TABLE S1. Strains used in this study

Species	**Strain**[a]	**Origin**
Lactic acid bacteria		
Lactococcus lactis subsp. *lactis*	S3+	Artisanal fresh cheese
Lactococcus lactis subsp. *lactis*	S3-	Protease-negative variant of S3+
Aerobic ripening bacteria		
Arthrobacter arilaitensis	Re117^T (= CIP 108037)	Reblochon cheese
Arthrobacter arilaitensis	2L34	Livarot cheese
Arthrobacter arilaitensis	Ep104	Epoisses cheese
Arthrobacter arilaitensis	3M03	Livarot cheese
Arthrobacter arilaitensis	Mu107	Munster cheese
Arthrobacter arilaitensis	Ma107	Maroilles cheese
Arthrobacter arilaitensis	GMPA29	Soft cheese
Brevibacterium aurantiacum	BLE3	Commercial ripening strain
Brevibacterium aurantiacum	ATCC 9174	Romadur cheese
Brevibacterium aurantiacum	2M23	Livarot cheese
Brevibacterium aurantiacum	ATCC 9175^T	Camembert cheese
Brevibacterium aurantiacum	BA 171	Beaufort cheese
Brevibacterium linens	ATCC 9172^T	Harzer cheese
Brevibacterium antiquum	CNRZ 918	Gruyère de Comté cheese
Corynebacterium casei	DPC 5298^T (= CIP 107182)	Gubbeen cheese
Corynebacterium casei	UCMA 3821	Livarot cheese
Corynebacterium variabile	Mu133	Vacherin cheese
Corynebacterium variabile	DPC 5310 (= CIP 107183)	Gubbeen cheese
Corynebacterium flavescens	Mu128	Munster cheese
Yeast		
Debaryomyces hansenii	304	Goat cheese

[a] Strains are from the following collections: American Type Culture Collection (ATCC), Rockville, MD, USA; Dairy products Research Centre (DPC), Moorepark, Fermoy, Ireland; Collection de l'Institut Pasteur (CIP), Paris, France; Centre National de Recherches Zootechniques (CNRZ): collection now transferred to the Centre International de Ressources Microbiennes (CIRM), Rennes, France. Stains 2L34, 3M03, UCMA 3821 and 2M23 are from LMILA (Laboratoire des Micro-organismes d'Intérêt Laitier et Alimentaire, Caen, France), and strain BLE3 is from Cargill (La Ferté-sous-Jouarre, France). The other strains are from the GMPA culture collection (Unité Mixte de Recherche Génie et Microbiologie des Procédés Alimentaires, Thiverval-Grignon, France).

