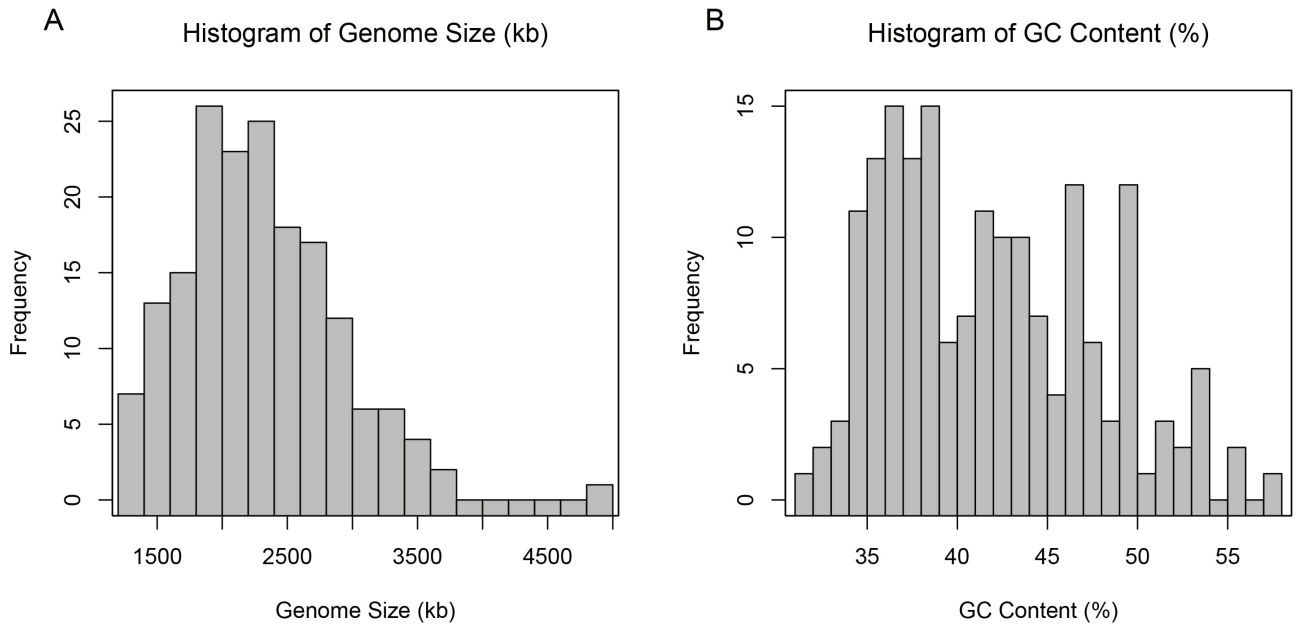
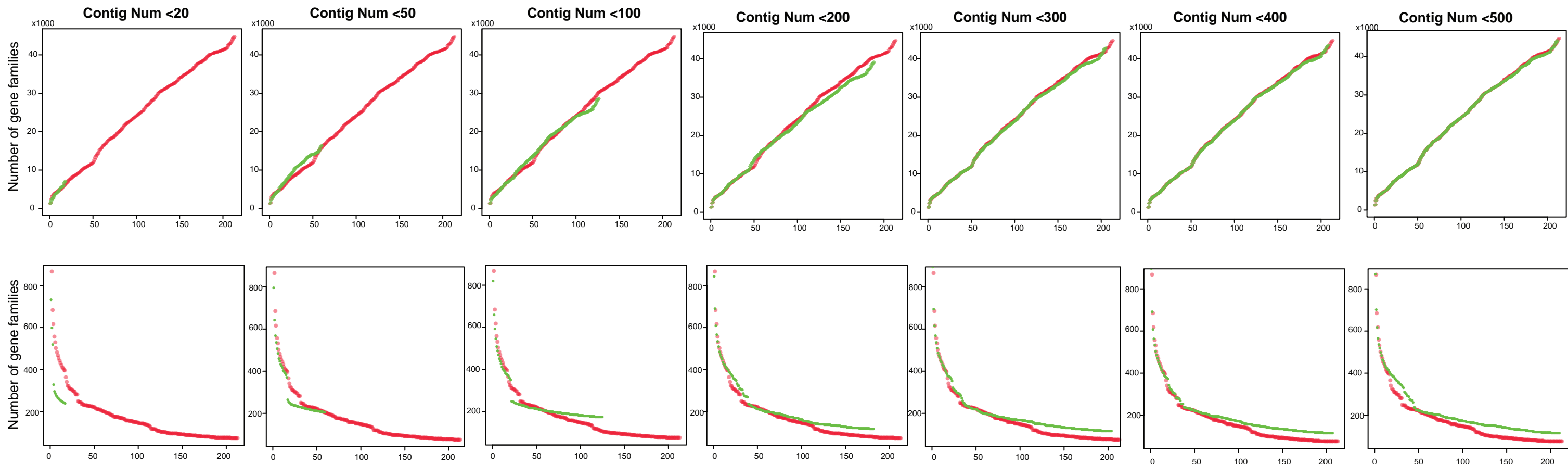


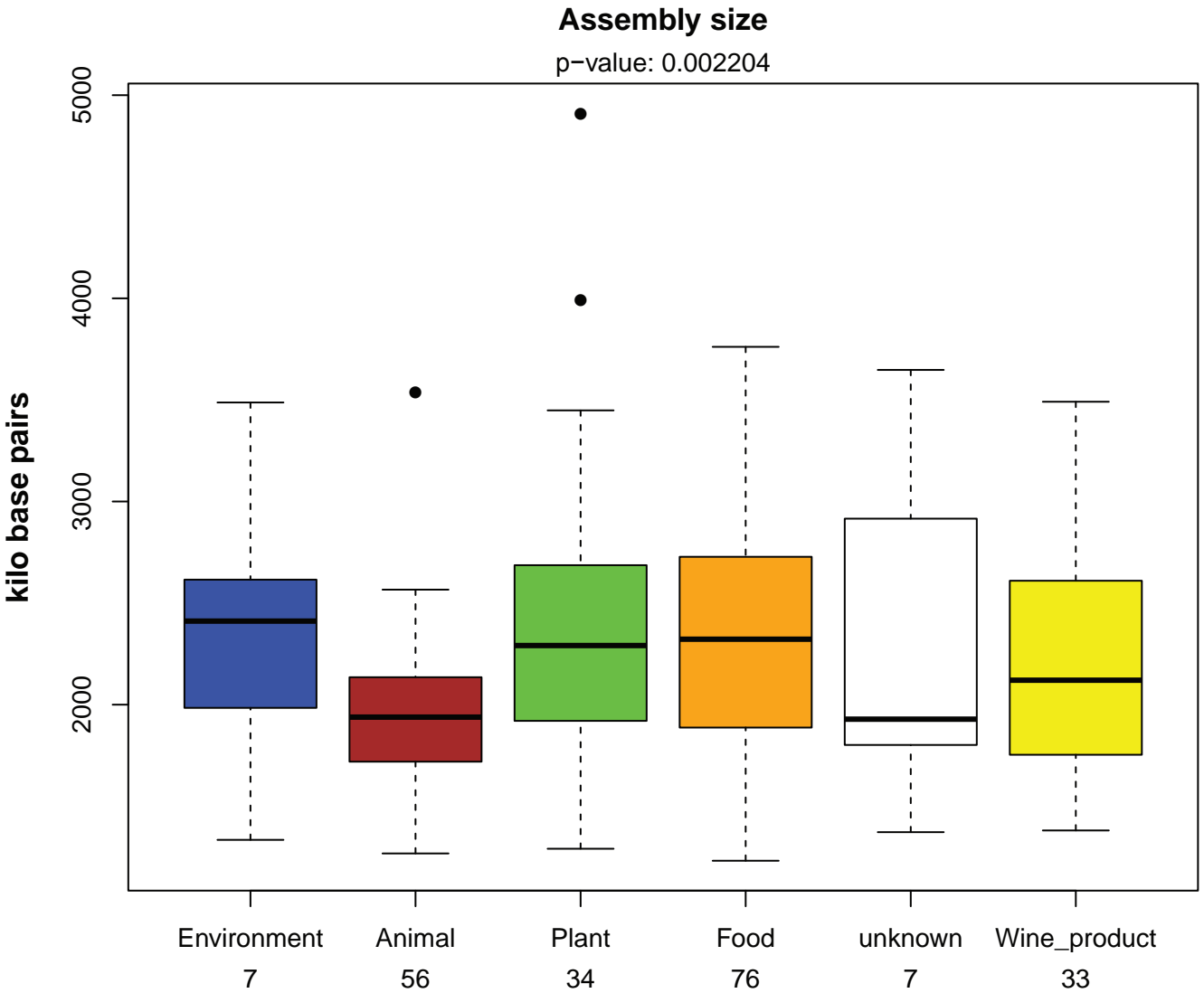
Supplementary Figures



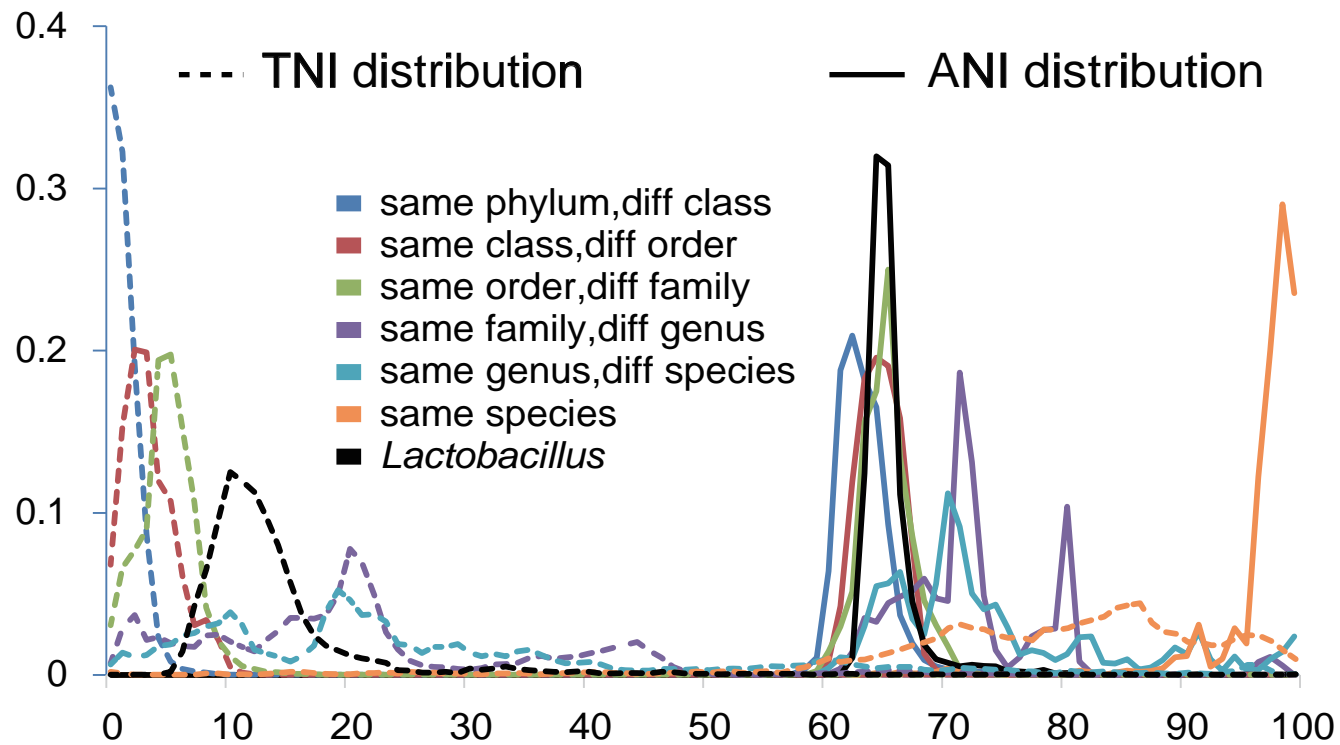
Supp. Figure 1. Histograms of genome size distribution (A) and GC% (B) for 175 *Lactobacillus* genomes.



Supp. Figure 2. Sizes of the pan-genome (top) and core-genomes (bottom) in all 213 genomes (red) and in all genomes with less than 20, 50, 100, 200, 300, 400 and 500 contigs (green).



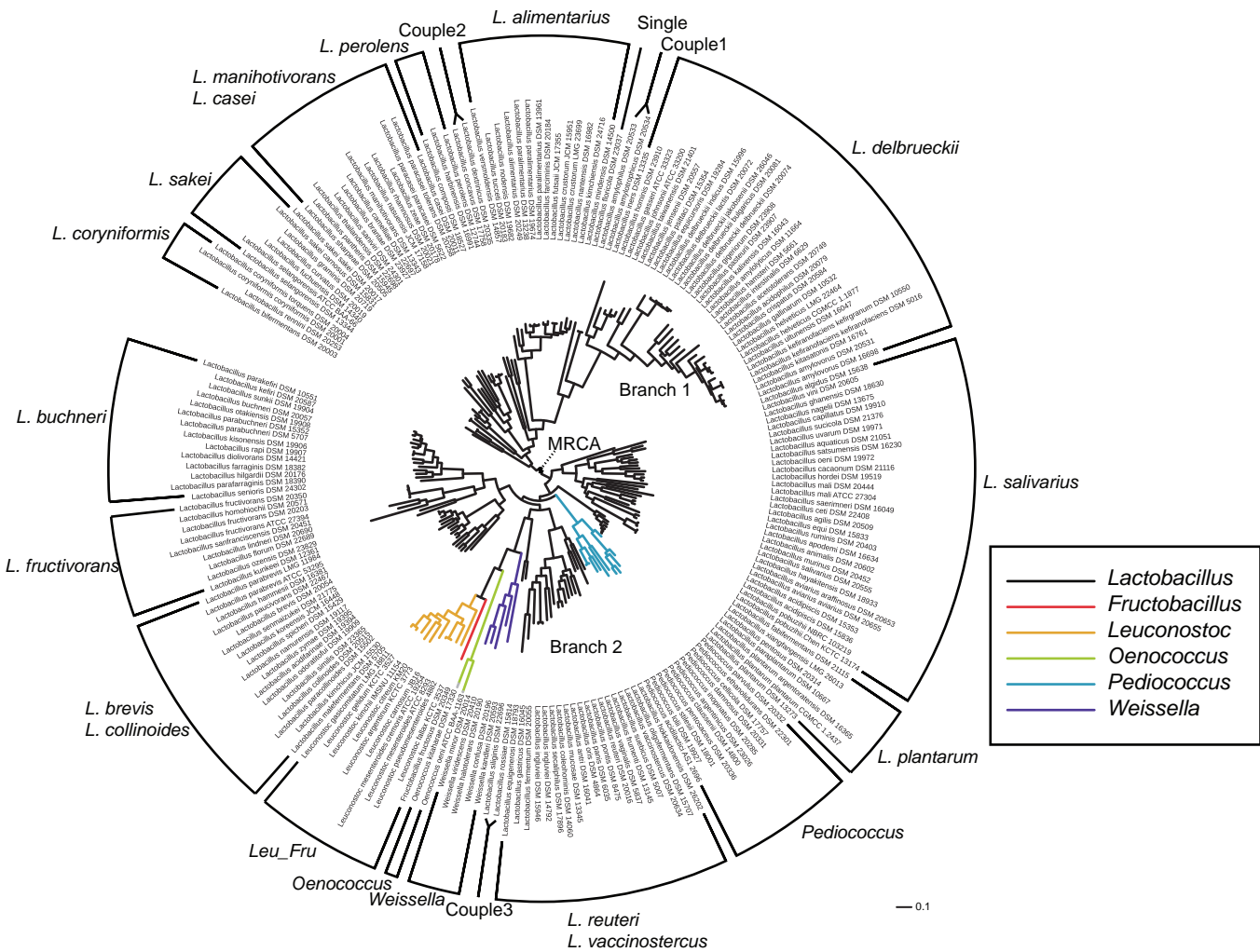
Supp. Figure 3. Analysis of genome assembly size as a function of niche. Niche categories are plotted on the x-axis and genome assembly size in kilobase pairs is plotted on the y-axis. Box-plots represent a five-point summary of the data in the following order (from bottom to top); minimum, first quartile, median, third quartile and maximum. Outliers are represented as individual points above or below the boxplot.



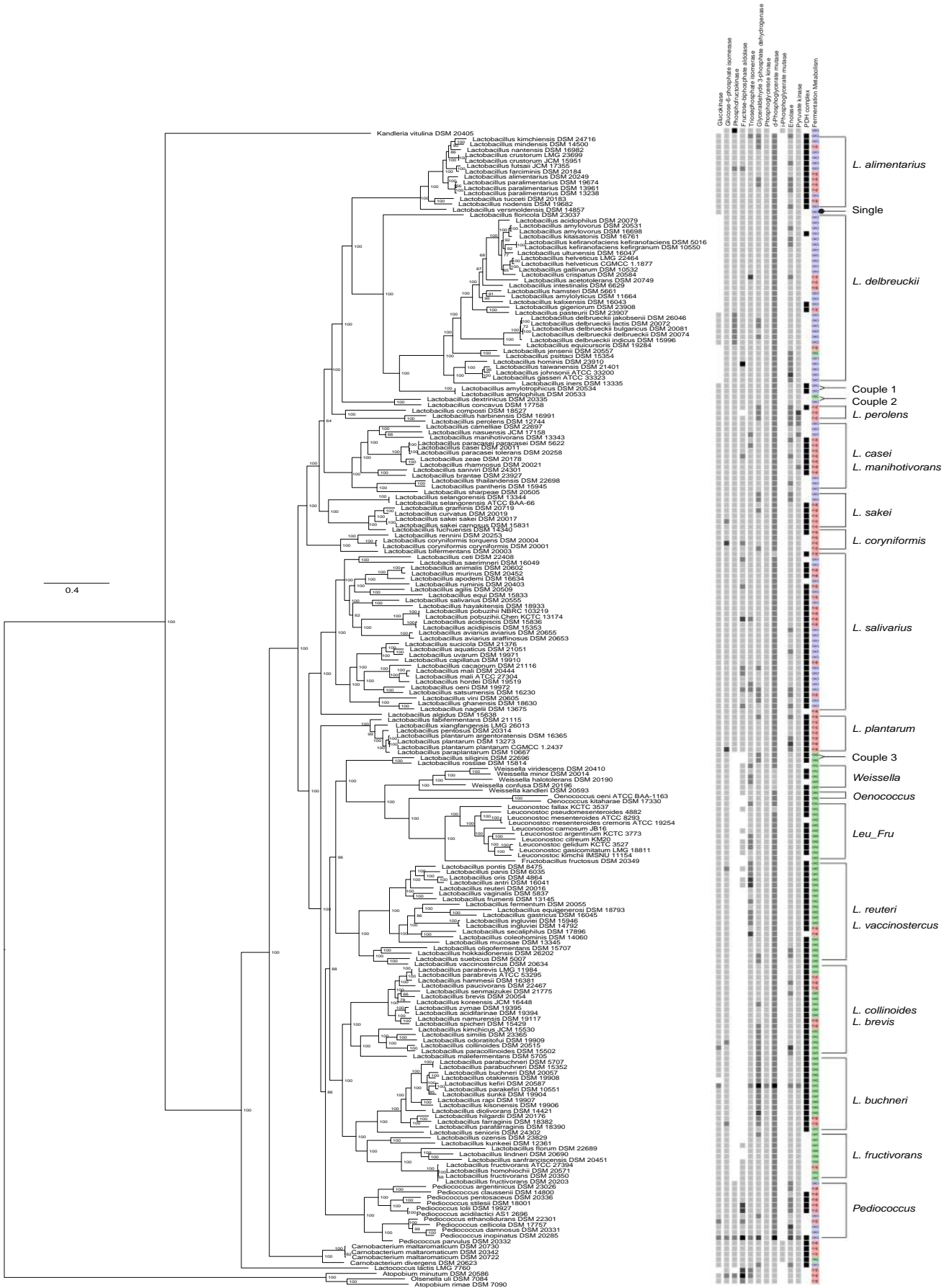
Supp. Figure 4. Frequency distribution of ANI and TNI values for the *Lactobacillus* species compared to those of traditionally defined taxonomic units. The black lines indicate the frequency distribution of values for the lactobacilli, which revealed lower values for both ANI and TNI than the majority of strains within the same family but in different genera.



Supp. Figure 5. Maximum Likelihood tree of published representative genomes that covers 452 genera. Published representative genomes that covered 452 genera from 26 phyla, as well as the 213 genomes sequenced in this research. The tree was built based on the concatenated amino acid sequences of 16 marker genes by using RAxML with 1000 bootstrap iterations. The numbers at nodes are bootstrap values and the genomes included in this study were indicated by red font.

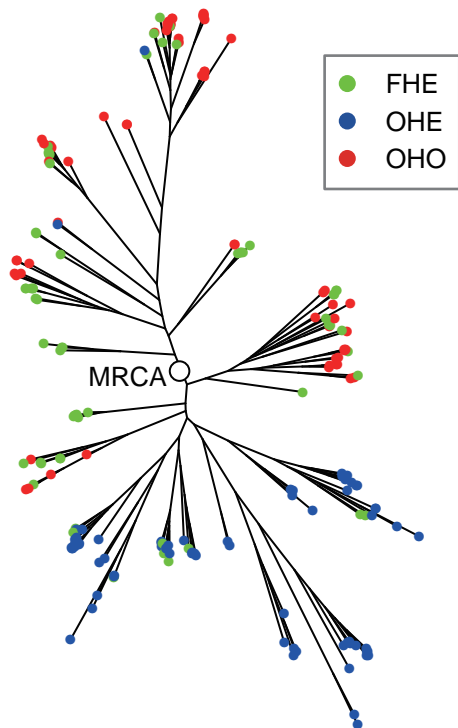


Supp. Figure 6. Maximum likelihood tree of strains of the *Lactobacillus* Genus Complex based on 73 core genes. The branch colors indicate different genera.

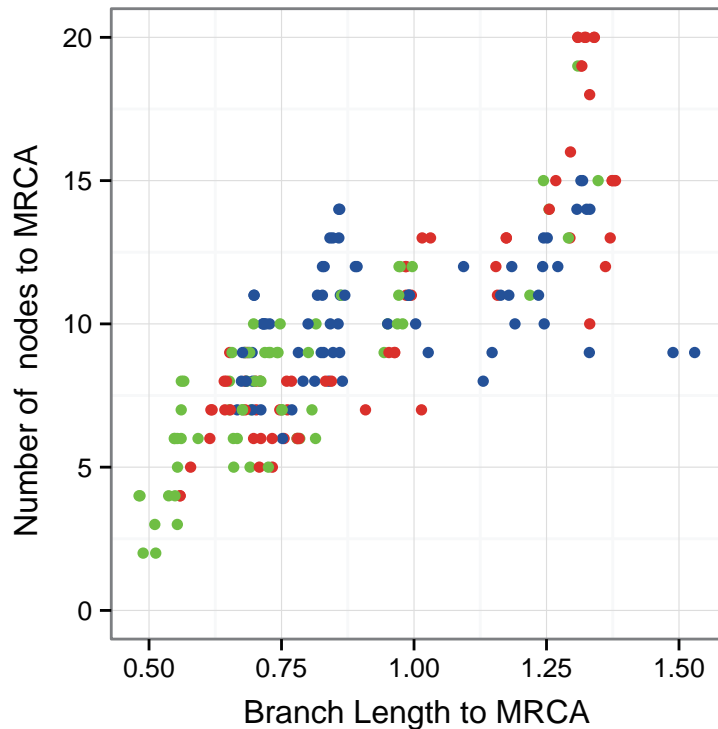


Supp. Figure 7. Distribution of glycolytic and pyruvate dehydrogenase genes across 213 lactobacilli and related species. The distribution of phosphoglycerate mutase is discriminated by the presence of genes encoding the cofactor-dependent (d) or the cofactor-independent (i) isofunctional enzymes. For all 10 core glycolytic enzymes, gene distribution is indicated in grey-scale from absence (white) to presence of 4 gene copies (black). For the pyruvate dehydrogenase operon (4 genes), presence of a functional complex is indicated in black, and absence of a functional complex in white. The fermentation metabolism phenotype is indicated as OHO: obligately homofermentative (purple), FHE: facultatively heterofermentative (pink) or OHE: obligately heterofermentative (green).

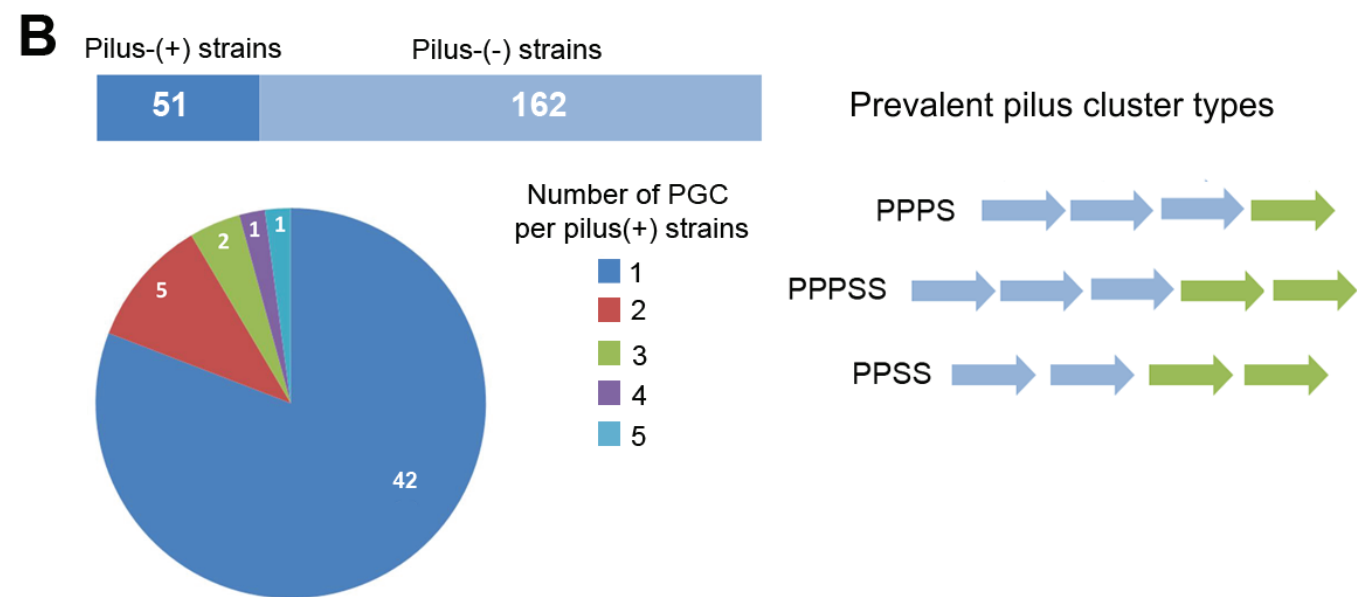
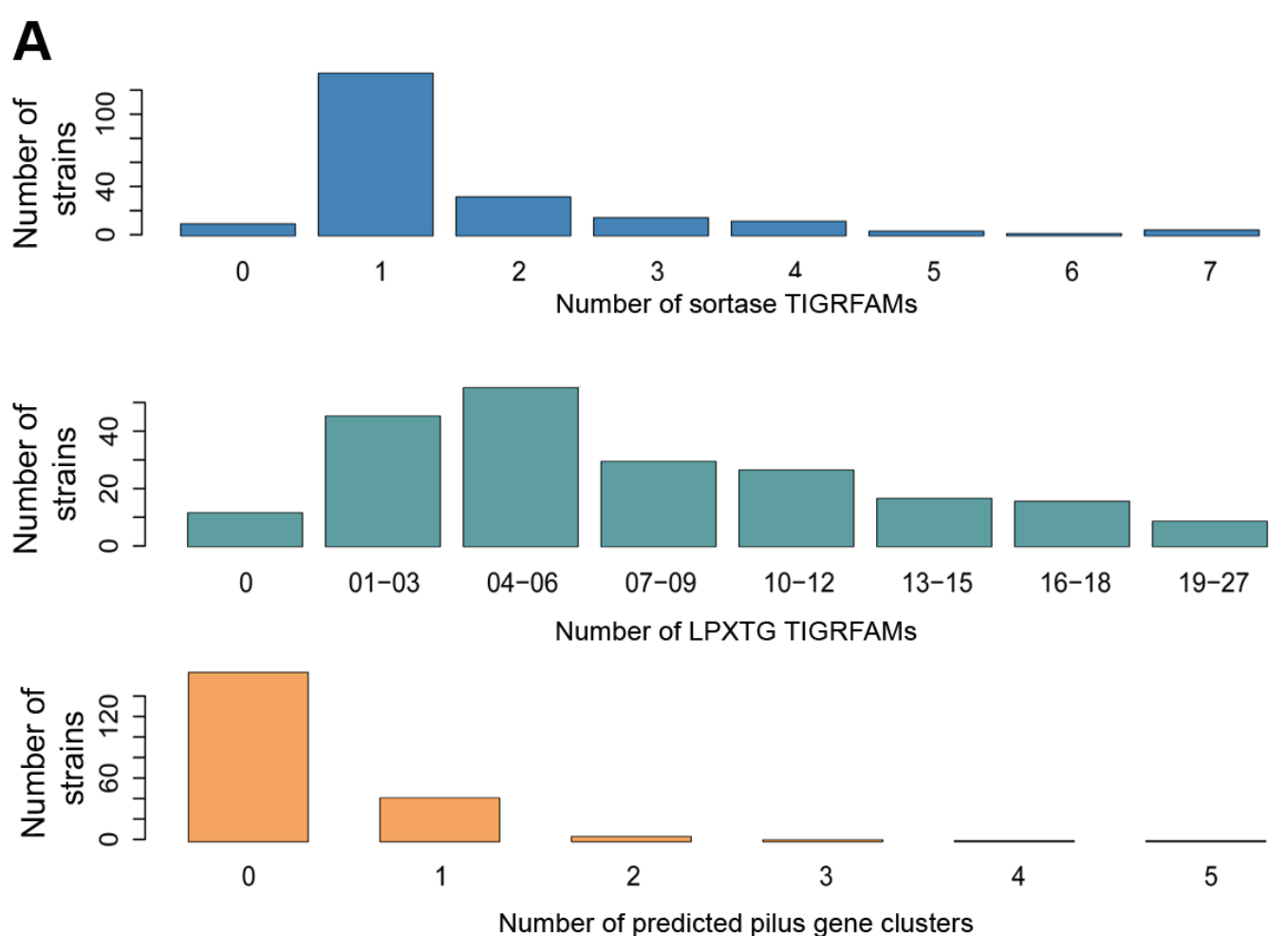
A



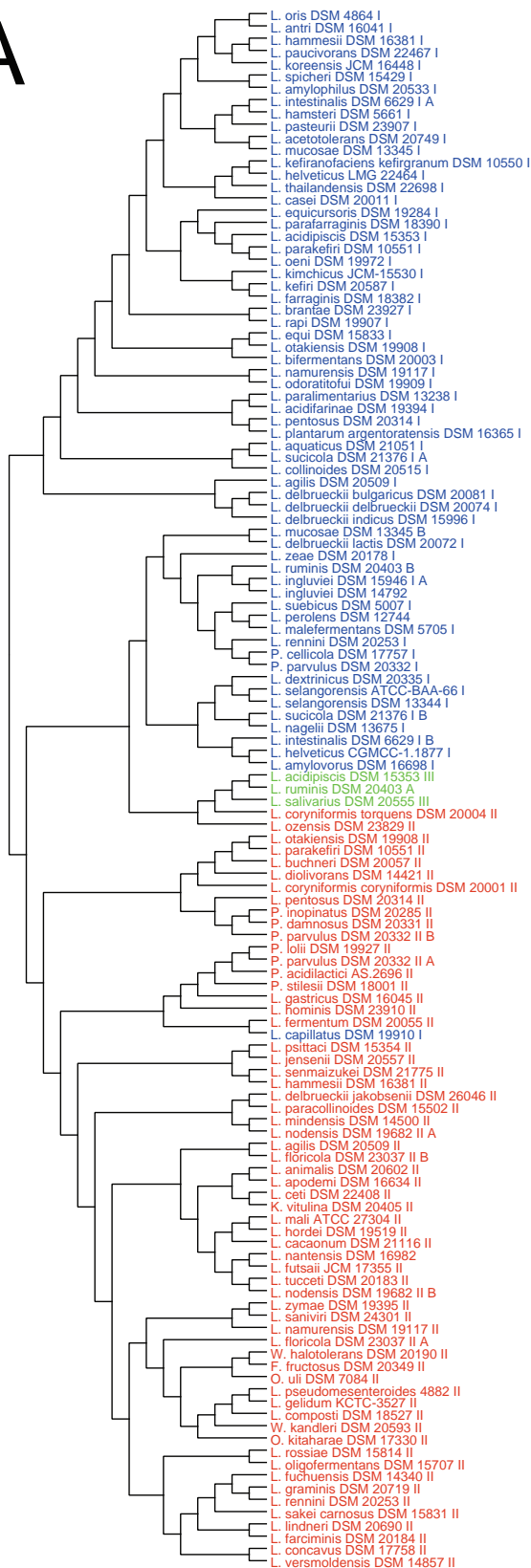
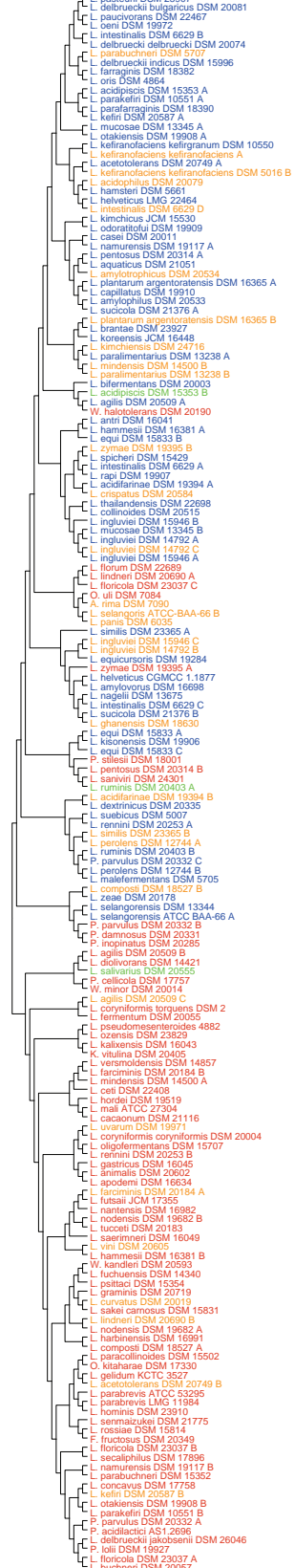
B



