

Table S1. Assembly statistics

	MES17	MES20	MES108	MES110	MES972
# paired-end reads	15,827,092	8,236,434	6,499,124	21,062,244	9,296,048
Sequencing depth	~400X	~210X	~170X	~540x	~230X
# contigs ^a	92	90	105	57	70
Total length ^a	5,858,763	5,857,725	5,668,879	5,808,840	6,081,788
GC (%) ^a	45.40	45.39	45.57	45.50	45.14
N50 ^a	259,003	265,343	261,401	413,718	235,203
Largest contig ^a	714,337	714,337	672,509	918,158	1,237,086
CDS ^b	5,286	5,288	5,120	5,175	5,536
tRNAs ^b	93	93	83	87	88
tmRNA ^b	1	1	1	1	1
rRNAs	incomplete	incomplete	incomplete	incomplete	incomplete

^aStatistics based on contigs of size \geq 500 bp (Quast report)

^bBased on Prokka annotation

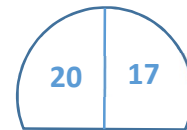
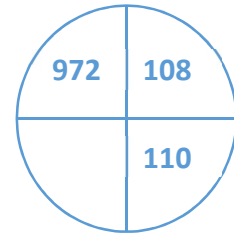
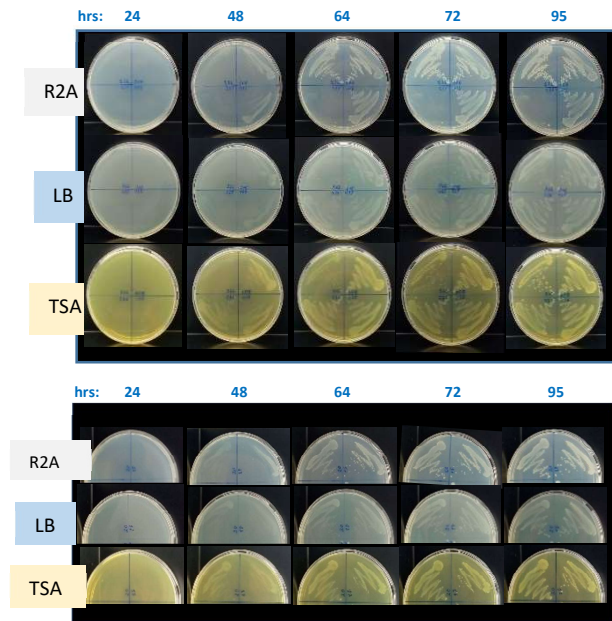
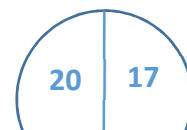
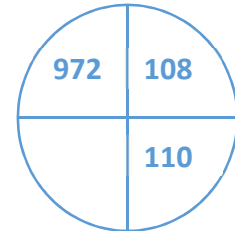
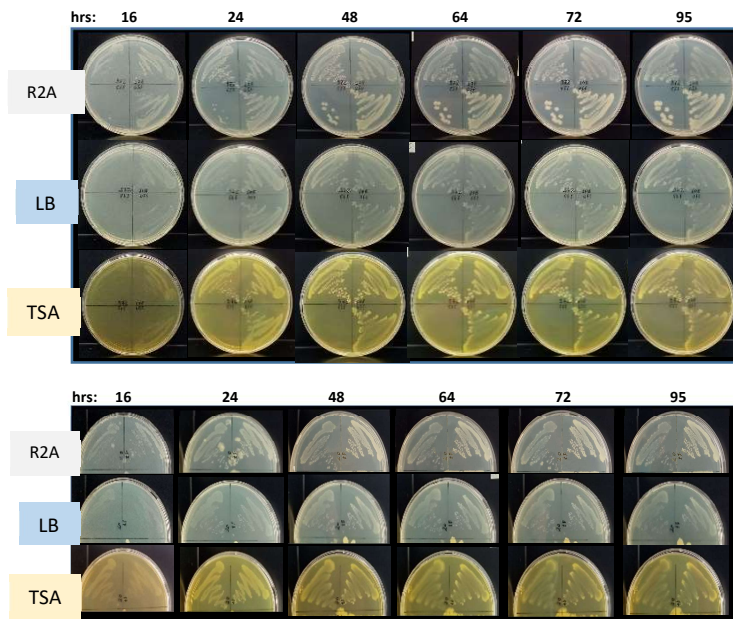
A**16°C****B****30°C**

Figure S1. Photographs of MES strains grown at the indicated time points on LB, TSA, or R2A media at 15°C (A) and 30°C (B). The accompanying diagram indicates which strain was grown on the respective section of the plate.

