

**Cell Host & Microbe, Volume 24**

**Supplemental Information**

**Bacterial Adaptation to the Host's Diet**

**Is a Key Evolutionary Force Shaping**

***Drosophila-Lactobacillus* Symbiosis**

**Maria Elena Martino, Pauline Joncour, Ryan Leenay, Hugo Gervais, Malay Shah, Sandrine Hughes, Benjamin Gillet, Chase Beisel, and François Leulier**

## Supplemental figure titles and legends

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### **Bacterial adaptation to diet is a key evolutionary force shaping *Drosophila-Lactobacillus* symbiosis**

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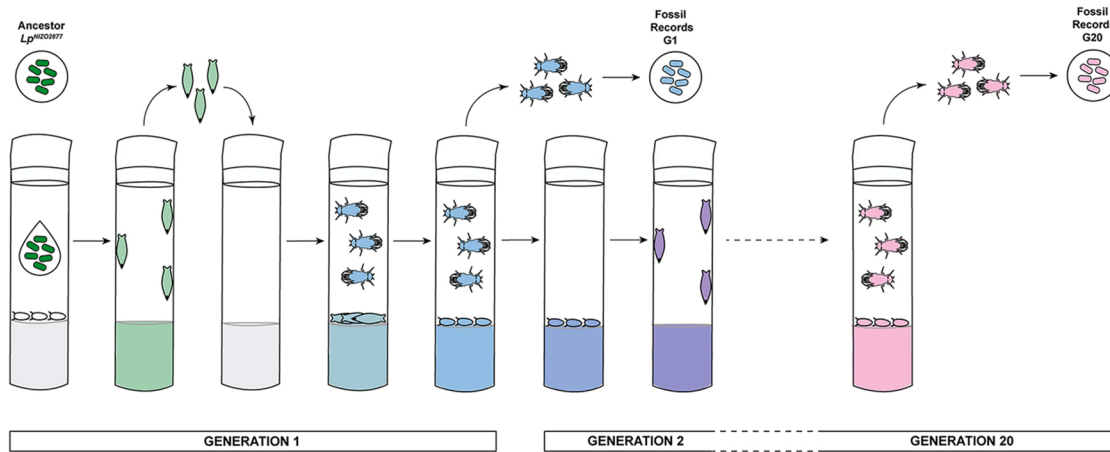
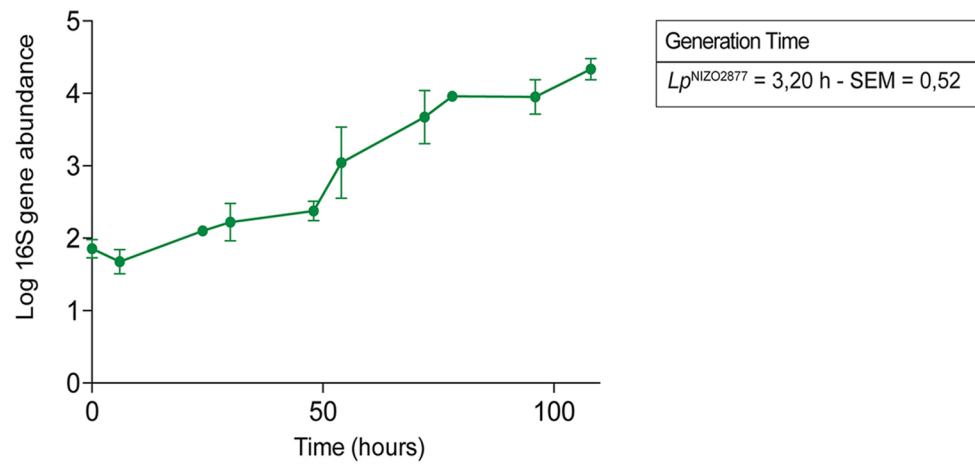
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**A****B****Figure S1**

**Supplemental Figure 1 (related to Fig. 1): Rationale and schematic representation of the experimental setup for studying *L. plantarum* adaptive evolution (AE) with *Drosophila melanogaster*.**

(A) The ancestor strain ( $Lp^{NIZO2877}$ ) was added to 40 germ-free (GF) *Drosophila* embryos at the beginning of the first *Drosophila* generation (Generation 1). The first 15 emerging pupae were transferred to a new sterile poor nutrient diet. This allowed the bacteria associated with the pupae to propagate and colonize the new environment. The 15 adults emerged from the 15 transferred pupae, mated and females laid eggs that became the founders of the following fly generation (Generation 2). Once the eggs were laid, the adults were collected and homogenized to isolate the evolved bacteria they carry (fossil records from generation 1). Generation 2 followed the same experimental cycle as Generation 1, with the exception that no further inoculation of the ancestor strain *L. plantarum*<sup>NIZO2877</sup> has been performed. Evolving bacteria were propagated through the transfer of the pupae during each generation. The experimental evolution lasted 20 *Drosophila* generations (313 days). Colour shading represents the evolution of the bacterial population during the experiment.

(B) 16S rRNA kinetics of  $Lp^{NIZO2877}$  in *Drosophila* Niche (*Drosophila* + Diet). The 16S rRNA gene quantification is shown in logarithmic scale. The mean generation time (h, hours) of  $Lp^{NIZO2877}$  in *Drosophila* niche  $\pm$  the standard error of the mean (SEM) are reported on the graph (see Methods).