TABLE S2. *Arthrobacter arilaitensis* Re117 gene primers used in this study

Gene[a]	Gene product	Primer sequence (5' → 3') F = forward, R = reverse
AARI_02870	iron-siderophore ABC transporter, substrate-binding protein	F: CTGATCGTGGTCTCCACCTC R: CTTCCAGTCCTTGTCACCGT
AARI_03970	iron-siderophore ABC transporter, substrate-binding protein	F: GAAGCTGTCATTGCGGAACAC R: CCGTTTGTTGGGCCGTA
AARI_03980	iron-siderophore ABC transporter, substrate-binding protein	F: CAATGAACTGCTGACGCAAAT R: AGGTCGTTCTCGGTGACAA
AARI_10870	iron-siderophore ABC transporter, substrate-binding protein	F: GGTTATCGGCACCGACAT R: CGCAGTATCCGCTGACG
AARI_15020	iron-siderophore ABC transporter, substrate-binding protein	F: GCCGAACTGGTGGCCTACA R: GTGATGGTGCCGACGTTTAC
AARI_26370	iron-siderophore ABC transporter, substrate-binding protein	F: ACCGCCTACGTCTACTCC R: ATCCGAGTCCCACTCGTTGA
AARI_30210	iron-siderophore ABC transporter, substrate-binding protein	F: GCGGTTGTCTCACTCGAATC R: GGAGAAGTCGGTCTTGAAGTCTG
AARI_32450	iron-siderophore ABC transporter, substrate-binding protein	F: CACCCTGATGCCGGACA R: GTCAACGGTAACGACCGATT
AARI_32790	iron-siderophore ABC transporter, substrate-binding protein	F: GGTGGTCAAGAACGAAGAAGC R: TCGGTGTACTGCGGGTAG
AARI_26120	iron/manganese/zinc ABC transporter, substrate-binding protein	F: CGGACGTGGTTCTGGCAAA R: GCGTGCATGAGCGTGAT
AARI_29890 and 30460	iron/manganese/zinc ABC transporter, substrate-binding protein	F: CTGCGAAAGCTGACCTGAT R: CGTCACTGACAACAGCGT
AARI_16210	putative divalent metal ion transporter	F: CATCTCCGGTGGCGACAA R: CGGCCCAGAAGCCAATC
AARI_18090	metal ion transporter	F: ATCAGCGCATTGCCTTG R: GGACGAGGTCTTCGACGAGTA
AARI_09570	pyridoxal-dependent amino acid decarboxylase	F: TGGACGGCATCGAGCAG R: GATTCAAGGGTTGGAGCGTT
AARI_09550	siderophore biosynthesis protein	F: CCCTGTCCAGCCACTGCTA R: TCGGTCATGGAGGATTCAATGAG
AARI_09560	L-lysine 6-monooxygenase (NADPH)	F: CGCGGAAATCTTCCTCGAC R: TCCAAGGTGAGCTTGGTGTA
AARI_32920	isochorismatase	F: AATGACGGTCGGGAAGAAATTAC R: CGCATCCATTCCTGGAGTT
AARI_32910	2,3-dihydro-2,3-dihydroxybenzoate dehydrogenase	F: GACCGCCGATATCAGTTCAC R: CCACATTGACCAGGCCTT
AARI_32900	isochorismate synthase	F: CGGGTCTCCTACTGCTGTC R: CATTCGCCTTCACCGTCTT
AARI_32890	non-ribosomal siderophore peptide synthetase component	F: CGGCGGCGAGAAGATCA R: GTGCGTTCGTTCGCCCA
AARI_26600	ferritin-like protein	F: GAAGATTGGCGAGCAACCAG R: CGAATCGCTTCGGAGACC
ideR (AARI_05610)	iron-dependent repressor IdeR	F: GCGTTGACGGAGAAAGGT R: ATGCTTCGTCATGGACGTATT
AARI_02510	ferric uptake regulation protein	F: ACCATTATTTCGGCAGTCCA R: GATCTGCCGGATGACGC
16S rRNA (AARI_36310, 3340, 36380, 36520, 36580, 36690)	16S ribosomal RNA	F: CCGTAGCTAACGCATTAAGTG R: CCGAAGGGAAACTCCATCT
tuf (AARI_23550)	Elongation factor Tu	F: CCAAGGTTCTGGCTGACAAGTA R: ATGTGCGAGATGTTGATGGTAAT
rpoA (AARI_23210)	DNA-directed RNA polymerase alpha chain	F: CTTCGGTGCGAAGTCCATT R: CATCGTCGATGGCGCTAC
rpoB (AARI_23600)	DNA-directed RNA polymerase beta chain	F: TGGAAGACGGCACTCCTTT R: ATTCAGGCTCGCCTTCAAT
gyrB (AARI_20200)	putative DNA gyrase subunit B	F: GACGTTGTTCTACCGCTACAT R: TTGGTCATCTCCGCCTCAG
ftsZ (AARI_20710)	cell division protein FtsZ	F: ATCGAATGATCGAAGTCGGTC R: TTCGCGTCCTACGTCTAGT
recA (ARI1_1010)	RecA bacterial DNA recombination protein	F: CCAACGCGGTCGGTAAC R: GTCGATGAGCGAACCTTCAC
dnaG (AARI_09340)	DNA primase	F: TGCCCAGACCTATGTCTGT R: ATCTTGCCGCCCTTGATGTA

[a] The *Arthrobacter arilaitensis* Re117 chromosome sequence is available in the EMBL database under accession number FQ311875.

