

Table S1. Complete predicted protein of AreR resulting from gene sequencing analysis of each isolate and the corresponding MIC of erythromycin ($\mu\text{g/ml}$), for 16 erythromycin resistant *Aliarcobacter butzleri* strains (MIC $>8 \mu\text{g/ml}$) and 56 susceptible strains.

Strain	MIC of erythromycin ($\mu\text{g/ml}$)	AreR protein sequence	Truncated protein
A11-2	32	LSTKNKIDKNYLNIIIEILLNDGISGLSIIKVATKANISIGG VQYIFGNKEGMIKAVFRKK*	Yes
AB 11/11	32	LSTKNKIDKNYLNIIIEILLNDGISGLSIRKVAYFNRWCSI YLWK*	Yes
AB 12/11	32	LSTKNKIDKNYLNIIIEILLNDGISGLSIRKVAYFNRWCSI YLWK*	Yes
AB 21/11	16	LSTKNKIDKNYLNIIIEILLNDGISGLSIRKVATKANISIGG VQYIFGNKEGMIKAVLEKNEEDYNRQIKILLKDDNSKYS QLKAHIEYISKHNDNEEFDKISKIITILLQEKVFEGLDQW YSASLNSIDTNTDEGKKLRLAFLFSEAMFTLMTLKYINIS PKEQKEIFEDLKTFL*	No
AB 26/11	16	LSTKNKIDKNYLNIIIEILLNDGISGLSIRKVATKANISIGG VQYIFGNKEGMIKAVLEKNEEDYNRQIKILLKDDNSKYS QLKAHIEYISKHNDNEEFDKISKIITILLQEKVFEGLDQW YSASLNSIDTNTDEGKKLRLAFLFSEAMFTLMTLKYINIS PKEQKEIFEDLKTFL*	No
AB_2811	32	LSTKNKIDKNYLNIIIEILLNDGISGLSIRKVATKANISIGG VQYIFGNKEGMIKAVLEKNEEDYNRQIKILLKDDNSKYS QLKAHIEYISKHNDNEEFDKISKIITILLQEKVFEGLDQW YSAS*	Yes
AB 33/11	32	LSTKNKIDKNYLNIIIEILLNDGISGLSIRKVATKANISIGG VQYIFGNKEGMIKAVLEKNEEDYNRQIKILLKDDNSKYS QLKAHIEYISKHNDNEEFDKISKIITILLQEKVFEGLQRL VEHIFKFY*	Yes
AB 46/11	32	LSTKNKILNFR*	Yes
AB 52/11	16	LSTKNKIDKNYLNIIIEILLNDGISGLSIRKVATKANISIGG VQYIFGNKEGMIKAVLEKNEEDYNRQIKILLKDDNSKYS QLKAHIEYISKHNDNEEFDKISKIITILLQEKVFEGLDQW YSASLNSIDTNTDEGKKLRLAFLFSEAMFTLMTLKYINIS PKEQKEIFEDLKTFL*	No
CR22-1A	16	LSTKNKIDKNYLNIIIEILLRRMHLATQMHKHLAS*	Yes
CR424	32	LSTKNKIDKNYLNIIIEILLNDGISGLSIRKVATKANISIGG VQYIFGNKEGMIKAVLEKNEEDYNRQIKILLKDDNSKYS QLKAHIEYISKHNDNEEFDKISKIITILLQEKVFVDTGTQRI WPPRAFTLGQLTHNDLAS*	Yes
CR502	32	LSTKNKIDKNYLNIIIEILLNDGISGLSIRKVATKANISIGG VQYIFGNKEGMIKAVLEKNEEDYNRQIKILLKDDNSKYS QLKAHIEYISKHNDNEEFDKISKIITILLQEHLV*	Yes
CR641	32	LSTKNKIDKNYLNIIIEILLNDGISGLSIRKVATKANISIGG VQYIFGNKEGMIKAVLEKNEEDYNRQIKILLKDDNSKYS QLKAHIEYISKHNDNEEFDKISKIITILLQEKVFEGLDQW YSASLNSIDTNTDEGKN*	Yes
CR88-1	16	LSTKNKIDKNYLNIIIEILLNDGISGLSIRKVATKANISIGG VQYIFGNKEGMIKAVLEKNEEDYNRQIKILLKDDNSKYS QLKAHIEYISKHNDNEEFDKISKIITILLQEKVFEGLDQW YSASLNSIDTNTDEGKN*	Yes
CR107-3	32	LSTKNKIDKNYLNIIIEILLNDGISGLSIRKVATKANISIGG VQYIFGNKEGMIKAVLEKNEEDYNRQIKILLKDDNSKYS	Yes

