

Table S1. Measurement of glutamate and GABA in *Levilactobacillus brevis* Lbr-6108, Lbr-35, and ATCC 14869. The p-value is the result of an ANOVA with Tukey's multiple comparison test comparing the ODs of each strain to at T48 to Lbr-6108 in the respective media.

Strain	Timepoint (hr)	Glutamate, MRS (µg/ml)		GABA, MRS (µg/ml)		OD, MRS (µg/ml)		p-value	Glutamate, MRS+MSG (µg/ml)		GABA, MRS+MSG (µg/ml)		OD, MRS+MSG (600nm)		p-value
		rep 1	rep 2	rep 1	rep 2	rep 1	rep 2		rep 1	rep 2	rep 1	rep 2	rep 1	rep 2	
Lbr-6108	0	660	670	50	50	0.139	0.434	89000	88000	50	50	0.137	0.133	>0.9999	
Lbr-6108	3	650	640	50	50	0.434	0.432	90000	86000	60	58	0.412	0.397		
Lbr-6108	6	620	590	66	70	0.667	0.671	86000	86000	100	100	0.615	0.602		
Lbr-6108	9	570	510	210	190	1.056	1.069	87000	83000	310	320	0.959	0.968		
Lbr-6108	12	360	350	340	350	1.291	1.320	81000	81000	620	630	1.217	1.226		
Lbr-6108	15	130	120	500	520	1.478	1.448	72000	76000	1200	1200	1.406	1.386		
Lbr-6108	18	100	100	500	500	1.638	1.611	63000	63000	1900	2000	1.542	1.540		
Lbr-6108	21	100	100	500	500	1.767	1.763	50000	51000	2800	2800	1.689	1.722		
Lbr-6108	24	100	100	500	500	1.816	1.833	37000	37000	4000	3800	1.789	1.774		
Lbr-6108	48	100	100	500	510	1.733	1.753	250	300	60000	60000	1.724	1.733		
Lbr-35	0	690	670	50	50	0.142	0.136	89000	88000	53	50	0.145	0.139		
Lbr-35	3	680	660	50	50	0.519	0.500	89000	90000	50	50	0.476	0.491		
Lbr-35	6	670	640	50	50	0.855	0.849	88000	86000	50	50	0.780	0.753		
Lbr-35	9	670	700	54	59	1.086	1.110	86000	89000	76	70	1.029	1.021		
Lbr-35	12	710	680	58	50	1.278	1.271	86000	90000	61	56	1.159	1.144		
Lbr-35	15	690	680	50	51	1.446	1.397	88000	89000	75	60	1.266	1.278		
Lbr-35	18	680	690	51	52	1.556	1.544	87000	89000	63	63	1.397	1.401		
Lbr-35	21	670	680	54	58	1.650	1.687	89000	95000	71	72	1.502	1.564		
Lbr-35	24	630	600	82	80	1.741	1.738	87000	88000	120	110	1.566	1.579		
Lbr-35	48	560	540	170	160	1.690	1.690	90000	89000	270	230	1.655	1.621		

Table S2. Glutamate utilization and GABA production by *Levilactobacillus brevis* Lbr-6108 in MRS with different concentrations of MSG.

Timepoint (hr)	MRS with 10,000 µg/mL MSG						MRS with 30,000 µg/mL MSG						MRS with 90,000 µg/mL MSG					
	Glu Drake (µg/mL)		GABA (µg/mL)		% Yield		Glu Drake (µg/mL)		GABA (µg/mL)		% Yield		Glu Drake (µg/mL)		GABA (µg/mL)		% Yield	
	rep 1	rep 2	rep 1	rep 2	rep 1	rep 2	rep 1	rep 2	rep 1	rep 2	rep 1	rep 2	rep 1	rep 2	rep 1	rep 2	rep 1	rep 2
5	5000.0	4500.0	50.0	50.0	10.0%	11.1%	10000.0	3400.0	50.0	50.0	5.0%	14.7%	5000.0	4740.0	50.0	50.0	1.0%	1.1%
24	4200.0	4290.0	2600.0	2620.0	61.9%	61.1%	6000.0	5920.0	2900.0	2930.0	48.3%	49.5%	4000.0	3790.0	1800.0	1830.0	45.0%	48.3%
48	8200.0	8160.0	5300.0	5310.0	64.6%	65.1%	16300.0	16270.0	10000.0	9970.0	61.3%	61.3%	24000.0	23530.0	13000.0	12680.0	54.2%	53.9%
72	8000.0	7980.0	6100.0	6075.0	76.3%	76.1%	18200.0	18405.0	12000.0	12140.0	65.9%	66.0%	28000.0	23530.0	16000.0	16450.0	57.1%	69.9%

Table S3. Gene List from Figure 4. Locus IDs are for *Levilactobacillus brevis* Lbr-6108 genome. Encoded protein functions are given for genes shown in Figure 4.