TABLE S3. Effect of the addition of iron and desferrioxamine B on the counts of *Debaryomyces hansenii* in the model cheeses. The cheese curds were inoculated with a yeast (*Debaryomyces hansenii*) and different strains of aerobic ripening bacteria. The values are the means of three biological replicates (separate cheeses). Values in bold correspond to significant differences (Student test, *P* < 0.05) between the cheeses supplemented with iron or desferrioxamine B and the corresponding control cheeses. SD = Standard deviation.

Aerobic ripening bacteria:	*Debaryomyces hansenii* at 12 days (cfu/g)						*Debaryomyces hansenii* at 16 days (cfu/g)					
	Control		+ Iron		+ Desferrio-xamine B		Control		+ Iron		+ Desferrio-xamine B	
	Mean	SD	Mean	SD	Mean	SD	Mean	SD	Mean	SD	Mean	SD
A. arilaitensis 3M03	2.6E+08	1.3E+08	4.5E+08	1.4E+08	1.4E+08	2.1E+07	2.9E+08	4.0E+07	3.3E+08	8.3E+07	3.2E+08	5.8E+07
A. arilaitensis Mu107	2.2E+08	1.0E+08	2.5E+08	4.3E+07	2.3E+08	1.3E+08	2.4E+08	3.2E+07	2.2E+08	9.6E+07	2.6E+08	1.1E+08
A. arilaitensis Ma107	1.7E+08	5.1E+07	3.3E+08	1.5E+08	2.3E+08	4.6E+07	2.1E+08	5.1E+07	3.8E+08	8.3E+07	3.1E+08	2.8E+07
A. arilaitensis GMPA29	1.9E+08	1.5E+08	2.6E+08	6.8E+07	1.3E+08	2.3E+07	2.3E+08	4.6E+07	2.4E+08	2.2E+07	2.0E+08	6.3E+07
A. arilaitensis 2L34	1.5E+08	2.3E+07	2.1E+08	3.8E+07	1.5E+08	3.4E+07	3.2E+08	8.7E+07	4.8E+08	2.1E+08	3.9E+08	1.1E+08
A. arilaitensis Ep104	1.4E+08	1.4E+07	1.5E+08	2.0E+07	1.9E+08	5.0E+07	3.2E+08	6.3E+07	2.8E+08	8.1E+07	2.0E+08	6.5E+07
A. arilaitensis Re117	1.6E+08	4.7E+07	1.9E+08	5.6E+07	2.3E+08	7.1E+07	2.4E+08	4.8E+07	5.9E+08	1.9E+08	1.9E+08	5.3E+07
C. casei DPC 5298	2.3E+08	1.3E+07	2.2E+08	2.8E+07	1.9E+08	5.4E+07	3.3E+08	7.1E+07	3.7E+08	1.6E+08	3.3E+08	6.0E+07
C. casei UCMA 3821	1.9E+08	3.2E+07	2.1E+08	7.6E+07	9.0E+07	4.0E+07	1.9E+08	2.9E+07	2.3E+08	2.0E+07	2.9E+08	7.5E+07
C. variabile DPC 5310	1.9E+08	3.5E+07	1.8E+08	6.3E+07	2.3E+08	6.9E+07	1.9E+08	2.9E+07	3.4E+08	9.8E+07	3.6E+08	9.7E+07
C. variabile Mu133	4.7E+08	2.6E+08	2.5E+08	6.6E+07	4.7E+08	1.2E+08	4.0E+08	5.9E+07	2.4E+08	8.9E+07	4.4E+08	1.8E+08
C. flavescens Mu128	2.4E+08	1.4E+08	2.6E+08	3.4E+07	2.6E+08	4.8E+07	3.2E+08	5.3E+07	3.7E+08	9.6E+07	3.0E+08	9.8E+07
B. aurantiacum BLE3	3.0E+08	9.8E+07	2.2E+08	4.1E+07	3.6E+08	5.4E+07	3.2E+08	7.0E+07	3.1E+08	1.2E+08	2.6E+08	4.9E+07
B. aurantiacum ATCC 9174	4.7E+08	2.0E+08	5.3E+08	1.4E+08	2.5E+08	5.7E+07	2.6E+08	7.5E+07	4.0E+08	7.5E+07	5.0E+08	1.7E+08
B. aurantiacum ATCC 9175	2.3E+08	8.5E+07	3.5E+08	1.0E+08	2.0E+08	4.6E+07	1.8E+08	3.0E+07	2.5E+08	4.0E+07	2.3E+08	4.4E+07
B. aurantiacum BA171	1.4E+08	4.6E+07	1.3E+08	4.3E+07	9.0E+07	1.5E+07	2.3E+08	7.5E+07	4.1E+08	1.3E+08	3.6E+08	1.2E+08
B. aurantiacum 2M23	9.3E+07	3.8E+07	5.0E+07	1.1E+07	1.8E+08	6.5E+07	2.4E+08	5.7E+07	2.3E+08	6.4E+07	2.9E+08	6.4E+07
B. antiquum 918	2.3E+08	7.6E+07	3.9E+08	1.5E+08	5.0E+08	1.8E+08	2.6E+08	6.7E+07	2.9E+08	7.6E+07	2.9E+08	8.4E+07
B. linens ATCC 9172	3.0E+08	4.2E+07	6.9E+08	2.5E+08	6.2E+08	2.6E+08	3.2E+08	8.5E+07	2.9E+08	8.6E+07	3.6E+08	6.4E+07