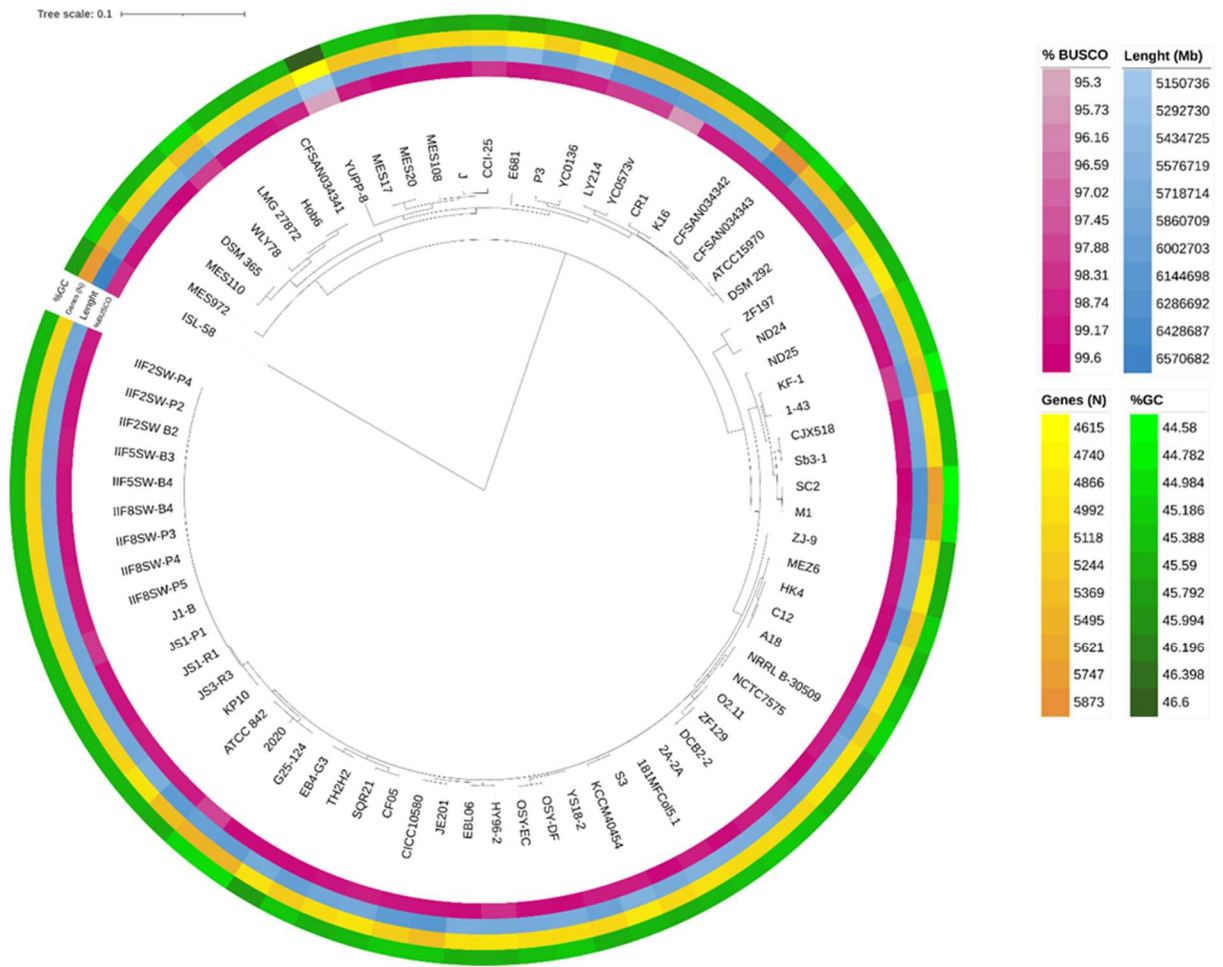
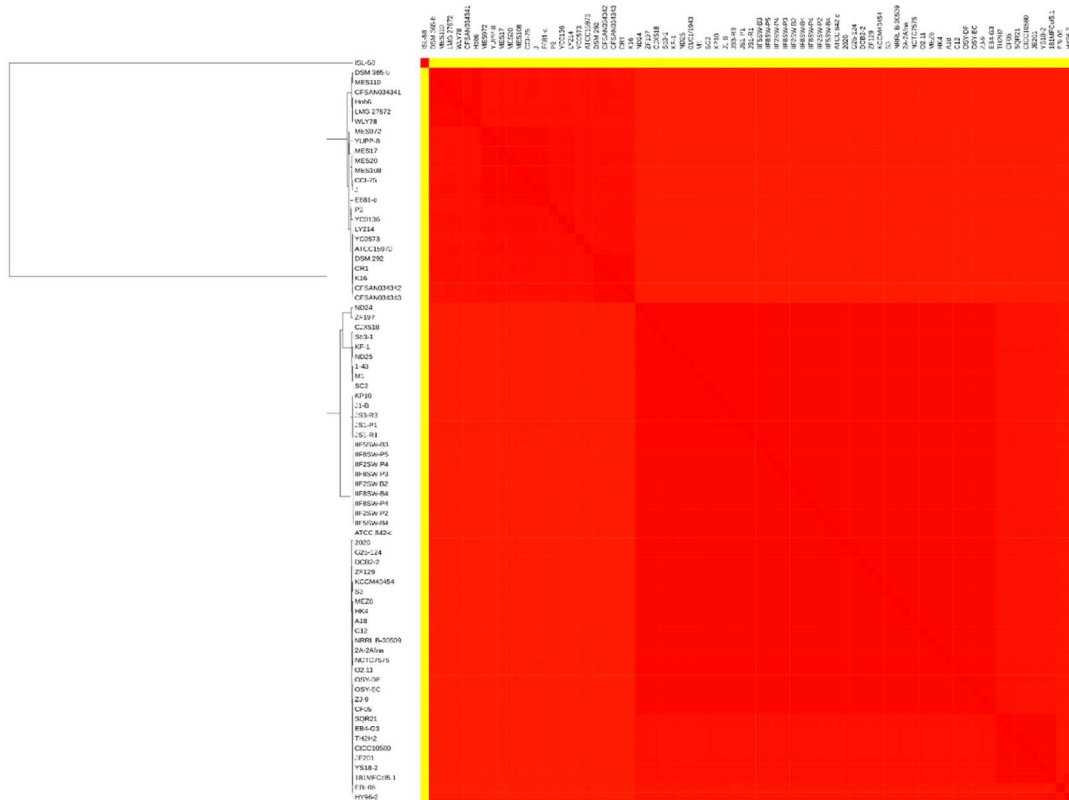
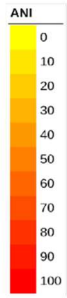


Figure S2. Phylogenetic tree features of the 76 strains of *P. polymyxa* obtained with Orthofinder. The circular heatmaps from inside to outside show the percentage of BUSCO, genome size, number of genes, and GC content, for each strain.

A

Tree scale: 100



B

Tree scale: 100

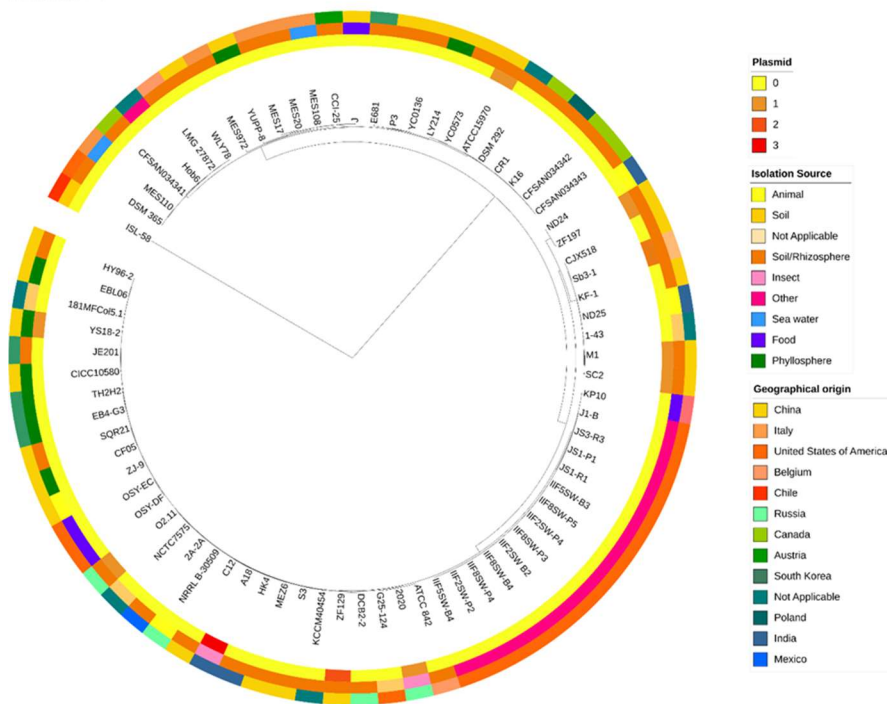
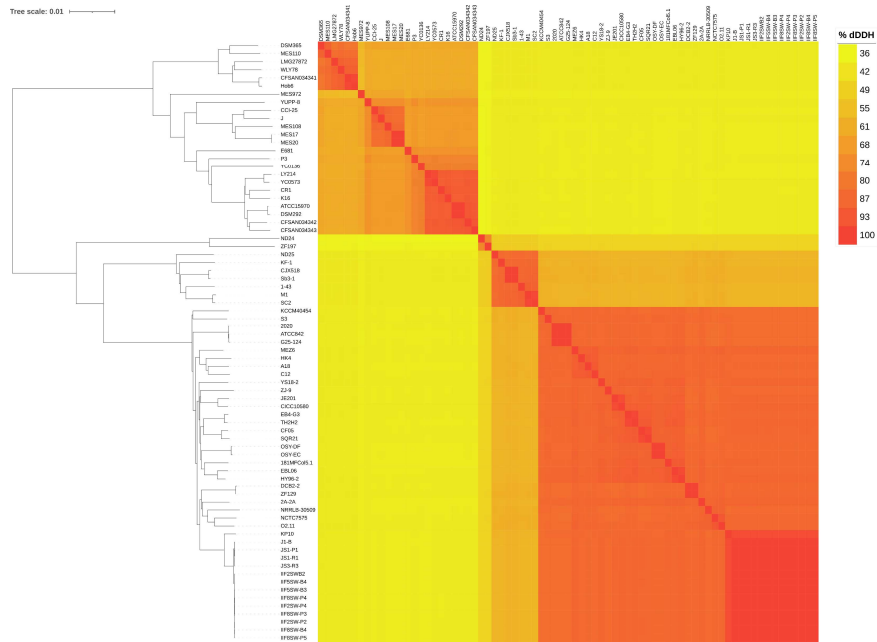