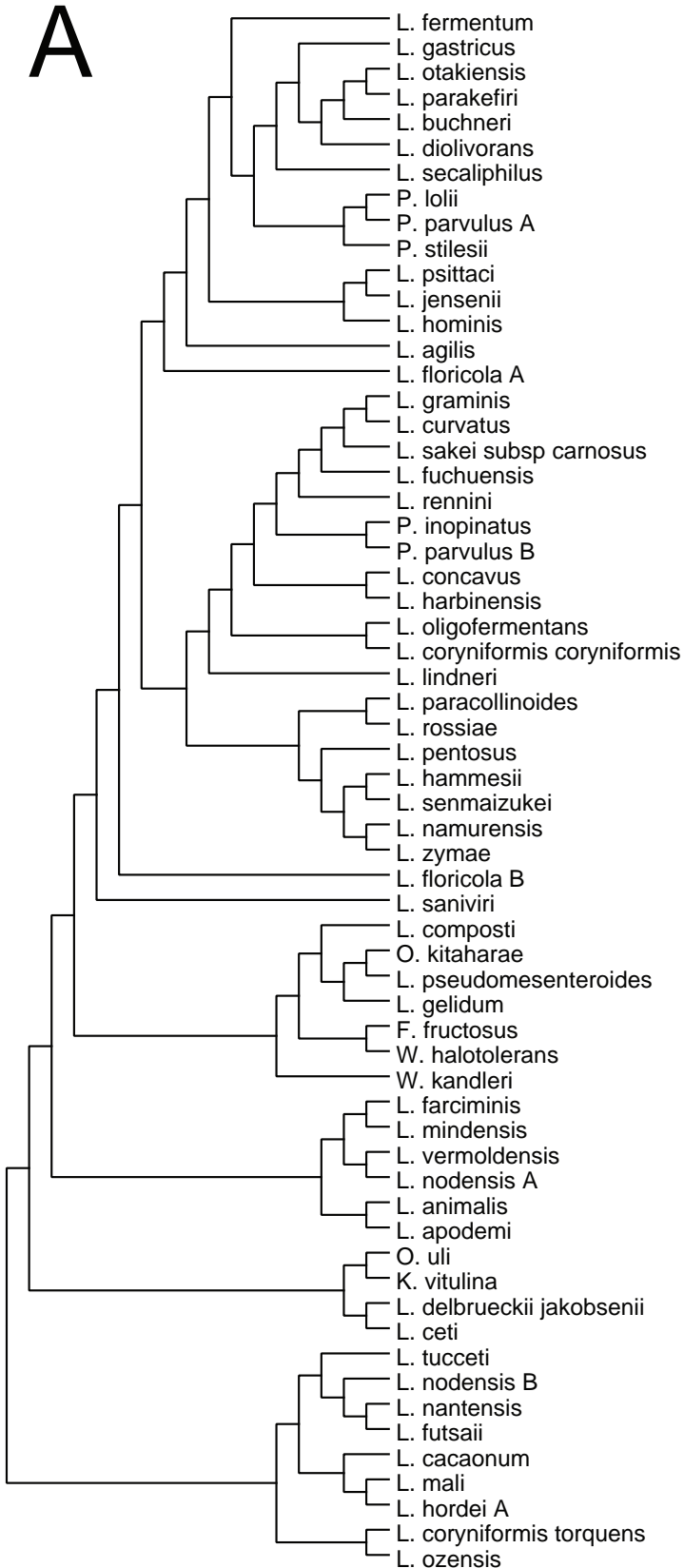
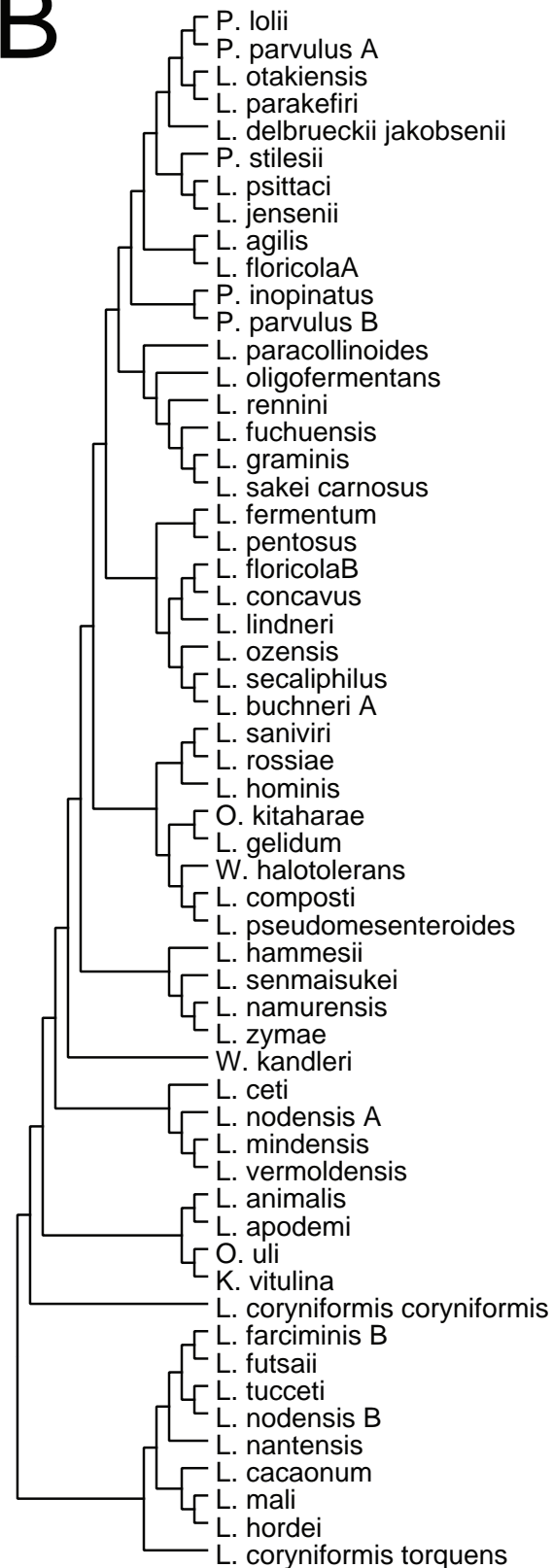
Supp. Figure 8. Evolution of carbohydrate metabolism in the *Lactobacillus* Genus Complex. A) Maximum likelihood tree of 204 strains of the *Lactobacillus* Genus Complex based on concatenated amino acid sequence of 73 core genes. The tree was built using RAxML with 100 bootstrap iterations. B) The number of nodes and the branch lengths to the MRCA for each strain/genome. The color of the branches in panel A and the dots in panel B indicate different fermentation types, with green representing FHE, blue representing OHE and red representing OHO.



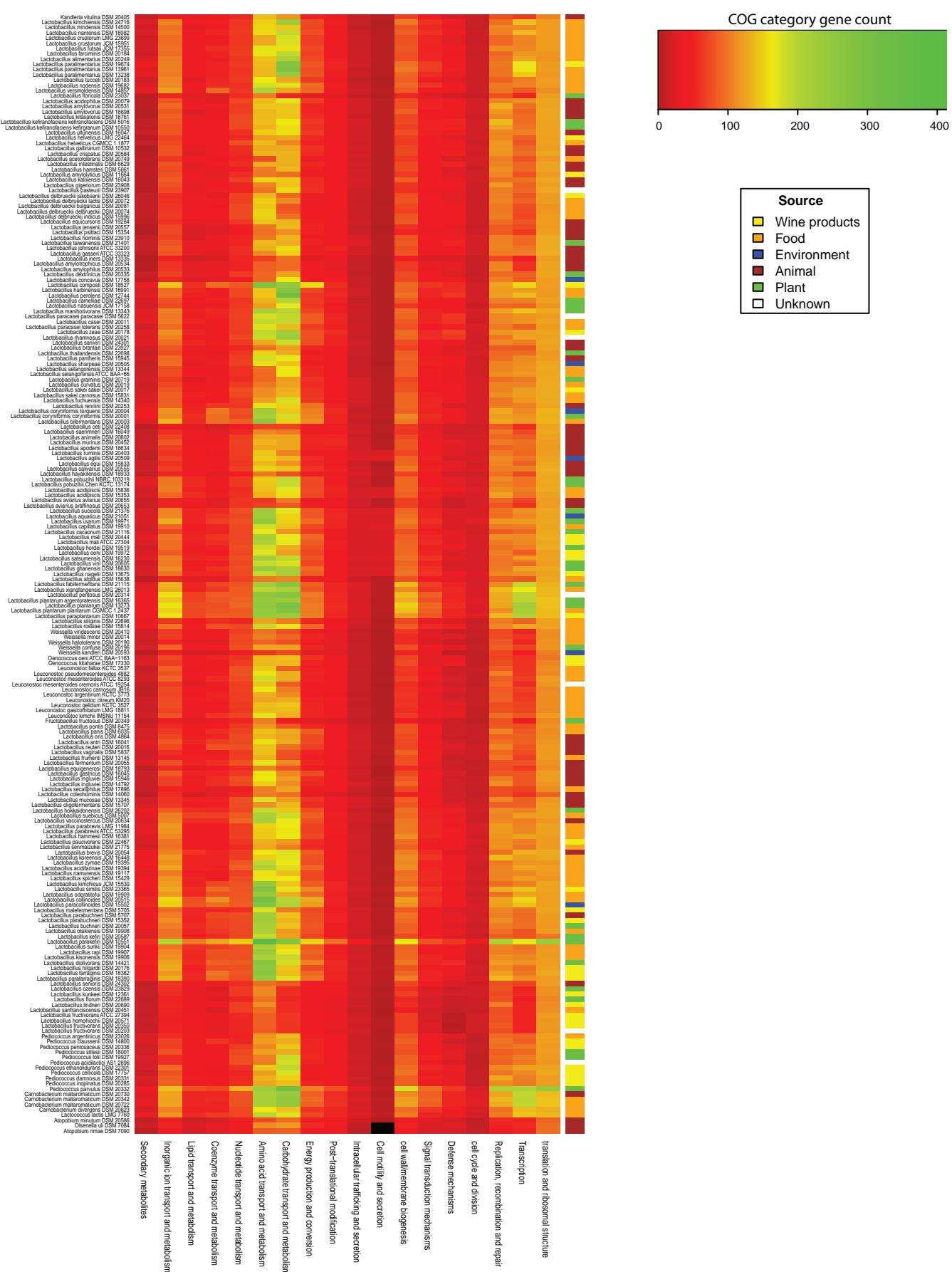
Supp. Figure 10. Distribution of LPXTG proteins, sortases and pilus gene clusters among the 213 genomes analysed. Panel A shows the pilus gene clusters (PGCs) that were found in 24% of all analyzed genomes and had prevalently one of the four types illustrated in Panel B Legend: green arrow = sortase gene; blue arrow = pilin gene.

A**B**

Supp. Figure 11. Comparative analysis of core CRISPR elements. The tree in panel A is derived from an alignment of the sequence of the universal Cas protein, Cas1, to create a phylogenetic tree showing the relatedness of all CRISPR-Cas systems in lactobacilli and closely related organisms (see Fig. 5A). The strain designation is followed by I, II, or III, corresponding to the respective CRISPR-Cas system type, using blue, red and green for Type I, II and III systems, respectively. Undefined systems are represented in orange. When multiple Cas1 proteins were found within a genome, they were differentiated by a letter. The tree in panel B is derived from an alignment of the CRISPR repeat sequences. All strain names correlate with the master CRISPR table (Supplementary Table 7). When a strain had multiple CRISPR repeats, they were given different letters to distinguish the repeats.

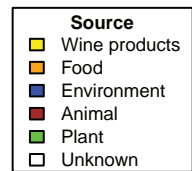
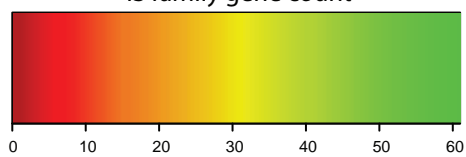
A**B**

Supp. Figure 12. Comparative analysis of Type II CRISPR-Cas systems. The tree in panel A is derived from an alignment of the sequence of the Type II signature Cas protein, Cas9, to create a phylogenetic tree showing the relatedness of Cas9 proteins from Type II-A and II-C systems (see Fig. 5B). The tree in panel B is derived from an alignment of the predicted tracrRNA sequences for Type II-A systems.

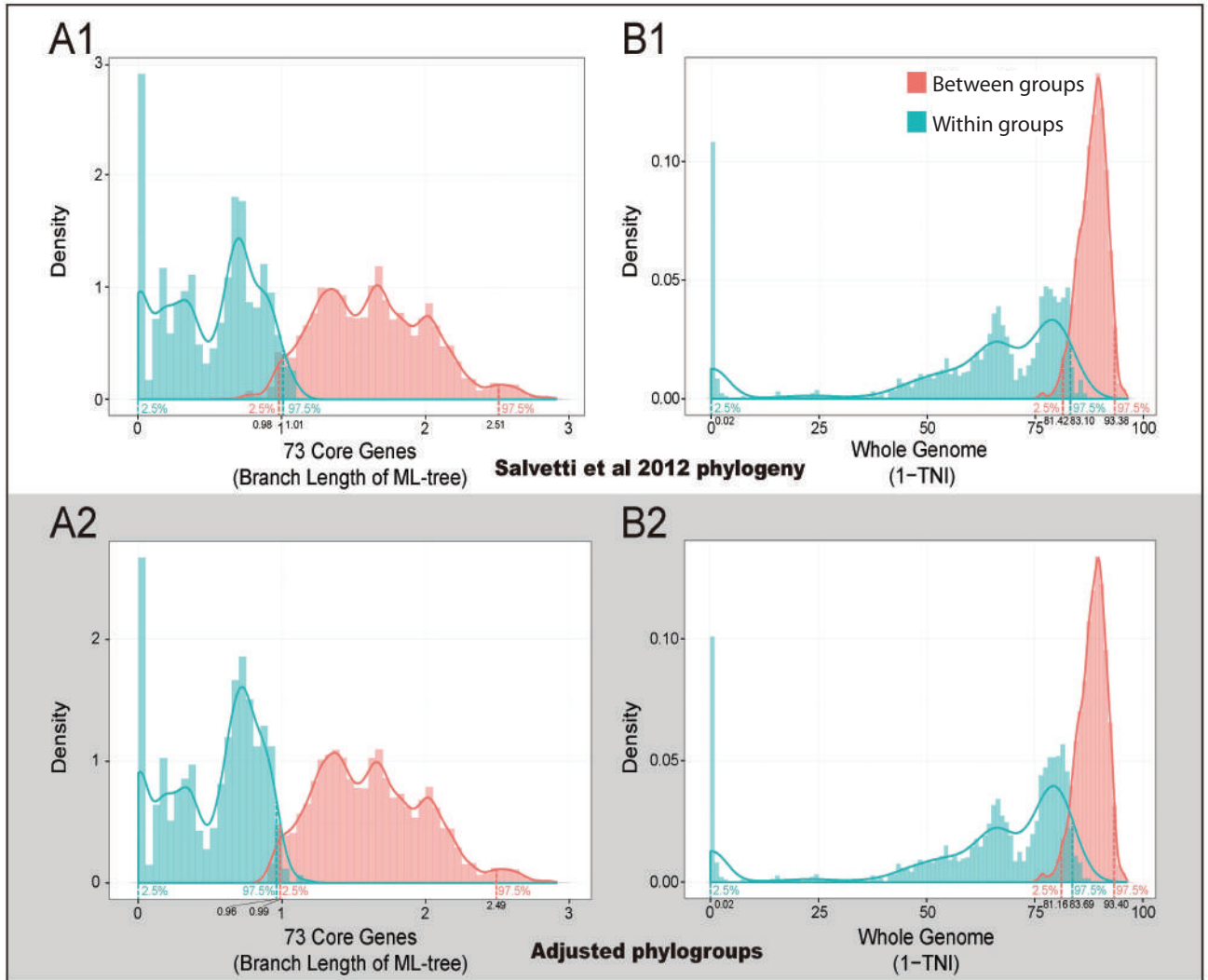


Supp. Figure 15. Heatmap of the distribution and abundance of 18 different COG categories across the 213 genomes. Number of genes assigned to each of the different COG categories is indicated by the color bar from black (absent) to green. Strains are ordered from top to bottom as they appear top-down in the phylogeny (Fig. 2) with source information by the color bar along the top of the heatmap.

IS family gene count



Supp. Figure 16. Heatmap of the distribution and abundance of 18 insertion sequence families across the 213 genomes. The number of genes assigned to each IS family is indicated by the color bar from black (absent) to green. The strains appear from top to bottom as they are featured top-down in the phylogeny (Fig. 2). Source information for each strain is indicated by a color bar along the top of the heatmap.



Supp. Figure 17. Branch length distribution and TNI value distribution (1-TNI). A current phylogrouping of the *Lactobacillus* Genus complex and a manually curated phylogrouping based on the maximum likelihood tree of 73 core genes (this study; see Supplementary Figure 18).



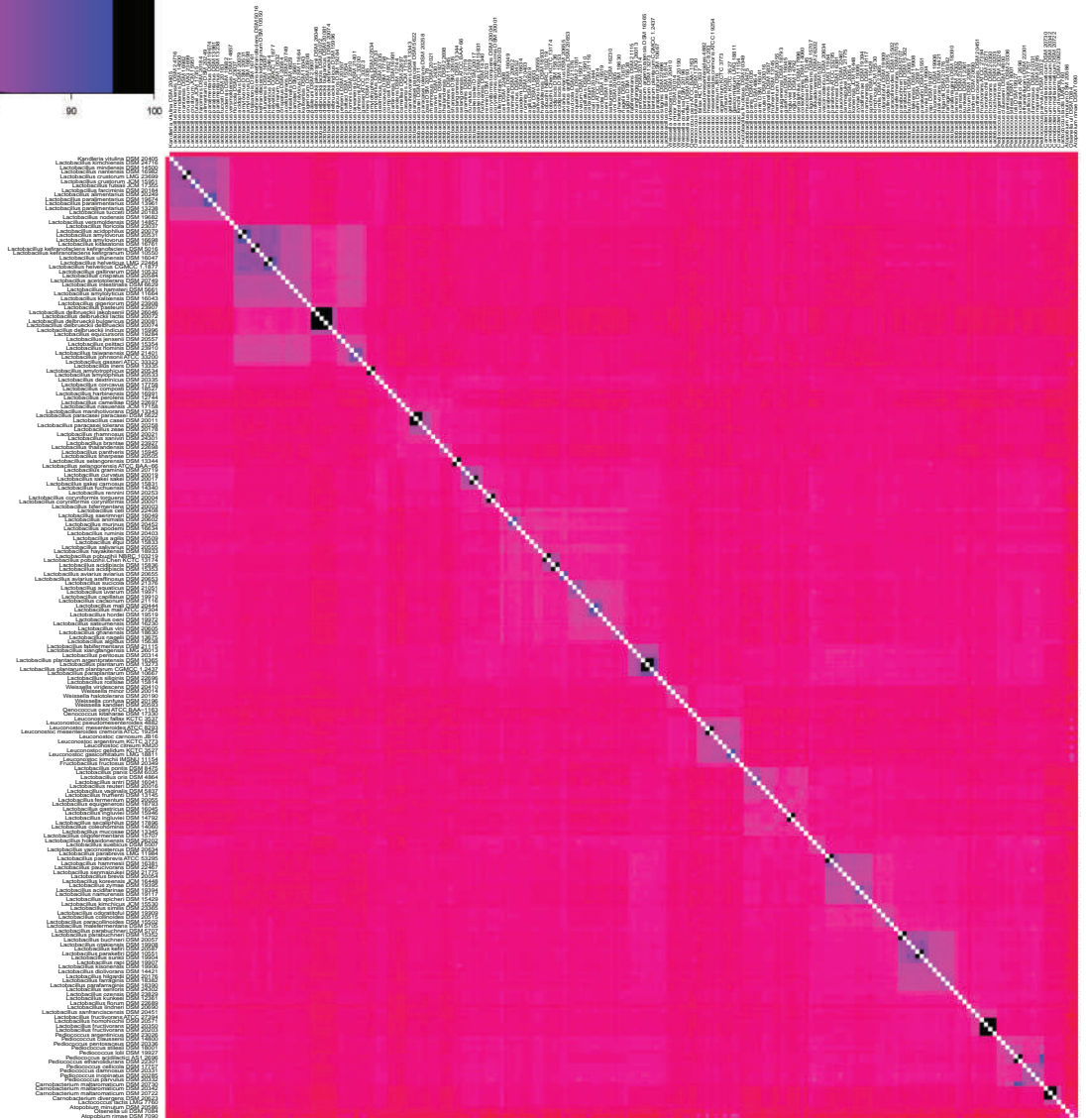
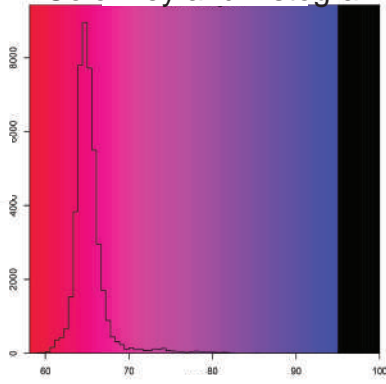
Supp. Figure 18. Manually curated phylogrouping of the *Lactobacillus* complex and associated genera based on 73 core genes maximum likelihood phylogeny. According to this revised phylogrouping, when the branch length between two strains is greater than 0.99, the probability is very high (>97.5%) that they belong to different phylogroups, and when the branch length is less than 0.96 between two strains, the probability that they belong to the same phylogroup is > 97.5%. Compared to the existing phylogrouping in Salveti et al., 2012, the adjustments made here are:

1. Two species, *L. amylotrophicus* and *L. amylophilus* that originally belonged to the *L. delbrueckii* group were excluded from *L. delbrueckii* and defined as a new Couple.
2. The single species *L. composti* was combined with the phylogroup *L. perolens*.
3. The phylogroup *L. casei* and *L. manihotivrans* were combined together with the previously defined single species, *L. camelliae*, *L. saniviri*, *L. brantae*, *L. sharpeae*, and the Couple that contained *L. thailandensis* and *L. pantheris*, was defined as a single phylogroup.
4. The single species *L. algidus* was combined with the phylogroup *L. salivarius*.
5. *Leuconostoc* and *Fructobacillus* were defined as a single phylogroup.
6. The phylogroups *L. reuteri* and *L. vaccinostercus* were combined together.
7. The phylogroups *L. brevis* and *L. collinoides* and a single species, *L. malefermentans*, were combined as a single phylogroup.
8. *L. senioris* was combined with the phylogroup *L. buchneri*.
9. The couple that contained *L. ozensis* and *L. kunkelii* was combined into the phylogroup *L. fructivorans*.



Supp. Figure 19. Phylogeny inferred from a 100 core gene dataset (27 partial + 73 complete core genes).

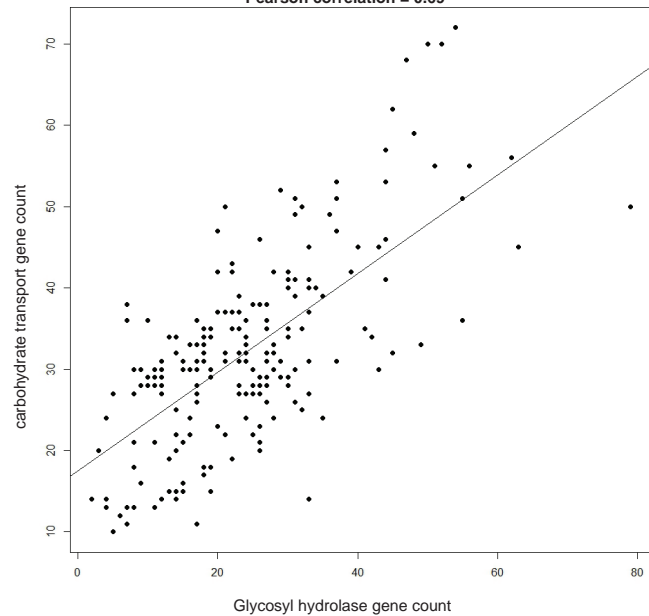
Color key and histogram



Supp. Figure 20. Heatmap of pairwise ANI values for 213 genomes. The order of the rows (top to bottom) and columns (left to right) is according to their position in the phylogenetic tree based on 73 core proteins (Fig. 2).

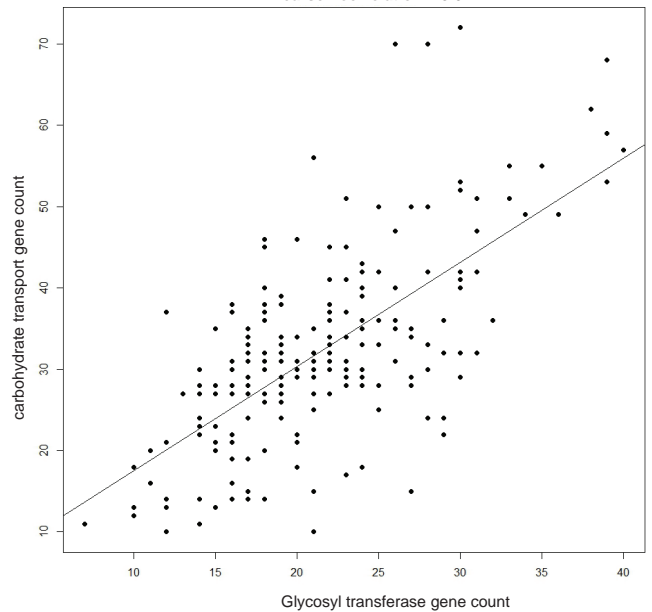
Carbohydrate transport against GHs

Pearson correlation = 0.69

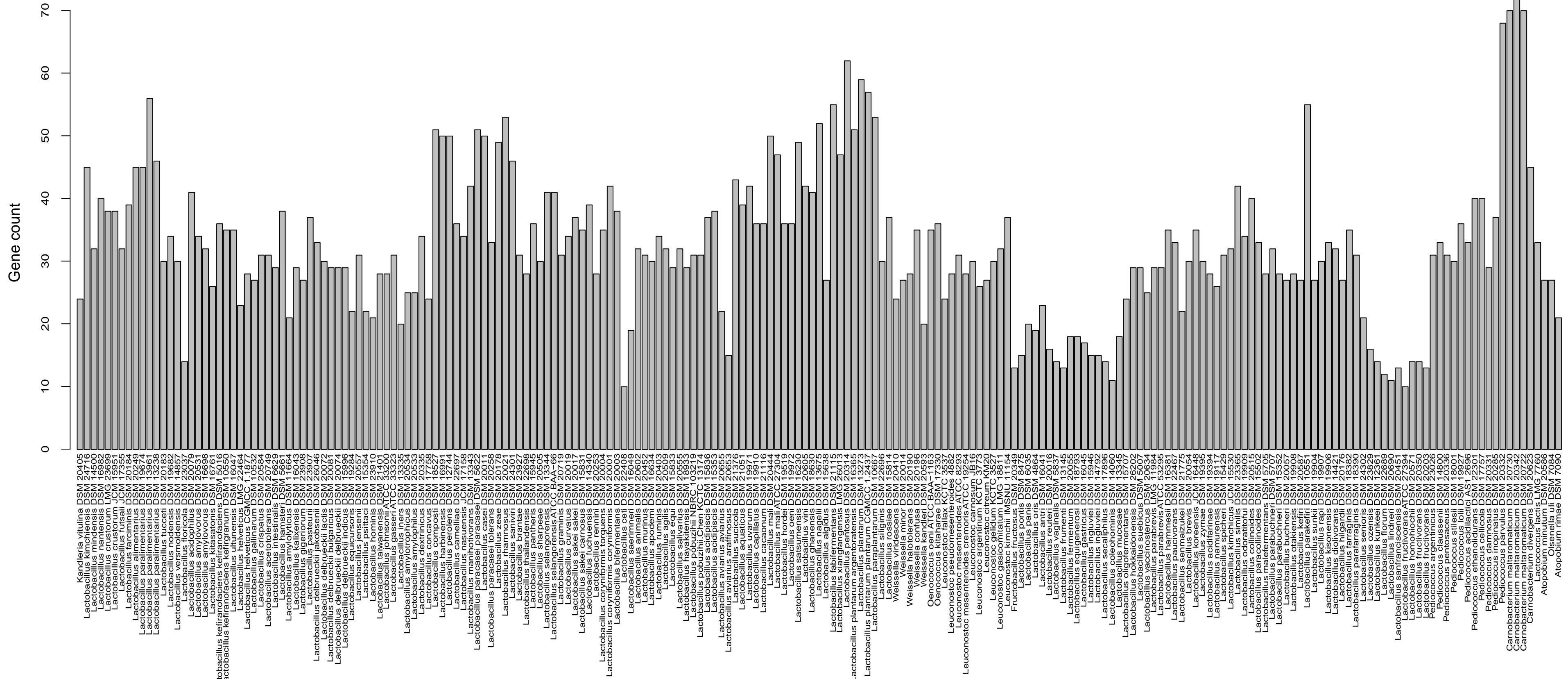


Carbohydrate transport against GTs

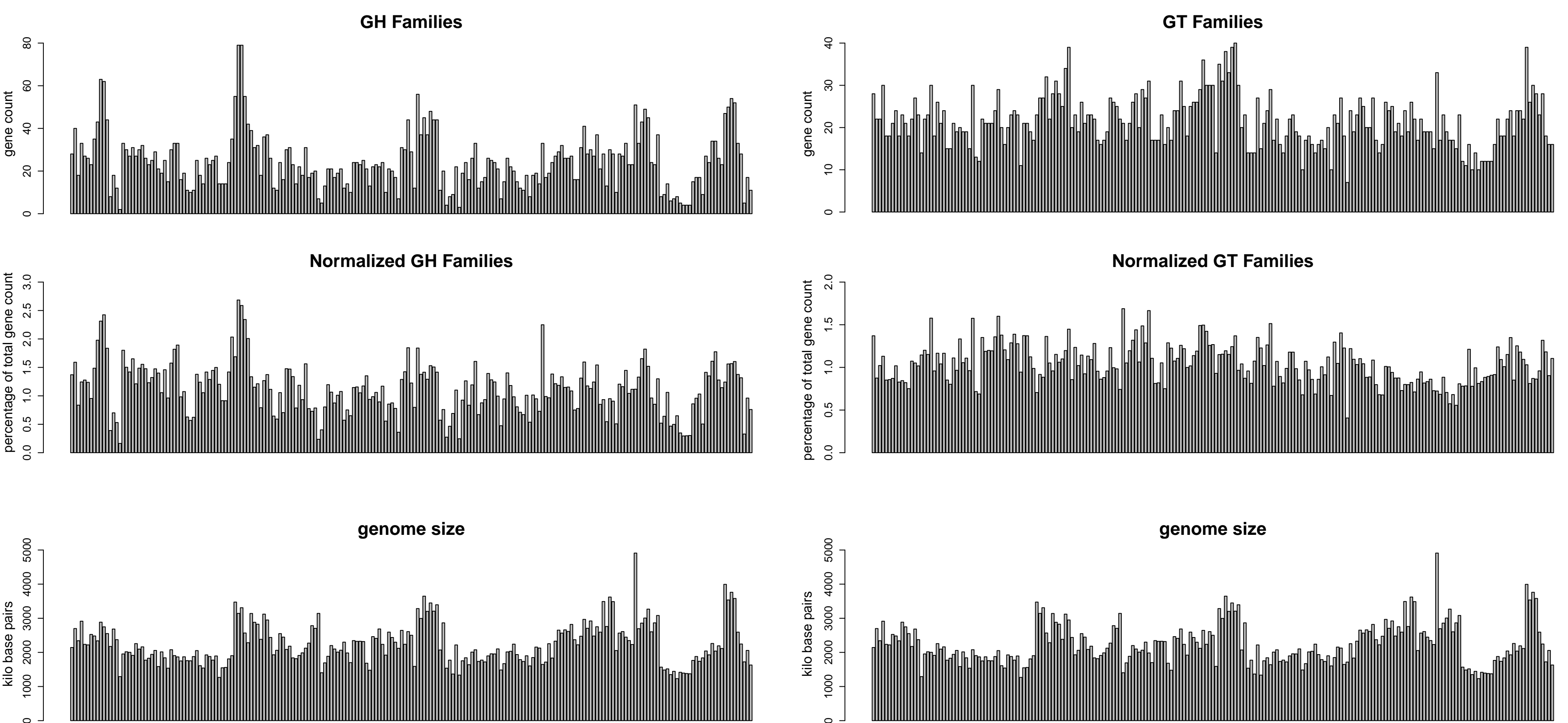
Pearson correlation = 0.67



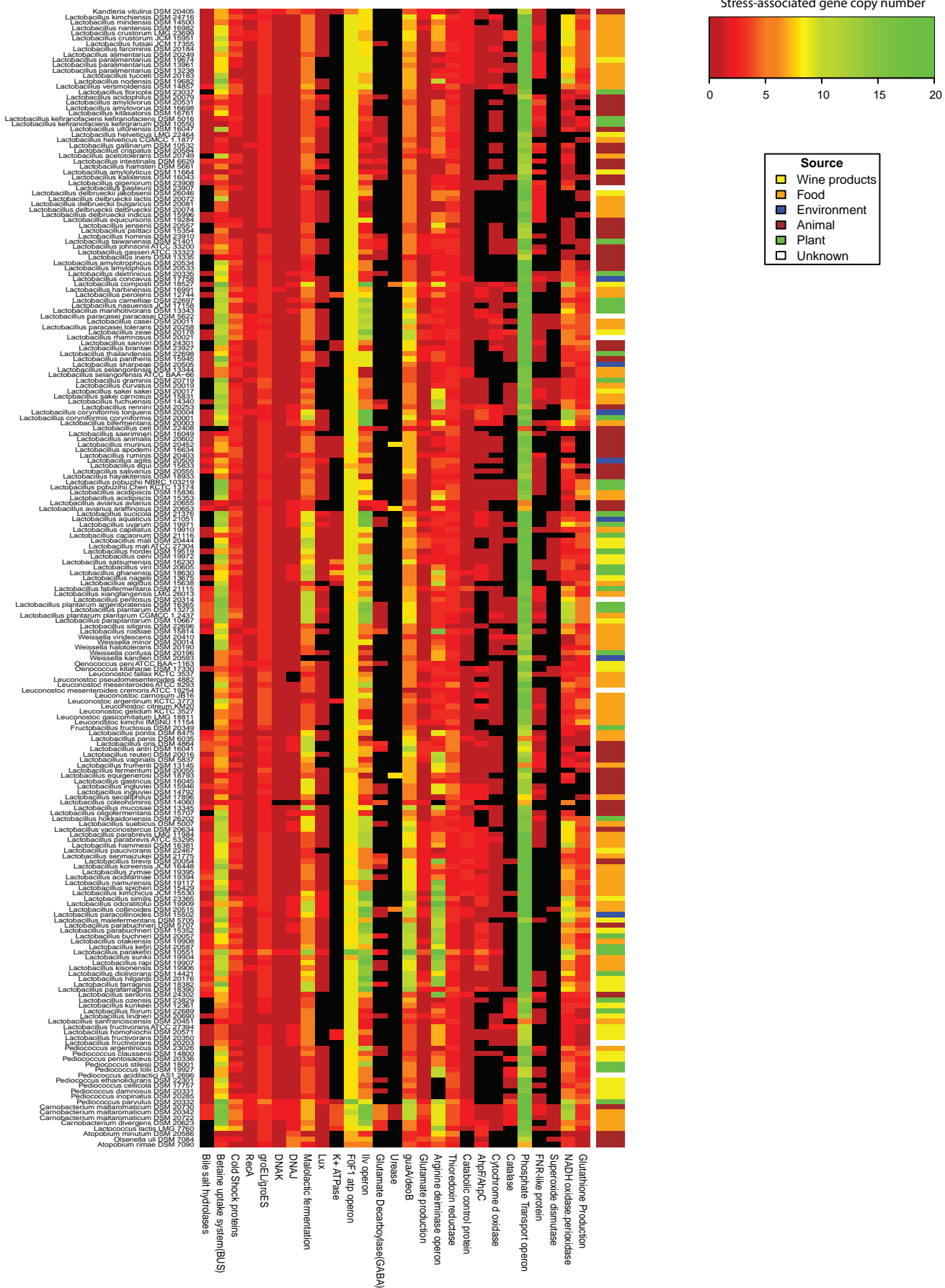
Supp. Figure 21. Scatterplots showing the correlation between the number of carbohydrate transport genes (y-axes) and the number of glycosyl hydrolase genes (x axis; left) and the number of glycosyl transferase genes (x-axis; right). The line of best fit for each plot was estimated using a least squares linear model.