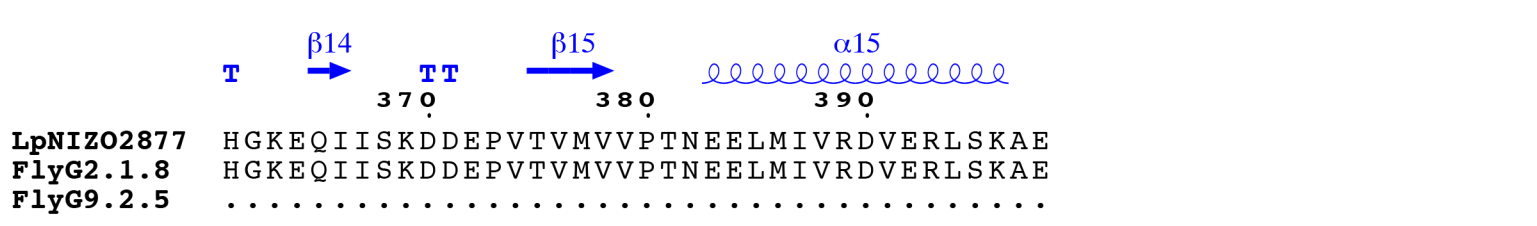
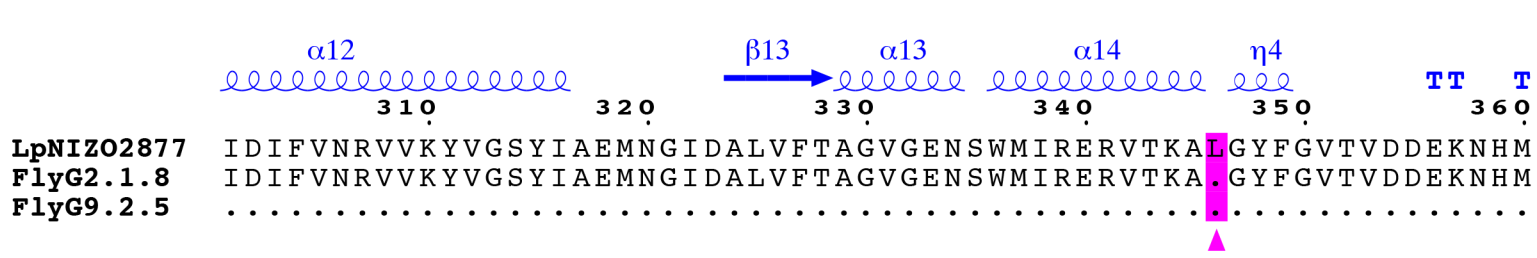
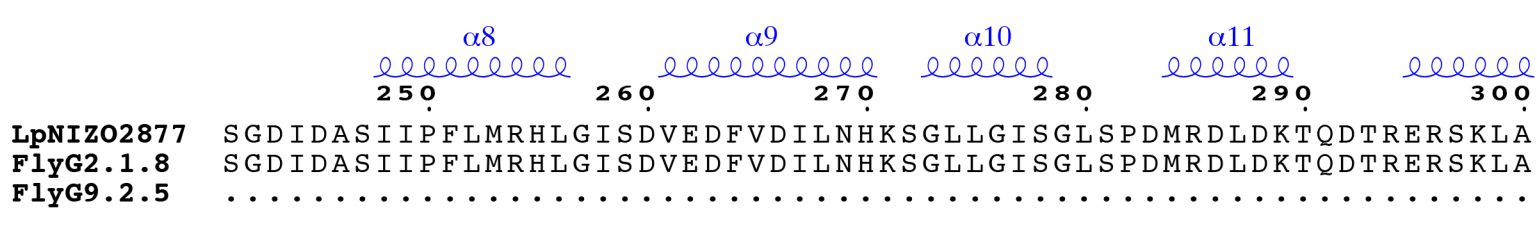
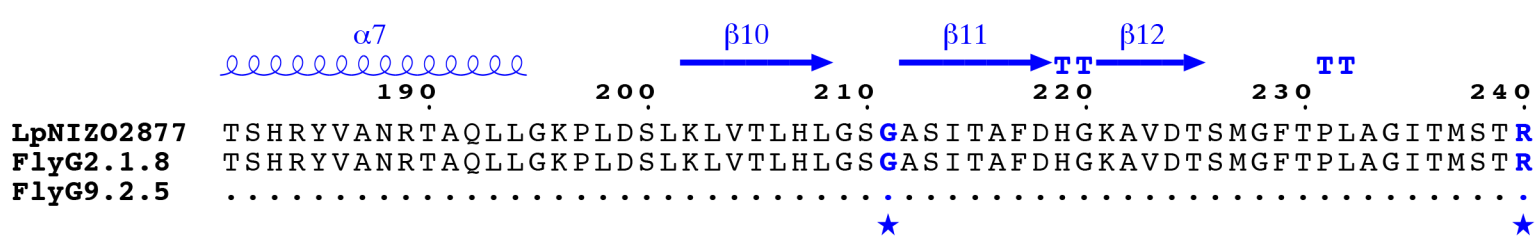
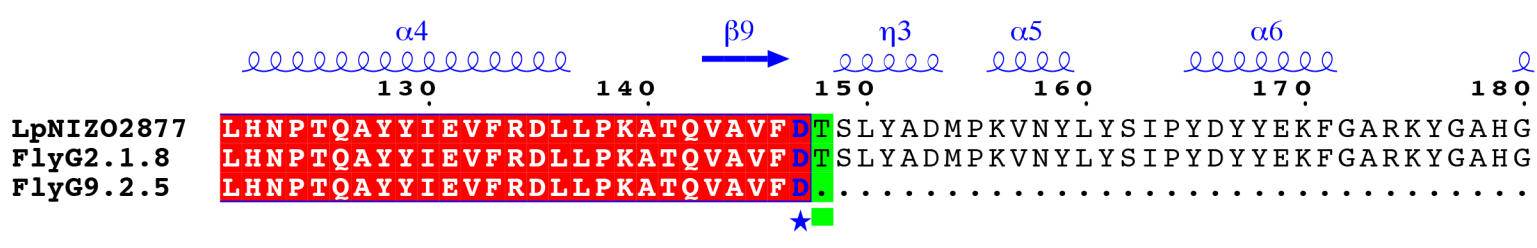
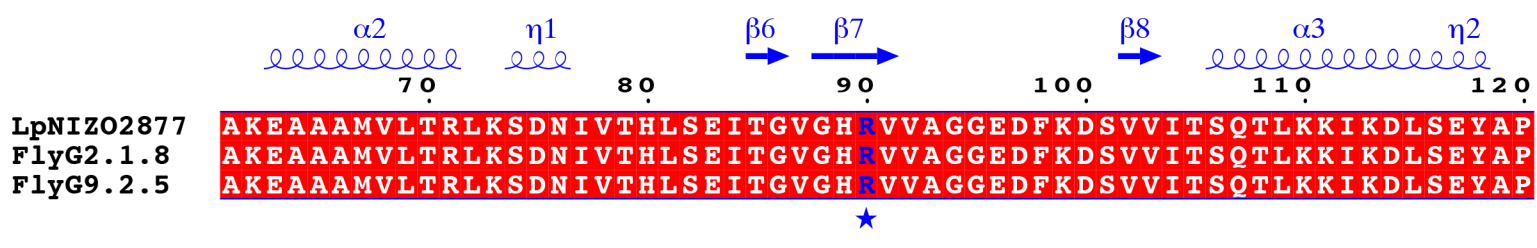
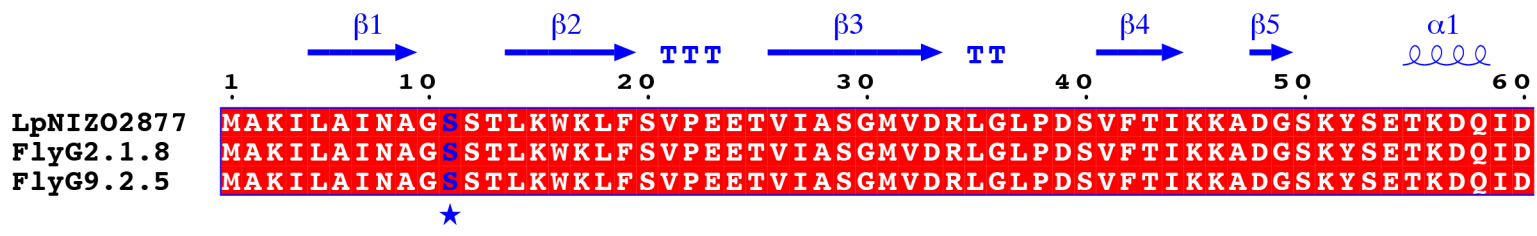
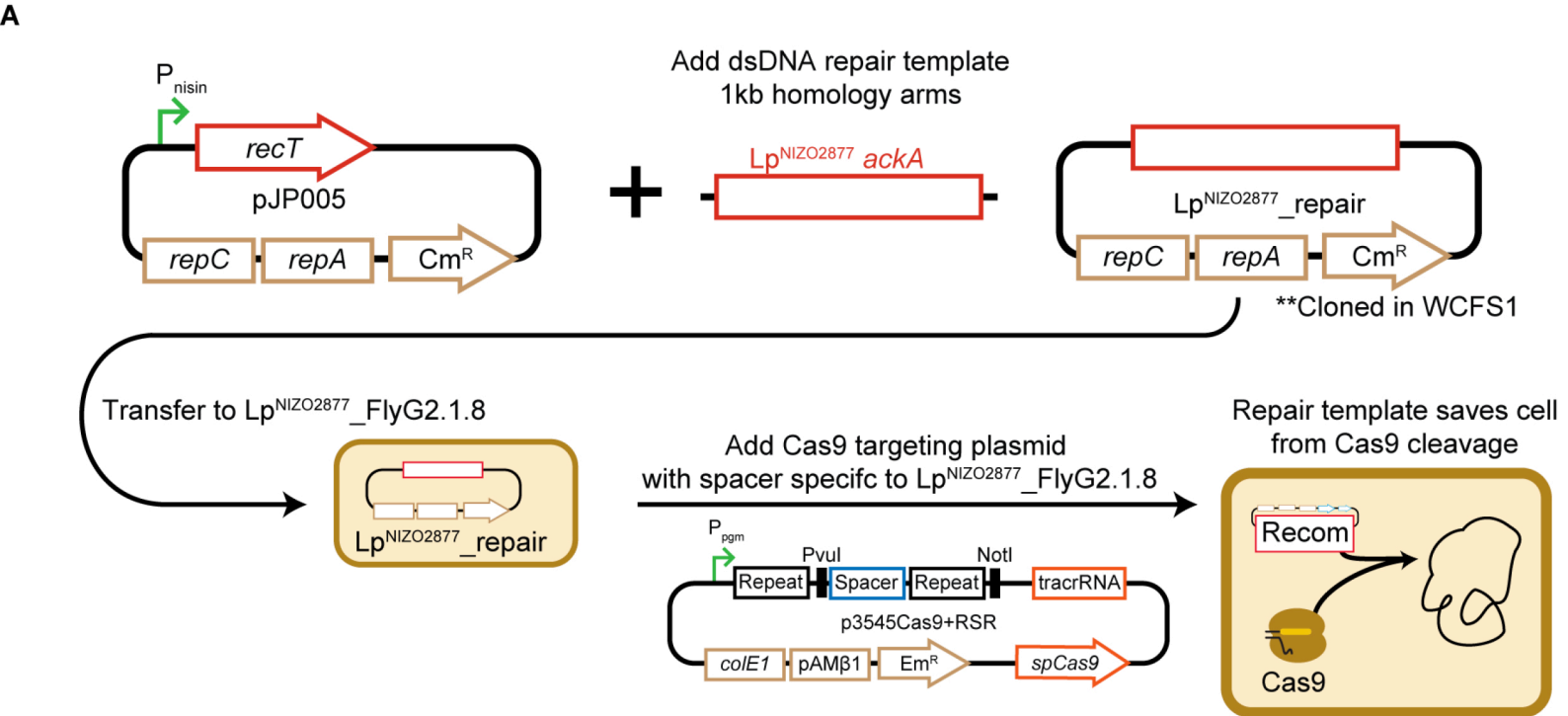
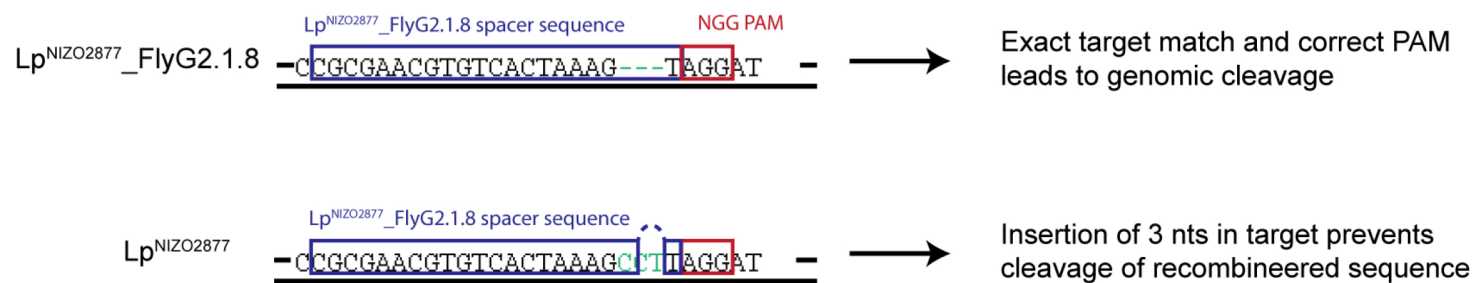