Figure S3. Correlation matrix of the 76 strains of *P. polymyxa* obtained with FastANI. A) In red strains with low nucleotide similarity, in yellow strains with high similarity. B) The circular heatmaps from inside to outside show the number of plasmids, isolation source and geographical origin, for each strain

A



B

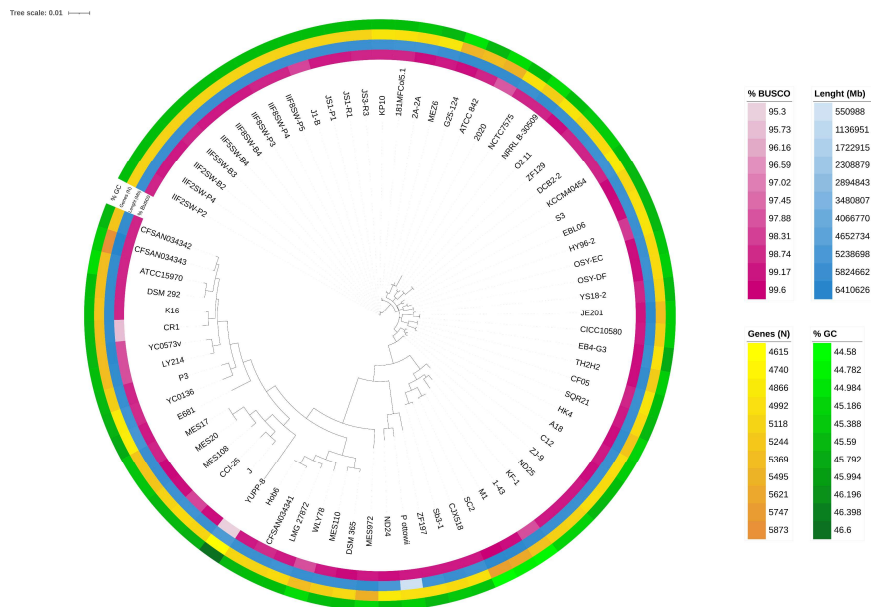
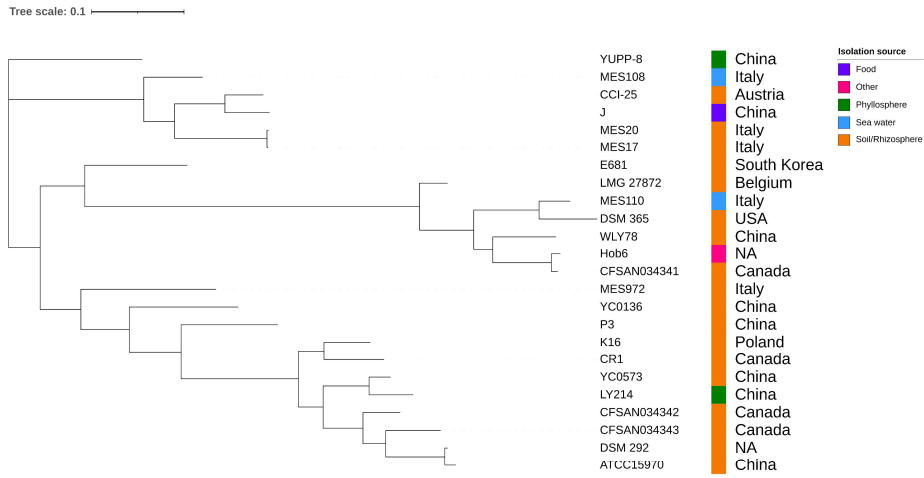


Figure S4. A) Heatmap of digital DNA-DNA hybridization values of the 75 genomes of *P. polymyxa*. B) Phylogenetic tree features of the 75 strains of *P. polymyxa* and *P. ottowii* obtained with OrthoFinder. The circular heatmap from inside to outside show the percentage of BUSCO, genome size, number of genes, and GC content, for each strain.

A



B

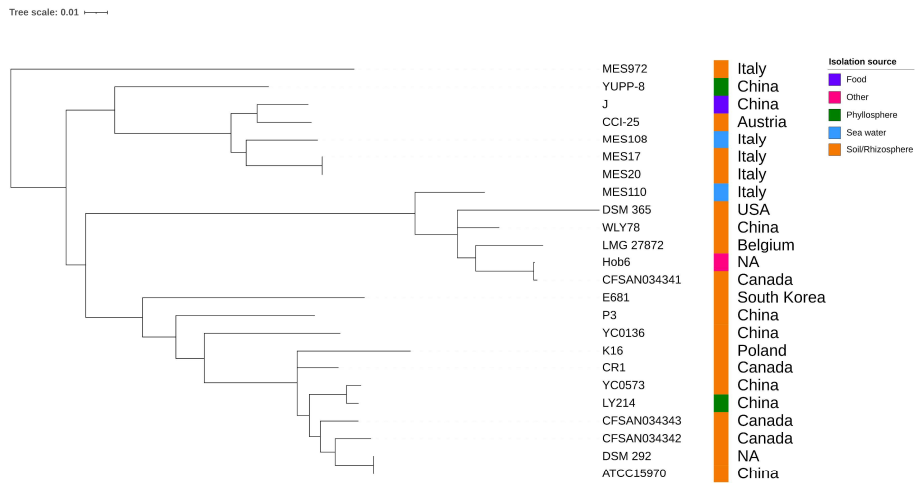
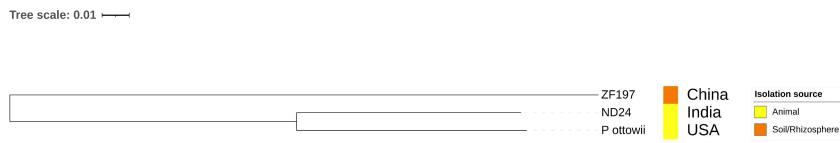


Figure S5. Phylogenetic relationships of Cluster 1 strains obtained with Roary (A) or Parsnp (B).