Locus ID	Gene name	Protein function	Operon / pathway	Panel in Figure 4
BGC39_04180	<i>gadA</i>	Glutamate decarboxylase (EC 4.1.1.15) GadA	L-Glutamate decarboxylase operon	A
BGC39_07245	<i>gadR</i>	Transcriptional regulator GadR	L-Glutamate decarboxylase operon	A
BGC39_07250	<i>gadC</i>	Glutamate/gamma-aminobutyrate antiporter	L-Glutamate decarboxylase operon	A
BGC39_07255	<i>gadB</i>	Glutamate decarboxylase (EC 4.1.1.15) GadB	L-Glutamate decarboxylase operon	A
BGC39_07260	<i>gltX</i>	Glutamyl-tRNA synthetase (EC 6.1.1.17; EC 6.1.1.24)	L-Glutamate decarboxylase operon	A
BGC39_05810	<i>hmpT</i>	Substrate-specific component HmpT of predicted hydroxymethylpyrimidine ECF transporter	Pyridoxal 5'-phosphate (PLP)	B
BGC39_05815	<i>thiD2</i>	Novel pyridoxal kinase, thiD family (EC 2.7.1.35)	Pyridoxal 5'-phosphate (PLP)	B
BGC39_05820	<i>norD</i>	Transcriptional regulator of pyridoxine metabolism / Pyridoxamine phosphate aminotransferase (EC 2.6.1.54)	Pyridoxal 5'-phosphate (PLP)	B
BGC39_05050	<i>argF</i>	Ornithine carbamoyltransferase (EC 2.1.3.3)	Arginine deiminase operon	C
BGC39_05055	<i>arcA</i>	Arginine deiminase (EC 3.5.3.6)	Arginine deiminase operon	C
BGC39_05060	<i>arcD</i>	Arginine/ornithine antiporter ArcD	Arginine deiminase operon	C
BGC39_06170	<i>aguA</i>	Agmatine deiminase (EC 3.5.3.12)	Agmatine deiminase operon	D
BGC39_06175	<i>aguD</i>	Agmatine/putrescine antiporter, associated with agmatine catabolism	Agmatine deiminase operon	D
BGC39_06180	<i>aguB</i>	Putrescine carbamoyltransferase (EC 2.1.3.6)	Agmatine deiminase operon	D
BGC39_06130	<i>mleP</i>	Malate permease	Malolactic fermentation operon	E

BGC39_06135	<i>mleS</i>	Malolactic enzyme (EC 4.1.1.101)	Malolactic fermentation operon	E
BGC39_06140	<i>mleR</i>	Malolactic regulator MleR	Malolactic fermentation operon	E
BGC39_06185	<i>nhaC2</i>	Predicted tyrosine transporter, NhaC family	Tyrosine decarboxylase operon	F
BGC39_06190	<i>tdcP</i>	Predicted tyrosine transporter, GadC family	Tyrosine decarboxylase operon	F
BGC39_06195	<i>tdcA</i>	L-tyrosine decarboxylase (EC 4.1.1.25) TDC	Tyrosine decarboxylase operon	F
BGC39_06200	<i>tyrS</i>	Tyrosyl-tRNA synthetase (EC 6.1.1.1)	Tyrosine decarboxylase operon	F

Figure S1. Culture purity testing by species- and strain-specific PCR for *Levilactobacillus brevis* Lbr-6108 and Lbr-35.

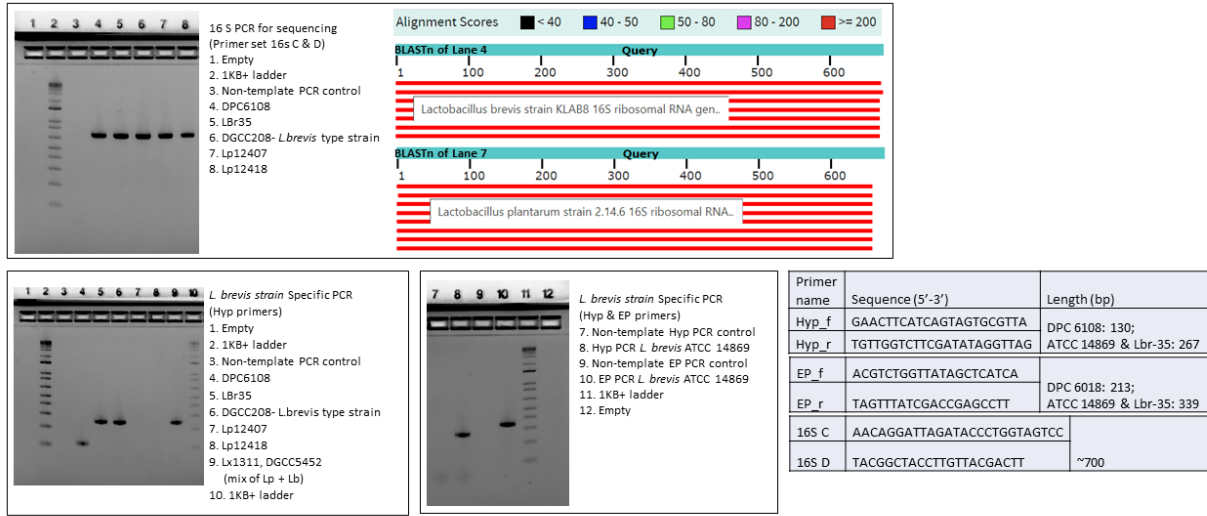


Figure S2. PCA plot of RNA-sequencing for *Levilactobacillus brevis* Lbr-6108 and Lbr-35.