INSA2808	32	QLKAHIEYISKHNDNEEFDKISKIITILLQEKVFVEGLQDW YSTSLNSIDTNTDEGKKLRLFFIFRSNVHINDFKIYKHIS* LSTKNKIDKNYLINIIEEILLNDGISGLSIRKVATKANISIGG VQYIFGNKEGMIKAVLEKMKRIIVK* LSTKNKIDKNYLINIIEEILLNDGISGLSIRKVATKANISIGG VQYIFGNKEGMIKAVLEKNEEDYNRQIKILLKDDNSKYS	Yes
DQ1dM1	2	QLKAHIEYISKHNDNEEFDKISKIITILLQEKVFVEGLQDW YSASLNSIDTNTDEGKKLRLAFLFSEAMFTLMTLKYINIS PKEQKEIFEDLKTFL* LSTKNKIDKNYLINIIEEILLNDGISGLSIRKVATKANISIGG VQYIFGNKEGMIKAVLEKNEEDYNRQIKILLKDDNSKYS	No
DQ13A1	4	---	---
DQ15A1	2	LSTKNKIDKNYLINIIEEILLNDGISGLSIRKVATKANISIGG VQYIFGNKEGMIKAVLEKNEEDYNRQIKILLKDDNSKYS QLKAHIEYISKHNDNEEFDKISKIITILLQEKVFVEGLQDW YSASLNSIDTNTDEGKKLRLAFLFSEAMFTLMTLKYINIS PKEQKEIFEDLKTFL* LSTKNKIDKNYLINIIEEILLNDGISGLSIRKVATKANISIGG VQYIFGNKEGMIKAVLEKNEEDYNRQIKILLKDDNSKYS	No
DQ19M1	2	QLKAHIEYISKHNDNEEFDKISKIITILLQEKVFVEGLQDW YSASLNSIDTNTDEGKKLRLAFLFSEAMFTLMTLKYINIS PKEQKEIFEDLKTFL* MSTKNKIDKNYLINIIEEILLNDGISGLSIRKVATKANISIG GVQYIFGNKEGMIKAVLEKNEEDYNRQIKILLKDDNSKY	No
DQ40A1	2	SQLKAHIEYISKHNDNEEFDKISKIITILLQEKVFVEGLQD WYSTSLNSIDTNTDEGKKLRLAFLFSEAMFTLMTLKYINI SPKEQKEIFEDLKTFL* LSTKNKIDKNYLINIIEEILLNDGISGLSIRKVATKANISIGG VQYIFGNKEGMIKAVLEKNEEDYNRQIKILLKDDNSKYS	No
DQ44M1	4	QLKAHIEYISKHNDNEEFDKISKIITILLQEKVFVEGLQDW YSTSLNSIDTNTDEGKKLRLAFLFSEAMFTLMTLKYINISP KEQKEIFEDLKTFL* LSTKNKIDKNYLINIIEEILLNDGISGLSIRKVATKANISIGG VQYIFGNKEGMIKAVLEKNEEDYNRQIKILLKDDNSKYS	No
DQ64A1	1	---	---
DQ46A2	2	LSTKNKIDKNYLINIIEEILLNDGISGLSIRKVATKANISIGG VQYIFGNKEGMIKAVLEKNEEDYNRQIKILLKDDNSKYS QLKAHIEYISKHNDNEEFDKISKIITILLQEKVFVEGLQDW YSASLNSIDTNTDEGKKLRLAFLFSEAMFTLMTLKYINIS PKEQKEIFEDLKTFL* LSTKNKIDKNYLINIIEEILLNDGISGLSIRKVATKANISIGG VQYIFGNKEGMIKAVLEKNEEDYNRQIKILLKDDNSKYS	No
DQ65A3	2	QLKAHIEYISKHNDNEEFDKISKIITILLQEKVFVEGLQDW YSTSLNSIDTNTDEGKKLRLAFLFSEAMFTLMTLKYINISP KEQKEIFEDLKTFL* LSTKNKIDKNYLINIIEEILLNDGISGLSIRKVATKANISIGG VQYIFGNKEGMIKAVLEKNEEDYNRQIKILLKDDNSKYS	No
DQ68M4	2	---	---
DQ72A1	2	LSTKNKIDKNYLINIIEEILLNDGISGLSIRKVATKANISIGG VQYIFGNKEGMIKAVLEKNEEDYNRQIKILLKDDNSKYS QLKAHIEYISKHNDNEEFDKISKIITILLQEKVFVEGLQDW YSASLNSIDTNTDEGKKLRLAFLFSEAMFTLMTLKYINIS PKEQKEIFEDLKTFL* LSTKNKIDKNYLINIIEEILLNDGISGLSIRRVATKANISIGG VQYIFGNKKGMIKAVLEKNEEDYNRQIKILLKDDNSKYS	No
A6-1	4	---	---
A8-1	2	LSTKNKIDKNYLINIIEEILLNDGISGLSIRRVATKANISIGG VQYIFGNKKGMIKAVLEKNEEDYNRQIKILLKDDNSKYS QLKAHIEYISKHNDNEEFDKISKIITILLQEKVFVEGLQDW YSTSLNSIDTNTDEGKKLRLAFLFSEAMFTLMTLKYINISP KEQKEIFEDLKTFL* LSTKNKIDKNYLINIIEEILLNDGISGLSIRRVATKANISIGG VQYIFGNKKGMIKAVLEKNEEDYNRQIKILLKDDNSKYS	No
A9-4	2	QLKAHIEYISKHNDNEEFDKISKIITILLQEKVFVEGLQDW YSASLNSIDTNTDEGKKLRLAFLFSEAMFTLMTLKYINIS PKEQKEIFEDLKTFL* LSTKNKIDKSYLINIIEEILLNDGISGLSIRKVATKANISIGG VQYIFGNKEGMIKAVLEKNEEDYNRQIKILLKDDNSKYS	No
A12-1	2	LSTKNKIDKSYLINIIEEILLNDGISGLSIRKVATKANISIGG VQYIFGNKEGMIKAVLEKNEEDYNRQIKILLKDDNSKYS	No