A



B



C



D

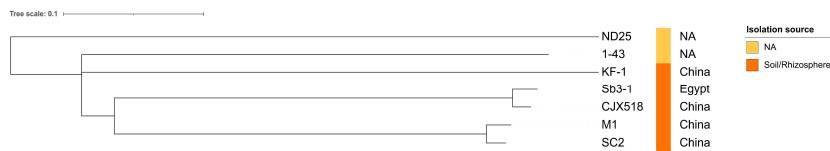
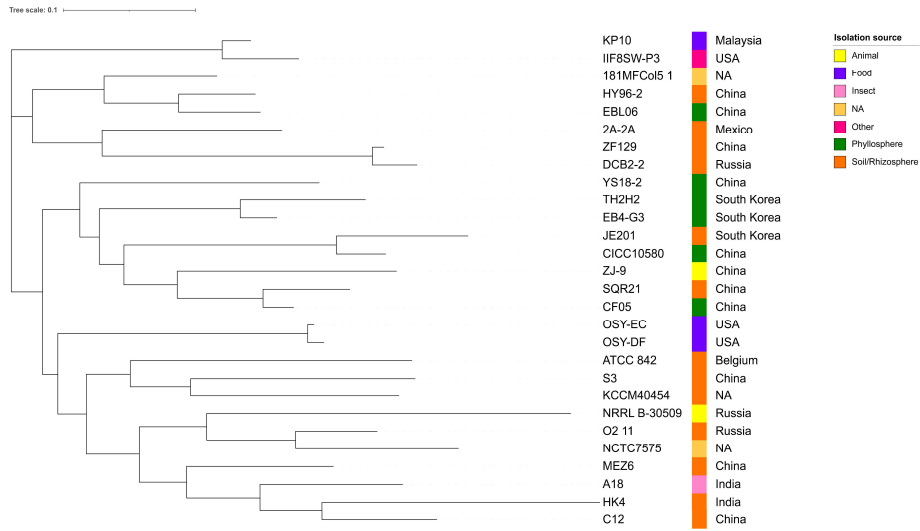


Figure S6. Phylogenetic relationships of Cluster 2 (A and B) and Cluster 3 (C and D) strains obtained with Roary (A and C) or Parsnp (B and D).

A



B

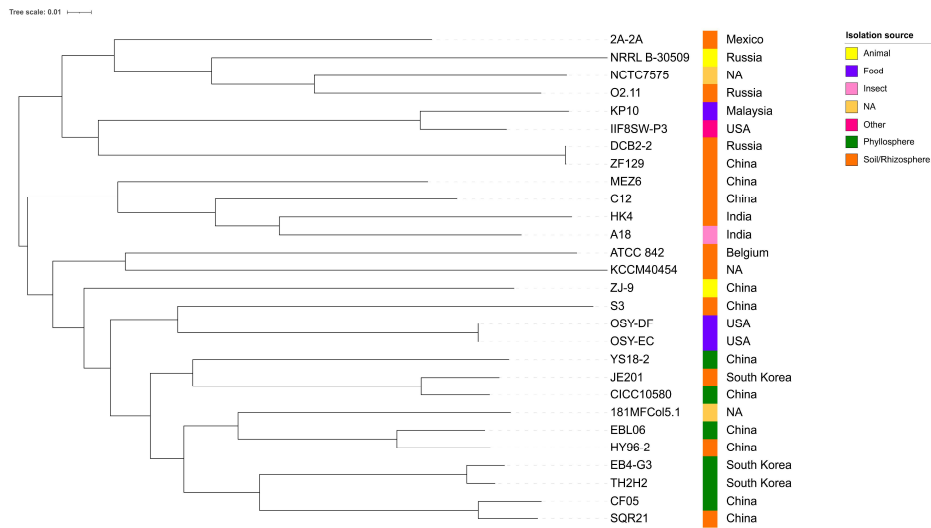


Figure S7. Phylogenetic relationships of Cluster 4 strains obtained with Roary (A) or Parsnp (B).


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WLY78 CTGAGACTTAAAGCTTACAGAGGCACTGAGCATCCACATGCAGCACAAAAACCTGAAGTTACGAACTTCGCGGATAA
MES110 CTGAGACTTAAAGCTTACAGAGGCACTGAGCATCCACATGCAGCACAAAAACCTGAAGTTACGAACTTCGCGGATAA
CFSAN034341 CTGAGACTTAAAGCTTACAGAGGCACTGAGCATCCACATGCAGCACAAAAACCTGAAGTTACGAACTTCGCGGATAA
Hob6 CTGAGACTTAAAGCTTACAGAGGCACTGAGCATCCACATGCAGCACAAAAACCTGAAGTTACGAACTTCGCGGATAA
LMG_27872 CTGAGACTTAAAGCTTACAGAGGCACTGAGCATCCACATGCAGCACAAAAACCTGAAGTTACGAACTTCGCGGATAA
E681 CTGAGACTTAAAGCTTACAGAGGCACTGAGCATCCACATGCAGCACAAAAACCTGAAGTTACGAACTTCGCGGATAA
J CTGAGACTTAAAGCTTACAGAGGCACTGAGCATCCACATGCAGCACAAAAACCTGAAGTTACGAACTTCGCGGATAA
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CR1 CTGAGACTTAAAGCTTACAGAGGCACTGAGCATCCACATGCAGCACAAAAACCTGAAGTTACGAACTTCGCGGATAA
K16 CTGAGACTTAAAGCTTACAGAGGCACTGAGCATCCACATGCAGCACAAAAACCTGAAGTTACGAACTTCGCGGATAA
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ATCC_15970 CTGAGACTTAAAGCTTACAGAGGCACTGAGCATCCACATGCAGCACAAAAACCTGAAGTTACGAACTTCGCGGATAA
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MES17 CTGAGACTTAAAGCTTACAGAGGCACTGAGCATCCACATGCAGCACAAAAACCTGAAGTTACGAACTTCGCGGATAA
MES108 CTGAGACTTAAAGCTTACAGAGGCACTGAGCATCCACATGCAGCACAAAAACCTGAAGTTACGAACTTCGCGGATAA
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P3 CTGAGACTTAAAGCTTACAGAGGCACTGAGCATCCACATGCAGCACAAAAACCTGAAGTTACGAACTTCGCGGATAA
CCI_25 CTGAGACTTAAAGCTTACAGAGGCACTGAGCATCCACATGCAGCACAAAAACCTGAAGTTACGAACTTCGCGGATAA
ND24 CTGAGACTTAAAGCTTACAGAGGTAACAGAGCATCCACATGCAGCACAAAAACCTGAAGTTACGAACTTCGCGGATAA
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ATCC_842 CTGAGACTTAAAGCTTACAGAGGTAACAGAGCATCCACATGCAGCACAAAAACCTGAAGTTACGAACTTCGCGGATAA
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O_211 CTGAGACTTAAAGCTTACAGAGGTAACAGAGCATCCACATGCAGCACAAAAACCTGAAGTTACGAACTTCGCGGATAA
HK4 CTGAGACTTAAAGCTTACAGAGGTAACAGAGCATCCACATGCAGCACAAAAACCTGAAGTTACGAACTTCGCGGATAA
A18 CTGAGACTTAAAGCTTACAGAGGTAACAGAGCATCCACATGCAGCACAAAAACCTGAAGTTACGAACTTCGCGGATAA
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ND25 CTGAGACTTAAAGCTTACAGAGGTAACAGAGCATCCACATGCAGCACAAAAACCTGAAGTTACGAACTTCGCGGATAA
I_43 CTGAGACTTAAAGCTTACAGAGGTAACAGAGCATCCACATGCAGCACAAAAACCTGAAGTTACGAACTTCGCGGATAA
SC2 CTGAGACTTAAAGCTTACAGAGGTAACAGAGCATCCACATGCAGCACAAAAACCTGAAGTTACGAACTTCGCGGATAA
M1 CTGAGACTTAAAGCTTACAGAGGTAACAGAGCATCCACATGCAGCACAAAAACCTGAAGTTACGAACTTCGCGGATAA
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Figure S8. Multiple alignment of the *rplM* gene. The nucleotide sequences were obtained from the strains belonging to Cluster 1 (yellow), Cluster 2 (gray), Cluster 3 (green), and Cluster 4 (cyan). The red asterisks indicate conserved regions that can be used to design primers for gene amplification. The consensus sequences of each Cluster are displayed in the box below the alignment. Cluster-specific SNVs are highlighted using the same colors of the Clusters.