Figure S2

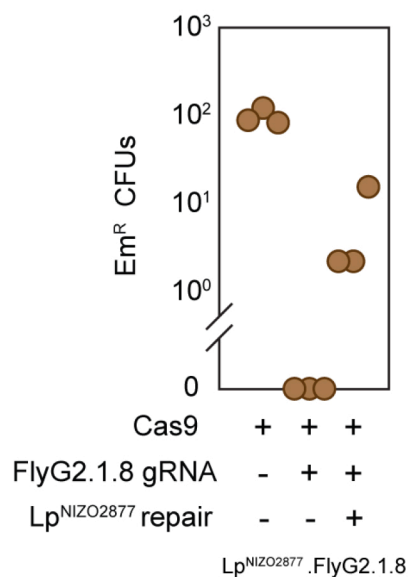
**Supplemental Figure 2 (related to Fig. 2): Sequence/structural analysis of *Lp*<sup>NIZO2877</sup> Acetate kinase A (AckA) protein aligned against the AckA of *Lp*<sup>NIZO2877</sup>-derived strains (FlyG2.1.8, FlyG9.2.5) evolved in *Drosophila* niche.** The secondary structure of the protein is indicated in blue above the sequence alignment. Catalytic residues of the predicted active site are shown in bold blue characters. The mutation sites are highlighted in pink and green for FlyG2.1.8 and FlyG9.2.5 strains respectively. The alignment was performed using Clustal Omega and drawn with ESPript.



