

## Additional file 1

**Table S1. Genebank identifiers of the nucleotide sequences of *atpA*, *pheS* and *rpoA* genes, used for the phylogenetic analyses.**

| Species   | <i>atpA</i>     | <i>pheS</i>     | <i>rpoA</i>     |
|---|-----------------|-----------------|-----------------|
| <i>Bacillus subtilis</i> 168 <sup>T</sup>                                 | NC_000964       | NC_000964       | NC_000964       |
| <i>L. carnosum</i> LMG 23898 <sup>T</sup>                                 | AM711275        | AM711282        | AM711353        |
| <i>L. citreum</i> LMG 9849 <sup>T</sup>                                   | AM711202        | AM711152        | AM711300        |
| <i>L. fallax</i> LMG 18975 <sup>T</sup>                                   | AM711284        | AM711193        | AM711343        |
| <i>L. gelidum</i> subsp. <i>aenigmaticum</i> POKY4-4                      | KF577554        | KF577556        | KF577561        |
| <i>L. gelidum</i> subsp. <i>aenigmaticum</i> POUF4d <sup>T</sup>          | KF577549        | KF577560        | KF577564        |
| <i>L. gelidum</i> subsp. <i>gasicomitatum</i> LMG 18811 <sup>T</sup>      | AM711180        | AM711150        | AM711318        |
| <i>L. gelidum</i> subsp. <i>gasicomitatum</i> LMG 18813                   | AM711201        | AM711162        | AM711317        |
| <i>L. gelidum</i> subsp. <i>gasicomitatum</i> KG16-1                      | LN890331        | LN890331        | LN890331        |
| <i>L. gelidum</i> subsp. <i>gelidum</i> LMG 18297 <sup>T</sup>            | AM711204        | AM711160        | AM711307        |
| <i>L. gelidum</i> subsp. <i>gelidum</i> JB7                               | CP003839        | CP003839        | CP003839        |
| <i>L. holzapfelii</i> LMG 23990 <sup>T</sup>                              | AM711273        | AM711209        | AM711354        |
| <i>L. inhae</i> LMG 22919 <sup>T</sup>                                    | AM711190        | AM711167        | AM711310        |
| <i>L. kimchii</i> LMG 23786 <sup>T</sup>                                  | AM711220        | AM711195        | AM711339        |
| <i>L. lactis</i> LMG 8894 <sup>T</sup>                                    | AM711253        | AM711267        | AM711311        |
| <i>L. mesenteroides</i> subsp. <i>mesenteroides</i> LMG 6893 <sup>T</sup> | AM711176        | AM711145        | AM711294        |
| <i>L. pseudomesenteroides</i> LMG 11482 <sup>T</sup>                      | AM711175        | AM711197        | AM711315        |
| <i>L. citreum</i> 1300_LCIT*  | NZ_JVUV01000032 | NZ_JVUV01000047 | NZ_JVUV01000055 |
| <i>L. gelidum</i> subsp. <i>gasicomitatum</i> 1301_LGAS**                 | NZ_JVUU01000022 | NZ_JVUU01000031 | NZ_JVUU01000023 |
| <i>L. inhae</i> LMG 22919 (= KCTC 3774, genome)***                        | NZ_AEMJ01000006 | NZ_AEMJ01000675 | NZ_AEMJ01000861 |
| <i>L. citreum</i> KM20  | NC_010471       | NC_010471       | NC_010471       |
| <i>L. argentinum</i> (later synonym of <i>L. lactis</i> [1]) KCTC 3773    | NZ_AEGQ01000052 | NZ_AEGQ01000042 | NZ_AEGQ01000003 |
| <i>L. lactis</i> KACC 91922   | NZ_JMEA01000009 | NZ_JMEA01000007 | NZ_JMEA01000004 |

\* Phylogenetic and pangenome analyses indicate the belonging of this genome to *L. lactis* species (see the main body of the article).

\*\* Phylogenetic and pangenome analyses indicate the belonging of this genome to *L. citreum* species (see the main body of the article).

\*\*\* Phylogenetic analysis indicates the belonging of this genome to *L. gelidum* subsp. *gasicomitatum* species (see the main body of the article).