OSY_DF	LRLKAYRGTEHPHAAQ K PEVYELRG
OSY_EC	LRLKAYRGTEHPHAAQ K PEVYELRG
ATCC_842	LRLKAYRGTEHPHAAQ K PEVYELRG
NRRL_B_30509	LRLKAYRGTEHPHAAQ K PEVYELRG
NCTC7575	LRLKAYRGTEHPHAAQ K PEVYELRG
MEZ6	LRLKAYRGTEHPHAAQ K PEVYELRG
O_211	LRLKAYRGTEHPHAAQ K PEVYELRG
HK4	LRLKAYRGTEHPHAAQ K PEVYELRG
A18	LRLKAYRGTEHPHAAQ K PEVYELRG
C12	LRLKAYRGTEHPHAAQ K PEVYELRG
TH2H2	LRLKAYRGTEHPHAAQ K PEVYELRG
EB4_G3	LRLKAYRGTEHPHAAQ K PEVYELRG
CICC_10580	LRLKAYRGTEHPHAAQ K PEVYELRG
JE201	LRLKAYRGTEHPHAAQ K PEVYELRG
DCB2	LRLKAYRGTEHPHAAQ K PEVYELRG
ZF129	LRLKAYRGTEHPHAAQ K PEVYELRG
KP10	LRLKAYRGTEHPHAAQ K PEVYELRG
IIF8SW	LRLKAYRGTEHPHAAQ K PEVYELRG
2A_2A	LRLKAYRGTEHPHAAQ K PEVYELRG
YS18	LRLKAYRGTEHPHAAQ K PEVYELRG
181MFCo151	LRLKAYRGTEHPHAAQ K PEVYELRG
EBL06	LRLKAYRGTEHPHAAQ K PEVYELRG
HY96	LRLKAYRGTEHPHAAQ K PEVYELRG
ZJ_9	LRLKAYRGTEHPHAAQ K PEVYELRG
SQR_21	LRLKAYRGTEHPHAAQ K PEVYELRG
CF05	LRLKAYRGTEHPHAAQ K PEVYELRG
KCCM_40454	LRLKAYRGTEHPHAAQ K PEVYELRG
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Sb3	LRLKAYRGTEHPHAAQ K PEVYELRG
CJX518	LRLKAYRGTEHPHAAQ K PEVYELRG
KF_1	LRLKAYRGTEHPHAAQ K PEVYELRG
ND25	LRLKAYRGTEHPHAAQ K PEVYELRG
1_43	LRLKAYRGTEHPHAAQ K PEVYELRG
SC2	LRLKAYRGTEHPHAAQ K PEVYELRG
M1	LRLKAYRGTEHPHAAQ K PEVYELRG
MES972	LRLKAYRGTEHPHAAQ K PEVYELRG
YC0573	LRLKAYRGTEHPHAAQ K PEVYELRG
LY214	LRLKAYRGTEHPHAAQ K PEVYELRG
CR1	LRLKAYRGTEHPHAAQ K PEVYELRG
K16	LRLKAYRGTEHPHAAQ K PEVYELRG
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CFSAN034342	LRLKAYRGTEHPHAAQ K PEVYELRG
ATCC_15970	LRLKAYRGTEHPHAAQ K PEVYELRG
DSM_292	LRLKAYRGTEHPHAAQ K PEVYELRG
WLY78	LRLKAYRGTEHPHAAQ K PEVYELRG
MES110	LRLKAYRGTEHPHAAQ K PEVYELRG
LMG_27872	LRLKAYRGTEHPHAAQ K PEVYELRG
CFSAN034341	LRLKAYRGTEHPHAAQ K PEVYELRG
Hob6	LRLKAYRGTEHPHAAQ K PEVYELRG
MES20	LRLKAYRGTEHPHAAQ K PEVYELRG
MES17	LRLKAYRGTEHPHAAQ K PEVYELRG
MES108	LRLKAYRGTEHPHAAQ K PEVYELRG
CCI_25	LRLKAYRGTEHPHAAQ K PEVYELRG
J	LRLKAYRGTEHPHAAQ K PEVYELRG
YUPP_8	LRLKAYRGTEHPHAAQ K PEVYELRG
E681	LRLKAYRGTEHPHAAQ K PEVYELRG
YC0136	LRLKAYRGTEHPHAAQ K PEVYELRG
P3	LRLKAYRGTEHPHAAQ K PEVYELRG
DSM_365	LRLKAYRGTEHPH <u>VAQ</u> KPEVYELRG
ZF197	LRLKAYRGTEHPHAAQ K PEVYELRG
ND24	LRLKAYRGTEHPHAAQ K PEVYELRG
P.ottowii	LRLKAYRGTEHPHAAQ K PEVYELRG

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Cluster 1,2,3,4	LRLKAYRGTEHPHAAQ K PEVYELRG
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Figure S9. Multiple alignment of protein L13. The sequences were obtained from the strains belonging to Cluster 1 (yellow), Cluster 2 (gray), Cluster 3 (green), and Cluster 4 (cyan). The consensus sequences of each Cluster are displayed in the box below the alignment. Cluster-specific amino acid substitutions are highlighted using the same colors of the Clusters. Strains DSM 365, MES972 and ZF197, have additional amino acid changes, which produce variability intra-clusters in position 117 (for DSM 365 and MES972) or 134 (for ZF197). The changed amino acids are in bold and underlined in the alignment.