**B**



**C**



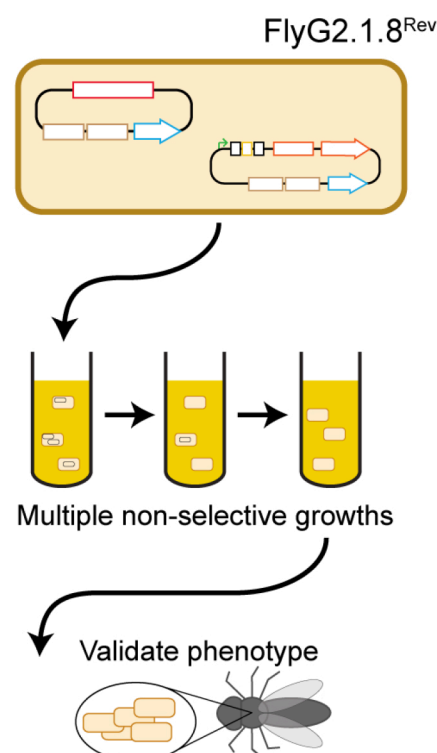
**D**

*ackA*

CCT

<i>Lp<sup>NIZO2877</sup></i>	---CCT---
<i>Lp<sup>NIZO2877</sup>.FlyG2.1.8</i>	-----
FlyG2.1.8 <sup>Rev</sup>	---CCT---
FlyG2.1.8 <sup>Rev1</sup>	No Amp <sup>1</sup>
FlyG2.1.8 <sup>Rev2</sup>	---CCT---
FlyG2.1.8 <sup>Rev3</sup>	-----
FlyG2.1.8 <sup>Rev4</sup>	---CCT---
FlyG2.1.8 <sup>Rev5</sup>	---CCT---
FlyG2.1.8 <sup>Rev6</sup>	---CCT---
FlyG2.1.8 <sup>Rev7</sup>	-----
FlyG2.1.8 <sup>Rev8</sup>	---CCT---
FlyG2.1.8 <sup>Rev9</sup>	---CCT---

**E**



**Figure S3**

**Supplemental Figure 3 (related to Fig. 3): CRISPR/Cas9 genome editing in *Lactobacillus plantarum* with a dsDNA repair template.**

(A) Construction of the repair template plasmid containing the dsDNA template. Following successful construct generation, cells containing the repair plasmid were transformed with the self-targeting Cas9 plasmid, thereby killing any cells that did not incorporate the repair template into the genome.

(B) Spacer design for targeting *ackA* in *Lp*<sup>NIZO2877</sup>\_FlyG2.1.8. The spacer will only successfully cleave *Lp*<sup>NIZO2877</sup>\_FlyG2.1.8, while allowing any edited survivors to evade cleavage due to a spacer mis-match and presence of a non-PAM.

(C) Transformation results after Cas9 self-targeting with the repair template plasmid. Presence of the repair template allowed for a total of 15 survivors clones to Cas9 killing.

(D) *ackA* locus sequencing results for 10 of the survivors. Two survivors contained the un-edited *ackA* gene in *Lp*<sup>NIZO2877</sup>.FlyG2.1.8, and one did not yield a PCR product (No Ampl.). Seven colonies contained the edited *ackA* sequence.

(E) Plasmid removal after editing. Successfully edited cells were passaged multiple times through non-selective media to remove the genome editing plasmids. After validation of plasmid removal, strains had their genomes sequenced and were analyzed for *in vivo* validation.

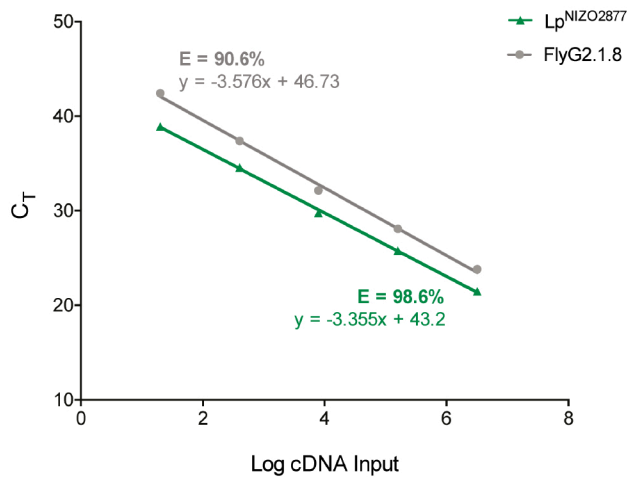
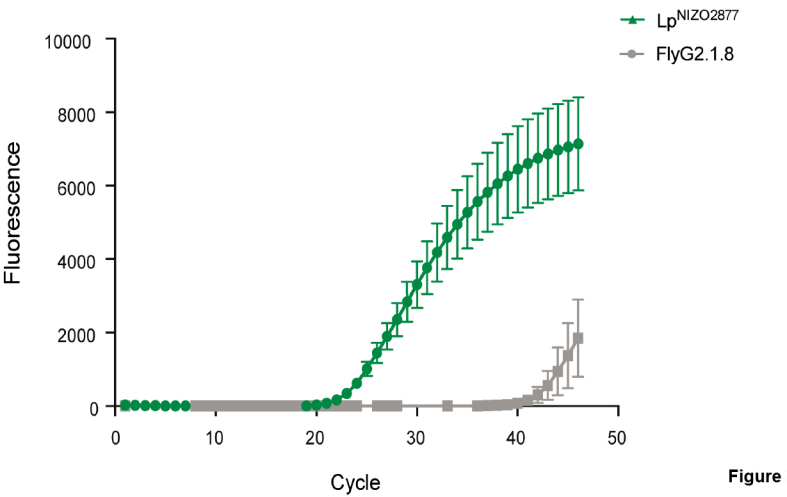
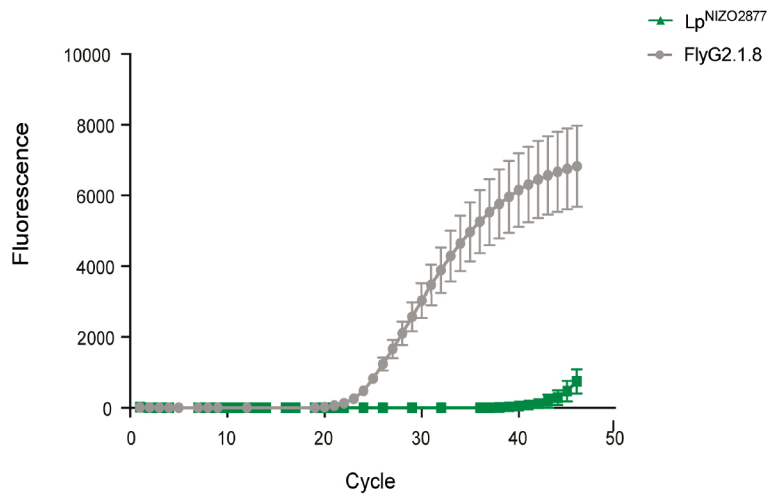
**A****B****C**

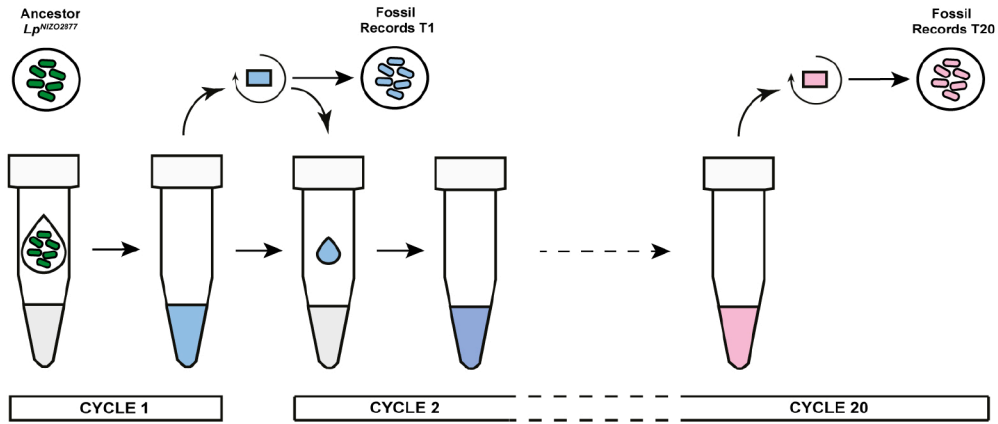
Figure S4

**Supplemental Figure 4 (related to Fig. 4): Development of two Real-Time PCR assays for the discrimination and quantification of *Lp*<sup>NIZO2877</sup> and *Lp*<sup>NIZO2877</sup>-evolved strain FlyG2.1.8.**