TABLE S4. Effect of the addition of iron and desferrioxamine B on the counts of *Lactococcus lactis* (lactic acid bacteria) in the model cheeses. The cheese curds were inoculated with a yeast (*Debaryomyces hansenii*) and different strains of aerobic ripening bacteria. The values are the means of three biological replicates (separate cheeses). Values in bold correspond to significant differences (Student test, $P < 0.05$) between the cheeses supplemented with iron or desferrioxamine B and the corresponding control cheeses. SD = Standard deviation.

Aerobic ripening bacteria:	*Lactococcus lactis* at 12 days (cfu/g)						*Lactococcus lactis* at 16 days (cfu/g)					
	Control		+ Iron		+ Desferrioxamine B		Control		+ Iron		+ Desferrioxamine B	
	Mean	SD	Mean	SD	Mean	SD	Mean	SD	Mean	SD	Mean	SD
A. arilaitensis 3M03	3.2E+07	1.9E+06	3.2E+07	6.4E+06	2.4E+07	9.1E+06	3.4E+07	9.1E+06	2.5E+07	5.5E+06	**1.0E+07**	2.5E+06
A. arilaitensis Mu107	3.9E+07	1.2E+07	3.2E+07	8.2E+06	3.4E+07	7.4E+06	2.7E+07	5.4E+06	3.4E+07	9.6E+06	2.6E+07	2.9E+06
A. arilaitensis Ma107	5.3E+07	1.5E+07	2.7E+07	1.2E+07	1.9E+07	9.9E+06	3.3E+07	7.9E+06	2.7E+07	7.3E+06	4.0E+07	1.8E+06
A. arilaitensis GMPA29	3.0E+07	6.1E+06	2.7E+07	9.4E+06	5.4E+07	1.1E+07	4.8E+07	1.1E+07	4.5E+07	1.3E+07	6.3E+07	1.3E+07
A. arilaitensis 2L34	2.4E+07	3.7E+06	4.0E+07	8.1E+06	2.5E+07	6.4E+06	4.4E+07	6.6E+06	1.1E+08	3.4E+07	9.3E+07	2.6E+07
A. arilaitensis Ep104	2.0E+07	5.0E+06	3.0E+07	2.7E+06	**6.6E+07**	1.2E+07	4.4E+07	5.7E+06	8.3E+07	2.2E+07	6.8E+07	1.8E+07
A. arilaitensis Re117	4.0E+07	2.2E+07	2.6E+07	1.0E+07	2.4E+07	6.5E+06	5.5E+07	3.6E+07	1.0E+08	4.5E+07	1.3E+08	2.5E+07
C. casei DPC 5298	1.3E+07	3.6E+06	1.8E+07	4.0E+06	1.2E+07	3.8E+06	2.5E+07	8.7E+06	3.4E+07	1.2E+07	1.6E+07	1.2E+06
C. casei UCMA 3821	3.8E+07	1.0E+07	4.7E+07	5.6E+06	1.6E+07	6.2E+06	4.2E+07	1.7E+07	3.7E+07	1.4E+07	3.6E+07	5.2E+06
C. variabile DPC 5310	3.0E+07	6.0E+06	2.7E+07	9.0E+06	4.0E+07	1.4E+07	2.7E+07	6.4E+05	5.9E+07	1.7E+07	3.7E+07	9.0E+06
C. variabile Mu133	3.1E+07	2.3E+06	2.7E+07	3.8E+06	3.2E+07	6.3E+06	4.7E+07	1.2E+07	**1.3E+07**	1.6E+06	7.9E+07	3.2E+07
C. flavescens Mu128	4.8E+06	7.0E+05	**1.2E+07**	1.2E+06	8.4E+06	1.9E+06	2.7E+07	2.7E+06	2.5E+07	8.1E+06	2.3E+07	8.0E+06
B. aurantiacum BLE3	2.3E+07	5.7E+06	1.6E+07	2.6E+06	2.4E+07	3.9E+06	4.5E+07	2.6E+06	4.7E+07	6.6E+06	3.4E+07	6.8E+06
B. aurantiacum ATCC 9174	3.3E+07	8.0E+06	6.2E+07	1.4E+07	1.9E+07	4.2E+06	3.7E+07	3.5E+06	4.8E+07	1.2E+07	5.0E+07	1.2E+07
B. aurantiacum ATCC 9175	2.5E+07	1.2E+06	2.8E+07	7.8E+06	2.2E+07	6.3E+06	2.9E+07	4.4E+06	2.9E+07	2.8E+06	2.0E+07	3.2E+06
B. aurantiacum BA171	2.4E+07	4.7E+06	2.0E+07	5.3E+06	2.1E+07	3.3E+06	3.0E+07	3.4E+06	3.1E+07	1.8E+06	2.0E+07	6.6E+06
B. aurantiacum 2M23	3.0E+07	5.4E+06	2.6E+07	8.6E+06	1.6E+07	5.2E+06	3.0E+07	1.4E+06	2.1E+07	5.6E+06	2.4E+07	3.3E+06
B. antiquum 918	2.5E+07	1.0E+07	2.7E+07	1.3E+07	2.0E+07	1.1E+07	3.1E+07	6.5E+06	3.4E+07	8.2E+06	2.5E+07	6.4E+06
B. linens ATCC 9172	3.4E+07	7.8E+06	2.3E+07	8.4E+06	1.8E+07	4.9E+06	5.6E+07	2.0E+07	2.9E+07	6.4E+06	4.1E+07	4.0E+06

TABLE S5. Effect of the addition of iron and desferrioxamine B on the growth of ripening bacteria in the model cheeses. The cheese curds were inoculated with a yeast (*Debaryomyces hansenii*) and different strains of aerobic ripening bacteria. The values are the counts of ripening bacteria in the cheeses supplemented with iron of desferrioxamine B, divided by the counts in the control cheeses (means of three biological replicates). Values in bold correspond to significant differences (counts; Student test, $P < 0.05$) between the cheeses supplemented with iron or desferrioxamine B and the corresponding control cheeses.