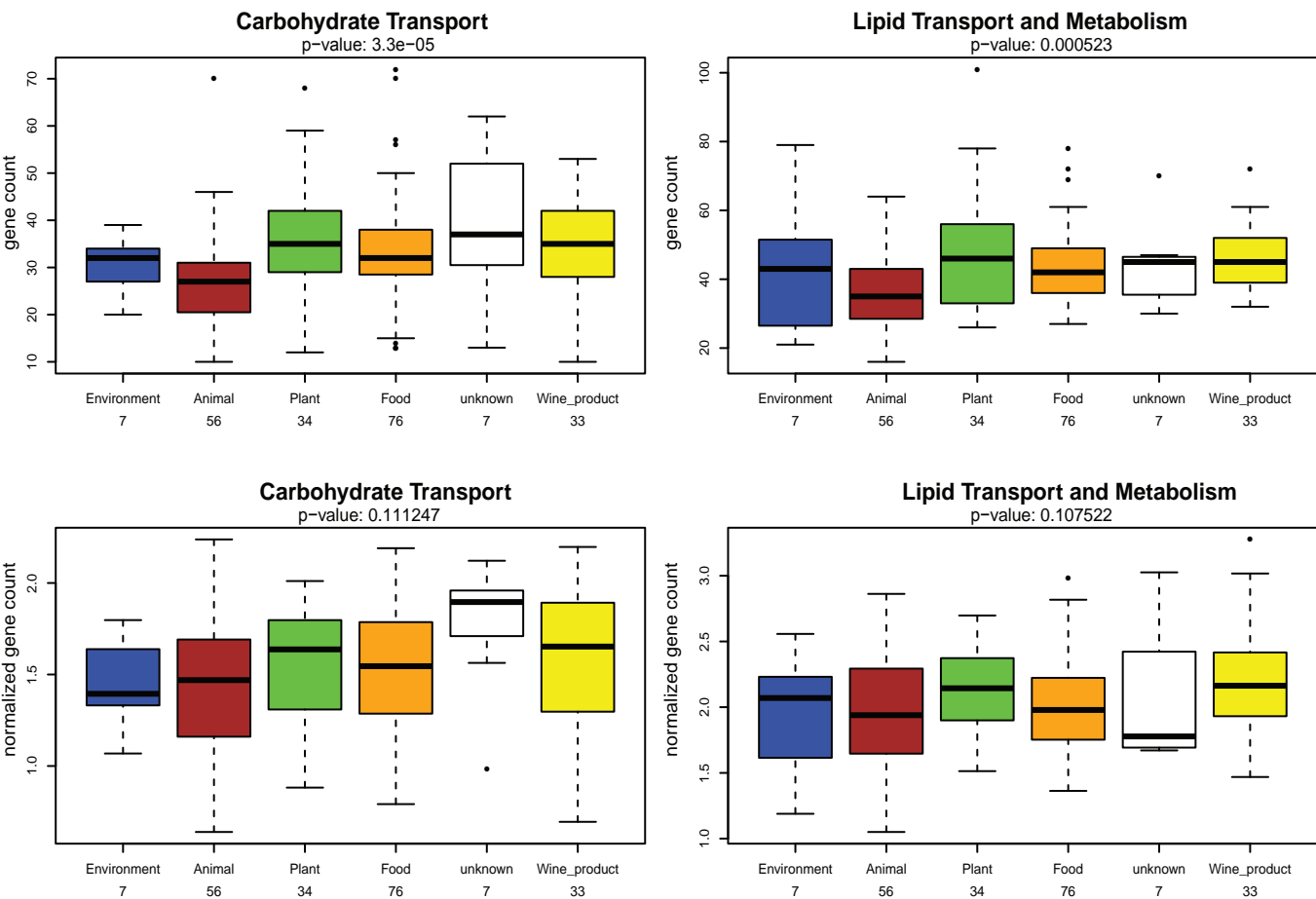
Supp. Figure 22. Barplot of the number of genes involved in carbohydrate transport for each strain. Strains are ordered according to the phylogenetic tree in Fig 2.



Supp. Figure 23. The effect of normalizing counts of GHs and GTs by genome size. The three bar-graphs on the left show, from top to bottom, GH gene counts, GH gene counts expressed as a percentage of the total gene count and genome size (in kbps). The equivalent for GTs is shown in the three bar-graphs on the right. Genome size is highly correlated with total number of genes per genome (Pearson; 0.99).



Supp. Figure 24. Heatmap of the distribution and abundance of stress response genes across the *Lactobacillus* Genus Complex and associated genera. Gene copy number for 27 stress-associated genes is indicated by the color key from black (absent) to green. Type of stress resistance is indicated by the names at the bottom of the figure. Strains are ordered from top to bottom as they appear top-down on the phylogeny (Fig. 2) with source information for each strain indicated by a color bar at the side of the heat-map.



Supp. Figure 25. Association of carbohydrate transport and lipid transport/metabolism with niche. Top panels display raw gene counts and bottom panels display gene counts normalized by total genes. Boxplots represent a five-point summary of the data in the following order (from bottom to top): minimum, first quartile, median, third quartile and maximum. Outliers are represented as individual points above or below the boxplot.

1 **Supplementary Tables**

2 **Supp. Table 1. Species analysed and their genomic features.**

3 **Supp. Table 2. Sequence information for the 73 core complete genes.** The core genome
4 was established based on genomes listed in Table 1. *Lactobacillus salivarius* genes are shown
5 as exemplars for sequence retrieval. Columns are protein ID numbers, gene designation,
6 locus tag, COG, annotation, co-ordinates in the *L. salivarius* UCC118 genome
7 (NC_007929.1), strand and gene length.

8 **Supp. Table 3. Genera used in building the tree of bacteria.**

9 **Supp. Table 4. Sixteen marker genes used to build the bacterial tree composed of 452**
10 **genera and 213 *Lactobacillus* genomes and *Lactobacillus* associated genera.**

11 **Supp. Table 5. Distribution of LPXTG-containing and sortase enzymes across the 213**
12 **genomes.**

13 **Supp. Table 6. Distribution and abundance of cell envelope proteases (CEPs) and**
14 **associated anchoring domains and motifs.**

15 **Supp. Table 7. CRISPR occurrence and diversity.** CRISPR-Cas system type designation
16 was determined by the presence of CRISPR repeats, spacers, the universal *cas1* gene, and
17 the signature for each type, namely *cas3*, *cas9*, and *cas10*, for Type I, II, and III, respectively.
18 A “Y” in the each of the gene columns designates that the gene was positioned next to the
19 CRISPR locus. In instances where only a partial gene was annotated, the symbol “Y*” is
20 shown. An N indicates that no *cas* gene was found. The type of the CRISPR-Cas system is
21 noted in the “Type” column. When multiple CRISPR loci of the same type were present in the
22 same genome, the type was then designated with a differential letter demarking their order in
23 identification. When *cas* genes could not be annotated, the CRISPR-Cas system type was
24 labeled “undefined.” Strains that contained neither CRISPR repeats nor *cas* genes were
25 labeled with the “N/A” designation. “DR length” corresponds to the number of nucleotides in
26 the CRISPR direct repeat. The number of spacers was also determined for each repeat-
27 spacer array.

28 **Supp. Table 8. Sequence information for the 27 core partial genes.**

29 **Supp. Table 9. Presence and absence of the complete pathways for production of the**
30 **20 standard amino acids.** A = auxotrophic; P = prototrophic.

31 **Supp. Table 10. Presence of sirtuin homologs in the 213 genomes analyzed.**

32 **Supp. Table 11. Genomic regions related to bacteriocin production identified in the**
33 **213 genomes.**

Table S1. Species analyzed and their genome features

Species Name	StrainID	Isolation year	Source	Genome Size (Mbp)	GC%	Predicted ORF number	Sequencing depth	Contig number	Short-read Archive	Genome Accession	Niche category	Phylogroup*
Atopobium minimum	DSM-20586	1987	Perineal abscess	1.72	48.69	1595	116.11	64	ERR339734	JQB00000000	Animal	Other
Atopobium rimosum	DSM-7900	1954	Human gingival crevice	1.63	49.26	1524	122.70	9	ICP00000000	JQD00000000	Animal	L. salivarius
Carnobacterium divergens	DSM-20623	1984	Human packaged minced beef	2.59	34.95	2451	77.13	51	ERR339727	JQB00000000	Food	Carnobacterium
Carnobacterium maltaromaticum	DSM-20342	1974	Milk with malty flavour	3.76	34.31	3369	53.17	155	ERR339700	JQB00000000	Food	Carnobacterium
Carnobacterium maltaromaticum	DSM-20722	1974	Vacuum-packaged meat	3.68	34.31	3541	55.86	64	ERR339702	JQB00000000	Food	Carnobacterium
Carnobacterium maltaromaticum	DSM-17370	1974	Disseminated rainbow trout	3.48	34.38	3389	56.57	56	ERR339703	JQB00000000	Food	Carnobacterium
Fructobacillus fructus	DSM-20349	1956	Flowers	1.48	44.56	1514	134.69	45	ERR339711	JQB00000000	Plant	Leu_Fru
Kandleria vinilina	DSM-20405	1973	Calf rumen	2.14	35.03	2126	93.31	138	ERR339782	JQB00000000	Animal	Other
Lactobacillus acidoterans	DSM-20749	1986	Fermented Vinegar Broth	1.59	36.26	1531	151.41	123	ERR339757	AYZ00000000	Food	L. salivarius
Lactobacillus acidoterans	DSM-19394	2001	Artisanal wheat sourdough	2.92	51.59	2735	47.57	47	AZD00000000	AZD00000000	Food	L. salivarius
Lactobacillus acidoterans	DSM-15353	2001	Artisanal wheat sourdough	2.32	39.06	2280	86.27	298	ERR339738	JQB00000000	Food	L. salivarius
Lactobacillus acidophilus	DSM-15836	2000	Fermented fish	2.33	39.07	2307	51.59	457	SRX456282	AZF00000000	Food	L. salivarius
Lactobacillus agilis	DSM-20079	1900	Human	1.95	34.59	1886	61.41	30	SRX456246	AZC00000000	Animal	L. delbrueckii
Lactobacillus agilis	DSM-20079	1900	Municipal sewage	1.74	34.04	1744	102.27	115	AYY00000000	AYY00000000	Environment	L. salivarius
Lactobacillus algalis	DSM-15638	2000	Vacuum-packed beef	1.59	36.03	1535	150.91	28	SRX456283	AZD00000000	Food	L. salivarius
Lactobacillus alimentarius	DSM-20249	1970	Marinated fish product	2.34	33.4	2223	102.65	58	ERR339701	AZD00000000	Food	L. alimentarius
Lactobacillus amylophilus	DSM-11664	1999	Acidified beer wort	1.54	38.24	1628	78.05	98	SRX456357	AZEF00000000	Wine product	L. delbrueckii
Lactobacillus amylophilus	DSM-20533	1981	Swine waste-corn fermentation	1.92	41.48	1910	124.56	112	ERR339717	AYY00000000	Animal	Couple1
Lactobacillus amylophilus	DSM-20534	2006	Swine waste-corn fermentation	1.55	43.59	1589	154.98	21	SRX456279	AZC00000000	Animal	Couple1
Lactobacillus amylovorus	DSM-16698	1981	Faeces, piglet intestine	2.00	37.82	2004	99.92	162	ERR339733	JQB00000000	Animal	L. delbrueckii
Lactobacillus amylovorus	DSM-20531	1981	Cattle waste-corn fermentation	2.02	37.77	2061	59.48	116	SRX456280	AZC00000000	Animal	L. delbrueckii
Lactobacillus animalis	DSM-20602	1983	Dental plaque of baboon	1.89	41.06	1813	127.29	93	ERR339783	AYY00000000	Animal	L. salivarius
Lactobacillus animalis	DSM-16641	2005	Gastric biopsies, Human stomach mucosa	2.24	51.11	2124	53.53	92	SRX456248	AZD00000000	Animal	L. reuteri, L. vaccinosus
Lactobacillus apodemus	DSM-11634	2006	Faeces of wild Japanese wood mouse	2.10	38.63	2009	114.35	109	ERR339737	AZD00000000	Animal	L. salivarius
Lactobacillus aquilinus	DSM-21051	2009	Surface of eutrophic freshwater pond	3.71	41.41	3279	99.53	61	ERR339743	AZD00000000	Environment	L. salivarius
Lactobacillus avarius subsp. avarius	DSM-20653	1986	Intestine of chicken	1.48	38.13	1429	162.40	49	ERR405609	AYZ00000000	Animal	L. salivarius
Lactobacillus avarius subsp. avarius	DSM-20655	1985	Faeces of chicken	1.68	40.12	1591	142.61	41	ERR339760	AYZ00000000	Animal	L. salivarius
Lactobacillus bifermans	DSM-20003	1945	Brown cheese	3.14	44.29	3088	76.38	205	ERR339761	AZD00000000	Food	L. reuteri, L. salivarius
Lactobacillus brevis	DSM-29227	1982	Faeces of Canada goose	2.17	45.48	2010	124.56	112	AYY00000000	AYY00000000	Animal	L. manihotivorus, L. casei
Lactobacillus brevis	DSM-20554	1919	Faeces	2.47	45.96	2425	48.50	11	SRX456278	AZCP00000000	Animal	L. brevis, L. collinoides
Lactobacillus buchneri	DSM-20057	1903	Tomato pulp	2.45	44.41	2349	49.05	90	SRX456296	AZD00000000	Plant	L. buchneri
Lactobacillus buchneri	DSM-21116	2009	Cocoa bean heap fermentation	1.92	33.87	1833	124.98	25	ERR339739	AZD00000000	Food	L. salivarius
Lactobacillus buchneri	DSM-22697	2007	Fermented tea leaves (niang)	2.57	45.39	2430	93.46	144	AYY00000000	AYY00000000	Food	L. manihotivorus, L. casei
Lactobacillus capillatus	DSM-19910	2008	Fermented brine used for stinky tofu production	2.24	37.63	2113	107.36	79	ERR339689	AZEF00000000	Food	L. salivarius
Lactobacillus casei	DSM-20011	1916	Cheese	2.83	46.45	2817	42.46	140	SRX456230	AZC00000000	Food	L. manihotivorus, L. casei
Lactobacillus casei	DSM-22408	2008	Lungs of a beaked whale	1.40	33.73	1258	142.46	69	ERR339740	JQB00000000	Animal	L. salivarius
Lactobacillus celastromis	DSM-14060	1981	Human vagina	2.02	40.81	1982	108.62	94	ERR339741	AZD00000000	Animal	L. salivarius
Lactobacillus celastromis	DSM-20515	1972	Fermenting apple juice	3.62	46.11	3380	66.27	165	ERR339741	AYY00000000	Food	L. brevis, L. collinoides
Lactobacillus compositus	DSM-18227	2007	Composting material of distilled sochu residue	3.47	43.95	3370	48.57	131	ERR339694	AZD00000000	Wine product	L. perolens
Lactobacillus compositus	DSM-17378	2009	Walks of a distilled spirit fermenting chile	1.90	43.3	1852	85.63	141	ERR339742	AZD00000000	Environment	Couple2
Lactobacillus coryniformis subsp. coryniformis	DSM-20001	1965	Silage	2.42	42.86	2623	44.36	198	SRX456340	AZC00000000	Animal	L. coryniformis
Lactobacillus coryniformis subsp. torques	DSM-20004	1965	Air of cow shed	2.78	42.99	2699	43.11	410	SRX456233	AZC00000000	Environment	L. coryniformis
Lactobacillus crispatus	DSM-20584	1955	Eye	2.06	36.59	2038	58.34	150	SRX456245	AZC00000000	Animal	L. delbrueckii
Lactobacillus crustorum	JCM-15951	2007	Wheat sourdough	1.95	41.55	2150	54.07	101	SRX456344	AZD00000000	Food	L. alimentarius
Lactobacillus crustorum	LMG-23699	2007	Wheat sourdough	2.24	34.99	2206	89.46	87	ERR339721	IQCK00000000	Food	L. alimentarius
Lactobacillus curvatus	DSM-20019	1903	Milk	1.82	41.97	1819	66.09	250	SRX456225	AZD00000000	Food	L. sakei
Lactobacillus delbrueckii subsp. bulgaricus	DSM-20081	1919	Bulgarian yoghurt	1.76	49.91	1707	113.73	80	ERR339756	QJAV00000000	Food	L. delbrueckii
Lactobacillus delbrueckii subsp. delbrueckii	DSM-20081	1919	Sour grain mash	1.76	49.91	1707	113.73	80	ERR339756	QJAV00000000	Food	L. delbrueckii
Lactobacillus delbrueckii subsp. indicus	DSM-15996	2005	Traditional dairy fermented product (Dahi type)	1.88	45.54	1884	126.93	69	AZD00000000	AZD00000000	Food	L. delbrueckii
Lactobacillus delbrueckii subsp. jacobsonii	DSM-20646	2013	Dolo wort (Alcoholic fermented beverage)	1.75	50.31	1715	102.89	135	SRX690302	JQCC00000000	Wine product	L. delbrueckii
Lactobacillus delbrueckii subsp. lactis	DSM-20072	1919	Emmental cheese	1.87	49.86	1842	61.26	223	ERR339627	AZD00000000	Food	L. delbrueckii
Lactobacillus delbrueckii subsp. lactis	DSM-20072	1919	Emmental cheese	1.87	49.86	1842	61.26	223	ERR339627	AZD00000000	Food	L. delbrueckii
Lactobacillus delbrueckii subsp. lactis	DSM-20072	1919	Emmental cheese	1.87	49.86	1842	61.26	223	ERR339627	AZD00000000	Food	L. delbrueckii
Lactobacillus delbrueckii subsp. lactis	DSM-20072	1919	Emmental cheese	1.87	49.86	1842	61.26	223	ERR339627	AZD00000000	Food	L. delbrueckii
Lactobacillus delbrueckii subsp. lactis	DSM-20072	1919	Emmental cheese	1.87	49.86	1842	61.26	223	ERR339627	AZD00000000	Food	L. delbrueckii
Lactobacillus delbrueckii subsp. lactis	DSM-20072	1919	Emmental cheese	1.87	49.86	1842	61.26	223	ERR339627	AZD00000000	Food	L. delbrueckii
Lactobacillus delbrueckii subsp. lactis	DSM-20072	1919	Emmental cheese	1.87	49.86	1842	61.26	223	ERR339627	AZD00000000	Food	L. delbrueckii
Lactobacillus delbrueckii subsp. lactis	DSM-20072	1919	Emmental cheese	1.87	49.86	1842	61.26	223	ERR339627	AZD00000000	Food	L. delbrueckii
Lactobacillus delbrueckii subsp. lactis	DSM-20072	1919	Emmental cheese	1.87	49.86	1842	61.26	223	ERR339627	AZD00000000	Food	L. delbrueckii
Lactobacillus delbrueckii subsp. lactis	DSM-20072	1919	Emmental cheese	1.87	49.86	1842	61.26	223	ERR339627	AZD00000000	Food	L. delbrueckii
Lactobacillus delbrueckii subsp. lactis	DSM-20072	1919	Emmental cheese	1.87	49.86	1842	61.26	223	ERR339627	AZD00000000	Food	L. delbrueckii
Lactobacillus delbrueckii subsp. lactis	DSM-20072	1919	Emmental cheese	1.87	49.86	1842	61.26	223	ERR339627	AZD00000000	Food	L. delbrueckii
Lactobacillus delbrueckii subsp. lactis	DSM-20072	1919	Emmental cheese	1.87	49.86	1842	61.26	223	ERR339627	AZD00000000	Food	L. delbrueckii
Lactobacillus delbrueckii subsp. lactis	DSM-20072	1919	Emmental cheese	1.87	49.86	1842	61.26	223	ERR339627	AZD00000000	Food	L. delbrueckii
Lactobacillus delbrueckii subsp. lactis	DSM-20072	1919	Emmental cheese	1.87	49.86	1842	61.26	223	ERR339627	AZD00000000	Food	L. delbrueckii
Lactobacillus delbrueckii subsp. lactis	DSM-20072	1919	Emmental cheese	1.87	49.86	1842	61.26	223	ERR339627	AZD00000000	Food	L. delbrueckii
Lactobacillus delbrueckii subsp. lactis	DSM-20072	1919	Emmental cheese	1.87	49.86	1842	61.26	223	ERR339627	AZD00000000	Food	L. delbrueckii
Lactobacillus delbrueckii subsp. lactis	DSM-20072	1919	Emmental cheese	1.87	49.86	1842	61.26	223	ERR339627	AZD00000000	Food	L. delbrueckii
Lactobacillus delbrueckii subsp. lactis	DSM-20072	1919	Emmental cheese	1.87	49.86	1842	61.26	223	ERR339627	AZD00000000	Food	L. delbrueckii
Lactobacillus delbrueckii subsp. lactis	DSM-20072	1919	Emmental cheese	1.87	49.86	1842	61.26	223	ERR339627	AZD00000000	Food	L. delbrueckii
Lactobacillus delbrueckii subsp. lactis	DSM-20072	1919	Emmental cheese	1.87	49.86	1842	61.26	223	ERR339627	AZD00000000	Food	L. delbrueckii
Lactobacillus delbrueckii subsp. lactis	DSM-20072	1919	Emmental cheese	1.87	49.86	1842	61.26	223	ERR339627	AZD00000000	Food	L. delbrueckii
Lactobacillus delbrueckii subsp. lactis	DSM-20072	1919	Emmental cheese	1.87	49.86	1842	61.26	223	ERR339627	AZD00000000	Food	L. delbrueckii
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Lactobacillus delbrueckii subsp. lactis	DSM-20072	1919	Emmental cheese	1.87	49.86	1842	61.26	223	ERR339627	AZD00000000	Food	L. delbrueckii
Lactobacillus delbrueckii subsp. lactis	DSM-20072	1919	Emmental cheese	1.87	49.86	1842	61.26	223	ERR339627	AZD00000000	Food	L. delbrueckii
Lactobacillus delbrueckii subsp. lactis	DSM-20072	1919	Emmental cheese	1.87	49.86	1842	61.26	223	ERR339627	AZD00000000	Food	L. delbrueckii
Lactobacillus delbrueckii subsp. lactis	DSM-20072	1919	Emmental cheese	1.87	49.86	1842	61.26	223	ERR339627	AZD00000000	Food	L. delbrueckii
Lactobacillus delbrueckii subsp. lactis	DSM-20072	1919	Emmental cheese	1.87	49.86	1842	61.26	223	ERR339627	AZD00000000	Food	L. delbrueckii
Lactobacillus delbrueckii subsp. lactis	DSM-20072	1919	Emmental cheese	1.87	49.86	1842	61.26	223	ERR339627	AZD00000000	Food	L. delbrueckii
Lactobacillus delbrueckii subsp. lactis	DSM-20072	1919	Emmental cheese	1.87	49.86	1842	61.26	223	ERR339627	AZD00000000	Food	L. delbrueckii
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Lactobacillus delbrueckii subsp. lactis	DSM-20072	1919	Emmental cheese	1.87	49.86	1842	61.26	223	ERR339627	AZD00000000	Food	L. delbrueckii
Lactobacillus delbrueckii subsp. lactis	DSM-20072	1919	Emmental cheese	1.87	49.86	1842	61.26	223	ERR339627	AZD00000000	Food	L. delbrueckii
Lactobacillus delbrueckii subsp. lactis	DSM-20072	1919	Emmental cheese	1.87	49.86	1842	61.26	223	ERR339627	AZD00000000	Food	L. delbrueckii
Lactobacillus delbrueckii subsp. lactis	DSM-20072	1919	Emmental cheese	1.87	49.86	1842	61.26	223	ERR339627	AZD00000000	Food	L. delbrueckii
Lactobacillus delbrueckii subsp. lactis												

Lactobacillus selangorensis	DSM-13344	2000	Chili bo	2.09	46.45	2082	95.83	32	SRX690300	QJAZ0000000	Food	L. sakei
Lactobacillus sensoris	DSM-24302	2012	Faeces of a healthy 100-year-old Japanese fema	1.57	39.09	1567	153.08	16	ERX359768	AYZR0000000	Animal	L. buchneri
Lactobacillus semmarinckei	DSM-21775	2008	Semmarincke, a Japanese pickle	2.22	48.04	1419	107.86	68	SRX456331	AYZH0000000	Food	L. brevis, L. collinoides
Lactobacillus sharaeae	DSM-20505	1982	Municipal sewage	2.45	53.38	2371	98.06	79	ERX359770	AYYO0000000	Environment	L. manihotivorum, L. casei
Lactobacillus siliginis	DSM-22696	2006	Wheat sourdough	2.07	44.08	2059	96.60	52	ERX359771	QJCB0000000	Food	Couple3
Lactobacillus similis	DSM-23365	2010	Fermented cane molasses at alcohol plants	3.49	46.99	3206	68.75	282	ERX359772	AYZM0000000	Wine product	L. brevis, L. collinoides
Lactobacillus spicheri	DSM-15429	2004	Rice sourdough	2.75	55.91	2494	87.23	51	ERX359773	AZFC0000000	Food	L. brevis, L. collinoides
Lactobacillus sacicola	DSM-21376	2009	Sap of an Oak tree	2.46	38.48	2335	97.51	31	ERX450947	AYZF0000000	Plant	L. salivarius
Lactobacillus saebicus	DSM-5007	1989	Apple mash	2.65	38.98	2517	45.26	81	SRX456334	AZGF0000000	Food	L. reuteri, L. vacciniostercus
Lactobacillus sunki	DSM-19904	2009	Sunki, a Japanese traditional pickle	2.69	42.06	2574	89.12	79	SRX456335	AZEA0000000	Food	L. buchneri
Lactobacillus taiwanensis	DSM-21401	2009	Silage cattle feed	1.88	33.97	1851	127.73	93	ERX359776	AYZG0000000	Plant	L. delbrueckii
Lactobacillus thailandensis	DSM-22698	2007	Fermented tea leaves (miang)	2.06	53.5	1943	116.47	23	SRX456337	AYZK0000000	Plant	L. manihotivorum, L. casei
Lactobacillus tucceti	DSM-20183	2009	Sausage	2.17	34.07	2093	110.40	51	ERX359779	AZDG0000000	Food	L. alimentarius
Lactobacillus ulmensis	DSM-16047	2005	Gastric biopsies, Human stomach mucosa	2.16	35.95	2113	55.51	105	SRX456274	AZFO0000000	Animal	L. delbrueckii
Lactobacillus uvorum	DSM-19971	2009	Mast of Bobal grape variety	2.69	36.88	2908	89.34	164	ERX359780	AZEG0000000	Plant	L. salivarius
Lactobacillus vacciniostercus	DSM-20634	1983	Cow dung	2.57	43.48	2485	93.56	112	ERX359731	AYYY0000000	Animal	L. reuteri, L. vacciniostercus
Lactobacillus vaginalis	DSM-5837	1989	Vaginal swab	1.79	40.46	1733	67.13	149	SRX456275	AZGL0000000	Animal	L. reuteri, L. vacciniostercus
Lactobacillus veromoldensis	DSM-14857	2003	Poultry salami	2.37	38.27	2319	50.56	62	SRX456244	AZFA0000000	Food	L. alimentarius
Lactobacillus vini	DSM-20605	2006	Mast of grape	2.24	37.54	2191	53.62	269	SRX456339	AYYX0000000	Plant	L. salivarius
Lactobacillus xiangfangensis	LMG-26013	2012	Pickles	3.00	45.1	2806	80.11	145	ERX359765	QJCL0000000	Food	L. plantarum
Lactobacillus zeae	DSM-20178	1959	Corn steep liquor	3.12	47.74	3043	38.45	55	SRX456369	AZCT0000000	Wine product	L. manihotivorum, L. casei
Lactobacillus zymae	DSM-16395	2005	Artisanal wheat sourdough	2.71	53.57	2460	88.66	75	ERX399772	AZDW0000000	Food	L. brevis, L. collinoides
Lactococcus lactis	LMG-1760	1873	Anchu mash	2.25	35.02	2237	89.07	45	ERX359766	QJCM0000000	Food	Other
Leuconostoc argentinum	KCTC-3773	1993	Raw milk	1.72	42.89	1821	NA	98	NA	AEQQ0000000	Food	Leu_Fru
Leuconostoc carnosum	JB16	1989	Kinchi	1.77	37.13	1711	NA	5	NA	T903S31 - CP0385	Food	Leu_Fru
Leuconostoc citrum	KM20	2008	Kinchi	1.90	38.87	1866	NA	5	NA	Q489736 - DQ48974	Food	Leu_Fru
Leuconostoc fallax	KCTC-3537	1992	Sauerkraut	1.64	37.53	1916	NA	30	NA	AELZ0000000	Food	Leu_Fru
Leuconostoc gasicomitatum	LMG-18811	2001	Tomato-marinated broiler meat strips	1.95	36.66	1929	NA	1	NA	FNS22744	Food	Leu_Fru
Leuconostoc gelidium	KCTC-3527	1989	Vacuum packaged beef	1.96	36.6	1951	NA	43	NA	AEMB0000000	Food	Leu_Fru
Leuconostoc kimchi	DSSN-11154	2000	Kinchi	2.10	37.91	2110	NA	6	NA	T901753 - CP00175	Food	Leu_Fru
Leuconostoc mesenteroides	ATCC-8293	1878	Fermenting olives	2.08	37.67	2056	NA	2	NA	C_008496_NC_0085	Food	Leu_Fru
Leuconostoc mesenteroides cremoris	ATCC-19254	1929	Hansen's dried starter powder	1.74	37.9	1791	NA	29	NA	C2K801	Unknown	Leu_Fru
Leuconostoc pseudomesenteroides	482	N/A	N/A	2.01	39.06	2180	NA	106	NA	CARKV0000000	Food	Leu_Fru
Oenococcus kitaharae	DSM-17330	2006	Distilled residue of shochu mashes	1.84	42.68	1900	NA	2	NA	AFVZ0000000	Wine product	Oenococcus
Oenococcus oeni	ATCC-BAA-1163	2002	Fermented beverages	1.75	37.94	2055	NA	62	NA	AAUV0000000	Wine product	Oenococcus
Olsenella uli	DSM-7084	1991	Human gingival crevice	2.06	64.69	1848	97.22	13	ERX399771	QJCO0000000	Animal	Other
Pediococcus acidilactici	ASI.2096	N/A	N/A	1.93	42.13	1849	51.85	18	SRX689743	QJQA0000000	Unknown	Pediococcus
Pediococcus argentinus	DSM-23026	2008	Fermented wheat flour	1.76	36.67	1772	56.66	93	SRX689746	QJQC0000000	Food	Pediococcus
Pediococcus cellicola	DSM-17757	2005	Distilled piri-fermenting cellar	2.04	39.04	1974	49.06	22	SRX689747	QJBR0000000	Wine product	Pediococcus
Pediococcus classeni	DSM-14800	2002	Spilled beer	1.88	36.74	1807	53.21	44	SRX689748	QJBB0000000	Wine product	Pediococcus
Pediococcus damnosus	DSM-20331	1903	Lager beer yeast	2.19	38.23	2085	45.63	201	SRX689749	QJBR0000000	Wine product	Pediococcus
Pediococcus ethanolifurans	DSM-22301	2006	Walls of a distilled-spirit-fermenting cellar	2.26	37.18	2180	44.23	66	SRX689750	QJBY0000000	Wine product	Pediococcus
Pediococcus inopinatus	DSM-20285	1988	Brewery yeast	2.11	38.61	2081	47.30	157	SRX689751	QJBC0000000	Wine product	Pediococcus
Pediococcus holi	DSM-19927	1887	Ryegrass silage	2.04	42.13	1971	49.00	31	SRX689752	QJCC0000000	Plant	Pediococcus
Pediococcus parvulus	DSM-20332	1961	Silage	3.99	40.38	3917	25.04	153	SRX689754	QJBE0000000	Plant	Pediococcus
Pediococcus pentosaceus	DSM-20336	1934	Dried American beer yeast	1.74	37.25	1887	57.49	28	SRX689755	QJBF0000000	Wine product	Pediococcus
Pediococcus stilesii	DSM-18001	2006	White maize grains	1.84	38.11	1834	54.41	47	SRX689756	QJBX0000000	Plant	Pediococcus
Weissella confusa	DSM-20396	1969	Sugar cane	2.22	44.73	2075	90.16	40	ERX359705	QJAV0000000	Plant	Weissella
Weissella halotolerans	DSM-20190	1983	Sausage	1.37	43.06	1341	146.41	12	ERX359698	QJBO0000000	Food	Weissella
Weissella kandleri	DSM-20593	1983	Desert spring	1.33	39.67	1281	149.88	21	ERX359708	QJBP0000000	Environment	Weissella
Weissella viridescens	DSM-20014	1983	Milking machine slime	1.77	39.29	1777	112.85	59	ERX359773	QJCD0000000	Food	Weissella
Weissella vinifera	DSM-20410	1957	Cured meat products	1.54	41.09	1525	130.11	8	ERX359781	QJBM0000000	Food	Weissella