(A) Real-time PCR standard curves obtained from the amplification of *Lp*<sup>NIZO2877</sup> (green) and FlyG2.1.8 (grey) strains. The graph shows the interpolated standard curves using determined threshold cycles ( $C_T$ ) values and known template numbers for five standard samples. All points represent the mean of triplicate PCR amplifications. The respective efficiency values and curve equations are reported on the graph.

(B, C) Fluorescence amplification plots obtained from the amplification of *Lp*<sup>NIZO2877</sup> and FlyG2.1.8 strains using *Lp*<sup>NIZO2877</sup>-specific (B) and FlyG2.1.8 specific (C) Real-time assays.

**A**



**B**

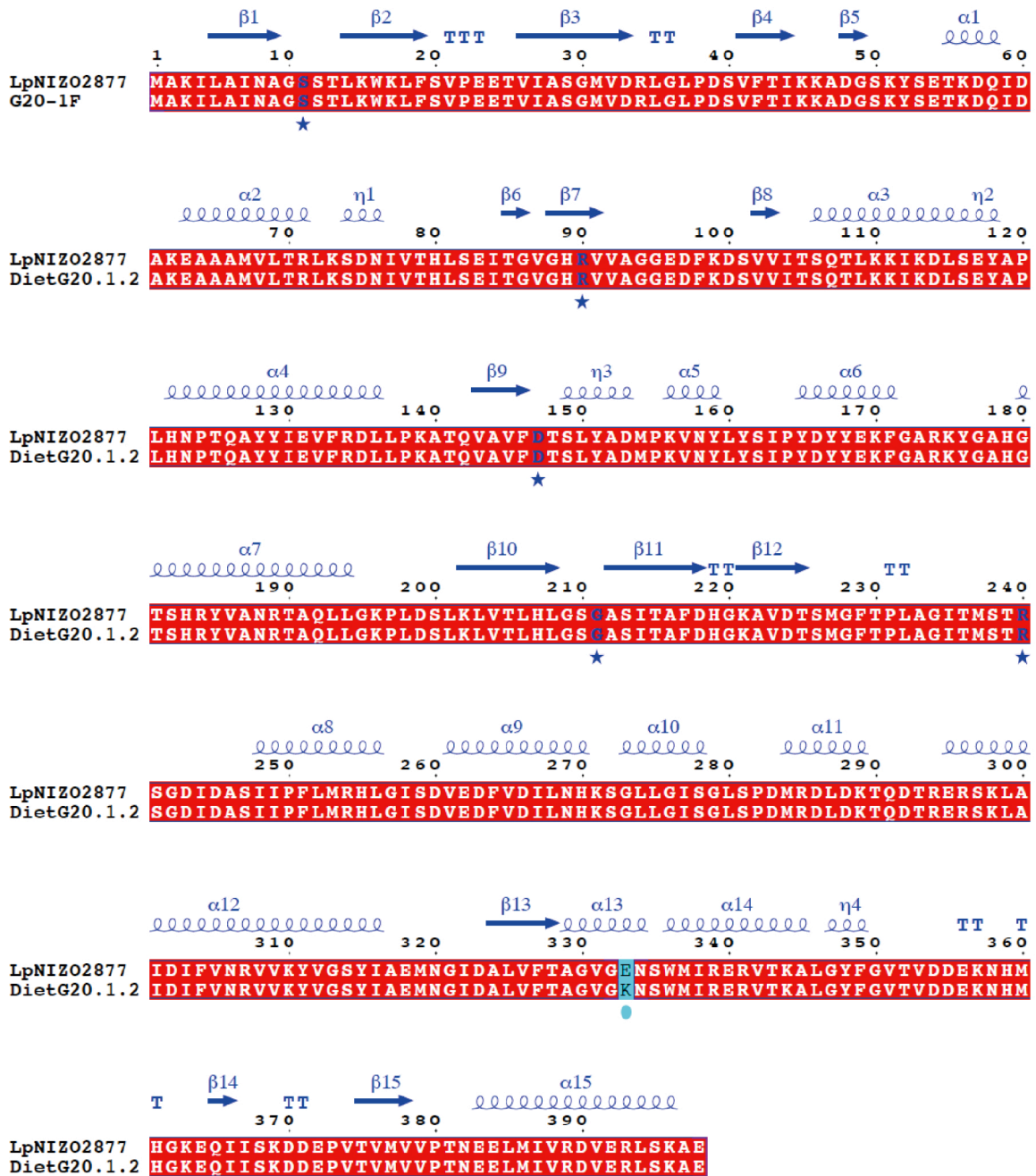


Figure S5

**Supplemental Figure 5 (related to Fig. 5): *L. plantarum* adaptive evolution (AE) in *Drosophila* diet without *Drosophila melanogaster*.**

(A) Rationale and schematic representation of the experimental setup. The ancestor ( $Lp^{NIZO2877}$ ) was added to sterile poor nutrient diet (Cycle 1). As soon as the microbial load reached the same value found on the 15 pupae used for propagating the bacterial population in the Niche adaptive evolution setup ( $10^7$  CFU/mL of diet; Figure S1A), part of the medium was crushed and transferred to a new sterile poor nutrient diet. Fossil records were isolated from the crushed medium at the end of each cycle. Cycle 2 followed the same experimental course as Cycle 1. *L. plantarum* experimental evolution on *Drosophila* diet lasted 20 cycles. Colour shading represents the evolution of the bacterial population during the experiment.

(B) Sequence/structural analysis of  $Lp^{NIZO2877}$  AckA protein aligned against AckA from  $Lp^{NIZO2877}$ -derived strain (DietG20.1.2) evolved in *Drosophila* diet. The secondary structure of the acetate kinase A protein is indicated in blue above the sequence alignment. The key catalytic residues of the predicted active sites are shown in bold blue characters. The mutation site is highlighted in cyan. The alignment was performed using Clustal Omega and drawn with ESPript.



