

## *Supplementary Material*

**Table S1.** 16S rRNA gene sequences (reads) obtained via next-generation sequencing from 18 soil samples before and after processing with DADA2 package v1.10.1

Sample ID	Number of raw reads	Forward reads after Dada2 cleaning	Reverse reads after Dada2 cleaning
S1	123 869	63 357	58 681
S2	131 245	58 830	60 679
S3	103 711	41 709	43 458
S4	111 339	56 431	59 223
S5	116 605	47 202	46 549
S6	159 638	89 881	85 511
S7	108 647	57 658	59 709
S8	131 019	69 780	68 206
S9	129 506	54 719	49 098
S10	105 476	38 149	41 579
S11	106 222	43 748	43 951
S12	103 640	40 121	37 806
S13	144 135	58 821	49 585
S14	103 131	52 692	55 162
S15	107 070	42 725	37 965
S16	123 938	68 436	66 687
S17	125 726	52 147	46 135
S18	125 565	51 579	45 595
Total reads (Forward and Reverse)	4 320 964	1 975 970	1 943 564

**Table S2.** Physicochemical properties and bacterial diversity metrics of the soil samples subjected to *Listeria* sp. detection via culture dependent and independent methods.

Sample ID	Sample source	<i>Listeria monocytogenes</i> isolation (serovar) <sup>1</sup>	<i>Listeria spp.</i> culture independent detection <sup>2</sup>	Soil physicochemical properties											Sample microbiological diversity <sup>2</sup>		
				*pH	EC (µS cm <sup>-1</sup> )	*H (g g <sup>-1</sup> )	S (g g <sup>-1</sup> )	C (g g <sup>-1</sup> )	N (g g <sup>-1</sup> )	C:N	Sand (%)	Silt (%)	Clay (%)	Texture class <sup>3</sup>	Chao1 Index	Simpson Index	Shannon Index
S1	CL	-	+ (9 reads)	5.2	228	0.0207	0.0011	0.0231	0.0024	9.5	33.3	39.9	26.8	Loam	6432.47	0.999	8.155
S2	CL	-	+ (19 reads)	5.6	75	0.0217	0.0011	0.0212	0.0022	9.6	72.0	24.0	4.0	Sandy Loam	6639.05	0.998	8.061