KF AAACCGCTTC TGGGTAACCTGAGATGGACCTGGGGACGTTAGACGCTGAAACAA GGTCTTGCTAACCTGAAATAG
 Sb3 AAACCGCTTC TGGGTAACCTGAGATGGACCTGGGGACGTTAGACGCTGAAACAA GGTCTTGCTAACCTGAAATAG
 CJX518 AAACCGCTTC TGGGTAACCTGAGATGGACCTGGGGACGTTAGACGCTGAAACAA GGTCTTGCTAACCTGAAATAG
 1_43 AAACCGCTTC TGGGTAACCTGAGATGGACCTGGGGACGTTAGACGCTGAAACAA GGTCTTGCTAACCTGAAATAG
 ZF197 AAACCGCTTC TGGGTAACCTGAGATGGACCTGGGGACGTTAGACGCTGAAACAA GGTCTTGCTAACCTGAAATAG
 ND24 AAACCGCTTC TGGGTAACCTGAGATGGACCTGGGGACGTTAGACGCTGAAACAA GGTCTTGCTAACCTGAAATAG
 P. ottowii AAACCGCTTC TGGGTAACCTGAGATGGACCTGGGGACGTTAGACGCTGAAACAA GGTCTTGCTAACCTGAAATAG
 181MFCo151 AAACCGCTTC TGGGTAACCTGAGATGGACCTGGGGACGTTAGACGCTGAAACAA GGTCTTGCTAACCTGAAATAG
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 DCB2 AAACCGCTTC TGGGTAACCTGAGATGGACCTGGGGACGTTAGACGCTGAAACAA GGTCTTGCTAACCTGAAATAG
 ZF129 AAACCGCTTC TGGGTAACCTGAGATGGACCTGGGGACGTTAGACGCTGAAACAA GGTCTTGCTAACCTGAAATAG
 KP10 AAACCGCTTC TGGGTAACCTGAGATGGACCTGGGGACGTTAGACGCTGAAACAA GGTCTTGCTAACCTGAAATAG
 S3 AAACCGCTTC TGGGTAACCTGAGATGGACCTGGGGACGTTAGACGCTGAAACAA GGTCTTGCTAACCTGAAATAG
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 OSY_DF AAACCGCTTC TGGGTAACCTGAGATGGACCTGGGGACGTTAGACGCTGAAACAA GGTCTTGCTAACCTGAAATAG
 OSY_EC AAACCGCTTC TGGGTAACCTGAGATGGACCTGGGGACGTTAGACGCTGAAACAA GGTCTTGCTAACCTGAAATAG
 2A_2A AAACCGCTTC TGGGTAACCTGAGATGGACCTGGGGACGTTAGACGCTGAAACAA GGTCTTGCTAACCTGAAATAG
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 ZJ_9 AAACCGCTTC TGGGTAACCTGAGATGGACCTGGGGACGTTAGACGCTGAAACAA GGTCTTGCTAACCTGAAATAG
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 C12 AAACCGCTTC TGGGTAACCTGAGATGGACCTGGGGACGTTAGACGCTGAAACAA GGTCTTGCTAACCTGAAATAG
 IIF85W AAACCGCTTC TGGGTAACCTGAGATGGACCTGGGGACGTTAGACGCTGAAACAA GGTCTTGCTAACCTGAAATAG
 SQR_21 AAACCGCTTC TGGGTAACCTGAGATGGACCTGGGGACGTTAGACGCTGAAACAA GGTCTTGCTAACCTGAAATAG
 CF05 AAACCGCTTC TGGGTAACCTGAGATGGACCTGGGGACGTTAGACGCTGAAACAA GGTCTTGCTAACCTGAAATAG
 MES972 AAACCGCTTC TGGGTAACCTGAGATGGACCTGGGGACGTTAGACGCTGAAACAA GGTCTTGCTAACCTGAAATAG
 WLY78 AAACCGCTTC TGGGTAACCTGAGATGGACCTGGGGACGTTAGACGCTGAAACAA GGTCTTGCTAACCTGAAATAG
 DSM_365 AAACCGCTTC TGGGTAACCTGAGATGGACCTGGGGACGTTAGACGCTGAAACAA GGTCTTGCTAACCTGAAATAG
 LMG_27872 AAACCGCTTC TGGGTAACCTGAGATGGACCTGGGGACGTTAGACGCTGAAACAA GGTCTTGCTAACCTGAAATAG
 CFSAN03434 AAACCGCTTC TGGGTAACCTGAGATGGACCTGGGGACGTTAGACGCTGAAACAA GGTCTTGCTAACCTGAAATAG
 Hob6 AAACCGCTTC TGGGTAACCTGAGATGGACCTGGGGACGTTAGACGCTGAAACAA GGTCTTGCTAACCTGAAATAG
 MES110 AAACCGCTTC TGGGTAACCTGAGATGGACCTGGGGACGTTAGACGCTGAAACAA GGTCTTGCTAACCTGAAATAG
 YC0136 AAACCGCTTC TGGGTAACCTGAGATGGACCTGGGGACGTTAGACGCTGAAACAA GGTCTTGCTAACCTGAAATAG
 YC0573 AAACCGCTTC TGGGTAACCTGAGATGGACCTGGGGACGTTAGACGCTGAAACAA GGTCTTGCTAACCTGAAATAG
 LY214 AAACCGCTTC TGGGTAACCTGAGATGGACCTGGGGACGTTAGACGCTGAAACAA GGTCTTGCTAACCTGAAATAG
 CR1 AAACCGCTTC TGGGTAACCTGAGATGGACCTGGGGACGTTAGACGCTGAAACAA GGTCTTGCTAACCTGAAATAG
 K16 AAACCGCTTC TGGGTAACCTGAGATGGACCTGGGGACGTTAGACGCTGAAACAA GGTCTTGCTAACCTGAAATAG
 CFSAN03434 AAACCGCTTC TGGGTAACCTGAGATGGACCTGGGGACGTTAGACGCTGAAACAA GGTCTTGCTAACCTGAAATAG
 CFSAN03434 AAACCGCTTC TGGGTAACCTGAGATGGACCTGGGGACGTTAGACGCTGAAACAA GGTCTTGCTAACCTGAAATAG
 ATCC_15970 AAACCGCTTC TGGGTAACCTGAGATGGACCTGGGGACGTTAGACGCTGAAACAA GGTCTTGCTAACCTGAAATAG
 DSM_292 AAACCGCTTC TGGGTAACCTGAGATGGACCTGGGGACGTTAGACGCTGAAACAA GGTCTTGCTAACCTGAAATAG
 E681 AAACCGCTTC TGGGTAACCTGAGATGGACCTGGGGACGTTAGACGCTGAAACAA GGTCTTGCTAACCTGAAATAG
 P3 AAACCGCTTC TGGGTAACCTGAGATGGACCTGGGGACGTTAGACGCTGAAACAA GGTCTTGCTAACCTGAAATAG
 MES20 AAACCGCTTC TGGGTAACCTGAGATGGACCTGGGGACGTTAGACGCTGAAACAA GGTCTTGCTAACCTGAAATAG
 MES17 AAACCGCTTC TGGGTAACCTGAGATGGACCTGGGGACGTTAGACGCTGAAACAA GGTCTTGCTAACCTGAAATAG
 MES108 AAACCGCTTC TGGGTAACCTGAGATGGACCTGGGGACGTTAGACGCTGAAACAA GGTCTTGCTAACCTGAAATAG
 CCI_25 AAACCGCTTC TGGGTAACCTGAGATGGACCTGGGGACGTTAGACGCTGAAACAA GGTCTTGCTAACCTGAAATAG
 J AAACCGCTTC TGGGTAACCTGAGATGGACCTGGGGACGTTAGACGCTGAAACAA GGTCTTGCTAACCTGAAATAG
 YUPP_8 AAACCGCTTC TGGGTAACCTGAGATGGACCTGGGGACGTTAGACGCTGAAACAA GGTCTTGCTAACCTGAAATAG