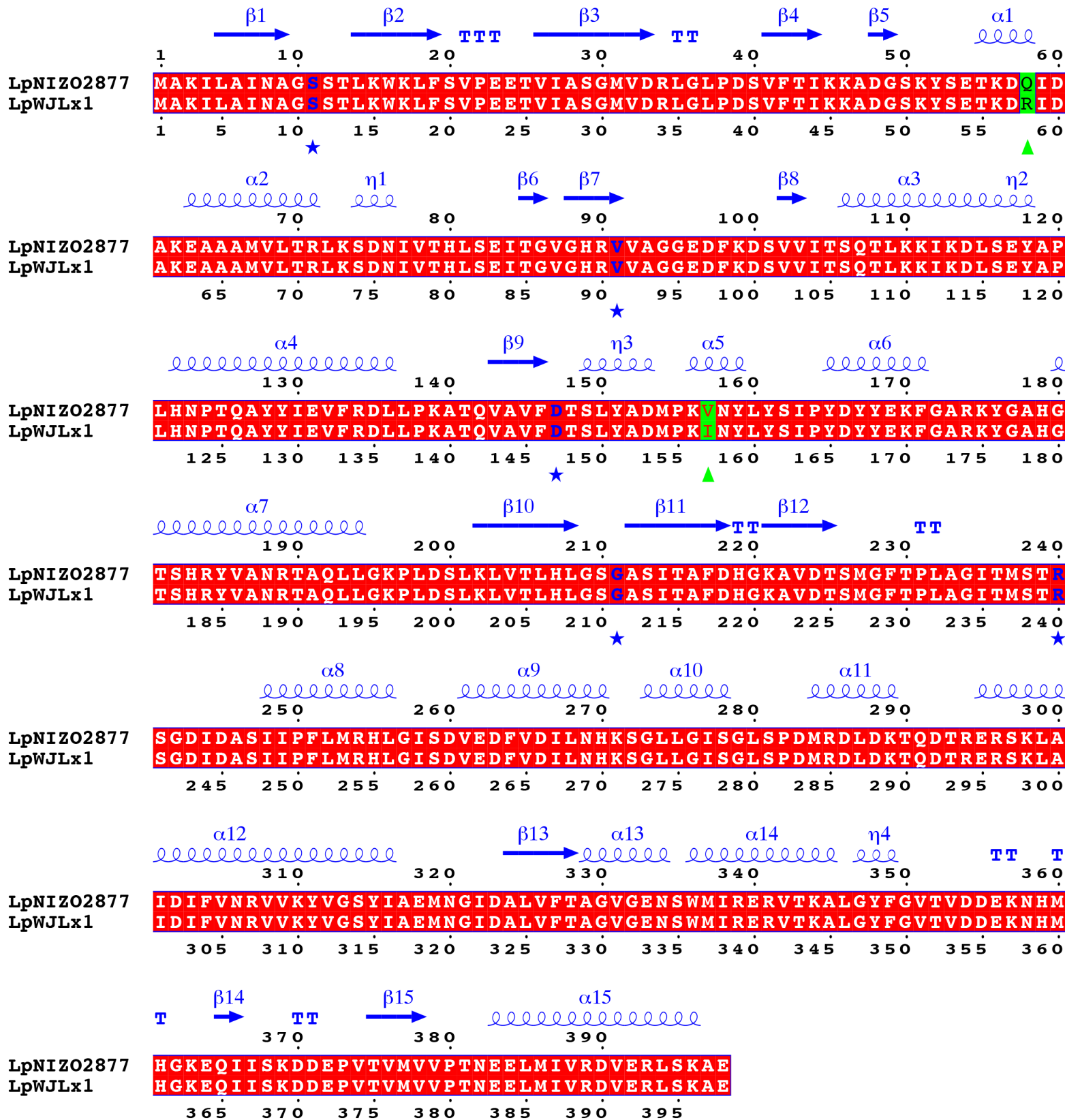


Figure S6

**Supplemental Figure 6 (related to Fig. 6): Sequence/structural analysis of *Lp*<sup>NIZO2877</sup> AckA protein aligned against AckA from *Lp*<sup>WJL</sup>.** The secondary structure of the acetate kinase A protein is indicated in blue above the sequence alignment. The key catalytic residues of the predicted active sites are shown in bold blue characters. The mutation sites are highlighted in green. The alignment was performed using Clustal Omega and drawn with ESPript.

### Supplemental tables Titles and Legends

**Table S1. Bacterial strains, Related to Figures 1, 2, 3, 5.** List of all *L. plantarum* strains used and sequenced in this study.

L. plantarum Strains	Description	Fly/Diet generation of isolation	Replicate	Accession Number	Reference
NIZO2877	Isolated from Vietnamese hotdog	-	-	LKHZ01000000	(Martino et al., 2015a)
WJL	Isolated from <i>Drosophila melanogaster</i> intestine	-	-	LKLZ00000000	(Martino et al., 2015b)
FlyG2.1.8	NIZO2877-evolved strain	2	1	PEBE00000000	This study
FlyG3.1.8	NIZO2877-evolved strain	3	1	PEGI00000000	This study
FlyG7.1.6	NIZO2877-evolved strain	7	1	PEGJ00000000	This study
FlyG8.1.1	NIZO2877-evolved strain	8	1	PEGK00000000	This study
FlyG8.1.2	NIZO2877-evolved strain	8	1	PEGL00000000	This study
FlyG9.1.4	NIZO2877-evolved strain	9	1	PEGM00000000	This study
FlyG10.1.5	NIZO2877-evolved strain	10	1	PEGN00000000	This study
FlyG10.1.9	NIZO2877-evolved strain	10	1	PEGO00000000	This study
FlyG11.1.2	NIZO2877-evolved strain	11	1	PEGP00000000	This study
FlyG11.1.6	NIZO2877-evolved strain	11	1	PEGQ00000000	This study
FlyG20.1.4	NIZO2877-evolved strain	20	1	PEGR00000000	This study
FlyG2.1.8Rev	NIZO2877-evolved strain	-	-	-	This study
FlyG9.2.5	NIZO2877-evolved strain	9	2	PEGS00000000	This study
FlyG11.2.6	NIZO2877-evolved strain	11	2	PEGT00000000	This study
FlyG20.2.6	NIZO2877-evolved strain	20	2	PEGU00000000	This study
DietG20.1.2	NIZO2877-evolved strain	20	1	PEGV00000000	This study
DietG20.2.2	NIZO2877-evolved strain	20	2	PEGW00000000	This study

**Table S1**

**Table S2. Summary of mutations detected across the experimental evolution of *L. plantarum*, related to Figures 1, 2, 3, 5.** List of all mutations detected in the *L. plantarum* experimental evolution replicates. §Locus tag refers to *L. plantarum* reference strain WCFS1 (Kleerebezem et al., 2003). nt: nucleotide; WGS: whole genome sequencing; SS: Sanger sequencing. Mutations identified by Sanger sequencing were confirmed from alignments of both forward and reverse reads.