**Table S2. NCBI assembly accession numbers/ INSDC identifiers for the comparative genomic analysis of *Leuconostoc* species (29.09.2015).**

| <b>Species</b>  | <b>NCBI assembly accession number/ INSDC identifiers</b> |
|---|--|
| <i>Leuconostoc argentinum</i> (later synonym of <i>L. lactis</i> [1]) KCTC 3773       | GCF_000179875.1  |
| <i>Leuconostoc carnosum</i> JB16  | GCF_000300135.1  |
| <i>Leuconostoc citreum</i> NRRL B-742   | GCF_000820965.1  |
| <i>Leuconostoc citreum</i> NRRL B-1299  | GCF_000820985.1  |
| <i>Leuconostoc citreum</i> KM20   | GCF_000026405.1  |
| <i>Leuconostoc citreum</i> LBAE C10   | GCF_000239895.2  |
| <i>Leuconostoc citreum</i> LBAE C11   | GCF_000239915.2  |
| <i>Leuconostoc citreum</i> LBAE E16   | GCF_000239935.2  |
| <i>Leuconostoc citreum</i> 1300_LCIT*   | GCF_001062635.1  |
| <i>Leuconostoc fallax</i> LMG 18975 <sup>T</sup> (= KCTC 3537)                        | GCF_000165675.2  |
| <i>Leuconostoc gelidum</i> subsp. <i>gasicomitatum</i> LMG 18811 <sup>T</sup>         | GCA_000196855.1  |
| <i>Leuconostoc gelidum</i> subsp. <i>gasicomitatum</i> KG16-1                         | LN890331- LN890334                                       |
| <i>Leuconostoc gelidum</i> subsp. <i>gasicomitatum</i> C120c                          | FBTC01000001-FBTC01000031                                |
| <i>Leuconostoc gelidum</i> subsp. <i>gasicomitatum</i> C122c                          | FBSY01000001-FBSY01000022                                |
| <i>Leuconostoc gelidum</i> subsp. <i>gasicomitatum</i> KSL4-2                         | FBTB01000001-FBTB01000023                                |
| <i>Leuconostoc gelidum</i> subsp. <i>gasicomitatum</i> PB1a                           | FBSX01000001-FBSX01000029                                |
| <i>Leuconostoc gelidum</i> subsp. <i>gasicomitatum</i> PB1e                           | FBDT01000001-FBDT01000022                                |
| <i>Leuconostoc gelidum</i> subsp. <i>gasicomitatum</i> PL111                          | FBTU01000001-FBTU01000029                                |
| <i>Leuconostoc gelidum</i> subsp. <i>gasicomitatum</i> 1301_LGAS**                    | GCF_001077275.1  |
| <i>Leuconostoc gelidum</i> subsp. <i>gelidum</i> JB7                                  | GCF_000298875.1  |
| <i>Leuconostoc gelidum</i> subsp. <i>gelidum</i> LMG 18297 <sup>T</sup> (= KCTC 3527) | GCF_000166715.2  |
| <i>Leuconostoc inhae</i> LMG 22919 (= KCTC 3774)***                                   | GCF_000166735.2  |
| <i>Leuconostoc kimchii</i> IMSNU 11154  | GCF_000092505.1  |
| <i>Leuconostoc kimchii</i> C2   | GCF_000219785.1  |
| <i>Leuconostoc lactis</i> KACC 91922  | GCF_000709265.1  |
| <i>Leuconostoc mesenteroides</i> Wikim17  | GCF_000787735.1  |
| <i>Leuconostoc mesenteroides</i> KFRI-MG  | GCF_000512955.1  |
| <i>Leuconostoc mesenteroides</i> P45  | GCF_000756355.1  |
| <i>Leuconostoc mesenteroides</i> subsp. <i>cremoris</i> LbT16                         | GCF_001184265.1  |
| <i>Leuconostoc mesenteroides</i> subsp. <i>cremoris</i> ATCC 19254                    | GCF_000160595.1  |
| <i>Leuconostoc mesenteroides</i> subsp. <i>cremoris</i> T26                           | GCF_000686485.1  |
| <i>Leuconostoc mesenteroides</i> subsp. <i>cremoris</i> TIFN8                         | GCF_000447945.1  |
| <i>Leuconostoc mesenteroides</i> subsp. <i>dextranicum</i> DSM 20484                  | GCF_001047695.1  |
| <i>Leuconostoc mesenteroides</i> subsp. <i>dextranicum</i> LbE15                      | GCF_001184245.1  |
| <i>Leuconostoc mesenteroides</i> subsp. <i>mesenteroides</i> LbE16                    | GCF_001184255.1  |
| <i>Leuconostoc mesenteroides</i> subsp. <i>mesenteroides</i> ATCC 8293                | GCF_000014445.1  |
| <i>Leuconostoc mesenteroides</i> subsp. <i>mesenteroides</i> J18                      | GCF_000234825.2  |
| <i>Leuconostoc pseudomesenteroides</i> 1159   | GCF_000686465.1  |
| <i>Leuconostoc pseudomesenteroides</i> 4882   | GCF_000297375.1  |
| <i>Leuconostoc pseudomesenteroides</i> LMG 11482 <sup>T</sup> (= KCTC 3652)           | GCF_000185065.2  |
| <i>Leuconostoc pseudomesenteroides</i> PS12   | GCF_000686505.1  |