S3	CL	-	+ (2 reads)	5.4	149	0.0198	0.0020	0.0202	0.0022	9.3	48.0	26.0	26.0	Sandy clay loam	7206.06	0.999	7.651
S4	CL	-	+ (4 reads)	5.6	87	0.0241	0.0010	0.0245	0.0029	8.4	60.0	19.2	20.8	Sandy clay loam	7248.94	0.999	8.024
S5	DB	4b	+ (2 reads)	7.8	27900	0.0194	0.0045	0.0704	0.0078	9.1	86.0	5.0	9.0	Loamy Sand	7760.02	0.998	7.527
S6	SH	4b	+ (6 reads)	6.1	480	0.0143	0.0025	0.0420	0.0035	11.9	73.3	17.1	9.6	Sandy Loam	7307.38	0.998	7.574
S7	SH	-	+ (2 reads)	5.5	500	0.0158	0.0018	0.0370	0.0032	11.6	56.8	27.5	15.7	Sandy Loam	7721.71	0.999	8.232
S8	SH	-	+ (4 reads)	6.1	430	0.0168	0.0016	0.0306	0.0103	3.0	54.0	39.3	6.7	Sandy Loam	7607.56	0.999	8.196
S9	DB	1/2b	+ (3 reads)	7.9	45000	0.0313	0.0061	0.1470	0.0150	9.8	65.9	9.3	24.8	Sandy clay loam	8458.93	0.999	8.013
S10	DB	1/2b	-	7.7	38100	0.0268	0.0076	0.1250	0.0137	9.1	57.9	15.3	26.8	Sandy clay loam	7556.58	0.998	7.664
S11	DB	4b	+ (3 reads)	8.0	6100	0.0333	0.0078	0.1654	0.0172	9.6	37.6	25.8	36.5	Clay loam	8112.78	0.997	7.550
S12	DB	1/2b	-	8.2	54500	0.0367	0.0089	0.1898	0.0199	9.6	58.4	5.4	36.2	Sandy clay	7678.87	0.998	7.569
S13	DB	1/2b	-	8.1	57000	0.0311	0.0082	0.1551	0.0178	8.7	53.2	13.2	33.6	Sandy clay loam	8299.71	0.998	7.721
S14	DB	-	+ (1 reads)	8.4	31300	0.0342	0.0078	0.1729	0.0182	9.5	65.9	5.9	28.2	Sandy clay loam	5979.21	0.999	7.740
S15	DB	4b	-	7.3	29800	0.0214	0.0038	0.0800	0.0085	9.4	72.0	5.9	22.2	Sandy clay loam	7733.04	0.997	7.280
S16	SH	-	+ (3 reads)	6.3	189	0.0153	0.0021	0.0336	0.0026	13.1	58.5	33.9	7.6	Sandy loam	7761.70	0.999	8.270
S17	DB	1/2b	-	8.7	41900	0.0269	0.0059	0.1311	0.0130	10.1	64.6	7.2	28.2	Sandy clay loam	8239.62	0.998	7.890
S18	DB	1/2b	-	8.0	59900	0.0322	0.0089	0.1510	0.0170	8.9	69.3	9.1	21.6	Sandy clay loam	8175.26	0.999	7.896