Table S2. Sequence information for the 73 core genes

PID*	Gene	locus tag*	COG	Annotation	Co-ordinates*	Strand*	Length*
90960992	<i>dnaN</i>	LSL_0002	COG0592L	DNA polymerase III subunit beta	1532..2671	+	1140
90960995	<i>gyrB</i>	LSL_0005	COG0187L	DNA gyrase subunit B	4451..6409	+	1959
90960996	<i>gyrA</i>	LSL_0006	COG0188L	DNA gyrase subunit A	6446..8998	+	2553
90960997	<i>rpsF</i>	LSL_0007	COG0360J	30S ribosomal protein S6	9217..9507	+	291
90960998	<i>ssb</i>	LSL_0008	COG0629L	Single-strand DNA binding protein	9548..10099	+	552
90960999	<i>rpsR</i>	LSL_0009	COG0238J	30S ribosomal protein S18	10121..10357	+	237
90961180	<i>rpoC</i>	LSL_0198	COG0086K	DNA-directed RNA polymerase subunit beta'	238653..242318	+	3666
90961182	<i>rpsL</i>	LSL_0200	COG0048J	30S ribosomal protein S12	243364..243777	+	414
90961184	<i>efg</i>	LSL_0202	COG0480J	elongation factor G	244403..246496	+	2094
90961200	<i>trpS</i>	LSL_0218	COG0180J	Tryptophanyl-tRNA synthetase II	271973..272992	+	1020
90961335	<i>murF</i>	LSL_0355	COG0770M	UDP-N-acetylmuramoyl-tripeptide--D-alanyl-D-alanine ligase	387857..389227	+	1371
90961453	-	LSL_0477	COG0537FGR	bis(5'-nucleosyl)-tetrphosphatase	525874..526302	-	429
90961460	-	LSL_0484	COG0073R	tRNA-binding domain-containing protein	530707..531357	+	651
90961464	<i>polA</i>	LSL_0488	COG0749L	DNA polymerase I	536545..539223	+	2679
90961470	<i>thrS</i>	LSL_0494	COG0441J	threonyl-tRNA synthetase	543759..545708	+	1950
90961471	<i>infC</i>	LSL_0495	COG0290J	translation initiation factor IF-3	545916..546440	+	525
90961480	-	LSL_0504	COG0799S	lojap-related protein	552036..552389	+	354
90961487	<i>rpsB</i>	LSL_0511	COG0052J	30S ribosomal protein S2	557234..558031	+	798
90961488	<i>tsf</i>	LSL_0512	COG0264J	elongation factor Ts	558125..559000	+	876
90961519	-	LSL_0543	COG0218R	GTP-binding protein	584473..585063	+	591
90961537	<i>pyrH</i>	LSL_0561	COG0528F	uridylate kinase	600230..600952	+	723
90961538	<i>frr</i>	LSL_0562	COG0233J	ribosome recycling factor	600955..601518	+	564
90961539	<i>uppS</i>	LSL_0563	COG0020I	undecaprenyl pyrophosphate synthetase	601653..602435	+	783
90961540	<i>cdsA</i>	LSL_0564	COG0575I	phosphatidate cytidylyltransferase	602438..603226	+	789
90961544	-	LSL_0568	COG0779S	hypothetical protein	610934..611407	+	474
90961545	<i>nusA</i>	LSL_0569	COG0195K	transcription elongation factor NusA	611433..612560	+	1128
90961567	-	LSL_0591	COG2890J	peptide release factor--glutamine N5-methyltransferase	634747..635586	+	840
90961569	<i>upp</i>	LSL_0593	COG0035F	uracil phosphoribosyltransferase	636708..637337	+	630
90961575	<i>atpG</i>	LSL_0599	COG0224C	FOF1 ATP synthase subunit gamma	641185..642114	+	930
90961576	<i>atpD</i>	LSL_0600	COG0055C	FOF1 ATP synthase subunit beta	642139..643545	+	1407
90961630	<i>typA</i>	LSL_0653	COG1217T	GTP-binding protein	697034..698875	+	1842
90961790	<i>pheS</i>	LSL_0813	COG0016J	phenylalanyl-tRNA synthetase subunit alpha	829184..830230	+	1047
90961836	<i>pfs</i>	LSL_0859	COG0775F	5'-methylthioadenosine nucleosidase	878731..879417	+	687
90962022	<i>ftsZ</i>	LSL_1047	COG0206D	cell division protein FtsZ	1070613..1071866	-	1254
90962026	<i>murD</i>	LSL_1051	COG0771M	UDP-N-acetylmuramoyl-L-alanyl-D-glutamate synthetase	1075412..1076788	-	1377
90962027	<i>mraY</i>	LSL_1052	COG0472M	phospho-N-acetylmuramoyl-pentapeptide-transferase	1076817..1077785	-	969
90962042	<i>mreC</i>	LSL_1067	COG1792M	rod shape-determining protein MreC	1089421..1090275	-	855
90962072	<i>obgE</i>	LSL_1097	COG0536R	GTPase ObgE	1125579..1126877	-	1299
90962084	-	LSL_1109	COG0816L	Holliday junction resolvase-like protein	1136102..1136533	-	432
90962100	<i>ruvB</i>	LSL_1125	COG2255L	Holliday junction DNA helicase RuvB	1153506..1154516	-	1011
90962101	<i>ruvA</i>	LSL_1126	COG0632L	Holliday junction DNA helicase RuvA	1154555..1155160	-	606
90962106	<i>pgsA</i>	LSL_1131	COG0558I	CDP--diacylglycerol--glycerol-3-phosphate 3-phosphatidyltransferase	1163042..1163629	-	588
90962110	<i>ftsK</i>	LSL_1135	COG1674D	cell division protein	1168139..1170418	-	2280
90962125	-	LSL_1150	COG0802R	ATP/GTP hydrolase	1183489..1183941	-	453
90962130	<i>smpB</i>	LSL_1155	COG0691O	SsrA-binding protein	1187273..1187740	-	468
90962160	<i>prfB</i>	LSL_1185	COG1186J	peptide chain release factor 2	1222388..1223455	-	1068
90962186	<i>groEL</i>	LSL_1211	COG0459O	molecular chaperone GroEL	1246385..1248007	-	1623
90962187	<i>groS</i>	LSL_1212	COG0234O	molecular chaperone GroES	1248037..1248321	-	285
90962191	<i>gcp</i>	LSL_1216	COG0533O	O-sialoglycoprotein endopeptidase	1252076..1253107	-	1032
90962198	<i>holB</i>	LSL_1223	COG2812L	DNA polymerase III subunit delta'	1257561..1258553	-	993
90962199	<i>tmk</i>	LSL_1224	COG0125F	thymidylate kinase	1258588..1259214	-	627
90962204	-	LSL_1229	COG0590FJ	cytosine/adenosine deaminase	1262491..1262991	-	501
90962212	<i>rplJ</i>	LSL_1238	COG0244J	50S ribosomal protein L10	1271311..1271814	-	504
90962215	<i>nusG</i>	LSL_1241	COG0250K	transcription antitermination protein	1273402..1273962	-	561
90962219	<i>spoU</i>	LSL_1245	COG0566J	tRNA/tRNA methyltransferase	1275013..1275759	-	747
90962221	<i>cysS</i>	LSL_1247	COG0215J	cysteinylyl-tRNA synthetase	1276159..1277571	-	1413
90962278	<i>ppnK</i>	LSL_1304	COG0061G	inorganic polyphosphate/ATP-NAD kinase	1351254..1352060	-	807
90962327	-	LSL_1355	COG0037D	tRNA(Ile)-lysine synthase TilS	1418710..1420068	-	1359
90962332	<i>mfd</i>	LSL_1360	COG1197LK	transcription-repair coupling factor	1422969..1426493	-	3525
90962333	<i>pth</i>	LSL_1361	COG0193J	peptidyl-tRNA hydrolase	1426515..1427072	-	558
90962374	<i>rplM</i>	LSL_1403	COG0102J	50S ribosomal protein L13	1478312..1478755	-	444
90962376	<i>chiQ</i>	LSL_1405	COG0619P	cobalt transport permease	1479676..1480470	-	795
90962380	<i>rpoA</i>	LSL_1409	COG0202K	DNA-directed RNA polymerase subunit alpha	1482888..1483832	-	945
90962387	<i>rplO</i>	LSL_1416	COG0200J	50S ribosomal protein L15	1487364..1487798	-	435
90962389	<i>rpsE</i>	LSL_1418	COG0098J	30S ribosomal protein S5	1488030..1488530	-	501
90962391	<i>rplF</i>	LSL_1420	COG0097J	50S ribosomal protein L6	1488953..1489489	-	537
90962392	<i>rpsH</i>	LSL_1421	COG0096J	30S ribosomal protein S8	1489522..1489920	-	399
90962394	<i>rplE</i>	LSL_1423	COG0094J	50S ribosomal protein L5	1490153..1490695	-	543
90962400	<i>rpsC</i>	LSL_1429	COG0092J	30S ribosomal protein S3	1492402..1493058	-	657
90962404	<i>rplW</i>	LSL_1433	COG0089J	50S ribosomal protein L23	1494625..1494909	-	285
90962405	<i>rplD</i>	LSL_1434	COG0088J	50S ribosomal protein L4	1494909..1495532	-	624
90962406	<i>rplC</i>	LSL_1435	COG0087J	50S ribosomal protein L3	1495557..1496180	-	624
90962696	<i>rplI</i>	LSL_1727	COG0359J	50S ribosomal protein L9	1809124..1809573	-	450

*These columns are provided according to the reference genome *L. salivarius* UCC118

Table S3. Genera used in building the tree of bacteria

Accession No.	Phylum	Class	Order	Family	Genus	Species	
NC_012483	Acidobacteria	Acidobacteria	Acidobacteriales	Acidobacteriaceae	<i>Acidobacterium</i>	<i>Acidobacterium capsulatum</i>	
NC_014963	Acidobacteria	Acidobacteria	Acidobacteriales	Acidobacteriaceae	<i>Terriglobus</i>	<i>Terriglobus saanensis</i>	
NC_015064	Acidobacteria	Acidobacteria	Acidobacteriales	Acidobacteriaceae	<i>Granulicella</i>	<i>Granulicella tundricola</i>	
NC_008536	Acidobacteria	Solibacteres	Solibacteriales	Solibacteriaceae	<i>Candidatus Solibacter</i>	<i>Candidatus Solibacter ustitatus</i>	
NC_008009	Acidobacteria	Unclassified	Unclassified	Unclassified	<i>Candidatus Koribacter</i>	<i>Candidatus Koribacter versatilis</i>	
NC_000962	Actinobacteria	Actinobacteria	Actinomycetales	Mycobacteriaceae	<i>Mycobacterium</i>	<i>Mycobacterium tuberculosis</i>	
NC_002935	Actinobacteria	Actinobacteria	Actinomycetales	Corynebacteriaceae	<i>Corynebacterium</i>	<i>Corynebacterium diphtheriae</i>	
NC_003155	Actinobacteria	Actinobacteria	Actinomycetales	Streptomycetaceae	<i>Streptomyces</i>	<i>Streptomyces avermitilis</i>	
NC_004307	Actinobacteria	Actinobacteria	Bifidobacteriales	Bifidobacteriaceae	<i>Bifidobacterium</i>	<i>Bifidobacterium longum</i>	
NC_004551	Actinobacteria	Actinobacteria	Actinomycetales	Unclassified	<i>Tropheryma</i>	<i>Tropheryma whipplei</i>	
NC_006085	Actinobacteria	Actinobacteria	Actinomycetales	Propionibacteriaceae	<i>Propionibacterium</i>	<i>Propionibacterium acnes</i>	
NC_006087	Actinobacteria	Actinobacteria	Actinomycetales	Microbacteriaceae	<i>Leifsonia</i>	<i>Leifsonia xyli</i>	
NC_006361	Actinobacteria	Actinobacteria	Actinomycetales	Nocardiaceae	<i>Nocardia</i>	<i>Nocardia farcinica</i>	
NC_007333	Actinobacteria	Actinobacteria	Actinomycetales	Nocardiopsaceae	<i>Thermobifida</i>	<i>Thermobifida fusca</i>	
NC_007777	Actinobacteria	Actinobacteria	Actinomycetales	Frankiaceae	<i>Frankia</i>	Unclassified	
NC_008148	Actinobacteria	Actinobacteria	Rubrobacterales	Rubrobacteraceae	<i>Rubrobacter</i>	<i>Rubrobacter xylanophilus</i>	
NC_008268	Actinobacteria	Actinobacteria	Actinomycetales	Nocardiaceae	<i>Rhodococcus</i>	<i>Rhodococcus jostii</i>	
NC_008541	Actinobacteria	Actinobacteria	Actinomycetales	Micrococcaceae	<i>Arthrobacter</i>	Unclassified	
NC_008578	Actinobacteria	Actinobacteria	Actinomycetales	Acidothermaceae	<i>Acidothermus</i>	<i>Acidothermus cellulolyticus</i>	
NC_008699	Actinobacteria	Actinobacteria	Actinomycetales	Nocardioidaceae	<i>Nocardioides</i>	Unclassified	
NC_009142	Actinobacteria	Actinobacteria	Actinomycetales	Pseudonocardiaceae	<i>Saccharopolyspora</i>	<i>Saccharopolyspora erythraea</i>	
NC_009380	Actinobacteria	Actinobacteria	Actinomycetales	Micromonosporaceae	<i>Salinispora</i>	<i>Salinispora tropica</i>	
NC_009480	Actinobacteria	Actinobacteria	Actinomycetales	Microbacteriaceae	<i>Clavibacter</i>	<i>Clavibacter michiganensis</i>	
NC_009664	Actinobacteria	Actinobacteria	Actinomycetales	Kineosporiaceae	<i>Kineococcus</i>	<i>Kineococcus radiotolerans</i>	
NC_010168	Actinobacteria	Actinobacteria	Actinomycetales	Micrococcaceae	<i>Renibacterium</i>	<i>Renibacterium salmoninarum</i>	
NC_010617	Actinobacteria	Actinobacteria	Actinomycetales	Micrococcaceae	<i>Kocuria</i>	<i>Kocuria rhizophila</i>	
NC_012669	Actinobacteria	Actinobacteria	Actinomycetales	Beutenbergiaceae	<i>Beutenbergia</i>	<i>Beutenbergia cavernae</i>	
NC_012803	Actinobacteria	Actinobacteria	Actinomycetales	Micrococcaceae	<i>Micrococcus</i>	<i>Micrococcus luteus</i>	
NC_013093	Actinobacteria	Actinobacteria	Actinomycetales	Pseudonocardiaceae	<i>Actinosynnema</i>	<i>Actinosynnema mirum</i>	
NC_013124	Actinobacteria	Actinobacteria	Actinomycetales	Acidimicrobiales	Acidimicrobiaceae	<i>Acidimicrobium</i>	<i>Acidimicrobium ferrooxidans</i>
NC_013131	Actinobacteria	Actinobacteria	Actinomycetales	Catenulisporaceae	<i>Catenulispora</i>	<i>Catenulispora acidiphila</i>	
NC_013159	Actinobacteria	Actinobacteria	Actinomycetales	Pseudonocardiaceae	<i>Saccharomonospora</i>	<i>Saccharomonospora viridis</i>	
NC_013165	Actinobacteria	Actinobacteria	Actinomycetales	Coriobacteriales	Coriobacteriaceae	<i>Slackia</i>	<i>Slackia heliotrinireducens</i>
NC_013169	Actinobacteria	Actinobacteria	Actinomycetales	Dermacoccaceae	<i>Kytococcus</i>	<i>Kytococcus sedentarius</i>	
NC_013170	Actinobacteria	Actinobacteria	Actinomycetales	Coriobacteriales	Coriobacteriaceae	<i>Cryptobacterium</i>	<i>Cryptobacterium curtum</i>
NC_013172	Actinobacteria	Actinobacteria	Actinomycetales	Dermabacteraceae	<i>Brachybacterium</i>	<i>Brachybacterium faecium</i>	
NC_013174	Actinobacteria	Actinobacteria	Actinomycetales	Jonesiaceae	<i>Jonesia</i>	<i>Jonesia dentrificans</i>	
NC_013203	Actinobacteria	Actinobacteria	Actinomycetales	Coriobacteriales	Atopobium	<i>Atopobium parvulum</i>	
NC_013204	Actinobacteria	Actinobacteria	Actinomycetales	Coriobacteriales	Coriobacteriaceae	<i>Eggerthella</i>	<i>Eggerthella lenta</i>
NC_013235	Actinobacteria	Actinobacteria	Actinomycetales	Nakamurellaceae	<i>Nakamurella</i>	<i>Nakamurella multipartita</i>	
NC_013510	Actinobacteria	Actinobacteria	Actinomycetales	Thermomonosporaceae	<i>Thermomonospora</i>	<i>Thermomonospora curvata</i>	
NC_013521	Actinobacteria	Actinobacteria	Actinomycetales	Sanguibacteraceae	<i>Sanguibacter</i>	<i>Sanguibacter keddicii</i>	
NC_013530	Actinobacteria	Actinobacteria	Actinomycetales	Promicromonosporaceae	<i>Xylanimonas</i>	<i>Xylanimonas cellulositytica</i>	
NC_013595	Actinobacteria	Actinobacteria	Actinomycetales	Streptosporangiaceae	<i>Streptosporangium</i>	<i>Streptosporangium roseum</i>	
NC_013715	Actinobacteria	Actinobacteria	Actinomycetales	Micrococcaceae	<i>Rothia</i>	<i>Rothia mucilaginosus</i>	
NC_013721	Actinobacteria	Actinobacteria	Actinomycetales	Bifidobacteriaceae	<i>Gardnerella</i>	<i>Gardnerella vaginalis</i>	
NC_013739	Actinobacteria	Actinobacteria	Actinomycetales	Solirubrobacteriales	Conexibacteraceae	<i>Conexibacter</i>	<i>Conexibacter woesei</i>
NC_013947	Actinobacteria	Actinobacteria	Actinomycetales	Glycomycetaceae	<i>Stackebrandtia</i>	<i>Stackebrandtia nassauensis</i>	
NC_014151	Actinobacteria	Actinobacteria	Actinomycetales	Cellulomonadaceae	<i>Cellulomonas</i>	<i>Cellulomonas flavigena</i>	
NC_014158	Actinobacteria	Actinobacteria	Actinomycetales	Tsukamurellaceae	<i>Tsukamurella</i>	<i>Tsukamurella paurometabola</i>	
NC_014165	Actinobacteria	Actinobacteria	Actinomycetales	Pseudonocardiaceae	<i>Thermobispora</i>	<i>Thermobispora bispora</i>	
NC_014168	Actinobacteria	Actinobacteria	Actinomycetales	Segniliparaceae	<i>Segniliparus</i>	<i>Segniliparus rotundus</i>	
NC_014218	Actinobacteria	Actinobacteria	Actinomycetales	Actinomycetaceae	<i>Arcanobacterium</i>	<i>Arcanobacterium haemolyticum</i>	
NC_014246	Actinobacteria	Actinobacteria	Actinomycetales	Actinomycetaceae	<i>Mobiluncus</i>	<i>Mobiluncus curtisii</i>	
NC_014318	Actinobacteria	Actinobacteria	Actinomycetales	Pseudonocardiaceae	<i>Amycolatopsis</i>	<i>Amycolatopsis mediterranei</i>	
NC_014363	Actinobacteria	Actinobacteria	Actinomycetales	Coriobacteriales	Coriobacteriaceae	<i>Olsenella</i>	<i>Olsenella uli</i>
NC_014830	Actinobacteria	Actinobacteria	Actinomycetales	Intrasporangiaceae	<i>Intrasporangium</i>	<i>Intrasporangium calvum</i>	
NC_015125	Actinobacteria	Actinobacteria	Actinomycetales	Microbacteriaceae	<i>Microbacterium</i>	<i>Microbacterium testaceum</i>	
NC_015312	Actinobacteria	Actinobacteria	Actinomycetales	Pseudonocardiaceae	<i>Pseudonocardia</i>	<i>Pseudonocardia dioxanivorans</i>	
NC_015389	Actinobacteria	Actinobacteria	Actinomycetales	Coriobacteriales	Coriobacteriaceae	<i>Coriobacterium</i>	<i>Coriobacterium glomerans</i>
NC_015564	Actinobacteria	Actinobacteria	Actinomycetales	Mycobacteriaceae	<i>Amycolicococcus</i>	<i>Amycolicococcus subflavus</i>	
NC_015588	Actinobacteria	Actinobacteria	Actinomycetales	Promicromonosporaceae	<i>Isoperitcola</i>	<i>Isoperitcola variabilis</i>	
NC_015635	Actinobacteria	Actinobacteria	Actinomycetales	Propionibacteriaceae	<i>Microclunatus</i>	<i>Microclunatus phosphovorius</i>	
NC_000918	Aquificae	Aquificae	Aquificales	Aquificaceae	<i>Aquifex</i>	<i>Aquifex aeolicus</i>	
NC_010730	Aquificae	Aquificae	Aquificales	Hydrogenothermaceae	<i>Sulfurihydrogenibium</i>	Unclassified	
NC_011126	Aquificae	Aquificae	Aquificales	Aquificaceae	<i>Hydrogenobaculum</i>	Unclassified	
NC_012440	Aquificae	Aquificae	Aquificales	Hydrogenothermaceae	<i>Persephonella</i>	<i>Persephonella marina</i>	
NC_013799	Aquificae	Aquificae	Aquificales	Aquificaceae	<i>Hydrogenobacter</i>	<i>Hydrogenobacter thermophilus</i>	
NC_013894	Aquificae	Aquificae	Aquificales	Aquificaceae	<i>Thermocrinis</i>	<i>Thermocrinis albus</i>	
NC_014926	Aquificae	Aquificae	Aquificales	Desulfurobacteriaceae	<i>Thermovibrio</i>	<i>Thermovibrio ammonificans</i>	
NC_015185	Aquificae	Aquificae	Aquificales	Desulfurobacteriaceae	<i>Desulfurobacterium</i>	<i>Desulfurobacterium thermolithotrophum</i>	
NC_002950	Bacteroidetes	Bacteroidia	Bacteroidales	Porphyromonadaceae	<i>Porphyromonas</i>	<i>Porphyromonas gingivalis</i>	
NC_003228	Bacteroidetes	Bacteroidia	Bacteroidales	Bacteroidaceae	<i>Bacteroides</i>	<i>Bacteroides fragilis</i>	
NC_009615	Bacteroidetes	Bacteroidia	Bacteroidales	Porphyromonadaceae	<i>Parabacteroides</i>	<i>Parabacteroides distans</i>	
NC_011565	Bacteroidetes	Bacteroidia	Bacteroidales	Unclassified	<i>Candidatus Azobacteroides</i>	<i>Candidatus Azobacteroides pseudotrichonymphae</i>	
NC_014033	Bacteroidetes	Bacteroidia	Bacteroidales	Prevotellaceae	<i>Prevotella</i>	<i>Prevotella ruminicola</i>	
NC_014734	Bacteroidetes	Bacteroidia	Bacteroidales	Porphyromonadaceae	<i>Paludibacter</i>	<i>Paludibacter propionicigenes</i>	
NC_015160	Bacteroidetes	Bacteroidia	Bacteroidales	Porphyromonadaceae	<i>Odoribacter</i>	<i>Odoribacter splanchnicus</i>	
NC_008255	Bacteroidetes	Cytophagia	Cytophagales	Cytophagaceae	<i>Cytophaga</i>	<i>Cytophaga hutchinsonii</i>	
NC_013037	Bacteroidetes	Cytophagia	Cytophagales	Cytophagaceae	<i>Dyadobacter</i>	<i>Dyadobacter fermentans</i>	
NC_013730	Bacteroidetes	Cytophagia	Cytophagales	Cytophagaceae	<i>Spirosoma</i>	<i>Spirosoma linguale</i>	
NC_014655	Bacteroidetes	Cytophagia	Cytophagales	Cytophagaceae	<i>Leadbetterella</i>	<i>Leadbetterella byssophila</i>	
NC_014759	Bacteroidetes	Cytophagia	Cytophagales	Flammeovirgaceae	<i>Marivirga</i>	<i>Marivirga tractuosa</i>	
NC_015703	Bacteroidetes	Cytophagia	Cytophagales	Cytophagaceae	<i>Runella</i>	<i>Runella slithyformis</i>	
NC_015914	Bacteroidetes	Cytophagia	Cytophagales	Cyclobacteriaceae	<i>Cyclobacterium</i>	<i>Cyclobacterium marinum</i>	
NC_008571	Bacteroidetes	Flavobacteria	Flavobacteriales	Flavobacteriaceae	<i>Gramella</i>	<i>Gramella forsetii</i>	
NC_009441	Bacteroidetes	Flavobacteria	Flavobacteriales	Flavobacteriaceae	<i>Flavobacterium</i>	<i>Flavobacterium johnsoniae</i>	

NC_013123	Bacteroidetes	Flavobacteria	Flavobacteriales	Unclassified	<i>Candidatus Sulcia</i>	<i>Candidatus Sulcia muelleri</i>
NC_013162	Bacteroidetes	Flavobacteria	Flavobacteriales	Flavobacteriaceae	<i>Capnocytophaga</i>	<i>Capnocytophaga ochracea</i>
NC_013222	Bacteroidetes	Flavobacteria	Flavobacteriales	Flavobacteriaceae	<i>Robiginitalea</i>	<i>Robiginitalea biformata</i>
NC_013418	Bacteroidetes	Flavobacteria	Flavobacteriales	Blattabacteriaceae	<i>Blattabacterium</i>	<i>Blattabacterium</i> sp. (<i>Periplaneta americana</i>)
NC_014041	Bacteroidetes	Flavobacteria	Flavobacteriales	Flavobacteriaceae	<i>Zunongwangia</i>	<i>Zunongwangia profunda</i>
NC_014230	Bacteroidetes	Flavobacteria	Flavobacteriales	Flavobacteriaceae	<i>Croceibacter</i>	<i>Croceibacter atlanticus</i>
NC_014472	Bacteroidetes	Flavobacteria	Flavobacteriales	Flavobacteriaceae	<i>Maribacter</i>	Unclassified
NC_014738	Bacteroidetes	Flavobacteria	Flavobacteriales	Flavobacteriaceae	<i>Riemerella</i>	<i>Riemerella anatipestifer</i>
NC_014934	Bacteroidetes	Flavobacteria	Flavobacteriales	Flavobacteriaceae	<i>Cellulophaga</i>	<i>Cellulophaga algicola</i>
NC_015144	Bacteroidetes	Flavobacteria	Flavobacteriales	Flavobacteriaceae	<i>Weeksella</i>	<i>Weeksella virosa</i>
NC_015321	Bacteroidetes	Flavobacteria	Flavobacteriales	Cryomorphaeae	<i>Fluviicola</i>	<i>Fluviicola taffensis</i>
NC_015496	Bacteroidetes	Flavobacteria	Flavobacteriales	Flavobacteriaceae	<i>Krokinobacter</i>	Unclassified
NC_015638	Bacteroidetes	Flavobacteria	Flavobacteriales	Flavobacteriaceae	<i>Lacinutrix</i>	Unclassified
NC_015844	Bacteroidetes	Flavobacteria	Flavobacteriales	Flavobacteriaceae	<i>Zobellia</i>	Unclassified
NC_015945	Bacteroidetes	Flavobacteria	Flavobacteriales	Flavobacteriaceae	<i>Muricauda</i>	<i>Muricauda ruestringensis</i>
NC_013061	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Sphingobacteriaceae	<i>Pedobacter</i>	<i>Pedobacter heparinus</i>
NC_013132	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Unclassified	<i>Chitinophaga</i>	<i>Chitinophaga pinensis</i>
NC_015277	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Sphingobacteriaceae	<i>Sphingobacterium</i>	Unclassified
NC_015510	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Saprospiraceae	<i>Haliscomenobacter</i>	<i>Haliscomenobacter hydrossis</i>
NC_007677	Bacteroidetes	Unclassified	Bacteroidetes Order II	Rhodothermaceae	<i>Salinibacter</i>	<i>Salinibacter ruber</i>
NC_010830	Bacteroidetes	Unclassified	Unclassified	Unclassified	<i>Candidatus Amoebophilus</i>	<i>Candidatus Amoebophilus asiaticus</i>
NC_015966	Bacteroidetes	Unclassified	Bacteroidetes Order II	Rhodothermaceae	<i>Rhodothermus</i>	<i>Rhodothermus marinus</i>
NC_000117	Chlamydiae	Chlamydia	Chlamydiales	Chlamydiaceae	<i>Chlamydia</i>	<i>Chlamydia trachomatis</i>
NC_003361	Chlamydiae	Chlamydia	Chlamydiales	Chlamydiaceae	<i>Chlamydomydia</i>	<i>Chlamydomydia caviae</i>
NC_005861	Chlamydiae	Chlamydia	Chlamydiales	Parachlamydiaceae	<i>Candidatus Protochlamydia</i>	<i>Candidatus Protochlamydia amoebophila</i>
NC_014225	Chlamydiae	Chlamydia	Chlamydiales	Waddliaceae	<i>Waddlia</i>	<i>Waddlia chondrophila</i>
NC_015702	Chlamydiae	Chlamydia	Chlamydiales	Parachlamydiaceae	<i>Parachlamydia</i>	<i>Parachlamydia acanthamoebae</i>
NC_015713	Chlamydiae	Chlamydia	Chlamydiales	Simkaniaceae	<i>Simkania</i>	<i>Simkania negevensis</i>
NC_002932	Chlorobiales	Chlorobia	Chlorobiales	Chlorobiaceae	<i>Chlorobaculum</i>	<i>Chlorobaculum tepidum</i>
NC_007514	Chlorobi	Chlorobia	Chlorobiales	Chlorobiaceae	<i>Chlorobium</i>	<i>Chlorobium chlorochromatii</i>
NC_011026	Chlorobi	Chlorobia	Chlorobiales	Chlorobiaceae	<i>Chloroherpeton</i>	<i>Chloroherpeton thalassium</i>
NC_011059	Chlorobi	Chlorobia	Chlorobiales	Chlorobiaceae	<i>Prosthecochloris</i>	<i>Prosthecochloris aestuarii</i>
NC_011060	Chlorobi	Chlorobia	Chlorobiales	Chlorobiaceae	<i>Pelodictyon</i>	<i>Pelodictyon phaeoclastratiforme</i>
NC_014960	Chloroflexi	Anaerolineae	Anaerolineales	Anaerolineaceae	<i>Anaerolinea</i>	<i>Anaerolinea thermophila</i>
NC_009523	Chloroflexi	Chloroflexi	Chloroflexales	Chloroflexaceae	<i>Roseiflexus</i>	Unclassified
NC_009972	Chloroflexi	Chloroflexi	Herpetosiphonales	Herpetosiphonaceae	<i>Herpetosiphon</i>	<i>Herpetosiphon aurantiacus</i>
NC_010175	Chloroflexi	Chloroflexi	Chloroflexales	Chloroflexaceae	<i>Chloroflexus</i>	<i>Chloroflexus aurantiacus</i>
NC_002936	Chloroflexi	Dehalococcoidia	Dehalococcoidales	Dehalococcoidaceae	<i>Dehalococcoides</i>	<i>Dehalococcoides mccartyi</i>
NC_014314	Chloroflexi	Dehalococcoidia	Unclassified	Unclassified	<i>Dehalogenimonas</i>	<i>Dehalogenimonas lykanthroporepellens</i>
NC_011959	Chloroflexi	Thermomicrobia	Thermomicrobiales	Thermomicrobiaceae	<i>Thermomicrobium</i>	<i>Thermomicrobium roseum</i>
NC_013523	Chloroflexi	Thermomicrobia	Sphaerobacterales	Sphaerobacteraceae	<i>Sphaerobacter</i>	<i>Sphaerobacter thermophilus</i>
NC_014836	Chrysiogenetes	Chrysiogenetes	Chrysiogenales	Chrysiogenaceae	<i>Desulfurispirillum</i>	<i>Desulfurispirillum indicum</i>
NC_005125	Cyanobacteria	Gloeobacteria	Gloeobacterales	Unclassified	<i>Gloeobacter</i>	<i>Gloeobacter violaceus</i>
NC_003272	Cyanobacteria	Unclassified	Nostocales	Nostocaceae	<i>Nostoc</i>	Unclassified
NC_004113	Cyanobacteria	Unclassified	Chroococcales	Unclassified	<i>Thermosynechococcus</i>	<i>Thermosynechococcus elongatus</i>
NC_005042	Cyanobacteria	Unclassified	Prochlorales	Prochlorococcaceae	<i>Prochlorococcus</i>	<i>Prochlorococcus marinus</i>
NC_005070	Cyanobacteria	Unclassified	Chroococcales	Unclassified	<i>Synechococcus</i>	Unclassified
NC_007413	Cyanobacteria	Unclassified	Nostocales	Nostocaceae	<i>Anabaena</i>	<i>Anabaena variabilis</i>
NC_008312	Cyanobacteria	Unclassified	Oscillatoriales	Unclassified	<i>Trichodesmium</i>	<i>Trichodesmium erythraeum</i>
NC_011726	Cyanobacteria	Unclassified	Chroococcales	Unclassified	<i>Cyanothece</i>	Unclassified
NC_014248	Cyanobacteria	Unclassified	Nostocales	Nostocaceae	<i>Trichormus</i>	<i>Trichormus azollae</i>
NC_013939	Deferribacteres	Deferribacteres	Deferribacterales	Deferribacteraceae	<i>Deferribacter</i>	<i>Deferribacter desulfuricans</i>
NC_013943	Deferribacteres	Deferribacteres	Deferribacterales	Deferribacteraceae	<i>Denitrovibrio</i>	<i>Denitrovibrio acetiphilus</i>
NC_014758	Deferribacteres	Deferribacteres	Deferribacterales	Deferribacteraceae	<i>Calditerrivibrio</i>	<i>Calditerrivibrio nitroreducens</i>
NC_015672	Deferribacteres	Deferribacteres	Deferribacterales	Deferribacteraceae	<i>Flexistipes</i>	<i>Flexistipes sinusarabici</i>
NC_001263	Deinococcus-Therm	Deinococci	Deinococcales	Deinococcaceae	<i>Deinococcus</i>	<i>Deinococcus radiodurans</i>
NC_005835	Deinococcus-Therm	Deinococci	Thermales	Thermaceae	<i>Thermus</i>	<i>Thermus thermophilus</i>
NC_013946	Deinococcus-Therm	Deinococci	Thermales	Thermaceae	<i>Meiothermus</i>	<i>Meiothermus ruber</i>
NC_014221	Deinococcus-Therm	Deinococci	Deinococcales	Trueperaceae	<i>Truepera</i>	<i>Truepera radiovictrix</i>
NC_014761	Deinococcus-Therm	Deinococci	Thermales	Thermaceae	<i>Oceanithermus</i>	<i>Oceanithermus profundus</i>
NC_015387	Deinococcus-Therm	Deinococci	Thermales	Thermaceae	<i>Marinithermus</i>	<i>Marinithermus hydrothermalis</i>
NC_011297	Dictyoglomi	Dictyoglomia	Dictyoglomales	Dictyoglomaceae	<i>Dictyoglomium</i>	<i>Dictyoglomium thermophilum</i>
NC_010644	Elusimicrobia	Elusimicrobia	Elusimicrobiales	Elusimicrobiaceae	<i>Elusimicrobium</i>	<i>Elusimicrobium minutum</i>
NC_013410	Fibrobacteres	Fibrobacteria	Fibrobacterales	Fibrobacteraceae	<i>Fibrobacter</i>	<i>Fibrobacter succinogenes</i>
NC_000964	Firmicutes	Bacilli	Bacillales	Bacillaceae	<i>Bacillus</i>	<i>Bacillus subtilis</i>
NC_002662	Firmicutes	Bacilli	Lactobacillales	Streptococcaceae	<i>Lactococcus</i>	<i>Lactococcus lactis</i>
NC_002737	Firmicutes	Bacilli	Lactobacillales	Streptococcaceae	<i>Streptococcus</i>	<i>Streptococcus pyogenes</i>
NC_002745	Firmicutes	Bacilli	Bacillales	Staphylococcaceae	<i>Staphylococcus</i>	<i>Staphylococcus aureus</i>
NC_004193	Firmicutes	Bacilli	Bacillales	Bacillaceae	<i>Oceanobacillus</i>	<i>Oceanobacillus iheyensis</i>
NC_004567	Firmicutes	Bacilli	Lactobacillales	Lactobacillaceae	<i>Lactobacillus</i>	<i>Lactobacillus plantarum</i>
NC_006510	Firmicutes	Bacilli	Bacillales	Bacillaceae	<i>Geobacillus</i>	<i>Geobacillus kaustophilus</i>
NC_008525	Firmicutes	Bacilli	Lactobacillales	Lactobacillaceae	<i>Pediococcus</i>	<i>Pediococcus pentosaceus</i>
NC_008528	Firmicutes	Bacilli	Lactobacillales	Leuconostocaceae	<i>Oenococcus</i>	<i>Oenococcus oeni</i>
NC_008531	Firmicutes	Bacilli	Lactobacillales	Leuconostocaceae	<i>Leuconostoc</i>	<i>Leuconostoc mesenteroides</i>
NC_008555	Firmicutes	Bacilli	Bacillales	Listeriaceae	<i>Listeria</i>	<i>Listeria welshimeri</i>
NC_010556	Firmicutes	Bacilli	Bacillales	Unclassified	<i>Exiguobacterium</i>	<i>Exiguobacterium sibiricum</i>
NC_011567	Firmicutes	Bacilli	Bacillales	Bacillaceae	<i>Anoxybacillus</i>	<i>Anoxybacillus flavithermus</i>
NC_011999	Firmicutes	Bacilli	Bacillales	Staphylococcaceae	<i>Macrocooccus</i>	<i>Macrocooccus caseolyticus</i>
NC_012491	Firmicutes	Bacilli	Bacillales	Paenibacillaceae	<i>Brevibacillus</i>	<i>Brevibacillus brevis</i>
NC_012914	Firmicutes	Bacilli	Bacillales	Paenibacillaceae	<i>Paenibacillus</i>	Unclassified
NC_013205	Firmicutes	Bacilli	Bacillales	Alicyclobacillaceae	<i>Alicyclobacillus</i>	<i>Alicyclobacillus acidocaldarius</i>
NC_014098	Firmicutes	Bacilli	Bacillales	Alicyclobacillaceae	<i>Kyrpidia</i>	<i>Kyrpidia tusciae</i>
NC_015278	Firmicutes	Bacilli	Lactobacillales	Aerococcaceae	<i>Aerococcus</i>	<i>Aerococcus urinae</i>
NC_015391	Firmicutes	Bacilli	Lactobacillales	Camobacteriaceae	<i>Camobacterium</i>	Unclassified
NC_015516	Firmicutes	Bacilli	Lactobacillales	Enterococcaceae	<i>Melissococcus</i>	<i>Melissococcus plutonius</i>
NC_015759	Firmicutes	Bacilli	Lactobacillales	Leuconostocaceae	<i>Weissella</i>	<i>Weissella koreensis</i>
NC_003030	Firmicutes	Clostridia	Clostridiales	Clostridiaceae	<i>Clostridium</i>	<i>Clostridium acetobutylicum</i>
NC_003869	Firmicutes	Clostridia	Thermoanaerobacterale	Thermoanaerobacteraceae	<i>Caldanaerobacter</i>	<i>Caldanaerobacter subterraneus</i>
NC_006177	Firmicutes	Clostridia	Clostridiales	Clostridiales Family XVIII	In <i>Symbiobacterium</i>	<i>Symbiobacterium thermophilum</i>
NC_007503	Firmicutes	Clostridia	Thermoanaerobacterale	Thermoanaerobacteraceae	<i>Carboxydotherrmus</i>	<i>Carboxydotherrmus hydrogenofmans</i>

