransferase	41162.42	8.23	*Prevotella ruminicola*	E= 3e-169; I= 276/360 (76%); P= 320/360 (88%)	YP_003574041.1
r_02-12	+	10360	11607	415	Histidine kinase	47176.97	5.21	*Prevotella ruminicola*	E= 4e-172; I= 291/409 (71%); P= 346/409 (84%)	YP_003574040.1
r_02-13	-	12157	12645	162	Hypothetical protein	16987.36	4.44	*Anopheles gambiae* str. PEST	E=0.18; I= 17/46 (37%); P= 29/46 (64%)	XP_317568.3
r_02-14	-	12705	13172	155	Alanyl-tRNA synthetase	18340.74	5.31	*Prevotella ruminicola*	E=8e-69; I=126/152 (82%); P=144/152 (94%)	YP_003574038.1
r_02-15	**-**	**13177**	**14682**	**501**	**alpha-Glucosidase (alpha-amylase) (GHF13)**	**56950.34**	**5.53**	***Prevotella ruminicola***	**E=0.0; I= 398/501 (79%); P= 436/501 (87%)**	**YP_003574036.1**
r_02-16	-	14819	15709	296	Malonyl CoA-acyl carrier protein	31591.42	5.04	*Prevotella ruminicola*	E=2e-164; I=283/296 (95%); P=289/296 (97%)	YP_003574035.1
r_02-17	-	15959	16300	113	Hypothetical protein	12599.67	8.51	*Trichoplax adhaerens*	E=0.45; I=22/57 (38%); P=32/57 (56%)	XP_002109933.1
r_02-18	-	16713	16955	80	Hypothetical protein	8357.08	4.6	*Ostreococcus tauri*	E=0.042; I=26/80 (33%); P=40/80 (50%)	XP_003074850.1
r_02-19	-	17262	17477	71	Hypothetical protein	7465.39	4.87	*Phaeodactylum tricornutum*	E=7.5; I=16/37 (43%); P=21/37 (56%)	XP_002177766.1
r_02-20	-	17792	20368	858	alpha-Glucan phosphorylase	99019.84	6	*Prevotella ruminicola*	E=0.0; I=766/856 (89%); P=819/856 (95%)	YP_003574031.1
r_02-21	-	20391	22082	563	alpha-Glycosyltransferase	64617.55	5.55	*Prevotella ruminicola*	E=0.0; I=466/576 (80%); P=503/576 (87%)	YP_003574030.1
r_02-22	+	22645	23139	164	Hypothetical protein	17633.17	8.14	*Prevotella ruminicola*	E=3e-77; I=140/157 (89%); P=152/157 (96%)	YP_003575276.1
r_02-23	-	23174	23518	114	50S ribosomal protein L20	13155.52	11.25	*Prevotella ruminicola*	E=4e-57; I=111/114 (97%); P=111/114 (97%)	YP_003573965.1
r_02-24	-	24594	25349	251	Hypothetical protein	28037.20	6.53	*Branchiostoma floridae*	E=4e-09; I=38/148 (25%); P=71/148 (47%)	XP_002611623.1
r_02-25	-	25357	26085	242	Threonine-tRNA ligase	27421.26	5.1	*Prevotella ruminicola*	E=5e-138; I=236/242 (97%); P=240/242 (99%)	YP_003573962.1

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

Table S2 (C) Fosmid *r_03*

Gene name	Strand	Left End	Right End	Length (AA)	Gene product name	MW (Da)	pI	Organism (best hit)	Expected Value (E). Identities (I). Positives (P)	Top homolog
r_03-01	+	1	3540	1148	Melibiase (CBM51)	119432.86	4.48	*Blastopirellula marina*	E=3e-06; I=43/150 (28%); P=77/150 (51%)	ZP_01089974.1
r_03-02	+	3626	5707	693	Histidine kinase	74948.66	5.96	*Chthononiobacter flavus*	E=2e-37; I=160/610 (26%); P=257/610 (42%)	ZP_03131882.1
r_03-03	+	6411	7748	445	Sugar transporter	47558.78	9.21	*Bacteriodes xylanisolvens*	E=2e-147; I=267/486 (54%); P=335/486 (68%)	CBK69517.1
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-Arabino-furanosidase (GHF43)**	**59988.12**	**7.20**	***Bacteroides xylanisolvens***	**E=7e-170; I288/527 (54%=); P=378/527 (71%)**	**ZP_06769240.1**
r_03-06	+	10683	12005	440	Aldose 1-epimerase	48897.69	9.46	*Opitutus terrae*	E=8e-96; I=172/357 (48%); P=228/357 (63%)	YP_001818271.1
r_03-07	-	12951	13232	93	Hypothetical protein	10227.92	11.45	*Arabidopsis lyrata*	E=6.0; I=20/58 (50%); P=29/58 (50%)	XP_002870203.1
r_03-08	+	13817	14239	140	TolR protein	15875.55	9.13	*Francisella tularensis*	E=2e-16; I=44/145 (30%); P=85/145 (58%)	YP_169843.1
r_03-09	+	14894	15172	92	Hypothetical protein	10218.49	11.66	*Rubrobacter xylanophilus*	E=7.3; I=21/49 (42%); P=26/49 (53%)	YP_643483.1
r_03-10	+	15612	18197	861	Aminotransferase	95115.21	11.55	*Desulfovibrio salexigens*	E=3e-87; I=172/369 (46%); P=235/369 (63%)	YP_002993204.1