Aerobic ripening bacteria:	12 days		16 days	
	Counts in iron-supplemented cheeses/counts in control cheeses	Counts in desferrioxamine-supplemented cheeses/counts in control cheeses	Counts in iron-supplemented cheeses/counts in control cheeses	Counts in desferrioxamine-supplemented cheeses/counts in control cheeses
A. arilaitensis 3M03	**3.5**	**3.5**	1.5	1.8
A. arilaitensis Mu107	1.2	**25.4**	**7.1**	**3.3**
A. arilaitensis Ma107	**20.3**	**20.9**	**4.9**	**4.0**
A. arilaitensis GMPA29	**7.6**	**221.4**	**3.7**	**2.7**
A. arilaitensis 2L34	**8.8**	**21.4**	**8.0**	**12.0**
A. arilaitensis Ep104	**45.1**	**76.0**	**12.9**	**9.9**
A. arilaitensis Re117	**3.2**	**12.1**	**10.9**	**14.9**
C. casei DPC 5298	**13.5**	**57.5**	**5.0**	**3.4**
C. casei UCMA 3821	**4.5**	1.1	1.4	**3.0**
C. variabile DPC 5310	2.0	**11.9**	2.7	**15.1**
C. variabile Mu133	2.3	**24.2**	**5.8**	**15.0**
C. flavescens Mu128	1.5	1.7	1.2	0.8
B. aurantiacum BLE3	**3.8**	**29.1**	1.0	1.2
B. aurantiacum ATCC 9174	0.4	**7.8**	**4.0**	**10.7**
B. aurantiacum ATCC 9175	2.2	**7.2**	2.4	2.1
B. aurantiacum BA171	**3.5**	**3.3**	1.0	1.2
B. aurantiacum 2M23	**7.0**	**74.0**	**37.7**	**212.2**
B. antiquum 918	**4.3**	**32.7**	1.6	**4.1**
B. linens ATCC 9172	1.6	**192.2**	**11.7**	**290.5**

TABLE S6. Effect of iron addition on the expression of *Arthrobacter arilaitensis* Re117 genes in model cheeses after 16 days of ripening. Values correspond to the biological replicates number 2 and number 3 (cheese replicates), and are the means obtained from three separate RNA extractions of a control cheese and of a cheese supplemented with 1 mg of iron per kg.

Gene	**Product**	**IdeR binding site**[a]	**NEL**[b] **biological replicate 2**		**NEL**[b] **biological replicate 3**	
			Mean	STD	Mean	STD
Siderophore biosynthesis genes:						
AARI_32900	isochorismate synthase, EC 5.4.4.2	upstream AARI_32920	0.28	0.02	0.17	0.01
iron/siderophore binding proteins:						
AARI_03970	iron-siderophore ABC transporter, substrate-binding protein	no	1.18	0.11	1.01	0.17
AARI_26370	iron-siderophore ABC transporter, substrate-binding protein	upstream AARI_26370	0.27	0.06	0.21	0.05
AARI_30210	iron-siderophore ABC transporter, substrate-binding protein	no	1.66	0.18	1.43	0.12
AARI_32790	iron-siderophore ABC transporter, substrate-binding protein	upstream AARI_32790	0.30	0.01	0.32	0.07

[a] Iron-dependent regulator binding site. Consensus sequence TTAGGTTAGGCTAACCTAA, up to five mismatches allowed.

[b] Normalized Expression Level: Expression of the considered gene in the cheese supplemented with iron, divided by the expression in the control cheese (calibrator), using *ftsZ*, *tuf* and *rpoB* as reference genes.