NC_007644	Firmicutes	Clostridia	Thermoanaerobacterale: Thermoanaerobacteraceae	<i>Moorella</i>	<i>Moorella thermoacetica</i>
NC_007907	Firmicutes	Clostridia	Clostridiales	<i>Desulfotobacterium</i>	<i>Desulfotobacterium hafniense</i>
NC_008346	Firmicutes	Clostridia	Clostridiales	<i>Syntrophomonadaceae</i>	<i>Syntrophomonas wolfei</i>
NC_009253	Firmicutes	Clostridia	Clostridiales	<i>Peptococcaceae</i>	<i>Desulfotomaculum</i>
NC_009437	Firmicutes	Clostridia	Thermoanaerobacterale: Thermoanaerobacterales Fami	<i>Caldicellulosiruptor</i>	<i>Caldicellulosiruptor saccharolyticus</i>
NC_009454	Firmicutes	Clostridia	Clostridiales	<i>Peptococcaceae</i>	<i>Pelotomaculum</i>
NC_009633	Firmicutes	Clostridia	Clostridiales	<i>Clostridiaceae</i>	<i>Alkaliphilus</i>
NC_010320	Firmicutes	Clostridia	Thermoanaerobacterale: Thermoanaerobacteraceae	<i>Thermoanaerobacter</i>	Unclassified
NC_010337	Firmicutes	Clostridia	Clostridiales	<i>Heliobacteriaceae</i>	<i>Heliobacterium</i>
NC_010376	Firmicutes	Clostridia	Clostridiales	<i>Clostridiales Family XI. Incer</i>	<i>Finegoldia</i>
NC_010424	Firmicutes	Clostridia	Clostridiales	<i>Peptococcaceae</i>	<i>Candidatus Desulforudis</i>
NC_010718	Firmicutes	Clostridia	Natranaerobiales	<i>Natranerobiaceae</i>	<i>Natranerobius</i>
NC_011295	Firmicutes	Clostridia	Thermoanaerobacterale: Thermodesulfobiaceae	<i>Coprothermobacter</i>	<i>Coprothermobacter proteolyticus</i>
NC_011899	Firmicutes	Clostridia	Halanaerobiales	<i>Halanaerobiaceae</i>	<i>Halothermothrix</i>
NC_012781	Firmicutes	Clostridia	Clostridiales	<i>Eubacteriaceae</i>	<i>Eubacterium</i>
NC_013171	Firmicutes	Clostridia	Clostridiales	<i>Clostridiales Family XI. Incer</i>	<i>Anaerococcus</i>
NC_013385	Firmicutes	Clostridia	Thermoanaerobacterale: Thermoanaerobacteraceae	<i>Ammonifex</i>	<i>Ammonifex degensii</i>
NC_014152	Firmicutes	Clostridia	Clostridiales	<i>Peptococcaceae</i>	<i>Thermincola</i>
NC_014220	Firmicutes	Clostridia	Clostridiales	<i>Syntrophomonadaceae</i>	<i>Syntrophothermus</i>
NC_014377	Firmicutes	Clostridia	Thermoanaerobacterale: Thermoanaerobacterales Fami	<i>Thermosediminibacter</i>	<i>Thermosediminibacter oceani</i>
NC_014378	Firmicutes	Clostridia	Halanaerobiales	<i>Halobacteroidaceae</i>	<i>Acetohalobium</i>
NC_014387	Firmicutes	Clostridia	Clostridiales	<i>Lachnospiraceae</i>	<i>Butyrivibrio</i>
NC_014410	Firmicutes	Clostridia	Thermoanaerobacterale: Thermoanaerobacterales Fami	<i>Thermoanaerobacterium</i>	<i>Thermoanaerobacterium thermosaccharolyticum</i>
NC_014654	Firmicutes	Clostridia	Halanaerobiales	<i>Halanaerobiaceae</i>	<i>Halanaerobium</i>
NC_014828	Firmicutes	Clostridia	Clostridiales	<i>Ruminococcaceae</i>	<i>Ethanoligenens</i>
NC_014831	Firmicutes	Clostridia	Clostridiales	<i>Clostridiales Family XVII. Inc</i>	<i>Thermaerobacter</i>
NC_014833	Firmicutes	Clostridia	Clostridiales	<i>Ruminococcaceae</i>	<i>Ruminococcus</i>
NC_015172	Firmicutes	Clostridia	Clostridiales	<i>Peptococcaceae</i>	<i>Syntrophobotulus</i>
NC_015275	Firmicutes	Clostridia	Clostridiales	<i>Lachnospiraceae</i>	<i>Cellulosilyticum</i>
NC_015499	Firmicutes	Clostridia	Thermoanaerobacterale: Thermodesulfobiaceae	<i>Thermodesulfobium</i>	<i>Thermodesulfobium narugense</i>
NC_015519	Firmicutes	Clostridia	Thermoanaerobacterale: Thermoanaerobacteraceae	<i>Tepidanaerobacter</i>	<i>Tepidanaerobacter acetatoxydans</i>
NC_015520	Firmicutes	Clostridia	Thermoanaerobacterale: Thermoanaerobacterales Fami	<i>Mahella</i>	<i>Mahella australiensis</i>
NC_015757	Firmicutes	Clostridia	Clostridiales	<i>Clostridiales Family XVII. Inc</i>	<i>Sulfobacillus</i>
NC_015913	Firmicutes	Clostridia	Clostridiales	<i>Clostridiaceae</i>	<i>Candidatus Arthromitus</i>
NC_015977	Firmicutes	Clostridia	Clostridiales	<i>Lachnospiraceae</i>	<i>Roseburia</i>
NC_015601	Firmicutes	Erysipelotrichia	Erysipelotrichales	<i>Erysipelotrichaceae</i>	<i>Erysipelothrix</i>
NC_013520	Firmicutes	Negativicutes	Selenomonadales	<i>Veillonellaceae</i>	<i>Veillonella</i>
NC_013740	Firmicutes	Negativicutes	Selenomonadales	<i>Acidaminococcaceae</i>	<i>Acidaminococcus</i>
NC_015437	Firmicutes	Negativicutes	Selenomonadales	<i>Veillonellaceae</i>	<i>Selenomonas</i>
NC_003454	Fusobacteria	Fusobacteria	Fusobacteriales	<i>Fusobacteriaceae</i>	<i>Fusobacterium</i>
NC_013192	Fusobacteria	Fusobacteria	Fusobacteriales	<i>Leptotrichiaceae</i>	<i>Leptotrichia</i>
NC_013515	Fusobacteria	Fusobacteria	Fusobacteriales	<i>Leptotrichiaceae</i>	<i>Streptobacillus</i>
NC_014632	Fusobacteria	Fusobacteria	Fusobacteriales	<i>Fusobacteriaceae</i>	<i>Ilyobacter</i>
NC_012489	Gemmatimonadetes	Gemmatimonadetes	Gemmatimonadales	<i>Gemmatimonadaceae</i>	<i>Gemmatimonas</i>
NC_011296	Nitrospirae	Nitrospira	Nitrospirales	<i>Nitrospiraceae</i>	<i>Thermodesulfovibrio</i>
NC_014355	Nitrospirae	Nitrospira	Nitrospirales	<i>Nitrospiraceae</i>	<i>Nitrospira</i>
NC_005027	Planctomycetes	Planctomycetia	Planctomycetales	<i>Planctomycetaceae</i>	<i>Rhodopirellula</i>
NC_013720	Planctomycetes	Planctomycetia	Planctomycetales	<i>Planctomycetaceae</i>	<i>Pirellula</i>
NC_014148	Planctomycetes	Planctomycetia	Planctomycetales	<i>Planctomycetaceae</i>	<i>Planctomyces</i>
NC_014962	Planctomycetes	Planctomycetia	Planctomycetales	<i>Planctomycetaceae</i>	<i>Isosphaera</i>
NC_000963	Proteobacteria	Alphaproteobacteria	Rickettsiales	<i>Rickettsiaceae</i>	<i>Rickettsia</i>
NC_002678	Proteobacteria	Alphaproteobacteria	Rhizobiales	<i>Phyllobacteriaceae</i>	<i>Mesorhizobium</i>
NC_002696	Proteobacteria	Alphaproteobacteria	Caulobacterales	<i>Caulobacteraceae</i>	<i>Caulobacter</i>
NC_003047	Proteobacteria	Alphaproteobacteria	Rhizobiales	<i>Rhizobiaceae</i>	<i>Sinorhizobium</i>
NC_003317	Proteobacteria	Alphaproteobacteria	Rhizobiales	<i>Brucellaceae</i>	<i>Brucella</i>
NC_003911	Proteobacteria	Alphaproteobacteria	Rhodobacterales	<i>Rhodobacteraceae</i>	<i>Ruegeria</i>
NC_004463	Proteobacteria	Alphaproteobacteria	Rhizobiales	<i>Bradyrhizobiaceae</i>	<i>Bradyrhizobium</i>
NC_005295	Proteobacteria	Alphaproteobacteria	Rickettsiales	<i>Anaplasmataceae</i>	<i>Ehrlichia</i>
NC_005296	Proteobacteria	Alphaproteobacteria	Rhizobiales	<i>Bradyrhizobiaceae</i>	<i>Rhodopseudomonas</i>
NC_005955	Proteobacteria	Alphaproteobacteria	Rhizobiales	<i>Bartonellaceae</i>	<i>Bartonella</i>
NC_006526	Proteobacteria	Alphaproteobacteria	Sphingomonadales	<i>Sphingomonadaceae</i>	<i>Zymomonas</i>
NC_006677	Proteobacteria	Alphaproteobacteria	Rhodospirillales	<i>Acetobacteraceae</i>	<i>Gluconobacter</i>
NC_007205	Proteobacteria	Alphaproteobacteria	Unclassified	Unclassified	<i>Candidatus Pelagibacter</i>
NC_007406	Proteobacteria	Alphaproteobacteria	Rhizobiales	<i>Bradyrhizobiaceae</i>	<i>Nitrobacter</i>
NC_007493	Proteobacteria	Alphaproteobacteria	Rhodobacterales	<i>Rhodobacteraceae</i>	<i>Rhodobacter</i>
NC_007626	Proteobacteria	Alphaproteobacteria	Rhodospirillales	<i>Rhodospirillaceae</i>	<i>Magnetospirillum</i>
NC_007643	Proteobacteria	Alphaproteobacteria	Rhodospirillales	<i>Rhodospirillaceae</i>	<i>Rhodospirillum</i>
NC_007722	Proteobacteria	Alphaproteobacteria	Sphingomonadales	<i>Erythrobacteraceae</i>	<i>Erythrobacter</i>
NC_007761	Proteobacteria	Alphaproteobacteria	Rhizobiales	<i>Rhizobiaceae</i>	<i>Rhizobium</i>
NC_007794	Proteobacteria	Alphaproteobacteria	Sphingomonadales	<i>Sphingomonadaceae</i>	<i>Novosphingobium</i>
NC_007797	Proteobacteria	Alphaproteobacteria	Rickettsiales	<i>Anaplasmataceae</i>	<i>Anaplasma</i>
NC_007798	Proteobacteria	Alphaproteobacteria	Rickettsiales	<i>Anaplasmataceae</i>	<i>Neorickettsia</i>
NC_007802	Proteobacteria	Alphaproteobacteria	Rhodobacterales	<i>Rhodobacteraceae</i>	<i>Jannaschia</i>
NC_008048	Proteobacteria	Alphaproteobacteria	Sphingomonadales	<i>Sphingomonadaceae</i>	<i>Sphingopyxis</i>
NC_008209	Proteobacteria	Alphaproteobacteria	Rhodobacterales	<i>Rhodobacteraceae</i>	<i>Roseobacter</i>
NC_008254	Proteobacteria	Alphaproteobacteria	Rhizobiales	<i>Phyllobacteriaceae</i>	<i>Chelativorans</i>
NC_008343	Proteobacteria	Alphaproteobacteria	Rhodospirillales	<i>Acetobacteraceae</i>	<i>Granulibacter</i>
NC_008347	Proteobacteria	Alphaproteobacteria	Rhodobacterales	<i>Hyphomonadaceae</i>	<i>Maricaulis</i>
NC_008358	Proteobacteria	Alphaproteobacteria	Rhodobacterales	<i>Hyphomonadaceae</i>	<i>Hyphomonas</i>
NC_008576	Proteobacteria	Alphaproteobacteria	Magnetococcales	<i>Magnetococcaceae</i>	<i>Magnetococcus</i>
NC_009484	Proteobacteria	Alphaproteobacteria	Rhodospirillales	<i>Acetobacteraceae</i>	<i>Acidiphilium</i>
NC_009488	Proteobacteria	Alphaproteobacteria	Rickettsiales	<i>Rickettsiaceae</i>	<i>Orientia</i>
NC_009511	Proteobacteria	Alphaproteobacteria	Sphingomonadales	<i>Sphingomonadaceae</i>	<i>Sphingomonas</i>
NC_009667	Proteobacteria	Alphaproteobacteria	Rhizobiales	<i>Brucellaceae</i>	<i>Ochrobactrum</i>
NC_009719	Proteobacteria	Alphaproteobacteria	Rhizobiales	<i>Rhodobiaceae</i>	<i>Parvibaculum</i>
NC_009720	Proteobacteria	Alphaproteobacteria	Rhizobiales	<i>Xanthobacteraceae</i>	<i>Xanthobacter</i>
NC_009937	Proteobacteria	Alphaproteobacteria	Rhizobiales	<i>Xanthobacteraceae</i>	<i>Azorhizobium</i>
NC_009952	Proteobacteria	Alphaproteobacteria	Rhodobacterales	<i>Rhodobacteraceae</i>	<i>Dinoroseobacter</i>
NC_010125	Proteobacteria	Alphaproteobacteria	Rhodospirillales	<i>Acetobacteraceae</i>	<i>Gluconacetobacter</i>
NC_010172	Proteobacteria	Alphaproteobacteria	Rhizobiales	<i>Methylobacteriaceae</i>	<i>Methylobacterium</i>

NC_010581	Proteobacteria	Alphaproteobacteria	Rhizobiales	Beijerinckiaceae	<i>Beijerinckia</i>	<i>Beijerinckia indica</i>
NC_011144	Proteobacteria	Alphaproteobacteria	Caulobacterales	Caulobacteraceae	<i>Phenylobacterium</i>	<i>Phenylobacterium zucineum</i>
NC_011386	Proteobacteria	Alphaproteobacteria	Rhizobiales	Bradyrhizobiaceae	<i>Oligotropha</i>	<i>Oligotropha carboxidovorans</i>
NC_011666	Proteobacteria	Alphaproteobacteria	Rhizobiales	Beijerinckiaceae	<i>Methylocella</i>	<i>Methylocella silvestris</i>
NC_011985	Proteobacteria	Alphaproteobacteria	Rhizobiales	Rhizobiaceae	<i>Agrobacterium</i>	<i>Agrobacterium tumefaciens</i>
NC_012982	Proteobacteria	Alphaproteobacteria	Rhodobacterales	Hyphomonadaceae	<i>Hirschia</i>	<i>Hirschia baltica</i>
NC_012985	Proteobacteria	Alphaproteobacteria	Rhizobiales	Rhizobiaceae	<i>Candidatus Liberibacter</i>	<i>Candidatus Liberibacter asiaticus</i>
NC_013209	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Acetobacteraceae	<i>Acetobacter</i>	<i>Acetobacter pasteurianus</i>
NC_014006	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	<i>Sphingobium</i>	<i>Sphingobium japonicum</i>
NC_014010	Proteobacteria	Alphaproteobacteria	Unclassified	Unclassified	<i>Candidatus Puniceispirillum</i>	<i>Candidatus Puniceispirillum marinum</i>
NC_014217	Proteobacteria	Alphaproteobacteria	Rhizobiales	Xanthobacteraceae	<i>Starkeya</i>	<i>Starkeya novella</i>
NC_014313	Proteobacteria	Alphaproteobacteria	Rhizobiales	Hyphomicrobiaceae	<i>Hyphomicrobium</i>	<i>Hyphomicrobium denitrificans</i>
NC_014375	Proteobacteria	Alphaproteobacteria	Caulobacterales	Caulobacteraceae	<i>Brevundimonas</i>	<i>Brevundimonas subvirbroides</i>
NC_014414	Proteobacteria	Alphaproteobacteria	Parvularculales	Parvularculaceae	<i>Parvularcula</i>	<i>Parvularcula bermudensis</i>
NC_014664	Proteobacteria	Alphaproteobacteria	Rhizobiales	Hyphomicrobiaceae	<i>Rhodomicrobium</i>	<i>Rhodomicrobium vannielii</i>
NC_002927	Proteobacteria	Betaproteobacteria	Burkholderiales	Alcaligenaceae	<i>Bordetella</i>	<i>Bordetella bronchiseptica</i>
NC_002946	Proteobacteria	Betaproteobacteria	Neisseriales	Neisseriaceae	<i>Neisseria</i>	<i>Neisseria gonorrhoeae</i>
NC_003295	Proteobacteria	Betaproteobacteria	Burkholderiales	Burkholderiaceae	<i>Ralstonia</i>	<i>Ralstonia solanacearum</i>
NC_004757	Proteobacteria	Betaproteobacteria	Nitrosomonadales	Nitrosomonadaceae	<i>Nitrosomonas</i>	<i>Nitrosomonas europaea</i>
NC_005085	Proteobacteria	Betaproteobacteria	Neisseriales	Neisseriaceae	<i>Chromobacterium</i>	<i>Chromobacterium violaceum</i>
NC_006350	Proteobacteria	Betaproteobacteria	Burkholderiales	Burkholderiaceae	<i>Burkholderia</i>	<i>Burkholderia pseudomallei</i>
NC_006513	Proteobacteria	Betaproteobacteria	Rhodocyclales	Rhodocyclaceae	<i>Aromatoleum</i>	<i>Aromatoleum aromaticum</i>
NC_007298	Proteobacteria	Betaproteobacteria	Rhodocyclales	Rhodocyclaceae	<i>Dechloromonas</i>	<i>Dechloromonas aromatica</i>
NC_007404	Proteobacteria	Betaproteobacteria	Hydrogenophilales	Hydrogenophilaceae	<i>Thiobacillus</i>	<i>Thiobacillus denitrificans</i>
NC_007614	Proteobacteria	Betaproteobacteria	Nitrosomonadales	Nitrosomonadaceae	<i>Nitrosospira</i>	<i>Nitrosospira multififormis</i>
NC_007908	Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae	<i>Albidiferax</i>	<i>Albidiferax ferrireducens</i>
NC_007947	Proteobacteria	Betaproteobacteria	Methylophilales	Methylophilaceae	<i>Methylobacillus</i>	<i>Methylobacillus flagellatus</i>
NC_007948	Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae	<i>Polaromonas</i>	Unclassified
NC_007973	Proteobacteria	Burkholderiales	Burkholderiales	Burkholderiaceae	<i>Cupriavidus</i>	<i>Cupriavidus metallidurans</i>
NC_008702	Proteobacteria	Betaproteobacteria	Rhodocyclales	Rhodocyclaceae	<i>Azoarcus</i>	Unclassified
NC_008752	Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae	<i>Acidovorax</i>	<i>Acidovorax citrulli</i>
NC_008786	Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae	<i>Verminephrobacter</i>	<i>Verminephrobacter eiseniae</i>
NC_008825	Proteobacteria	Betaproteobacteria	Burkholderiales	Unclassified	<i>Methylibium</i>	<i>Methylibium petroleiphilum</i>
NC_009379	Proteobacteria	Betaproteobacteria	Burkholderiales	Burkholderiaceae	<i>Polynucleobacter</i>	<i>Polynucleobacter necessarius</i>
NC_010002	Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae	<i>Delftia</i>	<i>Delftia acidovorans</i>
NC_010524	Proteobacteria	Betaproteobacteria	Burkholderiales	Unclassified	<i>Leptothrix</i>	<i>Leptothrix cholodnii</i>
NC_011662	Proteobacteria	Betaproteobacteria	Rhodocyclales	Rhodocyclaceae	<i>Thaueria</i>	Unclassified
NC_012559	Proteobacteria	Betaproteobacteria	Neisseriales	Neisseriaceae	<i>Laribacter</i>	<i>Laribacter hongkongensis</i>
NC_012791	Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae	<i>Variovorax</i>	<i>Variovorax paradoxus</i>
NC_012968	Proteobacteria	Betaproteobacteria	Methylophilales	Methylophilaceae	<i>Methylothera</i>	<i>Methylothera mobilis</i>
NC_012969	Proteobacteria	Betaproteobacteria	Methylophilales	Methylophilaceae	<i>Methylovorus</i>	<i>Methylovorus glucosotrophus</i>
NC_013194	Proteobacteria	Betaproteobacteria	Unclassified	Unclassified	<i>Candidatus Accumulibacter</i>	<i>Candidatus Accumulibacter phosphatis</i>
NC_013446	Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae	<i>Comamonas</i>	<i>Comamonas testosteroni</i>
NC_013959	Proteobacteria	Betaproteobacteria	Gallionellales	Gallionellaceae	<i>Sideroxydans</i>	<i>Sideroxydans lithotrophicus</i>
NC_014153	Proteobacteria	Betaproteobacteria	Burkholderiales	Unclassified	<i>Thiomonas</i>	<i>Thiomonas intermedia</i>
NC_014323	Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae	<i>Herbaspirillum</i>	<i>Herbaspirillum seropedicaceae</i>
NC_014394	Proteobacteria	Betaproteobacteria	Gallionellales	Gallionellaceae	<i>Gallionella</i>	<i>Gallionella capsijerriformans</i>
NC_014640	Proteobacteria	Betaproteobacteria	Burkholderiales	Alcaligenaceae	<i>Achromobacter</i>	<i>Achromobacter xylosoxidans</i>
NC_014910	Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae	<i>Alicyciphilus</i>	<i>Alicyciphilus denitrificans</i>
NC_014914	Proteobacteria	Betaproteobacteria	Burkholderiales	Alcaligenaceae	<i>Taylorella</i>	<i>Taylorella equigenitalis</i>
NC_015458	Proteobacteria	Betaproteobacteria	Burkholderiales	Alcaligenaceae	<i>Pusillimonas</i>	Unclassified
NC_015677	Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae	<i>Ramlibacter</i>	<i>Ramlibacter tataouinensis</i>
NC_015856	Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae	<i>Collimonas</i>	<i>Collimonas fungivorans</i>
NC_016002	Proteobacteria	Betaproteobacteria	Neisseriales	Neisseriaceae	<i>Pseudogulbenkiana</i>	Unclassified
NC_002937	Proteobacteria	Deltaproteobacteria	Desulfuovibrionales	Desulfuovibrionaceae	<i>Desulfovibrio</i>	<i>Desulfovibrio vulgaris</i>
NC_002939	Proteobacteria	Deltaproteobacteria	Desulfuromonadales	Geobacteraceae	<i>Geobacter</i>	<i>Geobacter sulfurreducens</i>
NC_005363	Proteobacteria	Deltaproteobacteria	Bdellovibrionales	Bdellovibrionaceae	<i>Bdellovibrio</i>	<i>Bdellovibrio bacteriovorus</i>
NC_007498	Proteobacteria	Deltaproteobacteria	Desulfuromonadales	Pelobacteraceae	<i>Pelobacter</i>	<i>Pelobacter carbinolicus</i>
NC_007759	Proteobacteria	Deltaproteobacteria	Syntrophobacterales	Syntrophaceae	<i>Syntrophus</i>	<i>Syntrophus aciditrophicus</i>
NC_007760	Proteobacteria	Deltaproteobacteria	Myxococcales	Myxococcaceae	<i>Anaeromyxobacter</i>	<i>Anaeromyxobacter dehalogenans</i>
NC_008011	Proteobacteria	Deltaproteobacteria	Desulfuovibrionales	Desulfuovibrionaceae	<i>Lawsonia</i>	<i>Lawsonia intracellularis</i>
NC_008095	Proteobacteria	Deltaproteobacteria	Myxococcales	Myxococcaceae	<i>Myxococcus</i>	<i>Myxococcus xanthus</i>
NC_008554	Proteobacteria	Deltaproteobacteria	Syntrophobacterales	Syntrophobacteraceae	<i>Syntrophobacter</i>	<i>Syntrophobacter fumaroxidans</i>
NC_009943	Proteobacteria	Deltaproteobacteria	Desulfobacterales	Desulfobacteraceae	<i>Desulfococcus</i>	<i>Desulfococcus oleovorans</i>
NC_010162	Proteobacteria	Deltaproteobacteria	Myxococcales	Polyangiaceae	<i>Sorangium</i>	<i>Sorangium cellulosum</i>
NC_011768	Proteobacteria	Deltaproteobacteria	Desulfobacterales	Desulfobacteraceae	<i>Desulfatibacillum</i>	<i>Desulfatibacillum alkenivorans</i>
NC_012108	Proteobacteria	Deltaproteobacteria	Desulfobacterales	Desulfobacteraceae	<i>Desulfobacterium</i>	<i>Desulfobacterium autotrophicum</i>
NC_013173	Proteobacteria	Deltaproteobacteria	Desulfuovibrionales	Desulfomicrobiaceae	<i>Desulfomicrobium</i>	<i>Desulfomicrobium baculatum</i>
NC_013223	Proteobacteria	Deltaproteobacteria	Desulfuovibrionales	Desulfohalobiaceae	<i>Desulfohalobium</i>	<i>Desulfohalobium retbaense</i>
NC_013440	Proteobacteria	Deltaproteobacteria	Myxococcales	Koffleriaceae	<i>Haliangium</i>	<i>Haliangium ochraceum</i>
NC_014216	Proteobacteria	Deltaproteobacteria	Desulfobacterales	Desulfobulbaceae	<i>Desulfurivibrio</i>	<i>Desulfurivibrio alkaliphilus</i>
NC_014365	Proteobacteria	Deltaproteobacteria	Desulfurculales	Desulfurculaceae	<i>Desulfurculus</i>	<i>Desulfurculus baarsii</i>
NC_014972	Proteobacteria	Deltaproteobacteria	Desulfobacterales	Desulfobulbaceae	<i>Desulfobulbus</i>	<i>Desulfobulbus propionicus</i>
NC_015318	Proteobacteria	Deltaproteobacteria	Desulfurellales	Desulfurellaceae	<i>Hippea</i>	<i>Hippea maritima</i>
NC_015388	Proteobacteria	Deltaproteobacteria	Syntrophobacterales	Syntrophaceae	<i>Desulfobacca</i>	<i>Desulfobacca acetoxidans</i>
NC_002163	Proteobacteria	Epsilonproteobacteria	Campylobacterales	Campylobacteraceae	<i>Campylobacter</i>	<i>Campylobacter jejuni</i>
NC_007575	Proteobacteria	Epsilonproteobacteria	Campylobacterales	Helicobacteraceae	<i>Sulfurimonas</i>	<i>Sulfurimonas denitrificans</i>
NC_009662	Proteobacteria	Epsilonproteobacteria	Unclassified	Unclassified	<i>Nitratiruptor</i>	Unclassified
NC_009663	Proteobacteria	Epsilonproteobacteria	Unclassified	Unclassified	<i>Sulfurovum</i>	Unclassified
NC_009850	Proteobacteria	Epsilonproteobacteria	Campylobacterales	Campylobacteraceae	<i>Arcobacter</i>	<i>Arcobacter butzleri</i>
NC_011333	Proteobacteria	Epsilonproteobacteria	Campylobacterales	Helicobacteraceae	<i>Helicobacter</i>	<i>Helicobacter pylori</i>
NC_012115	Proteobacteria	Epsilonproteobacteria	Nautiliales	Nautiliaceae	<i>Nautilia</i>	<i>Nautilia profundicola</i>
NC_013512	Proteobacteria	Epsilonproteobacteria	Campylobacterales	Campylobacteraceae	<i>Sulfurospirillum</i>	<i>Sulfurospirillum deleyianum</i>
NC_014762	Proteobacteria	Epsilonproteobacteria	Campylobacterales	Helicobacteraceae	<i>Sulfuricurvum</i>	<i>Sulfuricurvum kujiensae</i>
NC_014935	Proteobacteria	Epsilonproteobacteria	Campylobacterales	Unclassified	<i>Nitratifactor</i>	<i>Nitratifactor salsuginis</i>
NC_000907	Proteobacteria	Gammaproteobacteria	Pasteurellales	Pasteurellaceae	<i>Haemophilus</i>	<i>Haemophilus influenzae</i>
NC_000913	Proteobacteria	Gammaproteobacteria	Enterobacterales	Enterobacteriaceae	<i>Escherichia</i>	<i>Escherichia coli</i>
NC_002488	Proteobacteria	Gammaproteobacteria	Xanthomonadales	Xanthomonadaceae	<i>Xylella</i>	<i>Xylella fastidiosa</i>
NC_002516	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Pseudomonadaceae	<i>Pseudomonas</i>	<i>Pseudomonas aeruginosa</i>
NC_002528	Proteobacteria	Gammaproteobacteria	Enterobacterales	Enterobacteriaceae	<i>Buchnera</i>	<i>Buchnera aphidicola</i>

