

**Table S5. Conservation of regulatory RNAs in bacterial strains**

<b>Species</b>	<b>Strains</b>	<b>sRNAs</b>	<b>%</b>	<b>Riboswitches</b>	<b>%</b>
<i>C. difficile</i>	R20291	172	81%	57	79%
<i>C. difficile</i>	CD196	170	80%	57	79%
<i>C. difficile</i>	QCD-23m63	151	71%	51	71%
<i>C. difficile</i>	QCD-32g58	167	79%	41	57%
<i>C. difficile</i>	QCD-37x79	172	81%	54	75%
<i>C. difficile</i>	QCD-63q42	179	84%	52	72%
<i>C. difficile</i>	QCD-66c26	170	80%	54	75%
<i>C. difficile</i>	QCD-76w55	170	80%	52	72%
<i>C. difficile</i>	QCD-97b34	170	80%	49	68%
<i>C. difficile</i>	NAP07	145	68%	50	69%
<i>C. difficile</i>	NAP08	146	69%	50	69%
<i>C. difficile</i>	VPI	183	86%	51	71%
<i>C. difficile</i>	CD37*	174	82%	-	-
<i>C. acetobutylicum</i>	ATCC824	1	0.5%	4	5.6%
<i>C. beijerinckii</i>	NCIMB8052	4	1.9%	2	2.8%
<i>C. botulinum</i>	ATCC3502	3	1.4%	3	4.2%
<i>C. cellulolyticum</i>	ATCC35319	1	0.5%	0	0.0%
<i>C. cellulovorans</i>	743B	2	0.9%	4	5.6%
<i>C. kluyveri</i>	DSM555	1	0.5%	4	5.6%
<i>C. ljungdahlii</i>	ATCC49587	2	0.9%	4	5.6%
<i>C. novyi</i>	NT	1	0.5%	5	6.9%
<i>C. perfringens</i>	ATCC13124	5	2.4%	1	1.4%
<i>C. phytofermentans</i>	ISDg	2	0.9%	0	0.0%
<i>C. saccharolyticum</i>	WM1	1	0.5%	1	1.4%
<i>C. sticklandii</i>	DSM519	2	0.9%	4	5.6%
<i>C. tetani</i>	E88	4	1.9%	4	5.6%
<i>C. thermocellum</i>	ATCC27405	1	0.5%	1	1.4%
<i>B. subtilis</i>	168	0	0.0%	3	4.0%
<i>M. tuberculosis</i>	H37Rv	0	0.0%	0	0.0%
<i>E. coli</i>	K12	0	0.0%	0	0.0%
<i>H. pylori</i>	P12	0	0.0%	0	0.0%
<i>E. faecalis</i>	V583	0	0.0%	0	0.0%

\*Genome without annotation