		QLKAHIEYISKHNDNEEFDKISKIITILLQEKVFEGQLQDW YSASLNSIDTNTDEGKKLRLAFLFSEAMFTLMTLKYINIS PKEQKEIFEDLKTFL* LSTKNKIDKNYLINIIEILLNDGISGLSIRKVATKANISIGG VQYIFGNKEGMIKAVLEKNEEDYNRQIKILLKDDNSKYS	
AB 13/11	2	QLKAHIEYISKHNDNEEFDKISKIITILLQEKVFEGQLQDW YSTSLNSIDTNTDEGKKLRLAFLFSEAMFTLMTLKYINIS PKEQKEIFEDLKTFL* LSTKNKIDKNYLINIIEILLNDGISGLSIRRVATKANISIGG VQYIFGNKKGMIKAVLEKNEEDYNRQIKILLKDDNSKYS	No
AB_2211	2	QLKAHIEYISKHNDNEEFDKISKIITILLQEKVFLEGLQDW YNASLNSIDTNTDEGKKLRLAFLFSEAMFTLMTLKYINIS PKEQKEIFEDLKTFL* ---	No
AB 25/11	2	---	---
AB 30/11	2	LSTKNKIDKNYLINIIEILLNDGISGLSIRKVATKANISIGG VQYIFGNKEGMIKAVLEKNEEDYNRQIKILLKDDNSKYS QLKAHIEYISKHNDNEEFDKISKIITILLQEKVFEGQLQDW YSASLNSIDTNTDEGKKLRLAFLFSEAMFTLMTLKYINIS PKEQKEIFEDLKTFL* LSTKNKIDKNYLINIIEILLNDGISGLSIRKVATKANISIGG VQYIFGNKEGMIKAVLEKNEEDYNRQIKILLKDDNSKYS	No
AB 31/11	2	QLKAHIEYISKHNDNEEFDKISKIITILLQEKVFEGQLQDW YSASLNSIDTNTDEGKKLRLAFLFSEAMFTLMTLKYINIS PKEQKEIFEDLKTFL* LSTKNKIDKNYLINIIEILLNDGISGLSIRKVATKANISIGG VQYIFGNKEGMIKAVLEKNEEDYNRQIKILLKDDNSKYS	No
AB 32/11	2	QLKAHIEYISKHNDNEEFDKISKIITILLQEKVFEGQLQDW YSASLNSIDTNTDEGKKLRLAFLFSEAMFTLMTLKYINIS PKEQKEIFEDLKTFL* LSTKNKIDKNYLINIIEILLNDGISGLSIRKVATKANISIGG VQYIFGNKEGMIKAVLEKNEEDYNRQIKILLKDDNSKYS	No
AB 35/11	2	QLKAHIEYISKHNDNEEFDKISKIITILLQEKVFEGQLQDW YSASLNSIDTNTDEGKKLRLAFLFSEAMFTLMTLKYINIS PKEQKEIFEDLKTFL* LSTKNKIDKNYLINIIEILLNDGISGLSIRKVATKANISIGG VQYIFGNKEGMIKAVLEKNEEDYNRQIKILLKDDNSKYS	No
AB 38/11	2	QLKAHIEYISKHNDNEEFDKISKIITILLQEKVFEGQLQDW YSASLNSIDTNTDEGKKLRLAFLFSEAMFTLMTLKYINIS PKEQKEIFEDLKTFL* LSTKNKIDKNYLINIIEILLNDGISGLSIRKVATKANISIGG VQYIFGNKEGMIKAVLEKNEEDYNRQIKILLKDDNSKYS	No
AB 42/11	2	QLKAHIEYISKHNDNEEFDKISKIITILLQEKVFEGQLQDW YSASLNSIDTNTDEGKKLRLAFLFSEAMFTLMTLKYINIS PKEQKEIFEDLKTFL* LSTKNKIDKNYLINIIEILLNDGISGLSIRRVATKANISIGG VQYIFGNKKGMIKAVLEKNEEDYNRQIKILLKDDNSKYS	No
AB 43/11	2	QLKAHIEYISKHNDNEEFDKISKIITILLQEKVFLEGLQDW YSASLNSIDTNTDEGKKLRLAFLFSEAMFTLMTLKYINIS PKEQKEIFEDLKTFL* LSTKNKIDKNYLINIIEILLNDGISGLSIRRVATKANISIGG VQYIFGNKKGMIKAVLEKNEEDYNRQIKILLKDDNSKYS	No
Ab_4511	2	QLKAHIEYISKHNDNEEFDKISKIITILLQEKVFLEGLQDW YNASLNSIDTNTDEGKKLRLAFLFSEAMFTLMTLKYINIS PKEQKEIFEDLKTFL* LSTKNKIDKNYLINIIEILLNDGISGLSIRKVATKANISIGG VQYIFGNKEGMIKAVLEKNEEDYNRQIKILLKDDNSKYS	No
AB 47/11	2	QLKAHIEYISKHNDNEEFDKISKIITILLQEKVFEGQLQDW YSTSLNSIDTNTDEGKKLRLAFLFSEAMFTLMTLKYINIS PKEQKEIFEDLKTFL* ---	No
CR9-1	2	---	---