1: Based on multiplex PCR from isolated colonies

2: Based on 16S rRNA amplicon metagenomics from total soil DNA sequencing.

3: Based on the field guide to soil texture classes from the United States Department of Agriculture (USDA)

-: Negative detection/isolation

+: Positive detection

DB: Compacted soil of a dairy barn floor

SH: Soil collected near a slaughterhouse

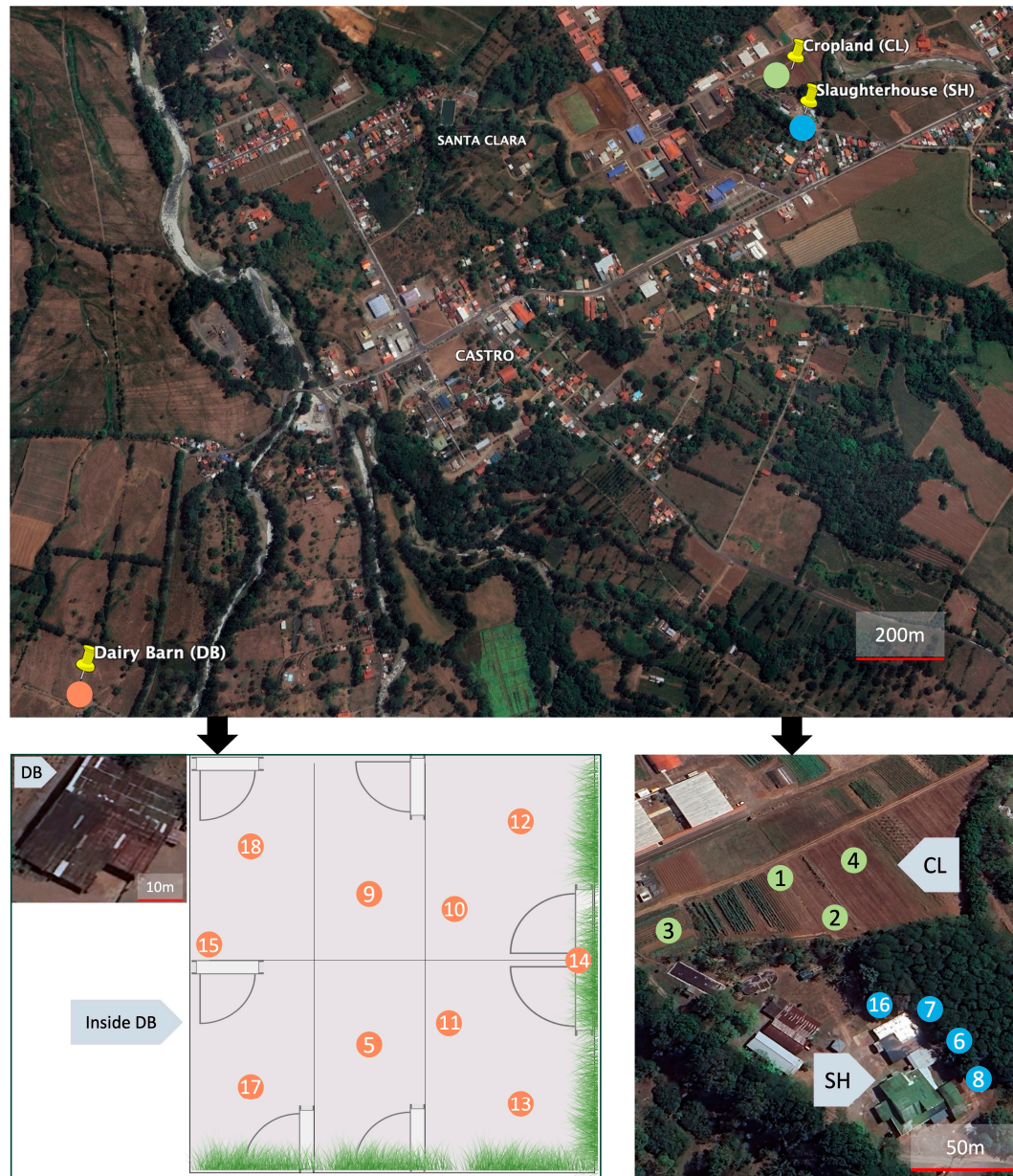
CL: Soil collected from croplands

\*Statistical significance using ANOVA of the Canonical Correspondence Analysis (CCA) with physicochemical factors as variables, p=0.002

**Table S3.** Analysis of variance (ANOVA) of the Canonical Correspondence Analysis (CCA) with physicochemical factors as variables.

