

Supplementary material

Table S1. Cleaning of the dataset (number of reads) of the metabarcoding of 16S rRNA of ruminal fluid of high-producing lactating dairy cows (n=64).

Sample ID	input	filtered	denoisedF	nonchim	Coverage
101	170205	94781	89929	84520	0.993265
102	166264	95724	91242	82939	0.993605
103	116868	62580	58610	55000	0.994762
104	163353	92456	87850	78031	0.994422
105	88338	48491	45564	41900	0.996327
106	89177	49590	46331	44482	0.99619
107	76846	43318	40810	38535	0.996871
108	103114	57607	53869	48698	0.99585
109	121048	72337	68624	63454	0.994898
110	166970	94519	90125	82415	0.994898
111	160318	93023	87608	82503	0.993265
112	184135	107527	102787	95036	0.994082
113	94601	53990	50755	47571	0.99517
114	194487	113033	107718	101427	0.991837
115	146675	84987	80977	74116	0.995102
116	226585	129744	123761	112656	0.991088
117	36763	19788	17671	16532	0.999728
118	90635	49743	46179	44201	0.995034
119	83505	48105	44666	43251	0.995986
120	91879	52277	49374	45065	0.995578
121	74272	42290	38857	37709	0.99483
122	110793	61937	58523	54937	0.99415
123	89500	49626	46049	44162	0.994558
124	100688	56425	52485	50448	0.993333
125	102792	60052	56639	52635	0.994694
126	196557	107468	101643	95157	0.993673
127	138804	78831	73753	68419	0.99415

128	164490	88045	82849	74340	0.993605
129	56425	31673	28644	27551	0.994762
130	50997	27988	24823	23824	0.996871
131	50960	30284	27698	26759	0.996803
132	53787	32554	29815	28455	0.996531
133	102755	58399	53144	50802	0.993946
134	98497	56561	51601	49123	0.993946
135	100602	56950	51590	50269	0.994354
136	123214	68850	63292	60844	0.994082
137	111123	61459	57178	53642	0.99483
138	94011	53081	48418	46202	0.992993
139	98917	56329	51123	48600	0.992721
140	93298	53084	48408	45822	0.995306
141	29543	16722	15148	14717	1
142	52090	30242	26672	26269	0.997211
143	88202	49101	44633	43534	0.995782
144	131897	74299	68204	64274	0.993197
145	111601	64232	58793	56802	0.994082
146	126115	72089	66334	64032	0.991837
147	120751	70236	64661	61127	0.992313
148	105353	60817	55541	53261	0.993061
149	102758	58560	53281	51008	0.994694
150	141180	79390	72727	67768	0.991973
151	102988	58878	52888	49563	0.993605
152	132316	74108	68716	63620	0.992245
153	77726	43710	39352	37669	0.995986
154	121031	67152	61410	58557	0.992925
155	116267	66851	61100	57575	0.993197
156	101922	58847	53655	50826	0.994218
157	130586	76084	69974	66841	0.991088
158	129472	75637	69657	65804	0.991905

159	106333	62340	56318	53627	0.993333
160	122261	68233	62201	58782	0.992993
161	135917	78448	71752	68186	0.993061
162	80862	45468	40151	37902	0.994898
163	128494	76865	70224	64986	0.992381
164	72475	43797	39832	38216	0.993129

Table S2. Output from *Aldex2* package, where relative differential abundance at genus level between liquid-associated microenvironment (LAM) and solid-associated microenvironment (SAM) samples was evaluated.

Phylum	Class	Order	Family	Genus	LAB	PAB	effect	overlap
Bacteroidota	Bacteroidia	Bacteroidales	Prevotellaceae	Prevotellaceae Ga6A1 group	3.46	5.68	1.41	0.06
Euryarchaeota	Methanobacteria	Methanobacteriales	Methanobacteriaceae	Methanosphaera	0.92	2.25	1.47	0.05
Fibrobacterota	Fibrobacteria	Fibrobacterales	Fibrobacteraceae	Fibrobacter	0.72	3.55	1.55	0.04
				Butyrivibrio	4.56	6.76	2.58	0.0005
				Lachnospiraceae XPB1014 group	1.69	3.90	2.19	0.004
				Oribacterium	1.40	3.57	1.75	0.03
				probable genus 10	1.99	4.18	1.34	0.04
				Catonella	-7.07	0.87	1.29	0.12
Firmicutes	Clostridia	Lachnospirales	Lachnospiraceae	Lachnospiraceae AC2044 group	1.36	3.66	1.17	0.07
				Acetitomaculum	4.03	5.30	1.09	0.11
				Lachnospiraceae NK3A20 group	5.10	5.97	1.08	0.12
		NA	Hungateiclostridiaceae	Saccharofermentans	3.60	5.57	1.89	0.01
	Negativicutes	Veillonellales-Selenomonadales	Selenomonadaceae	Anaerovibrio	2.18	3.75	1.15	0.09
Spirochaetota	Spirochaetia	Spirochaetales	Spirochaetaceae	Treponema	3.81	5.21	1.17	0.10

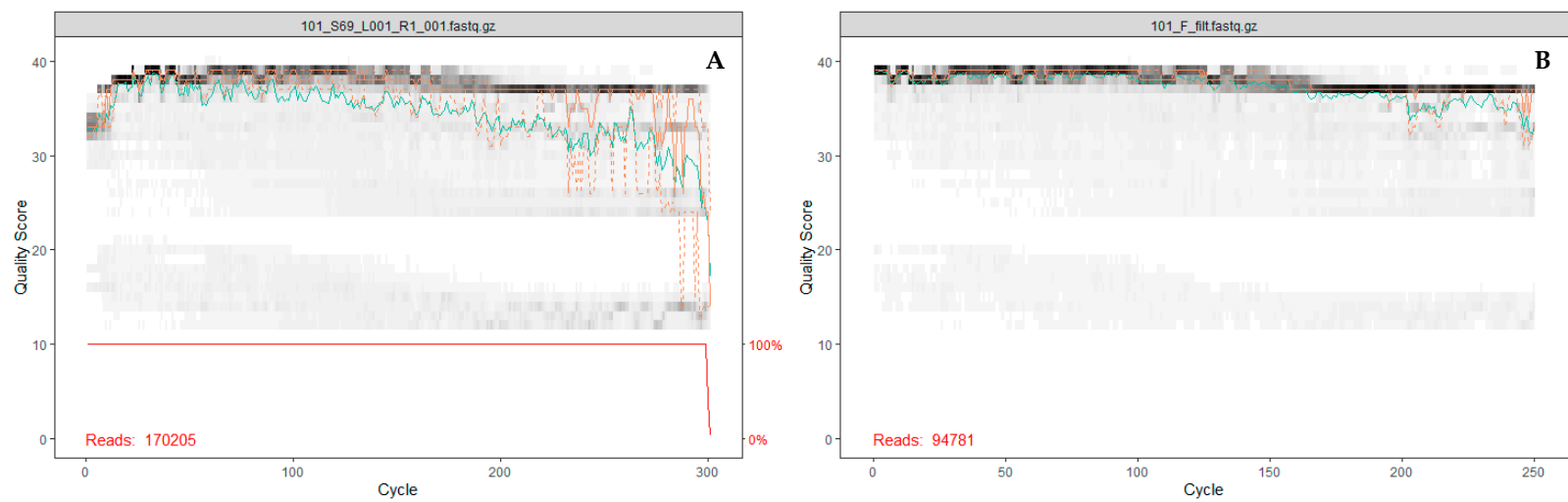


Figure S1. Sequencing quality check before (A) and after (B) cleaning and filterin