CR18-1	2	LSTKNKIDKNYLINIIEEILLNDGISGLSIRKVATKANISIGG VQYIFGNKEGMIKAVLEKNEEDYNRQIKILLKDDNSKYS QLKAHIEYISKHNDNEEFDKISKIITILLQEKVFEGLDW YSASLNSIDTNTDEGKKLRLAFLFSEAMFTLMTLKYINIS PKEQKEIFEDLKTFL* ---	No
CR20-1	0.5	---	---
CR21-1	2	LSTKNKIDKNYLINIIEEILLNDGISGLSIRKVATKANISIGG VQYIFGNKEGMIKAVLEKNEEDYNRQIKILLKDDNSKYS QLKAHIEYISKHNDNEEFDKISKIITILLQEKVFEGLDW YSASLNSIDTNTDEGKKLRLAFLFSEAMFTLMTLKYINIS PKEQKEIFEDLKTFL* ---	No
CR22-2	4	---	---
CR1-1	2	---	---
CR36-1	2	LSTKNKIDKNYLINIIEEILLNDGISGLSIRKVATKANISIGG VQYIFGNKEGMIKAVLEKNEEDYNRQIKILLKDDNSKYS QLKAHIEYISKHNDNEEFDKISKIITILLQEKVFEGLDW YSASLNSIDTNTDEGKKLRLAFLFSEAMFTLMTLKYINIS PKEQKEIFEDLKTFL* ---	No
CR40-1	1	LSTKNKIDKNYLINIIEEILLNDGISGLSIRKVATKANISIGG VQYIFGNKEGMIKAVLEKNEEDYNRQIKILLKDDNSKYS QLKAHIEYISKHNDNEEFDKISKIITILLQEKVFEGLDW YSTSLNSIDTNTDEGKKLRLAFLFSEAMFTLMTLKYINISP KEQKEIFEDLKTFL* ---	No
CR42-3	2	---	---
CR48-2	2	---	---
CR50-1	1	---	---
CR78-1	1	LSTKNKIDKNYLINIIEEILLNDGISGLSIRKVATKANISIGG VQYIFGNKEGMIKAVLEKNEEDYNRQIKILLKDDNSKYS QLKAHIEYISKHNDNEEFDKISKIITILLQEKVFEGLDW YSTSLNSIDTNTDEGKKLRLAFLFSEAMFTLMTLKYINISP KEQKEIFEDLKTFL* ---	No
CR90-2	2	---	---
CR101-1	1	---	---
CR1-4-1	4	---	---
CR1132	2	MSTKNKIDKNYLINIIEEILLNDGISGLSIRKVATKANISIG GVQYIFGNKEGMIKAVLEKNEEDYNRQIKILLKDDNSKY SQLKAHIEYISKHNDNEEFDKISKIITILLQEKVFEGLD WYSTSLNSIDTNTDEGKKLRLAFLFSEAMFTLMTLKYINI SPKEQKEIFEDLKTFL* ---	No
CR1143	4	MSTKNKIDKNYLINIIEEILLNDGISGLSIRRVATKANISIG GVQYIFGNKKGMIKAVLEKNEEDYNRQIKILLKDDNSKY SQLKAHIEYISKHNDNEEFDKISKIITILLQEKVFLEGLD WYSASLNSIDTNTDEGKKLRLAFLFSEAMFTLMTLKYINI SPKEQKEIFEDLKTFL* ---	No
Ab_1711	2	MSTKNKIDKNYLINIIEEILLNDGISGLSIRKVATKANISIG GVQYIFGNKEGMIKAVLEKNEEDYNRQIKILLKDDNSKY SQLKAHIEYISKHNDNEEFDKISKIITILLQEKVFEGLD WYSASLNSIDTNTDEGKKLRLAFLFSEAMFTLMTLKYINI SPKEQKEIFEDLKTFL* ---	No
Ab_4211	2	MSTKNKIDKNYLINIIEEILLNDGISGLSIRKVATKANISIG GVQYIFGNKEGMIKAVLEKNEEDYNRQIKILLKDDNSKY SQLKAHIEYISKHNDNEEFDKISKIITILLQEKVFEGLD WYSASLNSIDTNTDEGKKLRLAFLFSEAMFTLMTLKYINI SPKEQKEIFEDLKTFL* ---	No
CR891	2	MSTKNKIDKNYLINIIEEILLNDGISGLSIRKVATKANISIG GVQYIFGNKEGMIKAVLEKNEEDYNRQIKILLKDDNSKY SQLKAHIEYISKHNDNEEFDKISKIITILLQEKVFEGLD WYSTSLNSIDTNTDEGKKLRLAFLFSEAMFTLMTLKYINI SPKEQKEIFEDLKTFL* ---	No