TABLE S7. Effect of desferrioxamine B (siderophore) addition on the expression of *Arthrobacter arilaitensis* Re117 genes in model cheeses after 16 days of ripening. Values correspond to the biological replicates number 2 and number 3 (cheese replicates), and are the means obtained from three separate RNA extractions of a control cheese and of a cheese supplemented with 50 µmoles of desferrioxamine B per kg.

Gene	**Product**	**IdeR binding site**[a]	**NEL**[b] **biological replicate 2**		**NEL**[b] **biological replicate 3**	
			Mean	STD	Mean	STD
Siderophore biosynthesis genes:						
AARI_32900	isochorismate synthase, EC 5.4.4.2	upstream AARI_32920	1.55	0.13	1.36	0.04
iron/siderophore binding proteins:						
AARI_03970	iron-siderophore ABC transporter, substrate-binding protein	no	5.59	0.79	3.65	0.07
AARI_26370	iron-siderophore ABC transporter, substrate-binding protein	upstream AARI_26370	1.27	0.15	1.13	0.20
AARI_30210	iron-siderophore ABC transporter, substrate-binding protein	no	1.83	0.14	1.45	0.17
AARI_32790	iron-siderophore ABC transporter, substrate-binding protein	upstream AARI_32790	1.16	0.08	1.30	0.10

[a] Iron-dependent regulator binding site. Consensus sequence TTAGGTTAGGCTAACCTAA, up to five mismatches allowed.

[b] Normalized Expression Level: Expression of the considered gene in the cheese supplemented with desferrioxamine B, divided by the expression in the control cheese (calibrator), using *ftsZ*, *tuf* and *rpoB* as reference genes.

