SUPPLEMENTAL DATA

FIG S1: Alignment of the eight GH36 conserved motifs (M1 to M8) found in the Aga protein of *L. lactis* subsp. *lactis* strain A12 and strain KF147, and *L. raffinolactis* strain ATCC 43920. Amino acids specific to strain A12 are indicated in bold.

Motif 1		
	A12	E**NF**G**DCY**G**FN**LVYSGN
	KF147	E**F**TGTAIGLTLVYSGN
	ATCC 43920	E**L**TGTAIGLTLVYSGN
Motif 2		
	A12	**A**PEA**V**L**S**YS**AN**G**FAQL**SQ**N**FH
	KF147	SPEALLVYSDQGLNGMSQTFH
	ATCC 43920	SPEALLVYSDQGLNGMSQTFH
Motif 3		
	A12	PILINNWEATYFDF**T**
	KF147	PILINNWEATYFDFD
	ATCC 43920	PILINNWEATYFDFD
Motif 4		
	A12	**I**G**VDML**V**M**DDGWFGN
	KF147	LGIELFVLDDGWFGK
	ATCC 43920	LGIELFVLDDGWFGK
Motif 5		
	A12	FG**I**WFEPEMV**SEE**S**K**LF
	KF147	FGLWFEPEMVNADSDLF
	ATCC 43920	FGLWFEPEMVNADSDLF
Motif 6		
	A12	**V**LD**STN**I**E**Y**V**KWDMNR
	KF147	ILDTIDIDYIKWDMNR
	ATCC 43920	ILDTIDIDYIKWDMNR
Motif 7		
	A12	**N**IL**F**EGC**A**GGGGRFD**L**G
	KF147	HILWEGCSGGGGRFDAG
	ATCC 43920	HVLWEGCSGGGGRFDAG
Motif 8		
	A12	WTSDNTDAI**N**RL**K**IQYG
	KF147	WTSDNTDA**V**ERL**D**IQYG
	ATCC 43920	WTSDNTDAIERL**E**IQYG

TABLE S1: Phenotypic comparison of strains A12 and IL1403 by Biolog assay analysis. The values correspond to the difference between the heights of the kinetic curves of the strains at 24 h, 36 h and 48 h. Positive arbitrary values indicate phenotypes more pronounced in strain A12 and negative arbitrary values indicate those more pronounced in strain IL1403.

Microplate	Well	Test	24 h	36 h	48 h
PM01	A02	L-Arabinose	160	163	164
PM01	B08	D-Xylose	115	123	126
PM01	C11	D-Melibiose	149	151	152
PM02	D05	Stachyose	146	149	150
PM02	D01	D-Raffinose	140	143	140
PM01	B06	D-Gluconic Acid	138	145	148
PM01	D09	α-D-Lactose	99	110	112
PM01	D11	Sucrose	80	100	110
PM01	A06	D-Galactose	47	45	45
PM02	C07	β-Methyl-D-Galactoside	31	56	72
PM01	D08	α-Methyl-D-Galactoside	116	126	132
PM01	F11	D-Cellobiose	84	83	82
PM02	B08	Arbutin	84	75	72
PM02	C01	Gentiobiose	80	73	69
PM02	B04	Amygdalin	37	63	79
PM01	E08	β-Methyl-D-Glucoside	126	120	114
PM01	C09	α-D-Glucose	47	47	46
PM01	A10	D-Trehalose	68	66	65
PM01	G08	N-Acetyl-β-D-Mannosamine	75	75	75
PM01	A03	N-Acetyl-D-Glucosamine	73	72	72
PM01	A11	D-Mannose	64	61	59
PM01	C07	D-Fructose	53	51	50
PM09	E12	7% Urea	49	63	71
PM09	E11	6% Urea	124	134	137
PM09	E10	5% Urea	93	78	59
PM09	E09	4% Urea	104	90	72
PM09	F03	3% Sodium Lactate	47	65	74
PM13	H03	Cupric Chloride	76	86	91
PM02	A05	g-Cyclodextrin	-92	-53	-30
PM13	C04	t-Butyl Hydroquinone	-79	-61	-53
PM10	E04	pH 9.5 + L-Asparagine	-79	-73	
PM09	A07	6% NaCl	-66	-69	-70
PM09	A08	6.5% NaCl	-77	-84	-88
PM09	A09	7% NaCl	-59	-67	-71
PM09	B05	6% NaCl + Dimethyl Sulphonyl Propionate	-65	-66	-64
PM09	E06	6% Sodium Formate	-64	-61	-56
PM01	B03	Glycerol	-25	-37	-43