CR604	0.125	MSTKNKIDKNYLINIIEEILLNDGISGLSIRKVATKANISIG GVQYIFGNKEGMIAVLEKNEEDYNRQIKILLKDDNSKY SQLKAHIEYISKHNDNEEFDKISKIITILLQEKVFEGQLD WYSTSLNSIDTNTDEGKKLRLAFLFSEAMFTLMTLYINI SPKEQKEIFEDLKTFL* MSTKNKIDKNYLINIIEEILLNDGISGLSIRKVATKANISIG GVQYIFGNKEGMIAVLEKNEEDYNRQIKILLKDDNSKY SQLKAHIEYISKHNDNEEFDKISKIITILLQEKVFEGQLD WYSASLNSIDTNTDEGKKLRLAFLFSEAMFTLMTLYINI SPKEQKEIFEDLKTFL*	No
1426_2003	1	MSTKNKIDKNYLINIIEEILLNDGISGLSIRKVATKANISIG GVQYIFGNKEGMIAVLEKNEEDYNRQIKILLKDDNSKY SQLKAHIEYISKHNDNEEFDKISKIITILLQEKVFEGQLD WYSASLNSIDTNTDEGKKLRLAFLFSEAMFTLMTLYINI SPKEQKEIFEDLKTFL* MSTKNKIDKNYLINIIEEILLNDGISGLSIRKVATKANISIG GVQYIFGNKEGMIAVLEKNEEDYNRQIKILLKDDNSKY SQLKAHIEYISKHNDNEEFDKISKIITILLQEKVFEGQLD WYSASLNSIDTNTDEGKKLRLAFLFSEAMFTLMTLYINI SPEEQKEIFEDLKTFL*	No
CR892	2	MSTKNKIDKNYLINIIEEILLNDGISGLSIRKVATKANISIG GVQYIFGNKEGMIAVLEKNEEDYNRQIKILLKDDNSKY SQLKAHIEYISKHNDNEEFDKISKIITILLQEKVFEGQLD WYSASLNSIDTNTDEGKKLRLAFLFSEAMFTLMTLYINI SPEEQKEIFEDLKTFL*	No
A103	2	---	---
DQ31A1	4	MSTKNKIDKNYLINIIEEILLNDGISGLSIRKVATKANISIG GVQYIFGNKEGMIAVLEKNEEDYNRQIKILLKDDNSKY SQLKAHIEYISKHNDNEEFDKISKIITILLQEKVFEGQLD WYSTSLNSIDTNTDEGKKLRLAFLFSEAMFTLMTLYINI SPKEQKEIFEDLKTFL*	No
Ab_3711	1	---	---
CR461	1	---	---
A111	2	---	---
DQ20dA1	2	MSTKNKIDKNYLINIIEEILLNDGISGLSIRKVATKANISIG GVQYIFGNKEGMIAVLEKNEEDYNRQIKILLKDDNSKY SQLKAHIEYISKHNDNEEFDKISKIITILLQEKVFEGQLD WYSASLNSIDTNTDEGKKLRLAFLFSEAMFTLMTLYINI SPKEQKEIFEDLKTFL*	No

Isolates identified in bold correspond to predicted proteins deduced from previous whole genome sequencing (1).

--- No amplification of *areR*.

Table S2. Oligonucleotide sequences used in the current work.