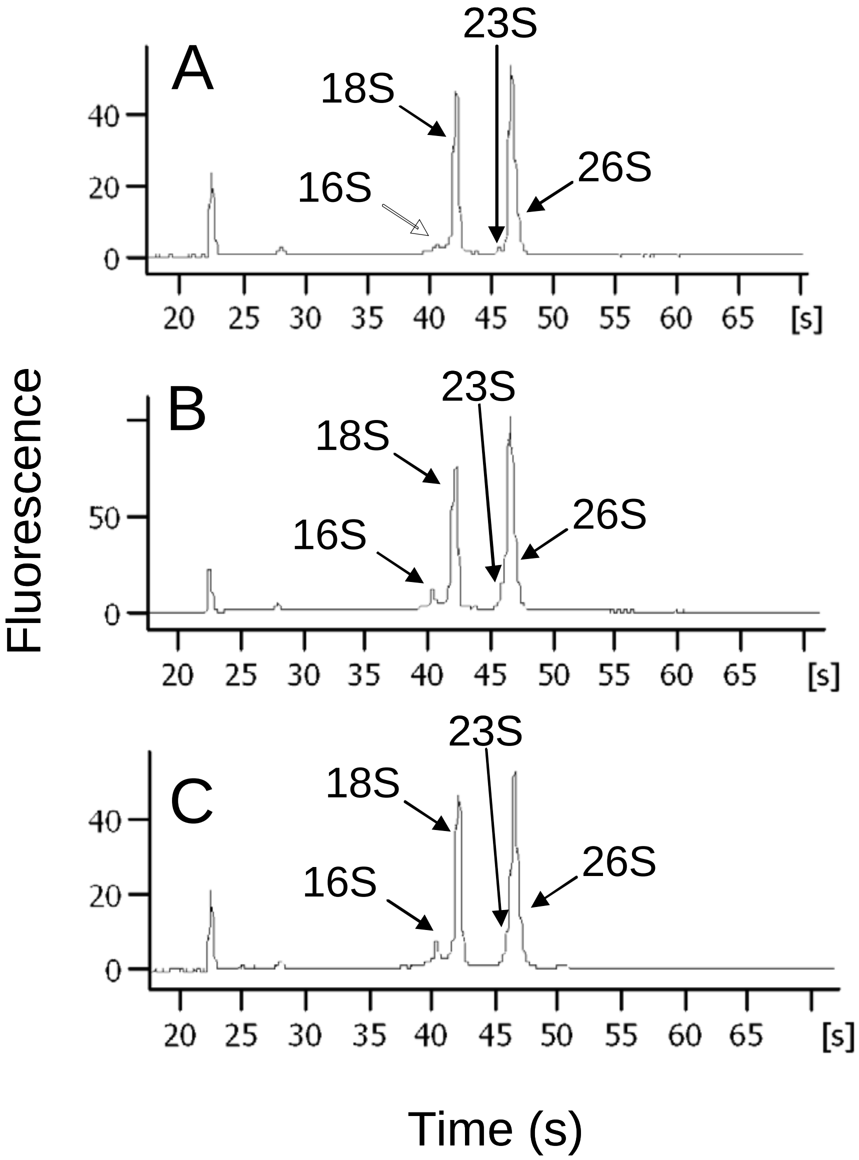

FIG. S1. Electrophoregrams of RNA preparations (Agilent Bioanalyzer) from cheeses after 16 days of ripening with the ripening strain, *Arthrobacter arilaitensis* Re117. A: control cheese; B: cheese supplemented with iron; C: cheese supplemented with desferrioxamine B.