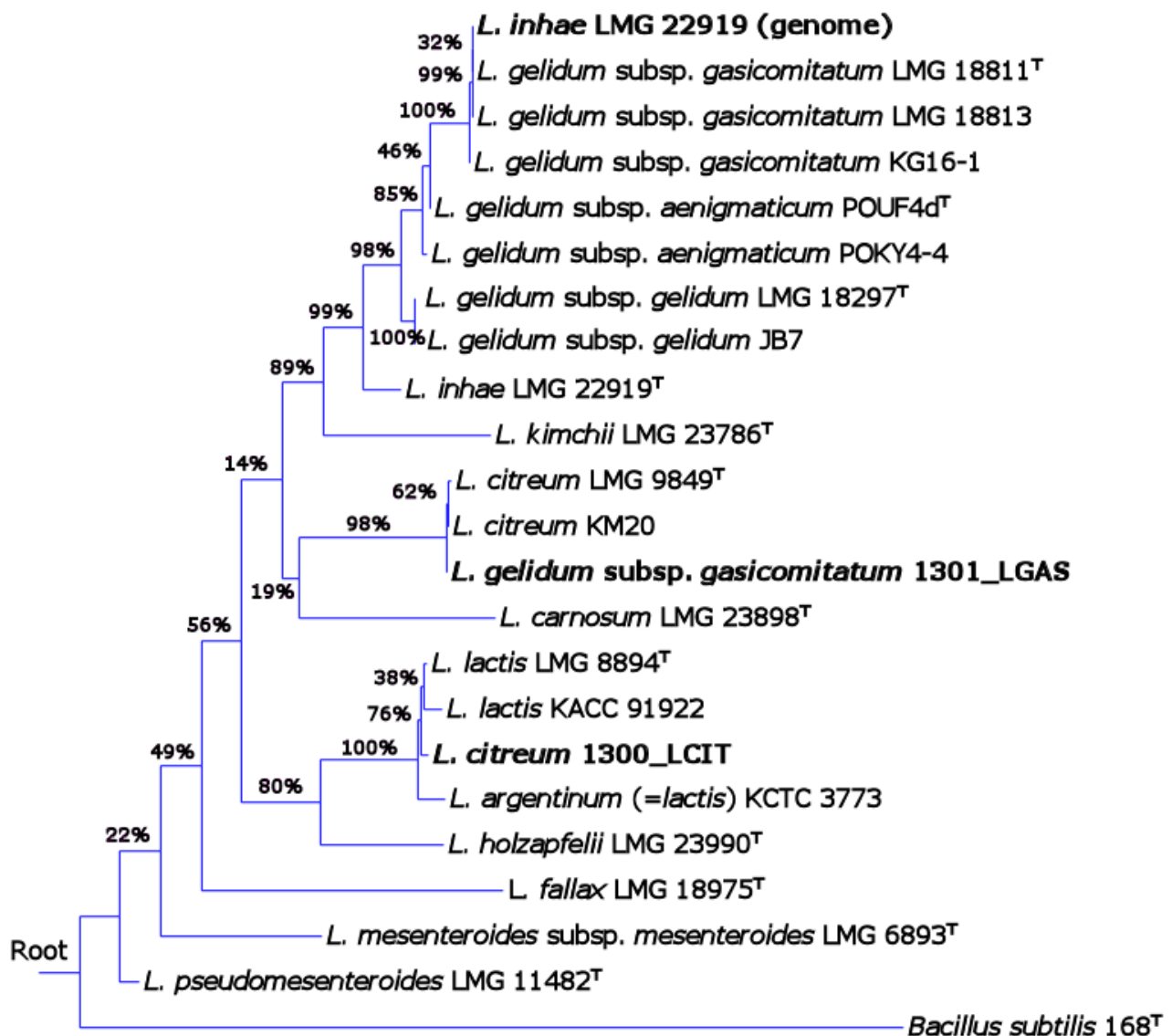
\* Phylogenetic and pangenome analyses indicate the belonging of this genome to *L. lactis* species (see the main body of the article).