Primer	Target gene	Sequence (5'→3')	Application
tetR_F1	tetR	gaataagaagttcYaaaatatgatgc	<i>tetR</i> amplification and sequencing <i>tetR</i> internal sequencing
tetR_R1		tccatcaatttgMggctaac	
tetR_seq		cattgaagagattctctta	
areB_A1	areB	ttgaaataagggtactactcagg	Isogenic <i>cmeB</i> mutant construction
areB_A2		<i>Ttattctcctagtagtca</i> ctccaacaccatctactcttgc	
areB_B1		<i>Tacctggagggaataatgatcc</i> attaggaattattgggcag	
areB_B2		gttcgctctggcttgcaaat	
areA_RTPCR_F1	areA	agttagaccgcaaattgatgg	Quantitative PCR
areA_RTPCR_R1		gcttagcatcatctgcttcttg	
areB_RTPCR_F1	areB	tggaaatggacaaaatgggtg	
areB_RTPCR_R1		tccaagccctggaatagaag	
areC_RTPCR_F1	areC	tcgattgatgcaaaagcaag	
areC_RTPCR_R1		ttgaagttgctgcgtattttg	

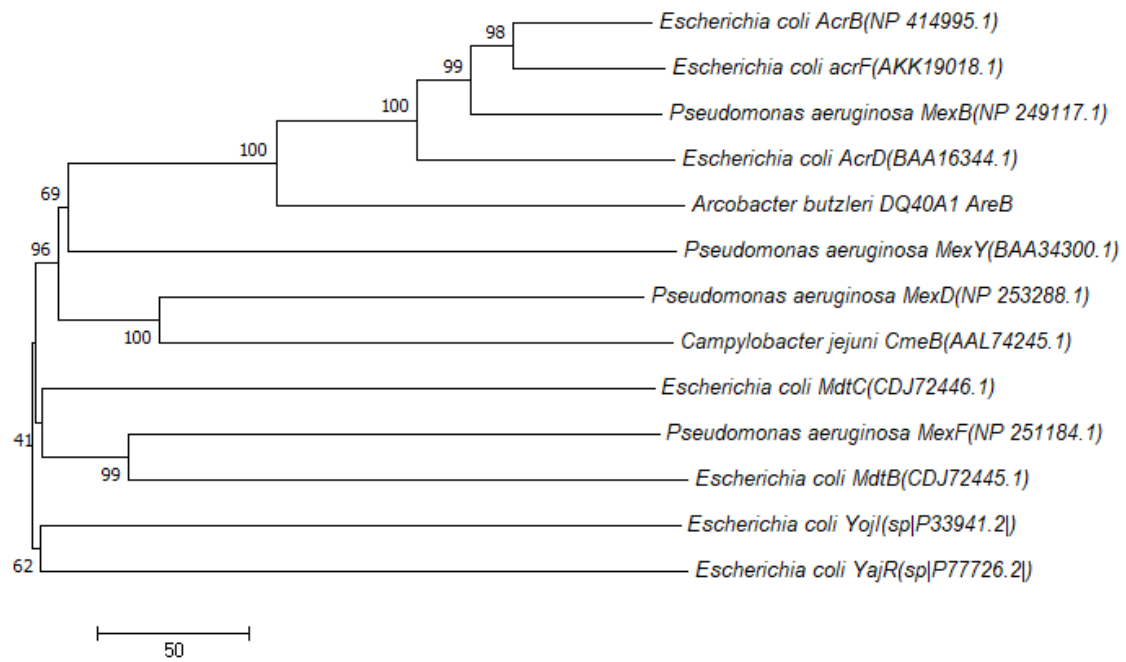


Figure S1. Neighbor-joining phylogenetic tree of AreB together with representatives of RND inner membrane components of *Escherichia coli*, *Pseudomonas aeruginosa* and *Campylobacter jejuni*. *Escherichia coli* MFS and ABC transporters were used in the analysis. The percentage of replicate trees in which the associated taxa clustered together in the bootstrap test (1000 replicates) are shown next to the branches. Accession numbers are shown in the parenthesis. Bar corresponds to 50 amino acid differences per sequence.