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

Table S2 (D) Plasmid *r_05*

Gene name	Strand	Left End	Right End	Length (AA)	Gene product name	MW (Da)*	pI	Organism (best hit)	Expected Value (E). Identities (I). Positives (P)	Top homolog
r_05-01	+	<1	312	104	Probable lipoprotein	11631.30	9.25	*Prevotella ruminicola*	E=3e-23; I=46/97 (47%); P=70/97 (72%)	YP_003575494.1
r_05-02	**-**	**309**	**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_05-03	-	1956	3791	611	Hypothetical protein	65171.72	4.65	*Bacteroides plebeius*	E=3e-48; I=127/360 (35%); P=197/360 (54%)	ZP_03210084.1
r_05-04	-	3831	>4637	267	Hypothetical protein	29364.18	4.57	*Bacteroides cellulosilyticus*	E=4e-54; I=127/293 (43%); P=168/293 (57%)	ZP_03678036.1

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

Table S2 (E) Plasmid *r_06*

Gene name	**Strand**	**Left End**	**Right End**	**Length (AA)**	**Gene product name**	**MW (Da)***	**pI**	**Organism (best hit)**	**Expected Value (E). Identities (I). Positives (P)**	**Top homolog**
r_06-01	+	<2	1456	483	Histidine kinase	55673.40	5.33	*Prevotella ruminicola*	E=6e-109; I=221/481 (45%); P=317/481 (65%)	YP_003575472.1
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_06-03	-	4439	5368	308	D-Phosphoglycerate dehydrogenase	32933.81	5.33	*Prevotella ruminicola*	E=2e-151; I=288/305 (94%); P=296/305 (97%)	YP_003574366.1
r_06-04	-	>5482	5805	106	Phosphoserine transaminase	11834.54	5.71	*Prevotella ruminicola*	E=3e-57; I=105/109 (96%); P=107/109 (98%)	YP_003574368.1

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

Table S2 (F) Plasmid *r_07*

Gene name	Strand	Left End	Right End	Length (AA)	Gene product name	MW (Da)*	pI	Organism (best hit)	Expected Value (E). Identities (I). Positives (P)	Top homolog
r_07-01	+	<2	202	79	Putative glycosyl hydrolase (GHF43)	8947.0	6.46	*Opitutus terrae* PB90-1	E=4e-12; I=34/69 (49%); P=46/69 (67%);	YP_001818251
r_07-02	**+**	**238**	**2721**	**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_07-03	+	2718	3560	280	beta-lactamase domain-containing protein	31172.3	5.41	*Clostridium sp. DL-VIII*	E=7e-42; I=92/279 (33%); P=133/279 (48%);	ZP_09205102
r_07-04	**+**	**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**

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

Table S2 (G) Plasmid *r_08*

Gene name	Strand	Left End	Right End	Length (AA)	Gene product name	MW (Da)*	pI	Organism (best hit)	Expected Value (E). Identities (I). Positives (P)	Top homolog
r_08-01	**+**	**258**	**3027**	**922**	**alpha-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**	**4073**	**346**	**alpha/beta Hydrolase**	**40359.5**	**4.95**	***Lysinibacillus sphaericus***	**E=7e-42; I=117/306 (38%); P=153/306 (50%)**	**YP_001698978.1**

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

Table S2 (H) Plasmid *r_09*

Gene name	**Strand**	**Left End**	**Right End**	**Length (AA)**	**Gene product name**	**MW (Da)***	**pI**	**Organism (best hit)**	**Expected Value (E). Identities (I). Positives (P)**	**Top homolog**
r_09-01	**-**	**<1**	**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**	**204**	**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