Cluster 1	AAACCGCTTC TGGGTAACCTGAGATGGACCTGGG GACGTTA ^{ca} CGTC TGAACAA
Cluster 2	AAACCGCTTC TGGGTAACCTGAGATGGACCTGGG GACGTTAG A CGTT TGAACAA
Cluster 3	AAACCGCTTC TGGGTAACCTGAGATGGACCTGG ^g GACGTTAG A CGTC TGAACAA
Cluster 4	AAACCGCTTC ^t TGGGTAACCTGAGATGGACCTGGG GACGTTAG A CGT ^g TGAACAA

Figure S11. Multiple alignment of the *rpmL* gene. The nucleotide sequences were obtained from the strains belonging to Cluster 1 (yellow), Cluster 2 (gray), Cluster 3 (green), and Cluster 4 (cyan). The red asterisks indicate conserved regions that can be used to design primers for gene amplification. The consensus sequences of each Cluster are displayed in the box below the alignment. Cluster-specific SNVs are highlighted using the same colors of the Clusters. SNVs common to Clusters 3 and 4 are indicated in blue.

Ribosomal protein L35

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OSY_DF      MPKMKTHSSLKGRFKITGTGKVTRYKAYRNHLLSHKSKRAKRVLTNPEMAPGDVRRLLKQGLANLK
OSY_EC      MPKMKTHSSLKGRFKITGTGKVTRYKAYRNHLLSHKSKRAKRVLTNPEMAPGDVRRLLKQGLANLK
ATCC_842    MPKMKTHSSLKGRFKITGTGKVTRYKAYRNHLLSHKSKRAKRVLTNPEMAPGDVRRLLKQGLANLK
NRRL_B_30509 MPKMKTHSSLKGRFKITGTGKVTRYKAYRNHLLSHKSKRAKRVLTNPEMAPGDVRRLLKQGLANLK
NCTC7575   MPKMKTHSSLKGRFKITGTGKVTRYKAYRNHLLSHKSKRAKRVLTNPEMAPGDVRRLLKQGLANLK
MEZ6       MPKMKTHSSLKGRFKITGTGKVTRYKAYRNHLLSHKSKRAKRVLTNPEMAPGDVRRLLKQGLANLK
O_211      MPKMKTHSSLKGRFKITGTGKVTRYKAYRNHLLSHKSKRAKRVLTNPEMAPGDVRRLLKQGLANLK
HK4        MPKMKTHSSLKGRFKITGTGKVTRYKAYRNHLLSHKSKRAKRVLTNPEMAPGDVRRLLKQGLANLK
A18        MPKMKTHSSLKGRFKITGTGKVTRYKAYRNHLLSHKSKRAKRVLTNPEMAPGDVRRLLKQGLANLK
C12        MPKMKTHSSLKGRFKITGTGKVTRYKAYRNHLLSHKSKRAKRVLTNPEMAPGDVRRLLKQGLANLK
TH2H2     MPKMKTHSSLKGRFKITGTGKVTRYKAYRNHLLSHKSKRAKRVLTNPEMAPGDVRRLLKQGLANLK
EB4_G3     MPKMKTHSSLKGRFKITGTGKVTRYKAYRNHLLSHKSKRAKRVLTNPEMAPGDVRRLLKQGLANLK
CICC_10580 MPKMKTHSSLKGRFKITGTGKVTRYKAYRNHLLSHKSKRAKRVLTNPEMAPGDVRRLLKQGLANLK
JE201     MPKMKTHSSLKGRFKITGTGKVTRYKAYRNHLLSHKSKRAKRVLTNPEMAPGDVRRLLKQGLANLK
DCB2      MPKMKTHSSLKGRFKITGTGKVTRYKAYRNHLLSHKSKRAKRVLTNPEMAPGDVRRLLKQGLANLK
ZF129     MPKMKTHSSLKGRFKITGTGKVTRYKAYRNHLLSHKSKRAKRVLTNPEMAPGDVRRLLKQGLANLK
KP10      MPKMKTHSSLKGRFKITGTGKVTRYKAYRNHLLSHKSKRAKRVLTNPEMAPGDVRRLLKQGLANLK
IIF85M    MPKMKTHSSLKGRFKITGTGKVTRYKAYRNHLLSHKSKRAKRVLTNPEMAPGDVRRLLKQGLANLK
2A_2A     MPKMKTHSSLKGRFKITGTGKVTRYKAYRNHLLSHKSKRAKRVLTNPEMAPGDVRRLLKQGLANLK
YS18      MPKMKTHSSLKGRFKITGTGKVTRYKAYRNHLLSHKSKRAKRVLTNPEMAPGDVRRLLKQGLANLK
181MFC0151 MPKMKTHSSLKGRFKITGTGKVTRYKAYRNHLLSHKSKRAKRVLTNPEMAPGDVRRLLKQGLANLK
EBL06     MPKMKTHSSLKGRFKITGTGKVTRYKAYRNHLLSHKSKRAKRVLTNPEMAPGDVRRLLKQGLANLK
HY96      MPKMKTHSSLKGRFKITGTGKVTRYKAYRNHLLSHKSKRAKRVLTNPEMAPGDVRRLLKQGLANLK
ZJ_9      MPKMKTHSSLKGRFKITGTGKVTRYKAYRNHLLSHKSKRAKRVLTNPEMAPGDVRRLLKQGLANLK
SQR_21    MPKMKTHSSLKGRFKITGTGKVTRYKAYRNHLLSHKSKRAKRVLTNPEMAPGDVRRLLKQGLANLK
CF05      MPKMKTHSSLKGRFKITGTGKVTRYKAYRNHLLSHKSKRAKRVLTNPEMAPGDVRRLLKQGLANLK
KCCM_40454 MPKMKTHSSLKGRFKITGTGKVTRYKAYRNHLLSHKSKRAKRVLTNPEMAPGDVRRLLKQGLANLK
S3        MPKMKTHSSLKGRFKITGTGKVTRYKAYRNHLLSHKSKRAKRVLTNPEMAPGDVRRLLKQGLANLK
ZF197     MPKMKTHSSLKGRFKITGTGKVTRYKAYRNHLLSHKSKRAKRVLTNPEMAPGDVRRLLKQGLANLK
ND24      MPKMKTHSSLKGRFKITGTGKVTRYKAYRNHLLSHKSKRAKRVLTNPEMAPGDVRRLLKQGLANLK