NC_002663	Proteobacteria	Gammaproteobacteria	Pasteurellales	Pasteurellaceae	<i>Pasteurella</i>	<i>Pasteurella multocida</i>
NC_002971	Proteobacteria	Gammaproteobacteria	Legionellales	Coxiellaceae	<i>Coxiella</i>	<i>Coxiella burnetii</i>
NC_003143	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	<i>Yersinia</i>	<i>Yersinia pestis</i>
NC_003197	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	<i>Salmonella</i>	<i>Salmonella enterica</i>
NC_003902	Proteobacteria	Gammaproteobacteria	Xanthomonadales	Xanthomonadaceae	<i>Xanthomonas</i>	<i>Xanthomonas campestris</i>
NC_003910	Proteobacteria	Gammaproteobacteria	Alteromonadales	Colwelliaceae	<i>Colwellia</i>	<i>Colwellia psycherythraea</i>
NC_004337	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	<i>Shigella</i>	<i>Shigella flexneri</i>
NC_004344	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	<i>Wigglesworthia</i>	<i>Wigglesworthia glossinidia</i>
NC_004347	Proteobacteria	Gammaproteobacteria	Alteromonadales	Shewanellaceae	<i>Shewanella</i>	<i>Shewanella oneidensis</i>
NC_004459	Proteobacteria	Gammaproteobacteria	Vibrionales	Vibrionaceae	<i>Vibrio</i>	<i>Vibrio vulnificus</i>
NC_004547	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	<i>Pectobacterium</i>	<i>Pectobacterium atrosepticum</i>
NC_005061	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	<i>Candidatus Blochmannia</i>	Unclassified
NC_005126	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	<i>Photorhabdus</i>	<i>Photorhabdus luminescens</i>
NC_005966	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Moraxellaceae	<i>Acinetobacter</i>	Unclassified
NC_006300	Proteobacteria	Gammaproteobacteria	Pasteurellales	Pasteurellaceae	<i>Basfia</i>	<i>Mannheimia succiniciproduens</i>
NC_006368	Proteobacteria	Gammaproteobacteria	Legionellales	Legionellaceae	<i>Legionella</i>	<i>Legionella pneumophila</i>
NC_006370	Proteobacteria	Gammaproteobacteria	Vibrionales	Vibrionaceae	<i>Photobacterium</i>	<i>Photobacterium profundum</i>
NC_006512	Proteobacteria	Gammaproteobacteria	Alteromonadales	Idiomarinaceae	<i>Idiomarina</i>	<i>Idiomarina loihiensis</i>
NC_006570	Proteobacteria	Gammaproteobacteria	Thiotrichales	Francisellaceae	<i>Francisella</i>	<i>Francisella tularensis</i>
NC_006840	Proteobacteria	Gammaproteobacteria	Vibrionales	Vibrionaceae	<i>Aliivibrio</i>	<i>Aliivibrio fischeri</i>
NC_007204	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Moraxellaceae	<i>Psychrobacter</i>	<i>Psychrobacter arcticus</i>
NC_007481	Proteobacteria	Gammaproteobacteria	Alteromonadales	Pseudoalteromonadaceae	<i>Pseudoalteromonas</i>	<i>Pseudoalteromonas haloplanktis</i>
NC_007484	Proteobacteria	Gammaproteobacteria	Chromatiales	Chromatiaceae	<i>Nitrosococcus</i>	<i>Nitrosococcus oceanii</i>
NC_007520	Proteobacteria	Gammaproteobacteria	Thiotrichales	Piscirickettsiaceae	<i>Thiomicrospira</i>	<i>Thiomicrospira crunigena</i>
NC_007645	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Hahellaceae	<i>Hahella</i>	<i>Hahella chejuensis</i>
NC_007912	Proteobacteria	Gammaproteobacteria	Alteromonadales	Alteromonadaceae	<i>Saccharophagus</i>	<i>Saccharophagus degradans</i>
NC_007963	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	<i>Chromohalobacter</i>	<i>Chromohalobacter salexigens</i>
NC_008260	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Alcanivoraceae	<i>Alcanivorax</i>	<i>Alcanivorax borkumensis</i>
NC_008309	Proteobacteria	Gammaproteobacteria	Pasteurellales	Pasteurellaceae	<i>Histophilus</i>	<i>Histophilus somni</i>
NC_008340	Proteobacteria	Gammaproteobacteria	Chromatiales	Ecotriorhodospiraceae	<i>Alkalilimnicola</i>	<i>Alkalilimnicola ehrlichii</i>
NC_008570	Proteobacteria	Gammaproteobacteria	Aeromonadales	Aeromonadaceae	<i>Aeromonas</i>	<i>Aeromonas hydrophila</i>
NC_008709	Proteobacteria	Gammaproteobacteria	Alteromonadales	Psychromonadaceae	<i>Psychromonas</i>	<i>Psychromonas ingrahamii</i>
NC_008740	Proteobacteria	Gammaproteobacteria	Alteromonadales	Alteromonadaceae	<i>Marinobacter</i>	<i>Marinobacter hydrocarbonoclasticus</i>
NC_008789	Proteobacteria	Gammaproteobacteria	Chromatiales	Ecotriorhodospiraceae	<i>Halorhodospira</i>	<i>Halorhodospira halophila</i>
NC_009053	Proteobacteria	Gammaproteobacteria	Pasteurellales	Pasteurellaceae	<i>Actinobacillus</i>	<i>Actinobacillus pleuropneumoniae</i>
NC_009436	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	<i>Enterobacter</i>	Unclassified
NC_009648	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	<i>Klebsiella</i>	<i>Klebsiella pneumoniae</i>
NC_009654	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Oceanospirillaceae	<i>Marinomonas</i>	Unclassified
NC_009778	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	<i>Cronobacter</i>	<i>Cronobacter sakazakii</i>
NC_009792	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	<i>Citrobacter</i>	<i>Citrobacter koseri</i>
NC_009832	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	<i>Serratia</i>	<i>Serratia proteamaculans</i>
NC_010554	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	<i>Proteus</i>	<i>Proteus mirabilis</i>
NC_010694	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	<i>Erwinia</i>	<i>Erwinia tasmaniensis</i>
NC_010943	Proteobacteria	Gammaproteobacteria	Xanthomonadales	Xanthomonadaceae	<i>Stenotrophomonas</i>	<i>Stenotrophomonas maltophilia</i>
NC_010995	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Pseudomonadaceae	<i>Cellvibrio</i>	<i>Cellvibrio japonicus</i>
NC_011206	Proteobacteria	Gammaproteobacteria	Acidithiobacillales	Acidithiobacillaceae	<i>Acidithiobacillus</i>	<i>Acidithiobacillus ferrooxidans</i>
NC_012560	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Pseudomonadaceae	<i>Azotobacter</i>	<i>Azotobacter vinelandii</i>
NC_012691	Proteobacteria	Gammaproteobacteria	Aeromonadales	Aeromonadaceae	<i>Tolumonas</i>	<i>Tolumonas auensis</i>
NC_012751	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	<i>Candidatus Hamiltonella</i>	<i>Candidatus Hamiltonella defensa</i>
NC_012880	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	<i>Dickeya</i>	<i>Dickeya dadantii</i>
NC_012913	Proteobacteria	Gammaproteobacteria	Pasteurellales	Pasteurellaceae	<i>Aggregatibacter</i>	<i>Aggregatibacter aphrophilus</i>
NC_012997	Proteobacteria	Gammaproteobacteria	Alteromonadales	Unclassified	<i>Teredinibacter</i>	<i>Teredinibacter turnerae</i>
NC_013166	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Alcanivoraceae	<i>Kangiella</i>	<i>Kangiella korensis</i>
NC_013422	Proteobacteria	Gammaproteobacteria	Chromatiales	Halothiobacillaceae	<i>Halothiobacillus</i>	<i>Halothiobacillus neapolitanus</i>
NC_013851	Proteobacteria	Gammaproteobacteria	Chromatiales	Chromatiaceae	<i>Allochroamatium</i>	<i>Allochroamatium vinosum</i>
NC_013889	Proteobacteria	Gammaproteobacteria	Chromatiales	Ecotriorhodospiraceae	<i>Thioalkalivibrio</i>	Unclassified
NC_013892	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	<i>Xenorhabdus</i>	<i>Xenorhabdus bovienii</i>
NC_013956	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	<i>Pantoea</i>	<i>Pantoea ananatis</i>
NC_014109	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	<i>Candidatus Riesia</i>	<i>Candidatus Riesia pediculicola</i>
NC_014147	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Moraxellaceae	<i>Moraxella</i>	<i>Moraxella catarrhalis</i>
NC_014532	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	<i>Halomonas</i>	<i>Halomonas elongata</i>
NC_014541	Proteobacteria	Gammaproteobacteria	Alteromonadales	Ferrimonadaceae	<i>Ferrimonas</i>	<i>Ferrimonas balearica</i>
NC_014924	Proteobacteria	Gammaproteobacteria	Xanthomonadales	Xanthomonadaceae	<i>Pseudoxanthomonas</i>	<i>Pseudoxanthomonas suwonensis</i>
NC_015061	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	<i>Rahnella</i>	Unclassified
NC_015460	Proteobacteria	Gammaproteobacteria	Pasteurellales	Pasteurellaceae	<i>Gallibacterium</i>	<i>Gallibacterium anatis</i>
NC_015497	Proteobacteria	Gammaproteobacteria	Alteromonadales	Alteromonadaceae	<i>Glaciicola</i>	Unclassified
NC_015554	Proteobacteria	Gammaproteobacteria	Alteromonadales	Alteromonadaceae	<i>Alteromonas</i>	Unclassified
NC_015572	Proteobacteria	Gammaproteobacteria	Methylococcales	Methylococcaceae	<i>Methylomonas</i>	<i>Methylomonas methanica</i>
NC_015581	Proteobacteria	Gammaproteobacteria	Thiotrichales	Piscirickettsiaceae	<i>Thioalkalimicrobium</i>	<i>Thioalkalimicrobium cyclicum</i>
NC_015735	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	<i>Candidatus Moranella</i>	<i>Candidatus Moranella endobia</i>
NC_000919	Spirochaetes	Spirochaetia	Spirochaetales	Spirochaetaceae	<i>Treponema</i>	<i>Treponema pallidum</i>
NC_001318	Spirochaetes	Spirochaetia	Spirochaetales	Spirochaetaceae	<i>Borrelia</i>	<i>Borrelia burgdorferi</i>
NC_004342	Spirochaetes	Spirochaetia	Spirochaetales	Leptospiraceae	<i>Leptospira</i>	<i>Leptospira interrogans</i>
NC_012225	Spirochaetes	Spirochaetia	Spirochaetales	Brachyspiraceae	<i>Brachyspira</i>	<i>Brachyspira hyodysenteriae</i>
NC_014364	Spirochaetes	Spirochaetia	Spirochaetales	Spirochaetaceae	<i>Spirochaeta</i>	<i>Spirochaeta smaragdinae</i>
NC_015152	Spirochaetes	Spirochaetia	Spirochaetales	Spirochaetaceae	<i>Sphaerochaeta</i>	<i>Sphaerochaeta globosa</i>
NC_013522	Synergistetes	Synergistia	Synergistales	Synergistaceae	<i>Thermanaerovibrio</i>	<i>Thermanaerovibrio acidaminovorans</i>
NC_014011	Synergistetes	Synergistia	Synergistales	Synergistaceae	<i>Aminobacterium</i>	<i>Aminobacterium colombiense</i>
NC_000908	Tenericutes	Mollicutes	Mycoplasmatales	Mycoplasmataceae	<i>Mycoplasma</i>	<i>Mycoplasma genitalium</i>
NC_002162	Tenericutes	Mollicutes	Mycoplasmatales	Mycoplasmataceae	<i>Ureaplasma</i>	<i>Ureaplasma parvum</i>
NC_005303	Tenericutes	Mollicutes	Acholeplasmatales	Acholeplasmataceae	<i>Candidatus Phytoplasma</i>	<i>Onion yellows phytoplasma</i>
NC_006055	Tenericutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	<i>Mesoplasma</i>	<i>Mesoplasma florum</i>
NC_010163	Tenericutes	Mollicutes	Acholeplasmatales	Acholeplasmataceae	<i>Acholeplasma</i>	<i>Acholeplasma laidlawii</i>
NC_015681	Thermodesulfobacteria	Thermodesulfobacteria	Thermodesulfobacteriales	Thermodesulfobacteriaceae	<i>Thermodesulfator</i>	<i>Thermodesulfator indicus</i>
NC_015682	Thermodesulfobacteria	Thermodesulfobacteria	Thermodesulfobacteriales	Thermodesulfobacteriaceae	<i>Thermodesulfobacterium</i>	<i>Thermodesulfobacterium geofontis</i>
NC_000853	Thermotogae	Thermotogae	Thermotogales	Thermotogaceae	<i>Thermotoga</i>	<i>Thermotoga maritima</i>
NC_009616	Thermotogae	Thermotogae	Thermotogales	Thermotogaceae	<i>Thermosipho</i>	<i>Thermosipho melanesiensis</i>
NC_009718	Thermotogae	Thermotogae	Thermotogales	Thermotogaceae	<i>Fervidobacterium</i>	<i>Fervidobacterium nodosum</i>
NC_010003	Thermotogae	Thermotogae	Thermotogales	Thermotogaceae	<i>Petrotoga</i>	<i>Petrotoga mobilis</i>
NC_012785	Thermotogae	Thermotogae	Thermotogales	Thermotogaceae	<i>Kosmotoga</i>	<i>Kosmotoga olearia</i>

NC_013525	Unclassified	Unclassified	Unclassified	Unclassified	<i>Thermobaculum</i>	<i>Thermobaculum terrenum</i>
NC_010571	Verrucomicrobia	Opiritae	Unclassified	Opiritaceae	<i>Opiritus</i>	<i>Opiritus terrae</i>
NC_014008	Verrucomicrobia	Opiritae	Puniceococcales	Puniceococcaceae	<i>Coraliomargarita</i>	<i>Coraliomargarita akajimensis</i>
NC_010794	Verrucomicrobia	Unclassified	Methylacidiphilales	Methylacidiphilaceae	<i>Methylacidiphilum</i>	<i>Methylacidiphilum infernorum</i>
NC_010655	Verrucomicrobia	Verrucomicrobiae	Verrucomicrobiales	Verrucomicrobiaceae	<i>Akkermansia</i>	<i>Akkermansia muciniphila</i>

Table S4. List of genes used in building the tree of bacteria

PID	Gene	Locus tag*	COG	Predicted product	Position*	Length (bp)*
90961179	<i>rpoB</i>	LSL_0197	COG0085K	DNA-directed RNA polymerase subunit beta	235025..238624	3600
90961471	<i>infC</i>	LSL_0495	COG0290J	translation initiation factor IF-3	545916..546440	525
90961487	<i>rpsB</i>	LSL_0511	COG0052J	30S ribosomal protein S2	557234..558031	798
90961488	<i>tsf</i>	LSL_0512	COG0264J	elongation factor Ts	558125..559000	876
90961538	<i>frr</i>	LSL_0562	COG0233J	ribosome recycling factor	600955..601518	564
90961545	<i>nusA</i>	LSL_0569	COG0195K	transcription elongation factor NusA	611433..612560	1128
90962130	<i>smpB</i>	LSL_1155	COG0691O	SsrA-binding protein	1187273..1187740	468
90962374	<i>rplM</i>	LSL_1403	COG0102J	50S ribosomal protein L13	1478312..1478755	444
90962389	<i>rpsE</i>	LSL_1418	COG0098J	30S ribosomal protein S5	1488030..1488530	501
90962391	<i>rplF</i>	LSL_1420	COG0097J	50S ribosomal protein L6	1488953..1489489	537
90962394	<i>rplE</i>	LSL_1423	COG0094J	50S ribosomal protein L5	1490153..1490695	543
90962399	<i>rplP</i>	LSL_1428	COG0197J	50S ribosomal protein L16	1491964..1492398	435
90962400	<i>rpsC</i>	LSL_1429	COG0092J	30S ribosomal protein S3	1492402..1493058	657
90962403	<i>rplB</i>	LSL_1432	COG0090J	50S ribosomal protein L2	1493766..1494599	834
90962405	<i>rplD</i>	LSL_1434	COG0088J	50S ribosomal protein L4	1494909..1495532	624
90962406	<i>rplC</i>	LSL_1435	COG0087J	50S ribosomal protein L3	1495557..1496180	624

*These columns are provided according to the reference genome *L. salivarius* UCC118

Table S5. Distribution of LPMXTG-containing and sortase enzymes across the 213 genomes

Species Name	StrainID	Prdms with LPMXTG motif	LPMXTG gene IDs	Sortase enzyme count	Sortase gene IDs	Initial LOCP output	Plus-positive strain*	Number of clusters	Locus tags
<i>Kandelia virens</i>	DSM 20438	4	DSM_20438G00656, DSM_20438G00657, DSM_20438G00658	7	DSM_20438G00648, DSM_20438G00649, DSM_20438G00650, DSM_20438G00651, DSM_20438G00652, DSM_20438G00653, DSM_20438G00654	Yes	1	1	DSM_20438G00648-DSM_20438G00657
<i>Lactobacillus kimchiensis</i>	DSM 14716	6	DSM_14716G00088, DSM_14716G00089, DSM_14716G00090, DSM_14716G00091, DSM_14716G00092, DSM_14716G00093	4	DSM_14716G00088, DSM_14716G00089, DSM_14716G00090, DSM_14716G00091	Yes	1	1	DSM_14716G00088-DSM_14716G00093
<i>Lactobacillus midlandis</i>	DSM 14500	9	DSM_14500G00041, DSM_14500G00042, DSM_14500G00043, DSM_14500G00044, DSM_14500G00045, DSM_14500G00046, DSM_14500G00047, DSM_14500G00048, DSM_14500G00049	10	DSM_14500G00041, DSM_14500G00042, DSM_14500G00043, DSM_14500G00044, DSM_14500G00045, DSM_14500G00046, DSM_14500G00047, DSM_14500G00048, DSM_14500G00049, DSM_14500G00050, DSM_14500G00051	No	0	0	
<i>Lactobacillus nesteri</i>	DSM 16982	8	DSM_16982G00249, DSM_16982G00250, DSM_16982G00251, DSM_16982G00252, DSM_16982G00253, DSM_16982G00254, DSM_16982G00255, DSM_16982G00256, DSM_16982G00257	10	DSM_16982G00249, DSM_16982G00250, DSM_16982G00251, DSM_16982G00252, DSM_16982G00253, DSM_16982G00254, DSM_16982G00255, DSM_16982G00256, DSM_16982G00257, DSM_16982G00258, DSM_16982G00259, DSM_16982G00260	No	0	0	
<i>Lactobacillus crustorum</i>	LMG 23699	6	LMG_23699G00127, LMG_23699G00128, LMG_23699G00129, LMG_23699G00130, LMG_23699G00131, LMG_23699G00132	6	LMG_23699G00127, LMG_23699G00128, LMG_23699G00129, LMG_23699G00130, LMG_23699G00131, LMG_23699G00132	No	0	0	
<i>Lactobacillus furci</i>	JCM 11951	5	JCM_11951G00051, JCM_11951G00052, JCM_11951G00053, JCM_11951G00054, JCM_11951G00055	5	JCM_11951G00051, JCM_11951G00052, JCM_11951G00053, JCM_11951G00054, JCM_11951G00055	No	0	0	
<i>Lactobacillus farci</i>	JCM 17355	5	JCM_17355G00149, JCM_17355G00150, JCM_17355G00151, JCM_17355G00152, JCM_17355G00153	5	JCM_17355G00149, JCM_17355G00150, JCM_17355G00151, JCM_17355G00152, JCM_17355G00153	No	0	0	
<i>Lactobacillus fuscus</i>	DSM 18184	5	DSM_18184G00034, DSM_18184G00035, DSM_18184G00036, DSM_18184G00037, DSM_18184G00038	5	DSM_18184G00034, DSM_18184G00035, DSM_18184G00036, DSM_18184G00037, DSM_18184G00038	No	0	0	
<i>Lactobacillus alimenteris</i>	DSM 20249	5	DSM_20249G00191, DSM_20249G00192, DSM_20249G00193, DSM_20249G00194, DSM_20249G00195	5	DSM_20249G00191, DSM_20249G00192, DSM_20249G00193, DSM_20249G00194, DSM_20249G00195	No	0	0	
<i>Lactobacillus paralimentarius</i>	DSM 19674	6	DSM_19674G00249, DSM_19674G00250, DSM_19674G00251, DSM_19674G00252, DSM_19674G00253, DSM_19674G00254	6	DSM_19674G00249, DSM_19674G00250, DSM_19674G00251, DSM_19674G00252, DSM_19674G00253, DSM_19674G00254	No	0	0	
<i>Lactobacillus paralimentarius</i>	DSM 13961	6	DSM_13961G00084, DSM_13961G00085, DSM_13961G00086, DSM_13961G00087, DSM_13961G00088, DSM_13961G00089	6	DSM_13961G00084, DSM_13961G00085, DSM_13961G00086, DSM_13961G00087, DSM_13961G00088, DSM_13961G00089	No	0	0	
<i>Lactobacillus paralimentarius</i>	DSM 13288	5	DSM_13288G00127, DSM_13288G00128, DSM_13288G00129, DSM_13288G00130, DSM_13288G00131	5	DSM_13288G00127, DSM_13288G00128, DSM_13288G00129, DSM_13288G00130, DSM_13288G00131	No	0	0	
<i>Lactobacillus necetti</i>	DSM 20183	6	DSM_20183G00143, DSM_20183G00144, DSM_20183G00145, DSM_20183G00146, DSM_20183G00147, DSM_20183G00148	6	DSM_20183G00143, DSM_20183G00144, DSM_20183G00145, DSM_20183G00146, DSM_20183G00147, DSM_20183G00148	No	0	0	
<i>Lactobacillus nodensis</i>	DSM 19682	7	DSM_19682G001072, DSM_19682G001073, DSM_19682G001074, DSM_19682G001075, DSM_19682G001076, DSM_19682G001077, DSM_19682G001078	7	DSM_19682G001072, DSM_19682G001073, DSM_19682G001074, DSM_19682G001075, DSM_19682G001076, DSM_19682G001077, DSM_19682G001078	No	0	0	
<i>Lactobacillus vromvoldensis</i>	DSM 14857	6	DSM_14857G001286, DSM_14857G001287, DSM_14857G001288, DSM_14857G001289, DSM_14857G001290, DSM_14857G001291	6	DSM_14857G001286, DSM_14857G001287, DSM_14857G001288, DSM_14857G001289, DSM_14857G001290, DSM_14857G001291	No	0	0	
<i>Lactobacillus florida</i>	DSM 23037	0		0		No	0	0	
<i>Lactobacillus acidophilus</i>	DSM 20079	11	DSM_20079G00040, DSM_20079G001512, DSM_20079G001513, DSM_20079G001514, DSM_20079G001515, DSM_20079G001516, DSM_20079G001517, DSM_20079G001518, DSM_20079G001519, DSM_20079G001520, DSM_20079G001521	11	DSM_20079G00040, DSM_20079G001512, DSM_20079G001513, DSM_20079G001514, DSM_20079G001515, DSM_20079G001516, DSM_20079G001517, DSM_20079G001518, DSM_20079G001519, DSM_20079G001520, DSM_20079G001521	No	0	0	
<i>Lactobacillus amylovorus</i>	DSM 20533	10	DSM_20533G00007, DSM_20533G001919, DSM_20533G001920, DSM_20533G001921, DSM_20533G001922, DSM_20533G001923, DSM_20533G001924, DSM_20533G001925, DSM_20533G001926, DSM_20533G001927	10	DSM_20533G00007, DSM_20533G001919, DSM_20533G001920, DSM_20533G001921, DSM_20533G001922, DSM_20533G001923, DSM_20533G001924, DSM_20533G001925, DSM_20533G001926, DSM_20533G001927	No	0	0	
<i>Lactobacillus amylovorus</i>	DSM 16698	6	DSM_16698G001813, DSM_16698G001814, DSM_16698G001815, DSM_16698G001816, DSM_16698G001817, DSM_16698G001818	6	DSM_16698G001813, DSM_16698G001814, DSM_16698G001815, DSM_16698G001816, DSM_16698G001817, DSM_16698G001818	No	0	0	
<i>Lactobacillus krasovskii</i>	DSM 16761	6	DSM_16761G001138, DSM_16761G001139, DSM_16761G001140, DSM_16761G001141, DSM_16761G001142, DSM_16761G001143	6	DSM_16761G001138, DSM_16761G001139, DSM_16761G001140, DSM_16761G001141, DSM_16761G001142, DSM_16761G001143	No	0	0	
<i>Lactobacillus kefirifaciens kefirifaciens</i>	DSM 5016	8	DSM_5016G001591, DSM_5016G001592, DSM_5016G001593, DSM_5016G001594, DSM_5016G001595, DSM_5016G001596, DSM_5016G001597, DSM_5016G001598	8	DSM_5016G001591, DSM_5016G001592, DSM_5016G001593, DSM_5016G001594, DSM_5016G001595, DSM_5016G001596, DSM_5016G001597, DSM_5016G001598	No	0	0	
<i>Lactobacillus kefirifaciens kefirifaciens</i>	DSM 10550	4	DSM_10550G001020, DSM_10550G002011, DSM_10550G002012, DSM_10550G002013	4	DSM_10550G001020, DSM_10550G002011, DSM_10550G002012, DSM_10550G002013	No	0	0	
<i>Lactobacillus alimenteris</i>	DSM 16047	3	DSM_16047G001070, DSM_16047G001071, DSM_16047G001072	3	DSM_16047G001070, DSM_16047G001071, DSM_16047G001072	No	0	0	
<i>Lactobacillus helveticus</i>	LMG 22660	9	LMG_22660G001772, LMG_22660G001951, LMG_22660G001952, LMG_22660G001953, LMG_22660G001954, LMG_22660G001955, LMG_22660G001956, LMG_22660G001957, LMG_22660G001958	9	LMG_22660G001772, LMG_22660G001951, LMG_22660G001952, LMG_22660G001953, LMG_22660G001954, LMG_22660G001955, LMG_22660G001956, LMG_22660G001957, LMG_22660G001958	No	0	0	
<i>Lactobacillus helveticus</i>	CGMCC 1.1877	5	CGMCC_1.1877G000568, CGMCC_1.1877G000569, CGMCC_1.1877G000570, CGMCC_1.1877G000571, CGMCC_1.1877G000572	5	CGMCC_1.1877G000568, CGMCC_1.1877G000569, CGMCC_1.1877G000570, CGMCC_1.1877G000571, CGMCC_1.1877G000572	No	0	0	
<i>Lactobacillus gallinarum</i>	DSM 10532	11	DSM_10532G001020, DSM_10532G000978, DSM_10532G000979, DSM_10532G000980, DSM_10532G000981, DSM_10532G000982, DSM_10532G000983, DSM_10532G000984, DSM_10532G000985, DSM_10532G000986, DSM_10532G000987	11	DSM_10532G001020, DSM_10532G000978, DSM_10532G000979, DSM_10532G000980, DSM_10532G000981, DSM_10532G000982, DSM_10532G000983, DSM_10532G000984, DSM_10532G000985, DSM_10532G000986, DSM_10532G000987	No	0	0	
<i>Lactobacillus crispatus</i>	DSM 10533	11	DSM_10533G000228, DSM_10533G000229, DSM_10533G000230, DSM_10533G000231, DSM_10533G000232, DSM_10533G000233, DSM_10533G000234, DSM_10533G000235, DSM_10533G000236, DSM_10533G000237, DSM_10533G000238	11	DSM_10533G000228, DSM_10533G000229, DSM_10533G000230, DSM_10533G000231, DSM_10533G000232, DSM_10533G000233, DSM_10533G000234, DSM_10533G000235, DSM_10533G000236, DSM_10533G000237, DSM_10533G000238	No	0	0	
<i>Lactobacillus acetotolerans</i>	DSM 20749	0		0		No	0	0	
<i>Lactobacillus intestinalis</i>	DSM 6629	13	DSM_6629G000082, DSM_6629G001159, DSM_6629G001160, DSM_6629G001161, DSM_6629G001162, DSM_6629G001163, DSM_6629G001164, DSM_6629G001165, DSM_6629G001166, DSM_6629G001167, DSM_6629G001168, DSM_6629G001169, DSM_6629G001170, DSM_6629G001171, DSM_6629G001172, DSM_6629G001173, DSM_6629G001174, DSM_6629G001175, DSM_6629G001176, DSM_6629G001177, DSM_6629G001178, DSM_6629G001179, DSM_6629G001180, DSM_6629G001181, DSM_6629G001182, DSM_6629G001183, DSM_6629G001184, DSM_6629G001185, DSM_6629G001186, DSM_6629G001187, DSM_6629G001188, DSM_6629G001189, DSM_6629G001190, DSM_6629G001191, DSM_6629G001192, DSM_6629G001193, DSM_6629G001194, DSM_6629G001195, DSM_6629G001196, DSM_6629G001197, DSM_6629G001198, DSM_6629G001199, DSM_6629G001200, DSM_6629G001201, DSM_6629G001202, DSM_6629G001203, DSM_6629G001204, DSM_6629G001205, DSM_6629G001206, DSM_6629G001207, DSM_6629G001208, DSM_6629G001209, DSM_6629G001210, DSM_6629G001211, DSM_6629G001212, DSM_6629G001213, 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Lactobacillus koreensis	JCM_16448	9	JCM_16448GL000085, JCM_16448GL001438, JCM_16448GL001439	3	JCM_16448GL001675, JCM_16448GL000224, JCM_16448GL000225	Yes	1	1	JCM_16448GL000222, JCM_16448GL000225
Lactobacillus arzyme	DSM_19395	16	DSM_19395GL002319, DSM_19395GL000381, DSM_19395GL000382	1	DSM_19395GL000034	No	0	0	
Lactobacillus acidifarinae	DSM_19394	14	DSM_19394GL001854, DSM_19394GL002248, DSM_19394GL002249	2	DSM_19394GL001800, DSM_19394GL000905	Yes	0	0	
Lactobacillus nummirensis	DSM_19117	15	DSM_19117GL000223, DSM_19117GL002162, DSM_19117GL002163	1	DSM_19117GL001722	No	0	0	
Lactobacillus spicheri	DSM_15429	15	DSM_15429GL000273, DSM_15429GL001364, DSM_15429GL001365	1	DSM_15429GL000043	No	0	0	
Lactobacillus kimcheicus	JCM_15350	7	JCM_15350GL002468, JCM_15350GL000731, JCM_15350GL000732	1	JCM_15350GL000783	No	0	0	
Lactobacillus similis	DSM_23365	21	DSM_23365GL001270, DSM_23365GL000121, DSM_23365GL000122	1	DSM_23365GL001158	Yes	0	0	
Lactobacillus odoraizoides	DSM_19909	23	DSM_19909GL000375, DSM_19909GL000334, DSM_19909GL000335	1	DSM_19909GL002358	Yes	0	0	
Lactobacillus collinsoniae	DSM_20515	10	DSM_20515GL000349, DSM_20515GL002667, DSM_20515GL002668	1	DSM_20515GL000897	Yes	0	0	
Lactobacillus paracollinoides	DSM_15502	15	DSM_15502GL003136, DSM_15502GL000710, DSM_15502GL000711	1	DSM_15502GL001533	Yes	0	0	
Lactobacillus maderfermentans	DSM_5705	12	DSM_5705GL001772, DSM_5705GL000489, DSM_5705GL000490	1	DSM_5705GL000241	No	0	0	
Lactobacillus parabuchneri	DSM_5707	9	DSM_5707GL002343, DSM_5707GL002311, DSM_5707GL002312	1	DSM_5707GL002384	No	0	0	
Lactobacillus parabuchneri	DSM_15352	11	DSM_15352GL001529, DSM_15352GL000299, DSM_15352GL000300	3	DSM_15352GL002182, DSM_15352GL001528, DSM_15352GL001529	Yes	1	1	DSM_15352GL001527, DSM_15352GL001531
Lactobacillus buchneri	DSM_20057	5	DSM_20057GL002290, DSM_20057GL002208, DSM_20057GL002209	1	DSM_20057GL002253	No	0	0	
Lactobacillus cackinasensis	DSM_19908	6	DSM_19908GL000970, DSM_19908GL000708, DSM_19908GL000709	1	DSM_19908GL002000	Yes	0	0	
Lactobacillus kefirii	DSM_20587	3	DSM_20587GL001017, DSM_20587GL001780, DSM_20587GL001781	1	DSM_20587GL001982	No	0	0	
Lactobacillus parakefirii	DSM_10551	6	DSM_10551GL001097, DSM_10551GL001348, DSM_10551GL001349	2	DSM_10551GL000796, DSM_10551GL004542	No	0	0	
Lactobacillus sunkii	DSM_19904	4	DSM_19904GL000561, DSM_19904GL001317, DSM_19904GL001318	1	DSM_19904GL000903	No	0	0	
Lactobacillus rapti	DSM_19907	6	DSM_19907GL001146, DSM_19907GL002649, DSM_19907GL002650	1	DSM_19907GL001524	No	0	0	
Lactobacillus kionensis	DSM_19906	6	DSM_19906GL002469, DSM_19906GL002006, DSM_19906GL002007	1	DSM_19906GL001744	No	0	0	
Lactobacillus diolivorans	DSM_14421	4	DSM_14421GL000349, DSM_14421GL002640, DSM_14421GL002641	2	DSM_14421GL002029, DSM_14421GL002101	Yes	0	0	
Lactobacillus ligandii	DSM_20176	2	DSM_20176GL001813, DSM_20176GL000973	1	DSM_20176GL000386	No	0	0	
Lactobacillus ferrireducens	DSM_18382	1	DSM_18382GL000356	1	DSM_18382GL002163	Yes	0	0	
Lactobacillus parafarraginis	DSM_18390	7	DSM_18390GL001600, DSM_18390GL000527, DSM_18390GL000528	2	DSM_18390GL002766, DSM_18390GL001314	No	0	0	
Lactobacillus senisensis	DSM_24302	3	DSM_24302GL001476, DSM_24302GL001193, DSM_24302GL001194	3	DSM_24302GL001196, DSM_24302GL001052, DSM_24302GL001053	Yes	1	1	DSM_24302GL001193, DSM_24302GL001196
Lactobacillus orezensis	DSM_23829	0		1	DSM_23829GL001214	No	0	0	
Lactobacillus kunkaei	DSM_12361	6	DSM_12361GL001115, DSM_12361GL001310, DSM_12361GL001311	1	DSM_12361GL001048	No	0	0	
Lactobacillus florani	DSM_22689	6	DSM_22689GL000154, DSM_22689GL000095, DSM_22689GL000096	1	DSM_22689GL000108	No	0	0	
Lactobacillus lindneri	DSM_20690	6	DSM_20690GL001120, DSM_20690GL001342, DSM_20690GL001343	1	DSM_20690GL000658	No	0	0	
Lactobacillus safraniae	DSM_20451	4	DSM_20451GL000977, DSM_20451GL002020, DSM_20451GL002021	1	DSM_20451GL000270	No	0	0	
Lactobacillus fructivorans	ATCC_27394	9	ATCC_27394GL000693, ATCC_27394GL000688, ATCC_27394	1	ATCC_27394GL000683	Yes	0	0	
Lactobacillus homohiochii	DSM_20571	9	DSM_20571GL000572, DSM_20571GL000664, DSM_20571GL000665	1	DSM_20571GL000680	Yes	0	0	
Lactobacillus fructivorans	DSM_20350	8	DSM_20350GL000774, DSM_20350GL000229, DSM_20350GL000230	1	DSM_20350GL001071	Yes	0	0	
Lactobacillus fructivorans	DSM_20203	8	DSM_20203GL001276, DSM_20203GL000494, DSM_20203GL000495	1	DSM_20203GL000504	Yes	0	0	
Podococcus argentinicus	DSM_23026	4	DSM_23026GL001175, DSM_23026GL000894, DSM_23026GL000895	1	DSM_23026GL000528	No	0	0	
Podococcus clausenii	DSM_14800	3	DSM_14800GL000637, DSM_14800GL001642, DSM_14800GL001643	2	DSM_14800GL001036, DSM_14800GL001113	Yes	1	1	DSM_14800GL001113, DSM_14800GL001115
Podococcus pentoseus	DSM_20356	3	DSM_20356GL000909, DSM_20356GL000913, DSM_20356GL000914	1	DSM_20356GL000314	No	0	0	
Podococcus stilisii	DSM_18001	0		1	DSM_18001GL000326	No	0	0	
Podococcus lotii	DSM_19927	3	DSM_19927GL001047, DSM_19927GL001900, DSM_19927GL001901	1	DSM_19927GL001675	Yes	0	0	
Podococcus acidilactici	ASI_2096G	3	ASI_2096GGL001049, ASI_2096GGL001783, ASI_2096GGL000415	1	ASI_2096GGL000951	No	0	0	
Podococcus ethanolidurans	DSM_22301	9	DSM_22301GL000128, DSM_22301GL000049, DSM_22301GL000050	4	DSM_22301GL001131, DSM_22301GL000126, DSM_22301GL001909	Yes	1	1	DSM_22301GL000125, DSM_22301GL001028
Podococcus cellicola	DSM_17357	7	DSM_17357GL000421, DSM_17357GL001523, DSM_17357GL001524	2	DSM_17357GL001526, DSM_17357GL001909	No	0	0	
Podococcus damnosus	DSM_20331	10	DSM_20331GL001090, DSM_20331GL001685, DSM_20331GL001686	3	DSM_20331GL001092, DSM_20331GL001093, DSM_20331GL001903	Yes	1	1	DSM_20331GL001090, DSM_20331GL001903
Podococcus inopinatus	DSM_20285	10	DSM_20285GL000864, DSM_20285GL000210, DSM_20285GL000211	4	DSM_20285GL001776, DSM_20285GL000520, DSM_20285GL000521	Yes	1	1	DSM_20285GL000546, DSM_20285GL000549
Podococcus parvulus	DSM_20332	10	DSM_20332GL002774, DSM_20332GL0013420, DSM_20332GL0013421	6	DSM_20332GL000316, DSM_20332GL001496, DSM_20332GL001497	Yes	1	2	DSM_20332GL000316, DSM_20332GL003316, DSM_20332GL003417
Carnobacterium malaromaticum	DSM_20370	22	DSM_20370GL003263, DSM_20370GL0010714, DSM_20370GL0010715	4	DSM_20370GL003099, DSM_20370GL003066, DSM_20370GL003067	Yes	0	0	
Carnobacterium malaromaticum	DSM_20342	27	DSM_20342GL002886, DSM_20342GL001571, DSM_20342GL001572	7	DSM_20342GL001625, DSM_20342GL002378, DSM_20342GL002379	Yes	1	1	DSM_20342GL002941, DSM_20342GL002944
Carnobacterium malaromaticum	DSM_20722	22	DSM_20722GL002044, DSM_20722GL001429, DSM_20722GL001430	7	DSM_20722GL000754, DSM_20722GL001730, DSM_20722GL001731	Yes	1	1	DSM_20722GL000754, DSM_20722GL000757
Carnobacterium divergens	DSM_20623	18	DSM_20623GL001163, DSM_20623GL000792, DSM_20623GL000793	4	DSM_20623GL001820, DSM_20623GL001147, DSM_20623GL001148	No	0	0	
Lactococcus lactis	LMG_7760	7	LMG_7760GL001946, LMG_7760GL001608, LMG_7760GL001609	2	LMG_7760GL001539, LMG_7760GL001947	Yes	1	1	LMG_7760GL001946, LMG_7760GL001949
Atopobium minutum	DSM_20586	9	DSM_20586GL001354, DSM_20586GL000632, DSM_20586GL000633	1	DSM_20586GL001167	No	0	0	
Olsenella sili	DSM_7084	5	DSM_7084GL001434, DSM_7084GL000839, DSM_7084GL000840	2	DSM_7084GL001746, DSM_7084GL001525	Yes	1	1	DSM_7084GL001746, DSM_7084GL001749
Atopobium ritae	DSM_7090	0		1	DSM_7090GL000687	No	0	0	
Total		1628		357			51	67	

Footnote: The gene sequences for all locus tags listed above are provided as supplementary datasets 3,4 and

* Cells colored in light gray indicate strain harboring at least 1 plus gene cluster with a similar gene order a *L. rhamnosus* strain GG.