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CR891      MSTKNKIDKNYLINIIIEILLNDGISGLSIRKVATKANISIGGVQYIFGNKEGMIKAVLE
DQ40A1    MSTKNKIDKNYLINIIIEILLNDGISGLSIRKVATKANISIGGVQYIFGNKEGMIKAVLE
CR604     MSTKNKIDKNYLINIIIEILLNDGISGLSIRKVATKANISIGGVQYIFGNKEGMIKAVLE
Ab_4511   MSTKNKIDKNYLINIIIEILLNDGISGLSIRKVATKANISIGGVQYIFGNKEGMIKAVLE
CR1132    MSTKNKIDKNYLINIIIEILLNDGISGLSIRKVATKANISIGGVQYIFGNKEGMIKAVLE
DQ31A1    MSTKNKIDKNYLINIIIEILLNDGISGLSIRKVATKANISIGGVQYIFGNKEGMIKAVLE
Ab_2211   MSTKNKIDKNYLINIIIEILLNDGISGLSIRKVATKANISIGGVQYIFGNKEGMIKAVLE
DQ20dA1   MSTKNKIDKNYLINIIIEILLNDGISGLSIRKVATKANISIGGVQYIFGNKEGMIKAVLE
CR1143    MSTKNKIDKNYLINIIIEILLNDGISGLSIRRVATKANISIGGVQYIFGNKKGMIKAVLE
Ab_1711   MSTKNKIDKNYLINIIIEILLNDGISGLSIRKVATKANISIGGVQYIFGNKEGMIKAVLE
Ab_4211   MSTKNKIDKNYLINIIIEILLNDGISGLSIRKVATKANISIGGVQYIFGNKEGMIKAVLE
1426_2003 MSTKNKIDKNYLINIIIEILLNDGISGLSIRKVATKANISIGGVQYIFGNKEGMIKAVLE
CR892     MSTKNKIDKNYLINIIIEILLNDGISGLSIRKVATKANISIGGVQYIFGNKEGMIKAVLE
CR641     MSTKNKIDKNYLINIIIEILLNDGISGLSIRKVATKANISIGGVQYIFGNKEGMIKAVLE
Ab_2811   MSTKNKIDKNYLINIIIEILLNDGISGLSIRKVATKANISIGGVQYIFGNKEGMIKAVLE
CR502     MSTKNKIDKNYLINIIIEILLNDGISGLSIRKVATKANISIGGVQYIFGNKEGMIKAVLE
CR424     MSTKNKIDKNYLINIIIEILLNDGISGLSIRKVATKANISIGGVQYIFGNKEGMIKAVLE
*****:*****:*****

CR891      KNEEDYNRQIKILLKDDNSKYSQLKAHIEYISKHNDNEEFDKISKIITILLQEKVFVEGL
DQ40A1    KNEEDYNRQIKILLKDDNSKYSQLKAHIEYISKHNDNEEFDKISKIITILLQEKVFVEGL
CR604     KNEEDYNRQIKILLKDDNSKYSQLKAHIEYISKHNDNEEFDKISKIITILLQEKVFVEGL
Ab_4511   KNEEDYNRQIKILLKDDNSKYSQLKAHIEYISKHNDNEEFDKISKIITILLQEKVFVEGL
CR1132    KNEEDYNRQIKILLKDDNSKYSQLKAHIEYISKHNDNEEFDKISKIITILLQEKVFVEGL
DQ31A1    KNEEDYNRQIKILLKDDNSKYSQLKAHIEYISKHNDNEEFDKISKIITILLQEKVFVEGL
Ab_2211   KNEEDYNRQIKILLKDDNSKYSQLKAHIEYISKHNDNEEFDKISKIITILLQEKVFVEGL
DQ20dA1   KNEEDYNRQIKILLKDDNSKYSQLKAHIEYISKHNDNEEFDKISKIITILLQEKVFVEGL
CR1143    KNEEDYNRQIKILLKDDNSKYSQLKAHIEYISKHNDNEEFDKISKIITILLQEKVFVEGL
Ab_1711   KNEEDYNRQIKILLKDDNSKYSQLKAHIEYISKHNDNEEFDKISKIITILLQEKVFVEGL
Ab_4211   KNEEDYNRQIKILLKDDNSKYSQLKAHIEYISKHNDNEEFDKISKIITILLQEKVFVEGL
1426_2003 KNEEDYNRQIKILLKDDNSKYSQLKAHIEYISKHNDNEEFDKISKIITILLQEKVFVEGL
CR892     KNEEDYNRQIKILLKDDNSKYSQLKAHIEYISKHNDNEEFDKISKIITILLQEKVFVEGL
CR641     KNEEDYNRQIKILLKDDNSKYSQLKAHIEYISKHNDNEEFDKISKIITILLQEKVFVEGL
Ab_2811   KNEEDYNRQIKILLKDDNSKYSQLKAHIEYISKHNDNEEFDKISKIITILLQEKVFVEGL
CR502     KNEEDYNRQIKILLKDDNSKYSQLKAHIEYISKHNDNEEFDKISKIITILLQEKVFD---
CR424     KNEEDYNRQIKILLKDDNSKYSQLKAHIEYISKHNDNEEFDKISKIITILLQEKVFD---
*****:*****:*****