\*\* Phylogenetic and pangenome analyses indicate the belonging of this genome to *L. citreum* species (see the main body of the article).

\*\*\* Phylogenetic analysis indicates the belonging of this genome to *L. gelidum* subsp. *gasicomitatum* species (see the main body of the article).

**Table S3. *L. gelidum* subsp. *gasicomitatum* draft genomes statistics.**

| <b>Strain</b> | <b>Genome size, Mb</b> | <b>Fold coverage</b> | <b>No of contigs</b> | <b>No of CDSs</b> | <b>Locus Tag</b> | <b>INSDC identifiers</b>  |
|---------------|------------------------|----------------------|----------------------|-------------------|------------------|---------------------------|
| <b>C120c</b>  | 2,00                   | 242                  | 31                   | 1962              | C120C            | FBTC01000001-FBTC01000031 |
| <b>C122c</b>  | 2,01                   | 631                  | 22                   | 2006              | C122C            | FBSY01000001-FBSY01000022 |
| <b>KSL4-2</b> | 2,01                   | 1634                 | 23                   | 2085              | KSL4             | FBTB01000001-FBTB01000023 |
| <b>PB1a</b>   | 2,09                   | 439                  | 29                   | 2061              | PB1A             | FBSX01000001-FBSX01000029 |
| <b>PB1e</b>   | 2,09                   | 1034                 | 22                   | 2107              | PB1E             | FBTD01000001-FBTD01000022 |
| <b>PL111</b>  | 2,06                   | 418                  | 29                   | 2020              | PL111            | FBTU01000001-FBTU01000029 |



**Figure S1.** Phylogenetic tree showing the relationship of *L. citreum* 1300\_LCIT, *L. gelidum* subsp. *gasicomitatum* 1301\_LGAS and *L. inhae* LMG 22919 genomes to other *Leuconostoc* species. The tree was built using T-REX web server [2] based on MUSCLE [3] aligned concatenated nucleotide sequences of *atpA*, *pheS* and *rpoA* genes (Genbank identifiers are listed in the Table S1 of Additional file 1). Poorly aligned positions were removed using Gblocks [4] with default parameters and the tree was inferred using RAxML program [5] with GTRCAT substitution model and *Bacillus subtilis* as an outgroup. Rapid bootstrap analysis was performed with 500 replicates. Type strains are identified with superscripted "T".

## References

1. Vancanneyt M, Zamfir M, De Wachter M, *et al.* Reclassification of *Leuconostoc argentinum* as a later synonym of *Leuconostoc lactis*. *Int. J. Syst. Evol. Microbiol.* 2006;**56**:213–6.
2. Boc A, Diallo AB, Makarenkov V. T-REX: a web server for inferring, validating and visualizing phylogenetic trees and networks. *Nucleic Acids Res.* 2012;**40**:W573–W579.
3. Edgar RC. MUSCLE: multiple sequence alignment with high accuracy and high throughput. *Nucleic Acid Res.* 2004;**32**:1792–1797.
4. Castresana J. Selection of conserved blocks from multiple alignments for their use in phylogenetic analysis. *Mol. Biol. Evol.* 2000;**17**:540–552.
5. Stamatakis A. RAxML-VI-HPC: maximum likelihood-based phylogenetic analyses with thousands of taxa and mixed models. *Bioinformatics* 2006;**22**:2688–2690.