TABLE S2: Number and name of strain A12 genes overlapping with the growth rate regulon (22) and genes differentially expressed when comparing two sugar sources. On the selected sugar couples, strain A12 displayed variable growth rates (Table 4). Gal: galactose; Glu: glucose; Ara: arabinose; Fru: fructose.

	Gal/Glu	**Fru/Glu**	**Ara/Glu**	**Ara/Fru**	**Ara/Gal**
Number of genes differentially expressed	178	37	56	159	18
Number of genes overlapping with the growth rate regulon	59	8	2	17	5
Name of overlapping genes	butB, ceo, dhal, dhaM, fmt, glpD, glpF2, metF, napC, pi244, ptbA, purl, rbsK, rliDB, yjdA, yjiB, ymgI, ymhC, ynfC, yphI, yrjB, yrjC, ytiA, yucG, ywgA, accD, apt, aroH, carA, dltC, guaA, ileS, infA, lysQ, metS, murA2, pepC, phnA, ps303, rplM, rplO, rpmE, rpsI, rpsJ, rpsS, thrA, ybfC, yfdB, yhcA, yjbC, ymeB, yneG, yneH, ynhD, yqaC, ythA, ythC, yvdF, yxdF,	carA, ileS, pgmB, ps303, pyrC, ythA, ythC, yxd	yrjB, ctrA	accD, atpG, ileS, optF, potD, ybfC, yldC, ytgG, ythA, ythC, mgtA, pi209, ycfH, yciA, yijG, ymhG, ypbB	accD, dltC, glpD, purM, yrjB

TABLE S3: Functions of genes specifically induced by *L. lactis* subsp. *lactis* strain A12 when grown on galactose (Gal), fructose (Fru), glucose (Glc), raffinose (Raff) or arabinose (Ara). Functional categories were defined according to (20). Ratio value analysis, obtained from four replicates, allowed genes with specific variation of expression in one sugar to be identified. Ratio values were associated with a p-value of less than 0.05 and a false discover rate below 0.1 or 0.05 (genes in bold). Experiments were performed in four replicates. *: genes lacking in strain IL1403.

Galactose

Gene	CAT	function	Gal/Glc ratio	Gal/Fru ratio	Gal/Ara ratio
galK	NRJsug	galactokinase	16.26	16.33	12.50
galM	NRJsug	aldose 1-epimerase	15.09	13.78	11.11
galT	NRJsug	galactose-1-phosphate uridylyltransferase	10.36	7.82	7.69
lacZ	NRJsug	beta-galactosidase	8.22	7.49	9.09
galE	NRJsug	UDP-glucose 4-epimerase	5.00	3.83	4.17
yugB	NRJaer	oxidoreductase	4.88	5.40	5.88
yugA	REGgen	transcription regulator	4.39	4.43	4.35
yrjB	NRJaer	oxidoreductase	2.31	1.91	1.52
glpD	NRJana	glycerol-3-phosphate dehydrogenase	1.66	1.60	1.45
scrK	NRJsug	fructokinase	1.65	2.28	1.82
argF	NRJAmi	ornithine carbamoyltransferase	1.62	1.58	1.61
pi318	OTHpha	prophage pi3 protein 18	1.56	1.35	1.45
ypcA	NRJsug	beta-glucosidase	1.56	2.24	1.41
ypcG	TSPcar	sugar ABC transporter permease protein	1.56	1.58	1.56
argE	AMIglu	acetylornithine deacetylase	1.54	2.63	2.38
ymjE	ENVsur	glycosyl transferase	1.52	1.32	1.19