CR891      QDWYSTSLNSIDTNTDEGKKLRLAFLFSEAMFTLMTLKYINISPKEQKEIFEDLKTFFLL
DQ40A1    QDWYSTSLNSIDTNTDEGKKLRLAFLFSEAMFTLMTLKYINISPKEQKEIFEDLKTFFLL
CR604     QDWYSTSLNSIDTNTDEGKKLRLAFLFSEAMFTLMTLKYINISPKEQKEIFEDLKTFFLL
Ab_4511   QDWYSTSLNSIDTNTDEGKKLRLAFLFSEAMFTLMTLKYINISPKEQKEIFEDLKTFFLL
CR1132    QDWYSTSLNSIDTNTDEGKKLRLAFLFSEAMFTLMTLKYINISPKEQKEIFEDLKTFFLL
DQ31A1    QDWYSTSLNSIDTNTDEGKKLRLAFLFSEAMFTLMTLKYINISPKEQKEIFEDLKTFFLL
Ab_2211   QDWYSTSLNSIDTNTDEGKKLRLAFLFSEAMFTLMTLKYINISPKEQKEIFEDLKTFFLL
DQ20dA1   QDWYSASLNSIDTNTDEGKKLRLAFLFSEAMFTLMTLKYINISPKEQKEIFEDLKTFFLL
CR1143    QDWYSASLNSIDTNTDEGKKLRLAFLFSEAMFTLMTLKYINISPKEQKEIFEDLKTFFLL
Ab_1711   QDWYSASLNSIDTNTDEGKKLRLAFLFSEAMFTLMTLKYINISPKEQKEIFEDLKTFFLL
Ab_4211   QDWYSASLNSIDTNTDEGKKLRLAFLFSEAMFTLMTLKYINISPKEQKEIFEDLKTFFLL
1426_2003 QDWYSASLNSIDTNTDEGKKLRLAFLFSEAMFTLMTLKYINISPKEQKEIFEDLKTFFLL
CR892     QDWYSASLNSIDTNTDEGKKLRLAFLFSEAMFTLMTLKYINISPKEQKEIFEDLKTFFLL
CR641     QDWYSASLNSIDTNTDEGKN-----
Ab_2811   QDWYSAS-----
CR502     -----
CR424     -----VGTQRIWPPRAFTLGQLTHNDLAS-----

```

Figure S2. Alignment of AreR from 17 *Aliarcobacter butzleri* strains.

Asterisks indicate amino acids that were common to all sequences, colons and dots indicate structurally similar amino acids as calculated by the Clustal W program.

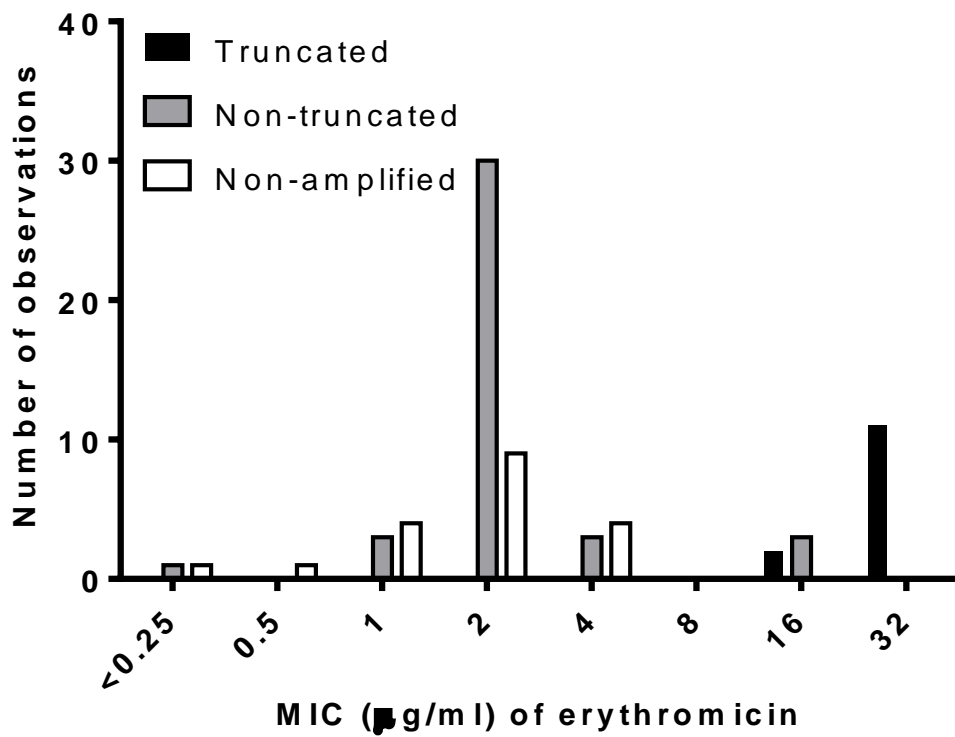


Figure S3. Distribution of minimum inhibitory concentration of erythromycin for *Aliarcobacter butzleri* isolates. Truncated indicates strains with a truncated predicted AreR, Non-truncated indicates strains with a non-truncated predicted AreR, Non-amplified depicts isolates for which no amplification was obtained.

Reference

1. Isidro J, Ferreira S, Pinto M, Domingues F, Oleastro M, Gomes JP, Borges V. 2020. Virulence and antibiotic resistance plasticity of *Arcobacter butzleri*: Insights on the genomic diversity of an emerging human pathogen. *Infect Genet Evol* 80:pii=104213. <https://doi.org/10.1016/j.meegid.2020.104213>