Table S6. Distribution and abundance of cell envelope proteins and associated anchoring domains and motifs

Species name	StrainID	CEPs	Cell anchor type		
			LPxTG	SLAP	T
Kandleria vitulina	DSM-20405	0	0	0	0
Lactobacillus kimchiensis	DSM-24716	0	0	0	0
Lactobacillus mindensis	DSM-14500	0	0	0	0
Lactobacillus nantensis	DSM-16982	0	0	0	0
Lactobacillus crustorum	LMG-23699	0	0	0	0
Lactobacillus crustorum	JCM-15951	0	0	0	0
Lactobacillus futsaii	JCM-17355	0	0	0	0
Lactobacillus farciminis	DSM-20184	0	0	0	0
Lactobacillus alimentarius	DSM-20249	0	0	0	0
Lactobacillus paralimentarius	DSM-19674	0	0	0	0
Lactobacillus paralimentarius	DSM-13961	0	0	0	0
Lactobacillus paralimentarius	DSM-13238	0	0	0	0
Lactobacillus tucseti	DSM-20183	0	0	0	0
Lactobacillus nodensis	DSM-19682	0	0	0	0
Lactobacillus versmoldensis	DSM-14857	0	0	0	0
Lactobacillus floricola	DSM-23037	0	0	0	0
Lactobacillus acidophilus	DSM-20079	1	0	1	0
Lactobacillus amylovorus	DSM-20531	0	0	0	0
Lactobacillus amylovorus	DSM-16698	0	0	0	0
Lactobacillus kitasatonis	DSM-16761	0	0	0	0
Lactobacillus kefiranofaciens kefiranofaciens	DSM-5016	2	0	2	0
Lactobacillus kefiranofaciens kefirgranum	DSM-10550	0	0	0	0
Lactobacillus ultunensis	DSM-16047	1	0	1	0
Lactobacillus helveticus	LMG-22464	1	0	1	0
Lactobacillus helveticus	CGMCC-1.1877	1	0	1	0
Lactobacillus gallinarum	DSM-10532	1	0	1	0
Lactobacillus crispatus	DSM-20584	0	0	0	0
Lactobacillus acetotolerans	DSM-20749	0	0	0	0
Lactobacillus intestinalis	DSM-6629	1	0	1	0
Lactobacillus hamsteri	DSM-5661	0	0	0	0
Lactobacillus amyolyticus	DSM-11664	0	0	0	0
Lactobacillus kalixensis	DSM-16043	1	0	1	0
Lactobacillus gigeriorum	DSM-23908	1	0	1	0
Lactobacillus pasteurii	DSM-23907	0	0	0	0
Lactobacillus delbrueckii jakobsenii	DSM-26046	1	0	1	0
Lactobacillus delbrueckii lactis	DSM-20072	1	0	1	0
Lactobacillus delbrueckii bulgaricus	DSM-20081	1	0	1	0
Lactobacillus delbrueckii delbrueckii	DSM-20074	1	0	1	0
Lactobacillus delbrueckii indicus	DSM-15996	1	0	1	0
Lactobacillus equicursoris	DSM-19284	1	0	1	0
Lactobacillus jensenii	DSM-20557	0	0	0	0
Lactobacillus psittaci	DSM-15354	0	0	0	0
Lactobacillus hominis	DSM-23910	1	0	1	0
Lactobacillus taiwanensis	DSM-21401	1	1	0	0
Lactobacillus johnsonii	ATCC-33200	0	0	0	0
Lactobacillus gasseri	ATCC-33323	0	0	0	0
Lactobacillus iners	DSM-13335	0	0	0	0
Lactobacillus amylophilus	DSM-20534	0	0	0	0
Lactobacillus amylophilus	DSM-20533	0	0	0	0
Lactobacillus dextrinicus	DSM-20335	0	0	0	0
Lactobacillus concavus	DSM-17758	1	1	0	0
Lactobacillus composti	DSM-18527	0	0	0	0
Lactobacillus harbinensis	DSM-16991	0	0	0	0
Lactobacillus perolens	DSM-12744	1	0	0	1
Lactobacillus camelliae	DSM-22697	2	2	0	0
Lactobacillus nasuensis	JCM-17158	1	1	0	0
Lactobacillus manihotivorans	DSM-13343	1	1	0	0
Lactobacillus paracasei paracasei	DSM-5622	2	2	0	0
Lactobacillus casei	DSM-20011	1	1	0	0
Lactobacillus paracasei tolerans	DSM-20258	0	0	0	0
Lactobacillus zeae	DSM-20178	2	2	0	0
Lactobacillus rhamnosus	DSM-20021	2	2	0	0
Lactobacillus saniviri	DSM-24301	0	0	0	0
Lactobacillus brantae	DSM-23927	0	0	0	0
Lactobacillus thailandensis	DSM-22698	0	0	0	0
Lactobacillus pantheris	DSM-15945	1	1	0	0
Lactobacillus sharpeae	DSM-20505	0	0	0	0
Lactobacillus selangorensis	DSM-13344	0	0	0	0
Lactobacillus selangorensis	ATCC-BAA-66	0	0	0	0
Lactobacillus graminis	DSM-20719	0	0	0	0
Lactobacillus curvatus	DSM-20019	0	0	0	0
Lactobacillus sakei sakei	DSM-20017	0	0	0	0
Lactobacillus sakei carnosus	DSM-15831	0	0	0	0
Lactobacillus fuchuensis	DSM-14340	0	0	0	0
Lactobacillus rennini	DSM-20253	0	0	0	0
Lactobacillus coryniformis torquens	DSM-20004	0	0	0	0
Lactobacillus coryniformis coryniformis	DSM-20001	0	0	0	0
Lactobacillus bifermmentans	DSM-20003	0	0	0	0
Lactobacillus ceti	DSM-22408	0	0	0	0
Lactobacillus saerimneri	DSM-16049	0	0	0	0
Lactobacillus animalis	DSM-20602	1	1	0	0
Lactobacillus murinus	DSM-20452	1	1	0	0
Lactobacillus apodemii	DSM-16634	1	1	0	0
Lactobacillus ruminis	DSM-20403	1	1	0	0
Lactobacillus agilis	DSM-20509	0	0	0	0
Lactobacillus equi	DSM-15833	1	1	0	0
Lactobacillus salivarius	DSM-20555	1	1	0	0
Lactobacillus hayakitensis	DSM-18933	0	0	0	0
Lactobacillus pobuzihii	NBRC-103219	0	0	0	0

Lactobacillus pobuzihii.Chen	KCTC-13174	0	0	0	0
Lactobacillus acidipiscis	DSM-15836	0	0	0	0
Lactobacillus acidipiscis	DSM-15353	0	0	0	0
Lactobacillus aviarius aviarius	DSM-20655	0	0	0	0
Lactobacillus aviarius araffinosus	DSM-20653	0	0	0	0
Lactobacillus sucicola	DSM-21376	0	0	0	0
Lactobacillus aquaticus	DSM-21051	0	0	0	0
Lactobacillus uvarum	DSM-19971	0	0	0	0
Lactobacillus capillatus	DSM-19910	0	0	0	0
Lactobacillus cacaonum	DSM-21116	0	0	0	0
Lactobacillus mali	DSM-20444	0	0	0	0
Lactobacillus mali	ATCC-27304	0	0	0	0
Lactobacillus hordei	DSM-19519	0	0	0	0
Lactobacillus oeni	DSM-19972	0	0	0	0
Lactobacillus satsumensis	DSM-16230	0	0	0	0
Lactobacillus vini	DSM-20605	0	0	0	0
Lactobacillus ghanensis	DSM-18630	0	0	0	0
Lactobacillus nagelii	DSM-13675	0	0	0	0
Lactobacillus algidus	DSM-15638	0	0	0	0
Lactobacillus fabifermentans	DSM-21115	0	0	0	0
Lactobacillus xiangfangensis	LMG-26013	0	0	0	0
Lactobacillus pentosus	DSM-20314	0	0	0	0
Lactobacillus plantarum argenteratensis	DSM-16365	0	0	0	0
Lactobacillus plantarum	DSM-13273	0	0	0	0
Lactobacillus plantarum plantarum	CGMCC-1.2437	0	0	0	0
Lactobacillus paraplantarum	DSM-10667	0	0	0	0
Lactobacillus siliginis	DSM-22696	0	0	0	0
Lactobacillus rossiae	DSM-15814	0	0	0	0
Weissella viridescens	DSM-20410	0	0	0	0
Weissella minor	DSM-20014	0	0	0	0
Weissella halotolerans	DSM-20190	0	0	0	0
Weissella confusa	DSM-20196	0	0	0	0
Weissella kandleri	DSM-20593	0	0	0	0
Oenococcus oeni	ATCC-BAA-1163	0	0	0	0
Oenococcus kitaharae	DSM-17330	0	0	0	0
Leuconostoc fallax	KCTC-3537	0	0	0	0
Leuconostoc pseudomesenteroides	4882-	1	0	0	1
Leuconostoc mesenteroides	ATCC-8293	0	0	0	0
Leuconostoc mesenteroides cremoris	ATCC-19254	0	0	0	0
Leuconostoc carnosum	JB16-	0	0	0	0
Leuconostoc argentinum	KCTC-3773	0	0	0	0
Leuconostoc citreum	KM20-	0	0	0	0
Leuconostoc gelidum	KCTC-3527	0	0	0	0
Leuconostoc gasicomitatum	LMG-18811	0	0	0	0
Leuconostoc kimchii	IMSNU-11154	0	0	0	0
Fructobacillus fructosus	DSM-20349	0	0	0	0
Lactobacillus pontis	DSM-8475	0	0	0	0
Lactobacillus panis	DSM-6035	0	0	0	0
Lactobacillus oris	DSM-4864	0	0	0	0
Lactobacillus antri	DSM-16041	0	0	0	0
Lactobacillus reuteri	DSM-20016	0	0	0	0
Lactobacillus vaginalis	DSM-5837	0	0	0	0
Lactobacillus frumenti	DSM-13145	0	0	0	0
Lactobacillus fermentum	DSM-20055	0	0	0	0
Lactobacillus equigenerosi	DSM-18793	0	0	0	0
Lactobacillus gastricus	DSM-16045	0	0	0	0
Lactobacillus ingluviei	DSM-15946	0	0	0	0
Lactobacillus ingluviei	DSM-14792	0	0	0	0
Lactobacillus secaliphilus	DSM-17896	0	0	0	0
Lactobacillus coleohominis	DSM-14060	0	0	0	0
Lactobacillus mucosae	DSM-13345	0	0	0	0
Lactobacillus oligofermentans	DSM-15707	0	0	0	0
Lactobacillus hokkaidonensis	DSM-26202	0	0	0	0
Lactobacillus suebicus	DSM-5007	0	0	0	0
Lactobacillus vaccinofermentans	DSM-20634	0	0	0	0
Lactobacillus parabravis	LMG-11984	0	0	0	0
Lactobacillus parabravis	ATCC-53295	0	0	0	0
Lactobacillus hammesii	DSM-16381	0	0	0	0
Lactobacillus paucivorans	DSM-22467	0	0	0	0
Lactobacillus senmaizukei	DSM-21775	0	0	0	0
Lactobacillus brevis	DSM-20054	0	0	0	0
Lactobacillus koreensis	JCM-16448	0	0	0	0
Lactobacillus zymae	DSM-19395	0	0	0	0
Lactobacillus acidifarinae	DSM-19394	0	0	0	0
Lactobacillus namurensis	DSM-19117	0	0	0	0
Lactobacillus spicheri	DSM-15429	0	0	0	0
Lactobacillus kimchicus	JCM-15530	0	0	0	0
Lactobacillus similis	DSM-23365	0	0	0	0
Lactobacillus odoratitofui	DSM-19909	0	0	0	0
Lactobacillus collinoides	DSM-20515	1	1	0	0
Lactobacillus paracollinoides	DSM-15502	0	0	0	0
Lactobacillus malefermentans	DSM-5705	0	0	0	0
Lactobacillus parabuchneri	DSM-5707	1	0	0	1
Lactobacillus parabuchneri	DSM-15352	1	0	0	1
Lactobacillus buchneri	DSM-20057	1	0	0	1
Lactobacillus otakiensis	DSM-19908	1	0	0	1
Lactobacillus kefir	DSM-20587	1	0	0	1
Lactobacillus parakefir	DSM-10551	2	0	0	2
Lactobacillus sunkii	DSM-19904	1	0	0	1
Lactobacillus rapi	DSM-19907	0	0	0	0
Lactobacillus kisonensis	DSM-19906	0	0	0	0
Lactobacillus diolivorans	DSM-14421	2	1	0	1
Lactobacillus hilgardii	DSM-20176	0	0	0	0
Lactobacillus farraginis	DSM-18382	1	0	0	1

Lactobacillus parafarraginis	DSM-18390	1	0	0	1
Lactobacillus senioris	DSM-24302	0	0	0	0
Lactobacillus ozensis	DSM-23829	0	0	0	0
Lactobacillus kunkeei	DSM-12361	0	0	0	0
Lactobacillus florum	DSM-22689	0	0	0	0
Lactobacillus lindneri	DSM-20690	0	0	0	0
Lactobacillus sanfranciscensis	DSM-20451	0	0	0	0
Lactobacillus fructivorans	ATCC-27394	0	0	0	0
Lactobacillus homohiochii	DSM-20571	0	0	0	0
Lactobacillus fructivorans	DSM-20350	0	0	0	0
Lactobacillus fructivorans	DSM-20203	0	0	0	0
Pediococcus argentiniticus	DSM-23026	0	0	0	0
Pediococcus clausenii	DSM-14800	0	0	0	0
Pediococcus pentosaceus	DSM-20336	0	0	0	0
Pediococcus stilesii	DSM-18001	0	0	0	0
Pediococcus lolii	DSM-19927	0	0	0	0
Pediococcus acidilactici	AS1-2696	0	0	0	0
Pediococcus ethanolidurans	DSM-22301	1	1	0	0
Pediococcus cellicola	DSM-17757	1	1	0	0
Pediococcus damnosus	DSM-20331	0	0	0	0
Pediococcus inopinatus	DSM-20285	0	0	0	0
Pediococcus parvulus	DSM-20332	0	0	0	0
Carnobacterium maltaromaticum	DSM-20730	1	1	0	0
Carnobacterium maltaromaticum	DSM-20342	1	1	0	0
Carnobacterium maltaromaticum	DSM-20722	1	1	0	0
Carnobacterium divergens	DSM-20623	1	1	0	0
Lactococcus lactis	LMG-7760	0	0	0	0
Atopobium minutum	DSM-20586	2	2	0	0
Olsenella uli	DSM-7084	0	0	0	0
Atopobium rimae	DSM-7090	0	0	0	0
Total		60	30	17	13

Table S7. CRISPR occurrence and diversity.

Species Name	StrainID	CRISPR Type	CRISPR Repeat Sequence	DR Length	No. of Spacers	Cas1	Cas3	Cas9	Cas10
<i>Kandelia vitulina</i>	DSM-20405	II	GTTTATAGAGTGGTATTATTGACAGATACAAAAC	36	43	Y		Y	
<i>Lactobacillus kimchiensis</i>	DSM-24716	Undefined	GTGTTCCCAATATACATGGGGATGATTCT	29	3				
<i>Lactobacillus mindensis A</i>	DSM-14500	II	GTTTATAGAAAGTAACTCACTCAATTAAGAACC	35	25	Y		Y	
<i>Lactobacillus mindensis B</i>	DSM-14500	Undefined	GTGCTCCCAATAAACATGGGGATGATTCT	29	3				
<i>Lactobacillus nantensis</i>	DSM-16982	II	GTTTTGTACTCTCAAAGATTAGAAACAGTAAAC	36	22	Y		Y	
<i>Lactobacillus crustorum</i>	LMG-23699	N/A	None found						
<i>Lactobacillus crustorum</i>	JCM-15951	N/A	None found						
<i>Lactobacillus fuscus</i>	JCM-17355	II	GTTTTGTACTCTAAAGAACTAGAAATAGTAAAC	36	19	Y		Y	
<i>Lactobacillus farcininis A</i>	DSM-20184	Undefined	GTTTTGTACTCTAAAGAACTAGAAATAGTAAAC	36	4				
<i>Lactobacillus farcininis B</i>	DSM-20184	II	GTTTTAGAAAGTATGTCTTCTATTACTTAAGAAC	36	11	Y		Y	
<i>Lactobacillus alimentarius</i>	DSM-20249	N/A	None found						
<i>Lactobacillus paralimentarius</i>	DSM-19674	N/A	None found						
<i>Lactobacillus paralimentarius</i>	DSM-13961	N/A	None found						
<i>Lactobacillus paralimentarius A</i>	DSM-13238	I	GTACTCCCATGTATATGGGGATGATTCC	29	11	Y	Y		
<i>Lactobacillus paralimentarius B</i>	DSM-13238	Undefined	GTACTCCCAATATACATGGGGATGATTCT	29	15				
<i>Lactobacillus tuceti</i>	DSM-20183	II	GTTTTGTACTCTTAAGGATTAGTAATGTAAC	36	15	Y		Y	
<i>Lactobacillus nodensis A</i>	DSM-19682	II	GTTTTAGAAAGTACGTCACTTCAATGTAAGAAC	36	9	Y		Y	
<i>Lactobacillus nodensis B</i>	DSM-19682	II	GTTTTAGTACTCTCAAGAAATAGTAACAGTAAAC	36	9	Y		Y	
<i>Lactobacillus versmoldensis</i>	DSM-14857	II	GTTTTAGATCTAAGTCACTCAATTAAGAAC	36	2	Y		Y	
<i>Lactobacillus floricola A</i>	DSM-23037	II	GTTTTAGAAAGTATGCAAACTCAATAGGTTAACC	36	5	Y		Y	
<i>Lactobacillus floricola B</i>	DSM-23037	II	GTTTCAGAAAGTATGCTATTGAAATAGTTAGGACT	36	5	Y		Y	
<i>Lactobacillus floricola C</i>	DSM-23037	Undefined	CITTTTTCTCCGCAATCCGGAGAGTGATCC	28	46				
<i>Lactobacillus acidophilus</i>	DSM-20079	Undefined	ATTTTCTCCAGTATGGAGGATGATCC	28	31				
<i>Lactobacillus amylovorus</i>	DSM-20531	N/A	None found						
<i>Lactobacillus amylovorus</i>	DSM-16698	I	GTTTTTATTAACCTAAGAGAAATGTAAT	30	53	Y	Y		
<i>Lactobacillus kitatonis</i>	DSM-16761	N/A	None found						
<i>Lactobacillus kefiranoferens kefiranoferens A</i>	DSM-5016	Undefined	GTGTTCTCCACGTATGGGAGGT	23	5				
<i>Lactobacillus kefiranoferens kefiranoferens B</i>	DSM-5016	Undefined	GTGTTCTCCACGTATGGGAGGTGATCCT	29	4				
<i>Lactobacillus kefiranoferens kefirgranum</i>	DSM-10550	I	GTGTTCTCCACGTATGGGAGGTGATCC	28	61	Y	Y		
<i>Lactobacillus ultunensis</i>	DSM-16047	N/A	None found						
<i>Lactobacillus helveticus</i>	LMG-22464	I	GTATTCTCCACGTATGGGAGGTGATCC	28	26	Y	Y		
<i>Lactobacillus helveticus</i>	CGMCC-1.1877	I	GTTTTTATTAACCTAAGAGAAATGTAAG	30	41	Y	Y		
<i>Lactobacillus gallinarum</i>	DSM-10532	N/A	None found						
<i>Lactobacillus crispatus</i>	DSM-20584	Undefined	GTATTCTCCACGTATGGGAGGTGATCC	28	3				
<i>Lactobacillus acetotolerans A</i>	DSM-20749	I	GTATTCTCCACGTATGGGAGGTGATCCT	29	45	Y	Y		
<i>Lactobacillus acetotolerans B</i>	DSM-20749	Undefined	GTTTTAGATGATTGATGATCAATGAGGTTAGACC	36	9				
<i>Lactobacillus intestinalis A</i>	DSM-6629	I	GTATTCCCAACGTATGGGAGGTGATCC	28	7	Y	Y		
<i>Lactobacillus intestinalis B</i>	DSM-6629	I	GTATTCCCAACGTATGGGAGGTGATCC	28	13	Y	Y		
<i>Lactobacillus intestinalis C</i>	DSM-6629	I	GTTTTTATTAACCTAAGAGAAATGTAAT	30	9	Y*	Y*		
<i>Lactobacillus intestinalis D</i>	DSM-6629	Undefined	GGATCACCTCCACATACGGGAGAACAC	28	11				
<i>Lactobacillus hamsteri</i>	DSM-5661	I	GTATTCTCCACGTATGGGAGGTGATCC	28	43	Y	Y		
<i>Lactobacillus amylolyticus</i>	DSM-11664	N/A	None found						
<i>Lactobacillus kalsxiensis</i>	DSM-16043	II	GTTTTAGACTGTGATGACTAGTAAAGTAAAC	36	4	Y*			
<i>Lactobacillus eigerorum</i>	DSM-23908	N/A	None found						
<i>Lactobacillus pasteurii</i>	DSM-23907	I	GTGTCACCACTAAGTGGGGGTGATCC	28	9	Y	Y		
<i>Lactobacillus delbrueckii jakobsenii</i>	DSM-26046	II	GTTTTAGAAAGTGTCTATTCAATAAGGTTAAACC	36	11	Y		Y	
<i>Lactobacillus delbrueckii lactis</i>	DSM-20072	Undefined	None found						
<i>Lactobacillus delbrueckii bulgaricus</i>	DSM-20081	I	GTATTCCCAACCAAGTGGGGGTGATCC	28	40	Y	Y		
<i>Lactobacillus delbrueckii delbrueckii</i>	DSM-20074	I	GTATTCCCAACCAAGTGGGGGTGATCC	28	40	Y	Y		
<i>Lactobacillus delbrueckii indicus</i>	DSM-15996	I	GTATTCCCAACCAAGTGGGGGTGATCC	28	39	Y	Y		
<i>Lactobacillus equicursoris</i>	DSM-19284	I	GTATTCCCTCGTATGAGGGGGTATCC	28	21	Y	Y		
<i>Lactobacillus jensenii</i>	DSM-20557	Undefined	None found						
<i>Lactobacillus pstitaci</i>	DSM-15354	II	GTTTTAGAAAGTGTAAATCAGTAAGTTGAAAAAC	36	42	Y		Y	
<i>Lactobacillus hominis</i>	DSM-23910	II	GTTTTAGTATGTTAGATCAATAAGGTTAGATC	36	9	Y	Y		
<i>Lactobacillus taiwanensis</i>	DSM-21401	N/A	None found						
<i>Lactobacillus johnsonii</i>	ATCC-33200	N/A	None found						
<i>Lactobacillus gasseri</i>	ATCC-33323	N/A	None found						
<i>Lactobacillus iners</i>	DSM-13335	N/A	None found						
<i>Lactobacillus amylophilus</i>	DSM-20534	Undefined	GTTTTCCCGCACAGGCGGGGTGATCC	28	52				
<i>Lactobacillus amylophilus</i>	DSM-20533	I	GTTTTCCCGCACAGGCGGGGTGATCC	28	52	Y	Y		
<i>Lactobacillus dextrinicus</i>	DSM-20335	I	GTTTTTATTAACAAGATTTGAATGTAAT	30	100	Y	Y		
<i>Lactobacillus concavus</i>	DSM-17758	II	GTTTTAGAAAGTGTCTTCAATAGGTTAAGACT	36	68	Y		Y*	
<i>Lactobacillus composti A</i>	DSM-18527	II	GTCTCGAAGATGTGATGATCAATGATTTCAAGGAC	36	10	Y		Y	
<i>Lactobacillus composti B</i>	DSM-18527	Undefined	CGCAACTCTGTAGTGGGGAATGAAAT	30	5				
<i>Lactobacillus harbinensis</i>	DSM-16991	II	GTCCCAATTTAGCCGATTTGGAAGGATCCAATAGC	36	60	Y*		Y	
<i>Lactobacillus perolens A</i>	DSM-12744	Undefined	TTAGGGGTGCGTGAATGAAAG	22	9				
<i>Lactobacillus perolens B</i>	DSM-12744	I	GTCCGATCCCTGGGGGTGCGTGAATGAAAG	31	9	Y	Y		
<i>Lactobacillus camelliae</i>	DSM-22697	N/A	None found						
<i>Lactobacillus nasuensis</i>	JCM-17158	N/A	None found						
<i>Lactobacillus manihotivorans</i>	DSM-13343	N/A	None found						
<i>Lactobacillus paracasei paracasei</i>	DSM-5622	N/A	None found						
<i>Lactobacillus casei</i>	DSM-20011	I	GTTTTCCCGCACAGGCGGGGTGATCC	28	20	Y	Y*		
<i>Lactobacillus paracasei tolerans</i>	DSM-20258	N/A	None found						
<i>Lactobacillus zeae</i>	DSM-20178	I	GTCCGAGTCTACGTGACTGCGTGAATGAAAT	32	86	Y	Y		
<i>Lactobacillus rhamnosus</i>	DSM-20021	N/A	None found						
<i>Lactobacillus saniviri</i>	DSM-24301	II	GTTTTAGTGGATGTGATCAATAGGTTAAGCAC	36	58	Y		Y	
<i>Lactobacillus brantae</i>	DSM-23927	I	GTATTCCCGTGCATACGGGGGTGATCC	28	45	Y	Y		
<i>Lactobacillus thailandensis</i>	DSM-22698	I	GTGTTCCCGCAGGTGGGGGTGATCC	28	73	Y	Y		
<i>Lactobacillus pantheris</i>	DSM-15945	N/A	None found						
<i>Lactobacillus sharpeae</i>	DSM-20505	N/A	None found						
<i>Lactobacillus selangorensis</i>	DSM-13344	I	GTTTTTATTAACAATATGGAATGTAAT	30	33	Y	Y		
<i>Lactobacillus selangorensis A</i>	ATCC-BAA-66	I	GTTTTTATTAACAATATGGAATGTAAT	30	37	Y	Y		
<i>Lactobacillus selangorensis B</i>	ATCC-BAA-66	Undefined	GTTTTTATTAACAATATGGAATGTAAT	30	8				
<i>Lactobacillus graminis</i>	DSM-20719	II	GTTTTAGAAAGTATCAATCAATGAGTGTCAAC	36	35	Y		Y	
<i>Lactobacillus curvatus</i>	DSM-20019	Undefined	GTTTTAGAAAGTATCAATCAATGAGTGTCAAC	36	6				
<i>Lactobacillus sakei sakei</i>	DSM-20017	N/A	None found						
<i>Lactobacillus sakei carnosus</i>	DSM-15831	II	GTTTTAGAAAGTATCAATCAATGAGTGTCAAC	36	21	Y		Y	
<i>Lactobacillus fuchuensis</i>	DSM-14340	II	GTTTTAGAAAGTATCAATCAATGAGTGTCAAC	36	27	Y		Y	
<i>Lactobacillus rennini A</i>	DSM-20253	I	GTCCGACTTATGATGGTGGTGAATGAAAT	32	24	Y	Y		
<i>Lactobacillus rennini B</i>	DSM-20253	II	GTTTTAGAAAGTATCAATCAATGAGTGTCAAC	36	12	Y		Y	
<i>Lactobacillus coryniformis torquens</i>	DSM-20004	II	GCTATTGATCTCTCAAGTTTCACGTAATAAGTAAAC	36	5	Y	Y		
<i>Lactobacillus coryniformis coryniformis</i>	DSM-20001	II	GTTTTAGAAAGTATCAATCAATGAGTGTCAAC	36	30	Y		Y	
<i>Lactobacillus bififormis</i>	DSM-20003	I	GTATTCCCGCACAGGCGGGGTGATCC	28	118	Y	Y		
<i>Lactobacillus cetii</i>	DSM-22408	II	GTTTAAAGACTATCGAAGAACACACTTCAAAAC	36	16	Y		Y	
<i>Lactobacillus saerimneri</i>	DSM-16049	II	GTTTTGTACTCTGAAGAATCTAGTAAAGTAAAC	36	8	Y*		Y*	
<i>Lactobacillus animalis</i>	DSM-20602	II	GTTTTAGACTATGTTTGTATGACTCCAAAAC	36	51	Y		Y	
<i>Lactobacillus murinus</i>	DSM-20452	N/A	None found						
<i>Lactobacillus apodemi</i>	DSM-16634	II	GTTTTAGACTATGATGTTTGTATGACTCCAAAAC	36	13	Y		Y	
<i>Lactobacillus ruminis A</i>	DSM-20403	III	GTTTTCGTCTCTCACTCGGAGATAGGTAATATC	36	13	Y			Y
<i>Lactobacillus ruminis B</i>	DSM-20403	I	ATTTCAACTCACGCCCTATACAGAGGGGAC	33	29	Y	Y		
<i>Lactobacillus agilis A</i>	DSM-20509	I	CTTCCCCACACTAGTGGGGTAAATCC	28	35	Y	Y		
<i>Lactobacillus agilis B</i>	DSM-20509	II	GTCTCAAGATGTGTTAAATCAATGATGTTAGTAC	36	32	Y		Y	
<i>Lactobacillus agilis C</i>	DSM-20509	Undefined	GTTTACAATCTCTTAAGTAAATAGATTC	30	4				
<i>Lactobacillus equi A</i>	DSM-15833	I	GTGTTCTCACTGATGAGGGGTAAATCC	28	13	Y*			
<i>Lactobacillus equi B</i>	DSM-15833	I	GTGTTCCCTGCTACGGGGGTGATCC	28	34	Y	Y		
<i>Lactobacillus equi C</i>	DSM-15833	Undefined	GTATTCCCTCACTGATGAGGGGTG	24	14				
<i>Lactobacillus salivarius</i>	DSM-20555	III	GTTTTGTCTCTTCACTCGGAGATATGTTCTTATT	36	11	Y			Y
<i>Lactobacillus hayakitensis</i>	DSM-18933	N/A	None found						
<i>Lactobacillus pobuzihii</i>	NBRC-103219	N/A	None found						
<i>Lactobacillus pobuzihii Chen</i>	KCTC-13174	N/A	None found						
<i>Lactobacillus acidipiscis</i>	DSM-15836	N/A	None found						
<i>Lactobacillus acidipiscis A</i>	DSM-15353	I	GTATTCCCAACGTATGGGGGTGATCC	28	22	Y	Y		
<i>Lactobacillus acidipiscis B</i>	DSM-15353	III	GTCTCTCCCTAATACCGGGGTATCTAATACC	36	39	Y			Y
<i>Lactobacillus avarius avarius</i>	DSM-20655	N/A	None found						
<i>Lactobacillus avarius araffinosus</i>	DSM-20653	N/A	None found						
<i>Lactobacillus succicola A</i>	DSM-21376	I	GTATTCCCGCGGTATGGGGGTGATCC	28	16	Y	Y		
<i>Lactobacillus succicola B</i>	DSM-21376	I	GTTTTTATTAACAATATGGAATGTAAT	30	41	Y	Y		
<i>Lactobacillus aquaticus</i>	DSM-21051	I	GTATTCCCGCACAGGCGGGGTGATCC	28	26	Y	Y		
<i>Lactobacillus uvarum</i>	DSM-19971	Undefined	GTTTTAGAAAGTGTGTTAAATCAATGAGTGTAGAAC	36	6				
<i>Lactobacillus capillatus</i>	DSM-19910	I	GTATTCCCGCACAGGCGGGGTGATCC	28	44	Y	Y		
<i>Lactobacillus cacoonum</i>	DSM-21116	II	GTTTTGTACTCTCAACATTTCTCATAGTAAAC	36	36	Y		Y	
<i>Lactobacillus mali</i>	DSM-20444	N/A	None found						
<i>Lactobacillus mali</i>	ATCC-27304	II	GTTTTGTACTCTCAACATTTCTCATAGTAAAC	36	21	Y		Y	

Table S8. Sequence information for the 27 core partial genes

PID*	<i>L. salivarius</i> locus		COG	Annotation	Co-ordinates*	Strand*	Length*
	Gene	tag*					
90960991	<i>dnaA</i>	LSL_0001	COG0593L	chromosomal replication initiation protein	1..1365	+	454
90960994	<i>recF</i>	LSL_0004	COG1195L	recombination protein F	3309..4448	+	379
90961461	<i>murC</i>	LSL_0485	COG0773M	UDP-N-acetylmuramyl-L-alanine ligase	533809..535140	+	443
90961551	<i>ribF</i>	LSL_0575	COG0196H	riboflavin kinase/FMN adenylyltransferase	616816..617772	+	318
90961553	<i>grpE</i>	LSL_0577	COG0576O	GrpE protein HSP-70 cofactor	618942..619538	+	198
90961554	<i>dnaK</i>	LSL_0578	COG0443O	molecular chaperone DnaK	619577..621424	+	615
90961556	<i>lepA</i>	LSL_0580	COG0481M	GTP-binding protein LepA	622843..624672	+	609
90961566	<i>prfA</i>	LSL_0590	COG0216J	peptide chain release factor 1	633672..634754	+	360
90961572	<i>atpF</i>	LSL_0596	COG0711C	ATP synthase subunit B	638577..639104	+	175
90961615	<i>rpsO</i>	LSL_0638	COG0184J	30S ribosomal protein S15	681489..681758	+	89
90962017	<i>ileS</i>	LSL_1042	COG0060J	isoleucyl-tRNA synthetase	1065203..1067998	-	931
90962030	<i>mraW</i>	LSL_1055	COG0275M	S-adenosyl-methyltransferase MraW	1080326..1081270	-	314
90962140	<i>pgk</i>	LSL_1165	COG0126G	phosphoglycerate kinase	1199234..1200436	-	400
90962149	<i>uvrA</i>	LSL_1174	COG0178L	excinuclease ABC subunit A	1208147..1210981	-	944
90962150	<i>uvrB</i>	LSL_1175	COG0556L	excinuclease ABC subunit B	1211000..1213000	-	666
90962161	<i>secA</i>	LSL_1186	COG0653U	preprotein translocase subunit SecA	1223594..1225957	-	787
90962203	<i>dnaX</i>	LSL_1228	COG2812L	DNA polymerase III subunit gamma/tau	1260545..1262284	-	579
90962211	<i>rplL</i>	LSL_1237	COG0222J	50S ribosomal protein L7/L12	1270871..1271239	-	122
90962242	<i>galU</i>	LSL_1268	COG1210M	UTP--glucose-1-phosphate uridylyltransferase	1304213..1305085	-	290
90962313	<i>trmA</i>	LSL_1341	COG2265J	tRNA (Uracil-5-) -methyltransferase	1392529..1393908	-	459
90962321	<i>pcrA</i>	LSL_1349	COG0210L	ATP-dependent DNA helicase	1403083..1405317	-	744
90962375	<i>truA</i>	LSL_1404	COG0101J	tRNA pseudouridine synthase A	1478890..1479660	-	256
90962386	<i>secY</i>	LSL_1415	COG0201U	preprotein translocase subunit SecY	1486063..1487361	-	432
90962403	<i>rplB</i>	LSL_1432	COG0090J	50S ribosomal protein L2	1493766..1494599	-	277
90962565	<i>parB</i>	LSL_1596	COG1475K	chromosome partitioning protein, DNA-binding protein	1676145..1677020	-	291
90962568	<i>gidB</i>	LSL_1599	COG0357M	16S rRNA methyltransferase GidB	1678668..1679393	-	241
90962695	<i>dnaB</i>	LSL_1726	COG0305L	replicative DNA helicase	1807560..1808951	-	463