Strain	Evolution	Replicate	Generation/	Detected mutation					
	Setup		Transfer	Gene/ Region	Locus Tag <sup>s</sup>	Annotation	Mutation	Position in Lp <sup>NIZ02877</sup>	Method
FlyG2.1.8	Niche	1	2	<i>ackA</i>	<i>lp_03010</i>	acetate kinase	deletion (Δ3)	2571613-5	WGS/SS
FlyG3.1.8	Niche	1	3	<i>ackA</i>	<i>lp_03010</i>	acetate kinase	deletion (Δ3)	2571613-5	WGS/SS
FlyG7.1.6	Niche	1	7	<i>int1</i>	-	intergenic region	1 nt substitution	504874	WGS/SS
				<i>cheY</i>	<i>lp_1544</i>	two-component system	1 nt substitution	1348923	WGS/SS
						response regulator			
<i>ackA</i>	<i>lp_03010</i>	acetate kinase	deletion (Δ3)	2571613-5	WGS				
FlyG8.1.1	Niche	1	8	<i>int1</i>	-	intergenic region	1 nt substitution	504874	WGS
				<i>cheY</i>	<i>lp_1544</i>	two-component system	1 nt substitution	1348923	WGS
						response regulator			
<i>ackA</i>	<i>lp_03010</i>	acetate kinase	deletion (Δ3)	2571613-5	WGS				
FlyG8.1.2	Niche	1	8	<i>int1</i>	-	intergenic region	1 nt substitution	504874	WGS
				<i>cheY</i>	<i>lp_1544</i>	two-component system	1 nt substitution	1348923	WGS
						response regulator			
<i>ackA</i>	<i>lp_03010</i>	acetate kinase	deletion (Δ3)	2571613-5	WGS				
FlyG9.1.4	Niche	1	9	<i>int1</i>	-	intergenic region	1 nt substitution	504874	WGS
				<i>cheY</i>	<i>lp_1544</i>	two-component system	1 nt substitution	1348923	WGS
						response regulator			
				<i>adhE</i>	<i>lp_3662</i>	alcohol dehydrogenase/ acetaldehyde dehydrogenase	1 nt substitution	2268660	WGS/SS
				<i>int2</i>	-	intergenic region	1 nt substitution	2456364	WGS/SS
<i>ackA</i>	<i>lp_03010</i>	acetate kinase	deletion (Δ3)	2571613-5	WGS				
FlyG10.1.5	Niche	1	10	<i>int1</i>	-	intergenic region	1 nt substitution	504874	WGS
				<i>cheY</i>	<i>lp_1544</i>	two-component system	1 nt substitution	1348923	WGS
						response regulator			
<i>ackA</i>	<i>lp_03010</i>	acetate kinase	deletion (Δ3)	2571613-5	WGS				
FlyG10.1.9	Niche	1	10	<i>int1</i>	-	intergenic region	1 nt substitution	504874	WGS
				<i>cheY</i>	<i>lp_1544</i>	two-component system	1 nt substitution	1348923	WGS
						response regulator			
<i>ackA</i>	<i>lp_03010</i>	acetate kinase	deletion (Δ3)	2571613-5	WGS				
FlyG11.1.2	Niche	1	11	<i>int1</i>	-	intergenic region	1 nt substitution	504874	WGS
				<i>cheY</i>	<i>lp_1544</i>	two-component system	1 nt substitution	1348923	WGS
						response regulator			
<i>ackA</i>	<i>lp_03010</i>	acetate kinase	deletion (Δ3)	2571613-5	WGS				
FlyG11.1.6	Niche	1	11	<i>int1</i>	-	intergenic region	1 nt substitution	504874	WGS
				<i>cheY</i>	<i>lp_1544</i>	two-component system	1 nt substitution	1348923	WGS
response regulator									

				-	<i>lp_0055</i>	<i>fumarate reductase, flavoprotein subunit</i>	1 nt substitution	2347322	WGS/SS
				<i>ackA</i>	<i>lp_03010</i>	<i>acetate kinase</i>	deletion (Δ3)	2571613-5	WGS
FlyG20.1.4	Niche	1	20	<i>pstB</i>	<i>lp_0749</i>	<i>phosphate ABC transporter</i>	1 nt substitution	120791	WGS/SS
						<i>ATP-binding protein</i>			
				-	<i>lp_0797</i>	<i>exoribonuclease II</i>	1 nt substitution	177140	WGS/SS
				<i>int1</i>	-	<i>intergenic region</i>	1 nt substitution	504874	WGS
				-	<i>lp_2499</i>	<i>ABC transporter</i>	1 nt substitution	947607	WGS
						<i>ATP-binding protein/permease</i>			
				-	<i>lp_1258</i>	<i>LysR family transcriptional regulator</i>	1 nt substitution	1105664	WGS/SS
				<i>cheY</i>	<i>lp_1544</i>	<i>two-component system</i>	1 nt substitution	1348923	WGS
						<i>response regulator</i>			
<i>int3</i>	-	<i>intergenic region</i>	1 nt substitution	1736935	WGS/SS				
<i>ackA</i>	<i>lp_03010</i>	<i>acetate kinase</i>	deletion (Δ3)	2571613-5	WGS				
FlyG9.2.5	Niche	2	9	<i>int4</i>	-	<i>intergenic region</i>	1 nt substitution	1982853	WGS/SS
				-	<i>lp_0197</i>	<i>cell surface protein precursor; LPXTG-motif cell wall anchor</i>	deletion (Δ6)	2471707-12	WGS/SS
				<i>ackA</i>	<i>lp_03010</i>	<i>acetate kinase</i>	1 nt substitution	2571025	WGS/SS
FlyG11.2.6	Niche	2	11	<i>int4</i>	-	<i>intergenic region</i>	1 nt substitution	1982853	WGS
				-	<i>lp_0197</i>	<i>cell surface protein precursor; LPXTG-motif cell wall anchor</i>	deletion (Δ6)	2471707-12	WGS
				<i>ackA</i>	<i>lp_03010</i>	<i>acetate kinase</i>	1 nt substitution	2571025	WGS
FlyG20.2.6	Niche	2	20	<i>cheY</i>	<i>lp_1544</i>	<i>two-component system</i>	1 nt substitution	1348886	WGS/SS
						<i>response regulator</i>			
				-	<i>lp_2212</i>	<i>NADH-flavin reductase</i>	1 nt substitution	1937136	WGS
				<i>int4</i>	-	<i>intergenic region</i>	1 nt substitution	1982853	WGS
				-	<i>lp_0197</i>	<i>cell surface protein precursor; LPXTG-motif cell wall anchor</i>	deletion (Δ6)	2471707-12	WGS
<i>ackA</i>	<i>lp_03010</i>	<i>acetate kinase</i>	1 nt substitution	2571025	WGS				
DietG20.1.2	Diet	1	20	<i>ackA</i>	<i>lp_03010</i>	<i>acetate kinase</i>	1 nt substitution	2571576	WGS/SS
DietG20.2.2	Diet	2	20	<i>int5</i>	-	<i>intergenic region</i>	1 nt substitution	2313069	WGS/SS
				<i>ackA</i>	<i>lp_03010</i>	<i>acetate kinase</i>	1 nt substitution	2571576	WGS/SS
				<i>int6</i>	-	<i>intergenic region</i>	1 nt substitution	1736935	WGS/SS