P.ottowii MPKMKTHSSLKGRFKITGTGKVTRYKAYRNHLLSHKSKRAKRVLTNPEMAPGDVRRLLKQGLANLK
Sb3       MPKMKTHSSLKGRFKITGTGKVTRYKAYRNHLLSHKSKRAKRVLTNPEMAPGDVRRLLKQGLANLK
CJX518    MPKMKTHSSLKGRFKITGTGKVTRYKAYRNHLLSHKSKRAKRVLTNPEMAPGDVRRLLKQGLANLK
KF_1     MPKMKTHSSLKGRFKITGTGKVTRYKAYRNHLLSHKSKRAKRVLTNPEMAPGDVRRLLKQGLANLK
ND25     MPKMKTHSSLKGRFKITGTGKVTRYKAYRNHLLSHKSKRAKRVLTNPEMAPGDVRRLLKQGLANLK
1_43     MPKMKTHSSLKGRFKITGTGKVTRYKAYRNHLLSHKSKRAKRVLTNPEMAPGDVRRLLKQGLANLK
SC2      MPKMKTHSSLKGRFKITGTGKVTRYKAYRNHLLSHKSKRAKRVLTNPEMAPGDVRRLLKQGLANLK
MI       MPKMKTHSSLKGRFKITGTGKVTRYKAYRNHLLSHKSKRAKRVLTNPEMAPGDVRRLLKQGLANLK
YC0573   MPKMKTHSSLKGRFKITGTGKVMRYKAYKNHLLSHKSKRAKRVLTNPEMAPGDVKRLKQGLANLK
LY214    MPKMKTHSSLKGRFKITGTGKVMRYKAYKNHLLSHKSKRAKRVLTNPEMAPGDVKRLKQGLANLK
CR1      MPKMKTHSSLKGRFKITGTGKVMRYKAYKNHLLSHKSKRAKRVLTNPEMAPGDVKRLKQGLANLK
K16      MPKMKTHSSLKGRFKITGTGKVMRYKAYKNHLLSHKSKRAKRVLTNPEMAPGDVKRLKQGLANLK
CFSAN034343 MPKMKTHSSLKGRFKITGTGKVMRYKAYKNHLLSHKSKRAKRVLTNPEMAPGDVKRLKQGLANLK
CFSAN034342 MPKMKTHSSLKGRFKITGTGKVMRYKAYKNHLLSHKSKRAKRVLTNPEMAPGDVKRLKQGLANLK
ATCC_15970 MPKMKTHSSLKGRFKITGTGKVMRYKAYKNHLLSHKSKRAKRVLTNPEMAPGDVKRLKQGLANLK
DSM_292   MPKMKTHSSLKGRFKITGTGKVMRYKAYKNHLLSHKSKRAKRVLTNPEMAPGDVKRLKQGLANLK
WLY78    MPKMKTHSSLKGRFKITGTGKVMRYKAYKNHLLSHKSKRAKRVLTNPEMAPGDVKRLKQGLANLK
DSM_365   MPKMKTHSSLKGRFKITGTGKVMRYKAYKNHLLSHKSKRAKRVLTNPEMAPGDVKRLKQGLANLK
LMG_27872 MPKMKTHSSLKGRFKITGTGKVMRYKAYKNHLLSHKSKRAKRVLTNPEMAPGDVKRLKQGLANLK
CFSAN034341 MPKMKTHSSLKGRFKITGTGKVMRYKAYKNHLLSHKSKRAKRVLTNPEMAPGDVKRLKQGLANLK
Hob6     MPKMKTHSSLKGRFKITGTGKVMRYKAYKNHLLSHKSKRAKRVLTNPEMAPGDVKRLKQGLANLK
MES110   MPKMKTHSSLKGRFKITGTGKVMRYKAYKNHLLSHKSKRAKRVLTNPEMAPGDVKRLKQGLANLK
MES20    MPKMKTHSSLKGRFKITGTGKVMRYKAYKNHLLSHKSKRAKRVLTNPEMAPGDVKRLKQGLANLK
MES17    MPKMKTHSSLKGRFKITGTGKVMRYKAYKNHLLSHKSKRAKRVLTNPEMAPGDVKRLKQGLANLK
MES108   MPKMKTHSSLKGRFKITGTGKVMRYKAYKNHLLSHKSKRAKRVLTNPEMAPGDVKRLKQGLANLK
CCI_25   MPKMKTHSSLKGRFKITGTGKVMRYKAYKNHLLSHKSKRAKRVLTNPEMAPGDVKRLKQGLANLK
J        MPKMKTHSSLKGRFKITGTGKVMRYKAYKNHLLSHKSKRAKRVLTNPEMAPGDVKRLKQGLANLK
YUYP_8   MPKMKTHSSLKGRFKITGTGKVMRYKAYKNHLLSHKSKRAKRVLTNPEMAPGDVKRLKQGLANLK
E681    MPKMKTHSSLKGRFKITGTGKVMRYKAYKNHLLSHKSKRAKRVLTNPEMAPGDVKRLKQGLANLK
YC0136   MPKMKTHSSLKGRFKITGTGKVMRYKAYKNHLLSHKSKRAKRVLTNPEMAPGDVKRLKQGLANLK
P3      MPKMKTHSSLKGRFKITGTGKVMRYKAYKNHLLSHKSKRAKRVLTNPEMAPGDVKRLKQGLANLK
MES972   MPKMKTHSSLKGRFKITGTGKVMRYKAYKNHLLSHKSKRAKRVLTNPEMAPGDVRRLLKQGLANLK
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Cluster 1	MPKMKTHSSLKGRFKITGTGKVTRYKAYRNHLLSHKSKRAKRVLTNP ^{EMAPGDVRRLLKQ} GLANLK
Cluster 2,3,4	MPKMKTHSSLKGRFKITGTGKVTRYKAYRNHLLSHKSKRAKRVLTNP ^{EMAPGDVRRLLKQ} GLANLK

Figure S12. Multiple alignment of ribosomal protein L35. The sequences were obtained from the strains belonging to Cluster 1 (yellow), Cluster 2 (gray), Cluster 3 (green), and Cluster 4 (cyan). The consensus sequences of each Cluster are displayed in the box below the alignment. Cluster-specific amino acid substitutions are highlighted using the same colors of the Clusters. The MES972 strain is underlined as it has an R at position 56, which is present in Clusters 1, 2, and 3, but is replaced by K in the other strains belonging to Cluster 1.