*These columns are provided according to the reference genome *L. salivarius* UCC118

Table S10. Presence of sirtuin homologs in the 213 genomes analyzed

Species Name	StrainID	SIR2 family proteins (homolog of mammalian SIRT1,
		SIR2L1, Sir2a)
Kandleria vitulina	DSM-20405	2
Lactobacillus kimchiensis	DSM-24716	1
Lactobacillus mindensis	DSM-14500	1
Lactobacillus nantensis	DSM-16982	1
Lactobacillus crustorum	LMG-23699	1
Lactobacillus crustorum	JCM-15951	1
Lactobacillus futsaii	JCM-17355	3
Lactobacillus farciminis	DSM-20184	2
Lactobacillus alimentarius	DSM-20249	2
Lactobacillus paralimentarius	DSM-19674	2
Lactobacillus paralimentarius	DSM-13961	2
Lactobacillus paralimentarius	DSM-13238	1
Lactobacillus tucseti	DSM-20183	2
Lactobacillus nodensis	DSM-19682	1
Lactobacillus versmoldensis	DSM-14857	3
Lactobacillus floricola	DSM-23037	0
Lactobacillus acidophilus	DSM-20079	1
Lactobacillus amylovorus	DSM-20531	1
Lactobacillus amylovorus	DSM-16698	1
Lactobacillus kitasatonis	DSM-16761	1
Lactobacillus kefirnofaciens kefirnofaciens	DSM-5016	3
Lactobacillus kefirnofaciens kefirgranum	DSM-10550	3
Lactobacillus ultunensis	DSM-16047	4
Lactobacillus helveticus	LMG-22464	3
Lactobacillus helveticus	CGMCC-1.1877	3
Lactobacillus gallinarum	DSM-10532	1
Lactobacillus crispatus	DSM-20584	1
Lactobacillus acetotolerans	DSM-20749	1
Lactobacillus intestinalis	DSM-6629	1
Lactobacillus hamsteri	DSM-5661	3
Lactobacillus amyolyticus	DSM-11664	1
Lactobacillus kalixensis	DSM-16043	1
Lactobacillus gigeriorum	DSM-23908	1
Lactobacillus pasteurii	DSM-23907	1
Lactobacillus delbrueckii jakobsenii	DSM-26046	1
Lactobacillus delbrueckii lactis	DSM-20072	1
Lactobacillus delbrueckii bulgaricus	DSM-20081	1
Lactobacillus delbrueckii delbrueckii	DSM-20074	1
Lactobacillus delbrueckii indicus	DSM-15996	1
Lactobacillus equicursoris	DSM-19284	1
Lactobacillus jensenii	DSM-20557	1
Lactobacillus psittaci	DSM-15354	1
Lactobacillus hominis	DSM-23910	1
Lactobacillus taiwanensis	DSM-21401	1

<i>Lactobacillus johnsonii</i>	ATCC-33200	2
<i>Lactobacillus gasseri</i>	ATCC-33323	1
<i>Lactobacillus iners</i>	DSM-13335	0
<i>Lactobacillus amylotrophicus</i>	DSM-20534	1
<i>Lactobacillus amylophilus</i>	DSM-20533	1
<i>Lactobacillus dextrinicus</i>	DSM-20335	1
<i>Lactobacillus concavus</i>	DSM-17758	1
<i>Lactobacillus composti</i>	DSM-18527	1
<i>Lactobacillus harbinensis</i>	DSM-16991	1
<i>Lactobacillus perolens</i>	DSM-12744	1
<i>Lactobacillus camelliae</i>	DSM-22697	1
<i>Lactobacillus nasuensis</i>	JCM-17158	1
<i>Lactobacillus manihotivorans</i>	DSM-13343	1
<i>Lactobacillus paracasei paracasei</i>	DSM-5622	1
<i>Lactobacillus casei</i>	DSM-20011	1
<i>Lactobacillus paracasei tolerans</i>	DSM-20258	1
<i>Lactobacillus zeae</i>	DSM-20178	2
<i>Lactobacillus rhamnosus</i>	DSM-20021	2
<i>Lactobacillus saniviri</i>	DSM-24301	1
<i>Lactobacillus brantae</i>	DSM-23927	1
<i>Lactobacillus thailandensis</i>	DSM-22698	1
<i>Lactobacillus pantheris</i>	DSM-15945	1
<i>Lactobacillus sharpeae</i>	DSM-20505	0
<i>Lactobacillus selangorensis</i>	DSM-13344	1
<i>Lactobacillus selangorensis</i>	ATCC-BAA-66	1
<i>Lactobacillus graminis</i>	DSM-20719	3
<i>Lactobacillus curvatus</i>	DSM-20019	3
<i>Lactobacillus sakei sakei</i>	DSM-20017	0
<i>Lactobacillus sakei carnosus</i>	DSM-15831	0
<i>Lactobacillus fuchuensis</i>	DSM-14340	0
<i>Lactobacillus rennini</i>	DSM-20253	1
<i>Lactobacillus coryniformis torquens</i>	DSM-20004	2
<i>Lactobacillus coryniformis coryniformis</i>	DSM-20001	1
<i>Lactobacillus bifermentans</i>	DSM-20003	1
<i>Lactobacillus ceti</i>	DSM-22408	1
<i>Lactobacillus saerimneri</i>	DSM-16049	0
<i>Lactobacillus animalis</i>	DSM-20602	0
<i>Lactobacillus murinus</i>	DSM-20452	0
<i>Lactobacillus apodemi</i>	DSM-16634	1
<i>Lactobacillus ruminis</i>	DSM-20403	1
<i>Lactobacillus agilis</i>	DSM-20509	1
<i>Lactobacillus equi</i>	DSM-15833	2
<i>Lactobacillus salivarius</i>	DSM-20555	1
<i>Lactobacillus hayakitensis</i>	DSM-18933	0
<i>Lactobacillus pobuzihii</i>	NBRC-103219	1
<i>Lactobacillus pobuzihii.Chen</i>	KCTC-13174	1
<i>Lactobacillus acidipiscis</i>	DSM-15836	1

<i>Lactobacillus acidipiscis</i>	DSM-15353	1
<i>Lactobacillus aviarius aviarius</i>	DSM-20655	1
<i>Lactobacillus aviarius araffinosus</i>	DSM-20653	1
<i>Lactobacillus sucicola</i>	DSM-21376	1
<i>Lactobacillus aquaticus</i>	DSM-21051	1
<i>Lactobacillus uvarum</i>	DSM-19971	1
<i>Lactobacillus capillatus</i>	DSM-19910	1
<i>Lactobacillus cacaonum</i>	DSM-21116	0
<i>Lactobacillus mali</i>	DSM-20444	0
<i>Lactobacillus mali</i>	ATCC-27304	0
<i>Lactobacillus hordei</i>	DSM-19519	0
<i>Lactobacillus oeni</i>	DSM-19972	1
<i>Lactobacillus satsumensis</i>	DSM-16230	1
<i>Lactobacillus vini</i>	DSM-20605	1
<i>Lactobacillus ghanensis</i>	DSM-18630	1
<i>Lactobacillus nagelii</i>	DSM-13675	1
<i>Lactobacillus algidus</i>	DSM-15638	0
<i>Lactobacillus fabifermentans</i>	DSM-21115	1
<i>Lactobacillus xiangfangensis</i>	LMG-26013	1
<i>Lactobacillus pentosus</i>	DSM-20314	1
<i>Lactobacillus plantarum argenteratensis</i>	DSM-16365	1
<i>Lactobacillus plantarum</i>	DSM-13273	1
<i>Lactobacillus plantarum plantarum</i>	CGMCC-1.2437	1
<i>Lactobacillus paraplantarum</i>	DSM-10667	1
<i>Lactobacillus siliginis</i>	DSM-22696	1
<i>Lactobacillus rossiae</i>	DSM-15814	1
<i>Weissella viridescens</i>	DSM-20410	0
<i>Weissella minor</i>	DSM-20014	0
<i>Weissella halotolerans</i>	DSM-20190	1
<i>Weissella confusa</i>	DSM-20196	1
<i>Weissella kandleri</i>	DSM-20593	0
<i>Oenococcus oeni</i>	ATCC-BAA-116	1
<i>Oenococcus kitaharae</i>	DSM-17330	1
<i>Leuconostoc fallax</i>	KCTC-3537	0
<i>Leuconostoc pseudomesenteroides</i>	4882	1
<i>Leuconostoc mesenteroides</i>	ATCC-8293	1
<i>Leuconostoc mesenteroides cremoris</i>	ATCC-19254	1
<i>Leuconostoc carnosum</i>	JB16	0
<i>Leuconostoc argentinum</i>	KCTC-3773	1
<i>Leuconostoc citreum</i>	KM20	1
<i>Leuconostoc gelidum</i>	KCTC-3527	0
<i>Leuconostoc gasicomitatum</i>	LMG-18811	0
<i>Leuconostoc kimchii</i>	IMSNU-11154	0
<i>Fructobacillus fructosus</i>	DSM-20349	1
<i>Lactobacillus pontis</i>	DSM-8475	1
<i>Lactobacillus panis</i>	DSM-6035	2
<i>Lactobacillus oris</i>	DSM-4864	1

Lactobacillus antri	DSM-16041	1
Lactobacillus reuteri	DSM-20016	1
Lactobacillus vaginalis	DSM-5837	1
Lactobacillus frumenti	DSM-13145	2
Lactobacillus fermentum	DSM-20055	1
Lactobacillus equigenerosi	DSM-18793	1
Lactobacillus gastricus	DSM-16045	1
Lactobacillus ingluviei	DSM-15946	1
Lactobacillus ingluviei	DSM-14792	1
Lactobacillus secaliphilus	DSM-17896	1
Lactobacillus coleohominis	DSM-14060	0
Lactobacillus mucosae	DSM-13345	1
Lactobacillus oligofermentans	DSM-15707	1
Lactobacillus hokkaidonensis	DSM-26202	1
Lactobacillus suebicus	DSM-5007	1
Lactobacillus vaccinofermentans	DSM-20634	1
Lactobacillus parabrevis	LMG-11984	1
Lactobacillus parabrevis	ATCC-53295	1
Lactobacillus hammesii	DSM-16381	1
Lactobacillus paucivorans	DSM-22467	1
Lactobacillus senmaizukei	DSM-21775	1
Lactobacillus brevis	DSM-20054	1
Lactobacillus korensis	JCM-16448	1
Lactobacillus zymae	DSM-19395	1
Lactobacillus acidifarinae	DSM-19394	1
Lactobacillus namurensis	DSM-19117	1
Lactobacillus spicheri	DSM-15429	1
Lactobacillus kimchicus	JCM-15530	1
Lactobacillus similis	DSM-23365	1
Lactobacillus odoratitofui	DSM-19909	1
Lactobacillus collinoides	DSM-20515	1
Lactobacillus paracollinoides	DSM-15502	1
Lactobacillus malefermentans	DSM-5705	1
Lactobacillus parabuchneri	DSM-5707	1
Lactobacillus parabuchneri	DSM-15352	1
Lactobacillus buchneri	DSM-20057	1
Lactobacillus otakiensis	DSM-19908	1
Lactobacillus kefirii	DSM-20587	1
Lactobacillus parakefirii	DSM-10551	2
Lactobacillus sunkii	DSM-19904	2
Lactobacillus rapi	DSM-19907	1
Lactobacillus kisonensis	DSM-19906	1
Lactobacillus diolivorans	DSM-14421	1
Lactobacillus hilgardii	DSM-20176	1
Lactobacillus farraginis	DSM-18382	1
Lactobacillus parafarraginis	DSM-18390	2
Lactobacillus senioris	DSM-24302	1

<i>Lactobacillus ozensis</i>	DSM-23829	1
<i>Lactobacillus kunkeei</i>	DSM-12361	1
<i>Lactobacillus florum</i>	DSM-22689	1
<i>Lactobacillus lindneri</i>	DSM-20690	1
<i>Lactobacillus sanfranciscensis</i>	DSM-20451	1
<i>Lactobacillus fructivorans</i>	ATCC-27394	1
<i>Lactobacillus homohiochii</i>	DSM-20571	1
<i>Lactobacillus fructivorans</i>	DSM-20350	1
<i>Lactobacillus fructivorans</i>	DSM-20203	1
<i>Pediococcus argentinicus</i>	DSM-23026	0
<i>Pediococcus clausenii</i>	DSM-14800	0
<i>Pediococcus pentosaceus</i>	DSM-20336	0
<i>Pediococcus stilesii</i>	DSM-18001	0
<i>Pediococcus lolii</i>	DSM-19927	0
<i>Pediococcus acidilactici</i>	AS1-2696	0
<i>Pediococcus ethanolidurans</i>	DSM-22301	0
<i>Pediococcus cellicola</i>	DSM-17757	0
<i>Pediococcus damnosus</i>	DSM-20331	0
<i>Pediococcus inopinatus</i>	DSM-20285	0
<i>Pediococcus parvulus</i>	DSM-20332	0
<i>Carnobacterium maltaromaticum</i>	DSM-20730	0
<i>Carnobacterium maltaromaticum</i>	DSM-20342	0
<i>Carnobacterium maltaromaticum</i>	DSM-20722	0
<i>Carnobacterium divergens</i>	DSM-20623	1
<i>Lactococcus lactis</i>	LMG-7760	0
<i>Atopobium minutum</i>	DSM-20586	0
<i>Olsenella uli</i>	DSM-7084	2
<i>Atopobium rimae</i>	DSM-7090	1

34 **Supplementary Notes**

35 **Supplementary Note 1**

36 ***Lactobacillus* relatedness to other genera**

37 We also sequenced genomes of type strains from other genera associated with lactic
38 acid bacteria (LAB) including *Carnobacterium* and *Lactococcus* and other genera previously
39 misidentified as LAB, namely, *Atopobium*, *Kandleria* and *Olsenella*. *Carnobacterium* and
40 *Lactococcus* form distinct branches and are classified in the families *Carnobacteriaceae* and
41 *Streptococcaceae*, respectively, revealing closer genetic relatedness to genera other than
42 *Lactobacillus*. *Carnobacterium* is closely related to *Melissococcus* and *Lactococcus* to
43 *Streptococcus* (Fig. 1). This indicates that all currently known LAB descend from the same
44 ancestor as proposed previously¹. The un-relatedness of *Kandleria*, *Atopobium* and *Olsenella*
45 and other LAB is confirmed, with a closer relationship of *Kandleria* with *Erysipelothrix* in the
46 family *Erysipelotrichaceae* of the *Clostridium* subphylum cluster XVII of *Firmicutes*. *Atopobium*
47 and *Olsenella* revealed the greatest genetic distance from the genus *Lactobacillus*; they
48 belong to another phylum, *Actinobacteria*, which belongs to the high-GC, Gram-positive
49 bacteria, the most closely related genus being *Coriobacterium*.

50 **Supplementary Note 2**

51 **Validation of the core genome phylogeny**

52 We validated the branching order of the 73 core gene tree using alternative subsets of
53 gene datasets. We inferred a tree of the *Lactobacillus* genus complex, rooted on *Lactococcus*
54 *lactis*, comprised of 117 genes, and another tree of the *Lactobacillus* genus complex, rooted
55 on the *Carnobacteria*, comprised of 121 genes. We found there were only 4 minor branching
56 alterations. The robustness of the 73 core gene tree was also assessed using a range of
57 different models. Models tested were the WAG, LG, JTT, mtREV and Dayhoff models. The
58 resulting branching order of the strains was consistent across all the models with the exception
59 of mtREV. With this model the positions of *L. salivarius* DSM_20555, *L. hayakitensis*
60 DSM_18933 and *L. acetotolerans* DSM_20749 underwent minor node exchanges within the
61 same clade.

62 The impact of adding partial genes to the core gene dataset was assessed by inferring
63 a phylogeny (Supplementary Fig. 19) from the 73 complete core genes with an additional 27
64 partial core genes (listed in Supplementary Table 8) added to the dataset. The inferred
65 topology was highly congruent with the 73 complete core gene tree with only three very minor
66 branching alterations. Specifically, *L. koreensis* moved one branch within the *L. brevis*/*L.*
67 *collinoides* group. Minor displacements were also observed for *L. kefiranofaciens* DSM_5016
68 and DSM_10550 within the *L. delbrueckii* group and *L. salivarius* and *L. hayakitensis* within
69 the *L. salivarius* group.

70 **Supplementary Note 3**
71 **Relatedness of *Lactobacillus* species**

72 At the species level, the combination of ANI value and core genome phylogeny could
73 be proposed as the basis for optimal taxonomic classification², and its application could shed
74 new light on several issues including species widely used in the food and probiotic industry. A
75 long-debated case has been that of the *L. casei* group³. We propose that the species *L. casei*
76 and *L. paracasei* should be combined into a single species, *L. casei*, because the pair-wise
77 ANI values between the type strains of *L. casei* and two *L. paracasei* are 98~99%, larger than
78 the “un-official” species’ cut-off value of 95%⁴, and these three strains clustered together as a
79 monophyletic group (Fig. 2; Supplementary Fig. 20). The designation of *L. zeae* has been
80 controversial and there are reports suggesting its classification into the species *L. casei*^{3,5}.
81 However, the ANI value between *L. casei* and *L. zeae* is only 77%~78%, which is similar to
82 the value between *L. casei* and another well-defined species, *L. rhamnosus*. Therefore, our
83 genomic analysis supports retaining *L. zeae* as a single species. Remarkably, ANI values
84 seem not to be related to total DNA-DNA hybridization data reported previously⁵ for similarities
85 of *L. casei* type strain ATCC 393, which corresponds to the strain DSM 20011 included in this
86 study.

87 The genus *Lactobacillus* was recently defined as 16 phylogroups (incl. *Pediococcus*),
88 4 couples (groups containing only two species) and 10 single species⁶. Such delineations are
89 generally supported by the phylogenetic relationships constructed here based on the core
90 proteins, but two modifications are suggested (Fig. 2; Supplementary Fig. 18). Firstly, *L.*
91 *camelliae* could be included in the *L. manihotivorans* group and not in the *L. delbrueckii* group,
92 supported by a mean TNI value of <15% to the group, which is far lower than that within the
93 other *L. delbrueckii* group species (79.5%). Moreover, *L. amylophilus* and *L. amylophilus*
94 should also be classified as a single species, *L. amylophilus*, as the two type strains have an
95 ANI value of approximately 100%, although multilocus analysis and DNA-DNA hybridization
96 values suggested their separation.

97 **Supplementary Note 4**
98 **Phylogenomics of glycolysis and hexose fermentation**

99 In species characterized by the presence of Pfk, the distribution of the pyruvate
100 dehydrogenase operon (*Pdh*; composed of 4 genes) reflected carbohydrate metabolism since
101 it is absent in 57% of obligately homofermentative species while it is present in facultatively
102 heterofermentative members. Consistency was observed between *Pdh* distribution and
103 phylogenetic groupings: 90% of the species of the *L. delbrueckii* group lack *pdh*, while
104 members of groups like *L. salivarius*, *L. plantarum*, *L. casei* or *L. alimentarius* are
105 characterized by presence of both *pfk* and *pdh*, although they belong to different phenotypic
106 categorizations. Additionally, 80% of the species within the *L. delbrueckii* group lack

107 glucokinase, the first enzyme of the glycolytic pathway, except for the monophyletic subgroup
108 formed by the *L. delbrueckii* and *L. equicursoris* species. For growth on glucose, a PTS
109 transport system may obviate the need for this enzyme⁷ and most of these species (79%) are
110 classified as obligately homofermentative. Thus, comparative genomic analysis of glycolysis
111 reveals that species inside the historically defined groups have a coherent genotypic
background despite metabolic heterogeneity.

112 **Supplementary Note 5**

113 **Carbohydrate active enzymes**

114 Some GH families are present more uniformly across the dataset, indicating the
115 importance of the biotransformations associated with these families. Included in this are
116 enzymes involved in the hydrolysis of peptidoglycan (GH25 and GH73⁸), which play an
117 important role in cell division, growth and preserving cell wall integrity. Bacterial autolysis can
118 have a positive impact in the dairy fermentation process through the enhancement of cheese
119 flavour upon the release of enzymes and amino acids⁹. Starch degradation enzymes are also
120 present almost uniformly across the genome set. α -amylase enzymes are catalysts in the
121 hydrolysis of the α -1,4 glycosidic linkages of starch with GH13 being the main GH family acting
122 on substrates with α -glucoside linkages. α -glucan metabolism is important in the breakdown
123 of resistant starch. Another universal family of GHs is GH65; this family is mainly composed
124 of phosphorylases, including maltose and trehalase phosphorylase, which are essential for
125 the survival of lactobacilli in sugar-rich environments such as sourdough, where maltose is the
126 predominant sugar¹⁰.

127 Six clades display unusually high GH abundance, namely, *L. (par)alimentarius*, *L.*
128 *perolens*, *L. plantarum*, *L. rafi*, *L. fructivorans* and *Carnobacterium* spp. The *Weissella* spp.
129 and *L. fructivorans* clade show an unusually low GH gene count. The most abundant GH
130 families are GH1, GH13, GH25 and GH73. GH73, an N-acetylmuramidase, is present in all
131 *Lactobacillus* species except *L. equi*. The four *Carnobacterium* genomes harbor several GH
132 families that are absent in all or most of the other genomes including GH18, GH24, GH84,
133 GH85 and GH119. GH18 enzymes are chitinases, GH24 are lysozymes while GH119
134 enzymes are involved in chitin binding.

135 Some rare GTs emerge in the dataset. *P. lolii* and *P. parvulus* are the only strains that
136 harbour genes for GT12, a ganglioside synthase. This activity is very interesting as it has been
137 reported in only 3 bacterial species and 28 eukaryotes. Production of GT11 may be a strain-
138 specific trait, because a single non-type strain of each of *L. johnsonii*, *L. amylovorus* and *L.*
139 *paraplantarum* also appear to encode this activity (http://www.cazy.org/GT11_bacteria.html).

140 A number of GT families are present almost uniformly across the dataset. These
141 include GT51, which is involved in peptidoglycan synthesis⁸ and only *L. coleohominis* lacks

142 GT28, a galactosyltransferase involved in cell wall metabolism, suggesting alternative cell wall
143 structure in this vaginal isolate. Other ubiquitous families include more broad-spectrum GTs
144 that have been termed “polyspecific” because of their diverse functionality. Examples include
145 GT4 and GT2, which encompass at least 12 functions including cellulose synthase, chitin
146 synthase and mannosyltransferase¹¹.

147 The abundance of genes encoding carbohydrate transporters correlates strongly with
148 GH abundance and less strongly with GT abundance (Supplementary Fig. 21). The clade
149 distribution of carbohydrate transporter gene counts (Supplementary Fig. 22) mirrors this
150 correlation and highlights the relative abundance of carbohydrate management machinery in
151 the *L. alimentarius*, *L. casei*, *L. mali*, *L. plantarum* and *L. collinoides* clades, the pediococci
152 and carnobacteria. Normalization for genome size (Supplementary Fig. 23) reduces the
153 apparent overabundance of GT genes in some species, but not GH genes (Supplementary
154 Fig. 23), and it is debatable if such normalization is biologically relevant.

155 **Supplementary Note 6**

156 **Metabolic diversity of the lactobacilli**

157 A general representation of the genome content of the lactobacilli as Clusters of
158 Orthologous Groups (COGs; Supplementary Fig 15) reveals unexpected diversity in
159 categories including Transcription, Cell wall biogenesis, Energy production, Co-enzyme
160 transport, and Inorganic ion transport. The *L. plantarum*-related species from *L.*
161 *fabifermentans* through *L. paraplantum* (in Fig. 2) are particularly endowed with genes for
162 carbohydrate and amino acid transport and metabolism. Members of the *L. salivarius* clade
163 have the highest number of genes involved in cell motility and secretion, as expected from
164 previous studies in our group¹². Forty nine (23%) of the genomes screened had none of the
165 complete pathways for production of the 20 standard amino acids (AA), while no single
166 genome harboured the genes to produce all 20 AAs. The highest number of pathways
167 encoded by any one species was sixteen in *L. similis* (Supplementary Table 9). Some
168 phylogenetic clades harbored genes for the production of one or two amino acids; these
169 include *Weissella*, *L. brevis*, *Pediococcus* and *L. sakei*. The clade containing *L. collinoides*
170 and *L. kimchicus* as well as the *L. coryniformis* clade (with the exception of *L. rennini*) are
171 predicted to be prototrophic for at least 14 AAs. In contrast, ten of the twelve dairy isolates
172 have genes for five or fewer complete AA pathways, reflecting their evolution to the AA-rich
173 dairy environment.

174

175 **Supplementary Note 7**

176 **Sortase-anchored proteins**

177 The distribution of LPXTG proteins was not clearly correlated with the evolutionary
178 relationship of lactobacilli. Rather, it seems that the decoration of the cell wall with anchored

179 proteins is a common feature, indicating that most lactobacilli can establish interactions with
180 the environment. In our dataset of 213 genomes, only twelve bacterial strains do not have
181 LPXTG proteins (Supplementary Table 5). In addition, most lactobacilli genomes harbor at
182 least one gene encoding sortase, presumably the housekeeping sortase. The copy number of
183 sortase genes could be associated to some extent with the presence of pilus gene clusters
184 (PGC) (Fig. 4). These PGCs were identified in 51 strains in total, mostly belonging to six
185 clades. The bacterial species with the most pilus gene clusters was *Lactobacillus sharpeae*, a
186 sewage isolate. We also observed a large diversity of PGCs in terms of gene organization and
187 numbers, suggesting they may have distinct gene order and functions (Supplementary Fig.
188 10). One of the most common PGC types consists of three pilin genes and one sortase gene,
189 which is similar to the PGC originally reported in *L. rhamnosus* GG¹³.

190 **Supplementary Note 8**

191 **The *Lactobacillus mobilome***

192 The mobile component of the bacterial genome can expand coding capacity as in the
193 case of plasmids and megaplasmids¹⁴ or may be associated with genome decay as in the
194 case of Insertion Sequence (IS) elements¹⁵. Some IS elements exhibit a very limited
195 distribution across the 213 genomes, for example, IS1 which is restricted to only *L. ingluvei*
196 and *L. equi* (Supplementary Fig. 16). IS91 is present in the genomes of only two species, both
197 of dairy-product origin (*L. casei* and *L. paracasei* subsp. *tolerans*), and IS481 is found in only
198 3 strains (*L. paracollinoides*, *L. farraginis* and *P. inopinatus*) all associated with brewing. IS3,
199 on the other hand, exhibits a much greater distribution being present in almost all groups, with
200 the exception of *Weissella/Leuconostoc*, *L. fructivorans*, some *L. delbrueckii* strains and a few
201 singletons. Some genomes apparently harbor no IS elements, perhaps indicating a more rigid
202 architecture and a selective pressure against the acquisition of such elements. These species
203 include *Atopobium minutum*, *L. fructivorans*, *L. florum*, *L. sensoris*, *Weissella viridescens*, *L.*
204 *cacaonum*, *L. apodemi*, *L. ceti* and *L. brantae*. Of the 18 IS families in this database, the largest
205 number of families found is 13, in the *L. parabuchneri* genome. It is clear that IS elements
206 have played a general role in shaping the diversification and evolution of the lactobacilli.

207 Phages were detected in the genomes of 195 of the 213 genomes (Supplementary
208 Fig. 13), and only the genomes of *L. floricola*, *L. ingluviei*, *L. psittaci*, *L. sakei* subsp. *sakei*, *L.*
209 *sanfranciscensis*, *P. cellicola*, *P. claussenii* and *W. halotolerans* lacked homologues of phage
210 proteins. Proteins corresponding to holins and endolysins, and fibers/fiber assembly proteins
211 were apparently under-represented; this is likely due to the fact that holins are not well
212 annotated, whereas fiber proteins are very divergent, and not always present in the phage. It
213 is likely that this analysis under-reports phage genes and that fine tuning of homology cut-offs
214 for individual genes will identify more temperate phage. We identified plasmids in 41% of the

215 213 genomes analysed (Supplementary. Fig. 14) with numbers ranging from zero to six. 58%
216 of the plasmid-related genes were of unknown function, emphasizing the need for functional
217 genomics to elucidate this gene repertoire. Given the desirability of finding new plasmid
218 vectors for genetically manipulating lactobacilli in the laboratory and for food-grade strain
219 construction, these genomic data represent a valuable resource. Of the 87 strains predicted
220 to have plasmids, 75 had identifiable replication genes. The other 12 may harbor new
221 replication types that would be compatible with existing plasmid vectors.

222 **Supplementary Note 9**

223 **Stress resistance**

224 The broad range of niches that lactobacilli occupy is reflected in the multiple stress
225 resistance mechanisms their genomes encode (Supplementary Fig. 24). Knowledge of the
226 differential abundance of these systems can be exploited for identifying species and strains
227 that can withstand production stress, storage stress or intestinal survival¹⁶. Superoxide
228 dismutase and catalase show very limited distribution, as does the gene encoding glutamate
229 decarboxylase involved in proton scavenging and acid resistance (Supplementary Fig. 24),
230 the last of which is concentrated in *L. helveticus* and related species. Urease genes were
231 present in only 8 species including 3 of the 4 *Carnobacteria* species. Bile salt hydrolases
232 contribute to bile resistance in lactobacilli¹⁷; the pattern of their distribution in this genome data
233 resource, viewed in conjunction with other stress resistance genes, allows rational
234 identification of species likely to survive intestinal transit.

235 Protein acetyltransferases of prokaryotes like *Escherichia coli* confer resistance to heat
236 and oxidative stress¹⁸, and it was recently reported that homologs of the eukaryotic sirtuin
237 protein acetyltransferases contribute to stress resistance in *Lactobacillus paracasei*¹⁹. Forty of
238 the 213 genomes analyzed here lack homologs of any of SIRT1, SIR2L1, or Sir2 α
239 (Supplementary Table 10). The remaining 173 genomes encode at least one homolog, with a
240 single species *L. ultunensis* harbouring 4 homologs, and 3 homologs being found in a large
241 number of food or intestinal lactobacilli. Since pre-treatment of *Lactobacillus paracasei* strains
242 with the sirtuin activator resveratrol (found in berries and red wine) alleviated growth inhibition
243 by cholate¹⁹, this presents the exciting prospect that some food ingredients might promote
244 shelf-life of lactobacilli in functional food products, or that certain prebiotics might rationally
245 promote survival and intestinal transit of lactobacilli administered in synbiotics.

246 **Supplementary Note 10**

247 **Niche association and genome content**

248 A search for associations between niche and genome content for the 213 genomes
249 revealed moderate trends. The strongest trends were detected for species isolated from
250 animal sources (n=56), which, as noted in the main text, also had the lowest number of

251 predicted genes and the smallest average genome size (Supplementary Fig. 25). This is
252 evident at a functional level where numerous functional gene groups displayed the lowest
253 abundances in the animal niche. These groups include genes for the transport and metabolism
254 of carbohydrates (Supplementary Fig. 25, top panel), amino acids, lipids (Supplementary Fig.
255 25, top panel), co-enzymes, nucleotides and inorganic acids. Normalization for genome size
256 brought the difference above the significance threshold (Supplementary Fig. 25, bottom
257 panels; p-values of 0.11 and 0.107 for carbohydrate transport and lipid metabolism,
258 respectively). Genes involved in transcription, cell wall/membrane biogenesis and secondary
259 metabolites also have the lowest average abundance in the animal niche. Gene decay is
260 commonly associated with host-adapted microbes and this is a possible explanation for the
261 trend observed in genomes that have been isolated from animal sources.

262 Across the broader range of niches/sources, the analyses failed to detect niche-
263 specific genomic associations in our study, but rather a general pattern of gene decay in
264 species from the animal niche. This study focuses largely on the comparison of type strains
265 within the genus *Lactobacillus* and associated species so it is likely that the diversity among
266 species in the dataset was too great to reveal niche-specific traits. Studies that focus on
267 multiple strains of the same species are more suited to discovering niche-specific genes.

268

269 **Supplementary Note 11**

270 **Targeting competing microbes**

271 Bacteriocins are small, ribosomally synthesized antimicrobial peptides that can be exploited
272 as antimicrobial-producing cultures in fermented foods, or the bacteriocins themselves added,
273 e.g. pediocin and carnobacteriocin used as biopreservatives²⁰. Bacteriocins may also
274 contribute to probiotic properties by limiting infection²¹ or signalling to the innate immune
275 system²². Of the 213 genomes analysed here, 107 (50.2%; Supplementary Table 11) harbored
276 at least one Area of Interest (AOI) relating to bacteriocin production by screening against the
277 BAGEL database²³. Over half of these were larger proteins (>10 kDa) of the
278 enterolysin/helveticin class, which are no longer considered classical bacteriocins²⁴. However,
279 their widespread distribution suggests a central function for these currently cryptic
280 antimicrobials. Manual inspection confirmed that 38 AOIs had the contiguous gene structure
281 expected for typical bacteriocin operons. No dominant bacteriocin type was identified,
282 although 58% of intact AOIs fell under the Unmodified Bacteriocin (Class II) category. Many
283 of these included homologs of well-known bacteriocin operons including plantaricin, sakacin,
284 salivaricin, subtilin, leucocin, carnobacteriocin and lacticin F. Surprisingly, AOIs were
285 identified in many species not previously associated with bacteriocin production. For example,
286 genes encoding pediocins were annotated in *L. kimchicus* and *L. taiwanensis* was found to
287 harbour the machinery to produce subtilin. Predicted bacteriocin loci were found across all

288 clades of the phylogenetic tree with the exception of *Weissella* and the *L. brevis/L.parabrevis*
289 clade. Overall, the data do not support strict associations between species niche, the presence
290 of a bacteriocin or type of bacteriocin. Moreover, the overall prevalence of bacteriocins was
291 unexpectedly low compared to the literature describing this area, suggesting that many more
292 *Lactobacillus* species can produce bacteriocins than those represented by their type strains
293 examined in this study (for example *L. salivarius*²⁵).

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288

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