**Table S2**

**Table S3. Metabolomic dataset of *Drosophila* diet inoculated with *Lp*<sup>NIZO2877</sup> and FlyG2.1.8 separately, Related to Figure 6.** Table of metabolites resulted to be significantly different between *Lp*<sup>NIZO2877</sup>- and FlyG2.1.8-associated *Drosophila* diets based on two-sided t-tests ( $p < 0.05$ ). Fold-changes (FC) are calculated with the ratio between means of *Lp*<sup>NIZO2877</sup> and FlyG2.1.8 replicates for each metabolite. Metabolites with a positive FC are overrepresented in FlyG2.1.8-associated samples and those with a negative FC are underrepresented in FlyG2.1.8-associated samples. FC detail: If  $\text{mean}(\text{FlyG2.1.8}) > \text{mean}(\text{Lp}^{\text{NIZO2877}})$ ,  $\text{FC} = \text{mean}(\text{FlyG2.1.8})/\text{mean}(\text{Lp}^{\text{NIZO2877}})$ ; If  $\text{mean}(\text{Lp}^{\text{NIZO2877}}) > \text{mean}(\text{FlyG2.1.8})$ ,  $\text{FC} = - \text{mean}(\text{Lp}^{\text{NIZO2877}})/\text{mean}(\text{FlyG2.1.8})$









**Table S4. Primers, Related to Figures 1, 2, 4, 5.** List of DNA oligonucleotide primers used in this study.

Name	DNA sequence (5'-3')	Annealing t°	Reference
ackA_F	TAAGACGCAAGATACCCGTG	62	This study
ackA_R	ACGCACAATCATCAGCTCTT	62	This study
int1_F	TTTAAAACATCGGCTACGGAAG	63	This study
int1_R	TTATTTATCGCCCGCCAAGA	62	This study
cheY_F	CTCGCTCGTGATGTCTTACT	59	This study
cheY_R	TAACAGCACTAGCCACGTTC	60	This study
adhE_F	GGCTCCCTTAATTCACAAAGG	62	This study
adhE_R	ATCCTTGAAAGCTAACCGGG	63	This study
int2_F	AGCGATATCCTCCTGTGAAC	60	This study
int2_R	CGCGTTGTGCTAGCTAATTT	61	This study
lp_0055_F	GCCATGTGTGTAAACGTGTC	61	This study
lp_0055_R	GTGATCCAAGGGGTCCAAT	62	This study
pstB_F	AAGACAATTAAGGACGGTTCAC	60	This study
pstB_R	TGGTCGATAAGCCACATTCTT	62	This study
lp_0797_F	ATTTTCAAAGTGTGATTCGGT	63	This study
lp_0797_R	ACTTTTCGATCATTGTTTCAGC	63	This study
lp_1258_F	GGCGTTAACGGATGAATCTAA	62	This study
lp_1258_R	GACCTTGTTCTCCGCAGT	60	This study
int3_F	TTCTTCACACTTGGTTTTTCGT	62	This study
int3_R	GCGAATGTCATAGTCGGAGA	62	This study
int4_F	GACGATTAGACTAGTCGCGG	61	This study
int4_R	CATTCAAGCTGATATTGTCGGT	62	This study
lp_0197_F	CCGCCATGTTGACATTGATT	63	This study
lp_0197_R	CGTTGTGCTAGATGATTGGG	63	This study
ackA2_F	GTGAAATCACTGGGGTTGGT	63	This study
ackA2_R	ACCATGATCAAAAGCCGTGA	65	This study
int5_F	CAACGCAGAAGTTACATGCT	60	This study
int5_R	GCAATCCTGCGTTCATCATC	62	This study
int6_F	GTTTCGACGTTATTTACGGAT	62	This study
int6_R	CATCACGAATAGGTGCCAAA	63	This study
16S_UniF	GTGSTGCAYGGYTGTCGCA	70	(Packey et al., 2013)
16S_UniR	ACGTCRTCCMCACCTTCCTC	68	(Packey et al., 2013)
ackA_NIZO	CGAACGTGTCACTAAAGCCTT	63	This study
ackA_FlyG2	GCGAACGTGTCACTAAAGTAGG	62	This study
ackA_R_RT	CACGCACAATCATCAGCTCT	63	This study

**Table S4**

**Table S5. Plasmids used in this work, Related to Figure 3.** List of plasmids used to engineer *Lp*<sup>NIZO2877</sup> with CRISPR-Cas9.

Plasmid	Description	Resistance	Source	Stock
pJP005	RecT protein under a nisin-inducible promoter, without nisR and nisK genes	Cm	(Van Pijkeren and Britton, 2012)	CB651
pMSP3545	Gram-positive bacterial shuttle vector for nisin-controlled inducible expression	EmR	Addgene CN#46888	pCB574
pCas9	Plasmid containing <i>Streptococcus pyogenes</i> Cas9 and its tracrRNA	Amp	Addgene CN# 42876	pCB339
p3545Cas9	Shuttle vector containing <i>S. pyogenes</i> Cas9 and its tracrRNA	EmR	This work	pCB577
p3545Cas9+RSR	Shuttle vector containing <i>S. pyogenes</i> Cas9, tracrRNA, and a repeat-spacer-repeat array for targeting	EmR	This work	pCB578
p3545Cas9+ackA_G2 target	Cas9 shuttle vector targeting the acetate kinase gene in NIZO.G2	EmR	This work	pCB579
pJP005_NIZO ackA	pJP005 vector with repair template for the ackA target	Cm	This work	CB711

**Table S5**

**Table S6. Oligonucleotides used to engineer *Lp*<sup>NIZO2877</sup> with CRISPR-Cas9, Related to Figure 3.**



Shorthand	Name	Sequence
oRL1	pCas9.Gibson.fwd	GATGATAAGCTGTCCAAACATGAGAATTCCTTACGAAATCATCCTGTGGAGCTTAG
oRL2	pCas9.Gibson.rev	ATTTTTAGGATAAAGTCTGCCCCACCTTTTTCAGTCACCTCCTAGCTGACTC
oRL3	pMSP3545.Gibson.fwd	ATTGATTTGAGTCAGCTAGGAGGTGACTGAAAAAGGTGGGCAGAAAGTTATCCTAA
oRL4	pMSP3545.Gibson.rev	CCTACTAAGCTCCACAGGATGATTTTCGTAAGGAATTCATGTTTGGACAGCTTATCATCG
oRL5	gBlockRSR.Gibson.fwd	TTGGTTCAAAGAAAGCTTGAGCTCTCGAGTCAGGGGTACCGATCA
oRL6	gBlockRSR.Gibson.rev	GGAGGCACTCACCATGGGTACTGCAAATGTCTGCAATGAGTTGATCGC
oRL7	Acet.Kin.pJP005.f	ATTTACTAGTGTTTTTTCATCATGATCGCCTC
oRL8	Acet.Kin.pJP005.r	TCGCGAGCTCACAACGCATCTATCAGGAAG
oRL9	pJP005.seq.rev	TGATTGTTCTATCGAAAGCGAA
oRL10	pJP005.seq.fwd	AATTGCTAGAAGGATTTCAAAGTC
oRL11	AcetKin.Outer.fwd	GGAGGAGGACAGCAAAGCC
oRL12	AcetKin.Outer.rev	TGCGCGTCAAAACGTTTGTGTT
oRL13	G2.Reversion.sgRNA.fwd	CCACCGCGAACGTGTCACATAAAGTGTITTAGAGCTATGCTGTTTTGAATGGTCCCAAAACATCGATCGAAGC
oRL14	G2.Reversion.sgRNA.rev	GGCCGCTTCGATCGATGTTTTGGGACCATTCAAACAGCATAGCTCTAAAACACTTATGACACGTTCCGGTGGAT

**Table S6**