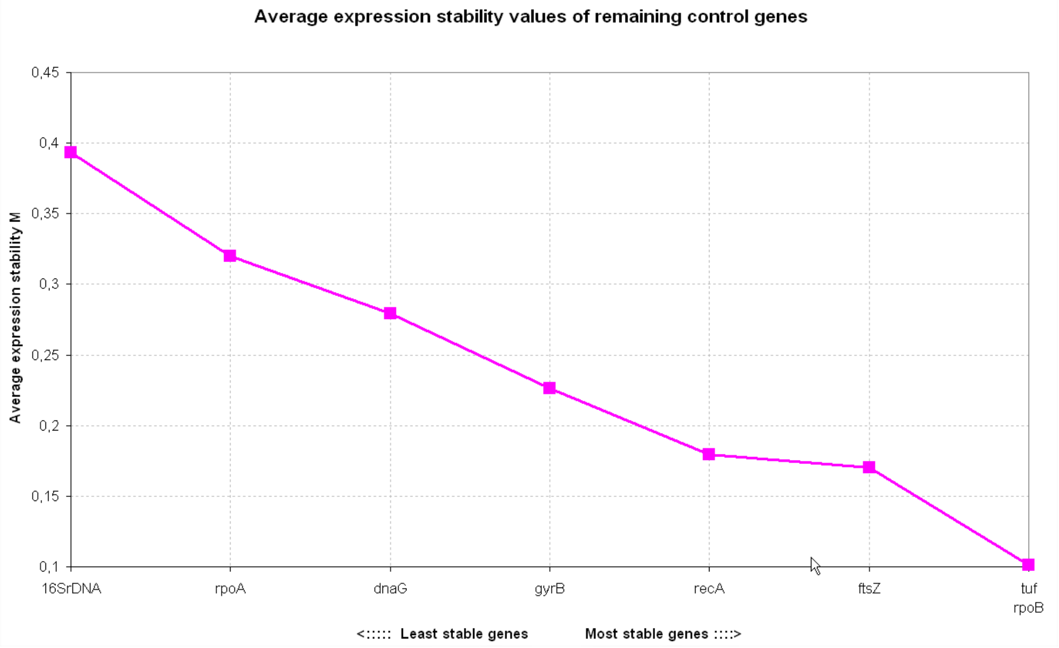

FIG. S2. Average expression stability values (*M*) of remaining control genes during stepwise exclusion of the least stable control genes (left point = all eight candidate reference genes; right point = reference genes *tuf* and *rpoB*).