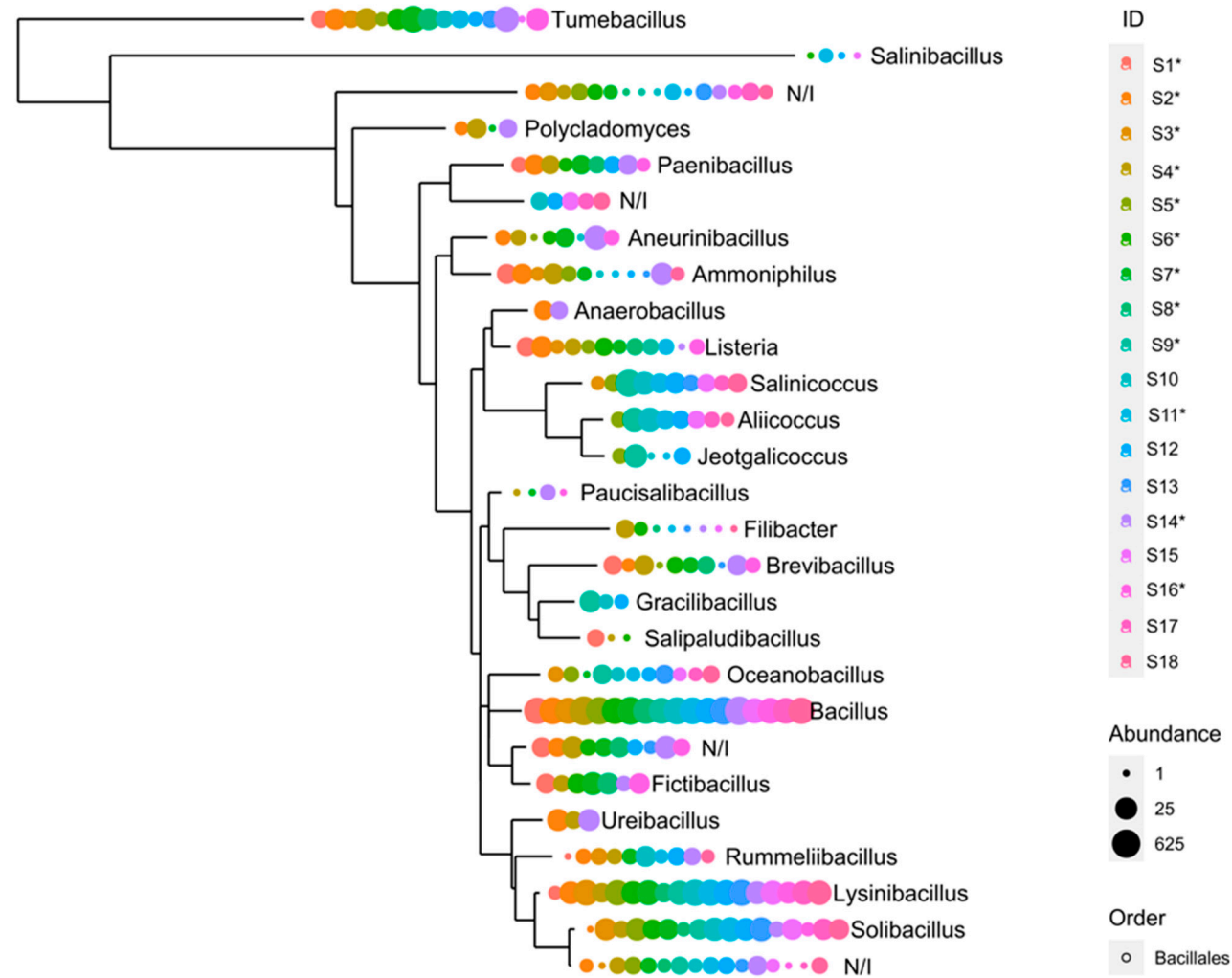
Variable	Df	ChiSquare	F	Pr(>F)
pH	1	0.5979	2.7648	0.002**
EC	1	0.1931	0.8929	0.569
CNS	1	0.1426	0.6594	0.888
H	1	0.5165	2.3885	0.002**
C:N	1	0.2285	1.0568	0.399
Sand	1	0.2459	1.1370	0.265
Silt	1	0.2687	1.2427	0.217
Clay	1	0.2318	1.0722	0.361
Residual	9	1.9463	NA	NA