bglH	NRJsug	beta-glucosidase	1.35	1.80	1.39
dnaJ	REPsyn	DnaJ	1.28	1.13	1.20
hom	AMIasp	homoserine dehydrogenase	0.67	0.70	0.79
busAA	TSPami	betaine ABC transporter ATP binding protein	0.56	0.36	0.50
blt	TSPmdr	multidrug efflux transporter	0.50	0.70	0.67
busAB	TSPami	betaine ABC transporter permease and substrate binding protein	0.50	0.32	0.44
lysA	AMIasp	diaminopimelate decarboxylase	0.50	0.65	0.65
lysP	TSPami	lysine specific permease	0.35	0.49	0.47

Fructose

Gene	**CAT**	**function**	**Fru/Glc ratio**	**Fru/Gal ratio**	**Fru/Ara ratio**
lacC=fruC	NRJsug	tagatose-6-phosphate kinase	4.73	5.26	4.17
glmS	INTami	glucosamine-fructose-6-phosphate aminotransferase	2.95	2.63	2.86
yjgB	UNK	hypothetical protein	2.91	4.00	3.13
yrbB	UNK	hypothetical protein	2.33	1.96	3.03
yuaE	UNK	hypothetical protein	1.89	2.00	1.92
LL2150*	UNK	hypothetical protein	1.71	1.82	1.82
radC	REPsyn	DNA repair protein RadC	1.69	1.59	1.75
busAB	TSPami	betaine ABC transporter permease and substrate binding protein	1.55	3.13	1.39
yqeD	UNK	hypothetical protein	1.45	1.47	1.54
LL1032*	TSPmdr	Putative ABC-type multidrug transport system, ATPase component	0.77	0.83	0.81
yucG	INTdeg	chitin binding protein	0.73	0.51	0.70
ackA1	NRJfer	acetate kinase	0.71	0.88	0.80
adhE	NRJfer	alcohol-acetaldehyde dehydrogenase	0.56	0.66	0.55
yrcA	NRJsug	phospho-beta-glucosidase	0.52	0.44	0.58
adhA	NRJfer	alcohol dehydrogenase	0.44	0.37	0.44

Glucose

Gene	**CAT**	**function**	**Glc/Gal ratio**	**Glc/Fru ratio**	**Glc/Ara ratio**
metE	AMIasp	5-methionine synthase	0.47	0.33	0.49

Raffinose

Gene	**CAT**	**function**	**Raff/Fru ratio**	**Raff/Gal ratio**	**Raff/Glu ratio**
aga*	NRJsug	Putative alpha galactosidase (GH 36)	10.51	5.23	10.61
LL2138*	TSPcar	Putative Na+/raffinose symporter	8.45	4.18	9.34
sucP*	NRJsug	Putative sucrose phosphorylase (GH 13)	4.32	3.21	5.15

Arabinose

Gene	**CAT**	**function**	**Ara/Fru ratio**	**Ara/glu ratio**	**Ara/Gal ratio**
araD*	NRJsug	Putative L-ribulose-5-phosphate 4-epimerase	9.61	14.04	11.81
araA*	NRJsug	Putative L-arabinose isomerase	8.46	10.34	9.53
araT*	NRJsug	Putative arabinose transporter	8.41	12.3	9.7
araB*	NRJsug	Putative Carbohydrate kinase, possible xylulose kinase	7.23	8.99	7.11
ptk	NRJpen	phosphoketolase	3.52	5.89	3.44
xylT	TPScar	D-xylose proton-symporter	2.83	2.49	2.4
xylX	NRJsug	putative acetyltransferase	2.34	2.62	2.18
araR*	NRJsug	Putative Regulatory protein	2.21	3.16	3.33
arcB	NRJami	ornithine carbamoyltransferase	1.49	1.98	1.5