Significance levels: \*\*\*:  $P < 0.001$ ; \*\*:  $P < 0.01$ ; \*:  $P < 0.05$

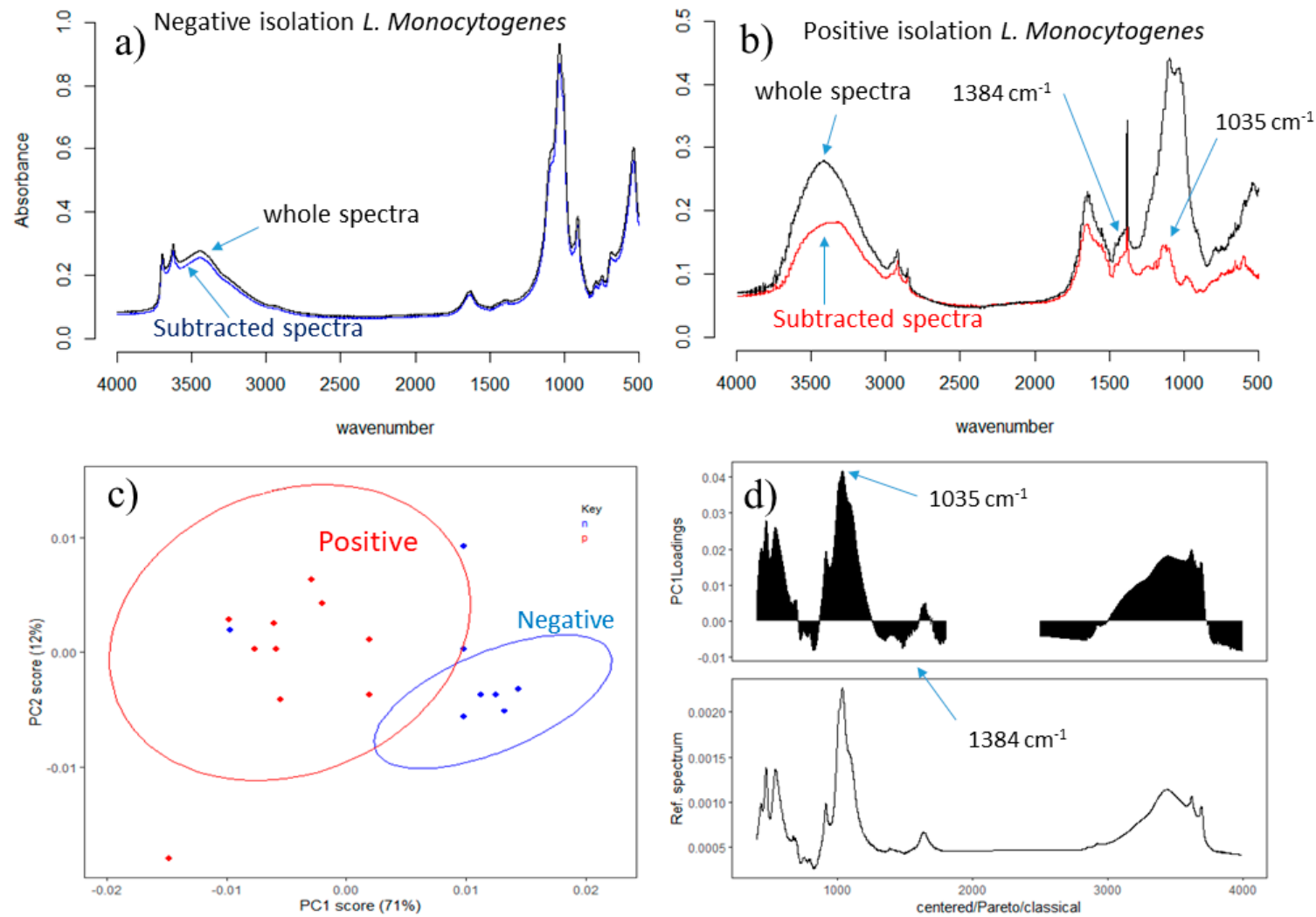


**Figure S1.** Sampling sites included in this study. The image on top shows the three sampled areas: a dairy barn (DB) where the animals were kept for feeding and/or milking; a slaughterhouse holding pen (SH), where livestock (pigs and cattle) are kept before sacrifice; and a nearby cropland (CL) of plantain, bean, and cassava crops and a fallow field. The images at the bottom show each sampling point at the different locations. *Satellite images obtained through Google Earth*





**Figure S2.** Phylogenetic tree of genera belonging to the order Bacillales based on the Illumina sequencing of the 16S rRNA gene showing the total abundance of each unique amplicon sequence variant (ASV) in 18 soil samples. \*Isolates positive for *Listeria* spp. ASV detection (CL: S1-S4; DB: S5, S9-15, S17-S18; SH: S6-S8, S16).



**Figure S3.** Transformed Fourier spectroscopic analysis of soil samples with the positive and negative isolation of *L. monocytogenes*, a) S3 as an example of negative isolation, b) S13 as an example of positive isolation, c) principal component analysis for subtracted spectra of OM-enriched samples and d) loading of the second component PC2 (12%) and its reference spectra.