**Table S3**. Region of sequence difference (RDs) identified in ST104 (ID24525)

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| **RDs** | **Size (bp)** | **% GC content**  | **ST1** | **ST7** | **ST25** | **Product** |
| **P1/7****BM407****GZ1****ID26154** | **SC84****98HAH33****05ZYH33** | **89-1591** |
| 1 | 12,979 | 38.26 | - | - | - | 1. Phage integrase2. Prophage antirepressor3. Phage protein4. DNA replication protein5. Phage/plasmid primase |
| 2 | 6,149 | 37.57 | - | - | + | 1. Class C3 sortase family proteins (srtG cluster)2. LPXTG-motif cell wall anchor domain protein |
| 3 | 820 | 43.78 | - | - | + | 1. Filamentation induced by cAMP protein Fic |
| 4 | 1,511 | 41.96 | - | - | + | 1. PTS system, sucrose-specific IIBC subunit |
| 5 | 19,828 | 41.01 | - | - | + | 1. Glycoside hydrolase family 1 (6-phospho-beta-glucosidase)2. PTS system lactose-specific EIICB component 3. PTS modulated transcriptional regulator, MtlR family4. AraC family transcriptional regulator5. PTS system, beta-glucoside-specific IIABC subunit6. Transcriptional antiterminator, BglG7. Cof-like hydrolase |
| 6 | 9,775 | 41.62 | - | - | + (78%) | 1. Integrase family protein2. Phage associated protein3. Phage protein4. Primase5. Phage/plasmid primase, P4 family |
| 7 | 3,502 | 41.95 | - | - | - | 1. Glutamine amidotransferase, class 12. Putative amino acid ABC transporter substrate-binding protein3. Polar amino acid ABC transporter, inner membrane subunit4. Glutamine transporter, ATP-binding protein |
| 8 | 2,989 | 39.61 | - | - | + | 1. Hypothetical protein |
| 9 | 1,001 | 34.97 | - | - | - | 1. Hypothetical protein |
| 10 | 718 | 41.64 | - | - | - | 1. Hypothetical protein |
| 11 | 3,090 | 30.94 | - | - | - | 1. ABC transporter-like protein2. Serine/threonine protein kinase related protein3. Transcriptional regulator |

**Table S3**. Region of difference (RDs) identified in ST104 (ID24525) (continued)

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| **RDs** | **Size (bp)** | **% GC content** | **ST1** | **ST7** | **ST25** | **Product** |
| **P1/7****BM407****GZ1****ID26154** | **SC84****98HAH33****05ZYH33** | **89-1591** |
| 12 | 2,989 | 42.09 | - | - | - | 1. Aldo/keto reductase family protein2. Transposase IS204/IS1001/IS1096/IS1165 family protein |
| 13 | 1,207 | 28.83 | - | - | + | 1. Hypothetical protein |
| 14 | 1,528 | 42.41 | - | - | - | 1. Hypothetical protein |
| 15 | 757 | 46.24 | - | - | + | 1. GCN5-related N-acetyltransferase |
| 16 | 535 | 44.86 | - | - | + | 1. Hypothetical protein |
| 17 | 630 | 27.14 | - | - | - | 1. Hypothetical protein |
| 18 | 1,563 | 37.04 | - | - | - | 1. FtsK/SpoIIIE family |
| 19 | 9,514 | 39.44 | - | - | - | 1. CRISPR-associated helicase2. CRISPR-associated protein (Cas5\_I superfamily)3. CRISPR-associated protein, Csd1 family4. CRISPR-associated protein Csd2 (Cas 7\_I-C superfamily)5. CRISPR-associated protein cas46. CRISPR-associated protein cas17. CRISPR-associated protein cas2 |
| 20 | 466 | 40.99 | - | - | + | 1. Transposase IS4 family protein |
| 21 | 1,181 | 41.57 | - | - | + | 1. Hypothetical protein |
| 22 | 1,048 | 35.11 | - | - | + | 1. Hypothetical protein |
| 23 | 8,191 | 37.96 | - | - | - | 1. Hypothetical protein2. Gram positive anchored-protein3. Cadmium resistance protein4. Cadmium resistance accessory protein CadX5. Phosphoesterase-like protein6. Transposase IS4 family protein |
| 24 | 847 | 31.40 | - | - | + | 1. Transcriptional regulator, XRE family |
| 25 | 1,855 | 37.63 | - | - | + | 1. ABC-2 type transporter2. ABC transporter related protein |
| 26 | 1,024 | 34.77 | - | - | + | 1. Phosphoribosylaminoimidazole carboxylase ATPase subunit |

**Table S3**. Region of difference (RDs) identified in ST104 (ID24525) (continued)

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| **RDs** | **Size (bp)** | **% GC content** | **ST1** | **ST7** | **ST25** | **Product** |
| **P1/7****BM407****GZ1****ID26154** | **SC84****98HAH33****05ZYH33** | **89-1591** |
| 27 | 3,574 | 34.44 | - | - | + | 1. Type II site-specific deoxyribonuclease2. DNA adenine methylase |
| 28 | 1,410 | 33.40 | - | - | + | 1. Hypothetical protein |
| 29 | 4,825 | 33.93 | - | - | + | 1. Hypothetical protein2. Type III restriction protein res subunit |
| 30 | 6,427 | 39.40 | - | - | - | 1. Class C1 sortase family proteins (srtF cluster)2. LPXTG-motif cell wall anchor domain-containing protein or cell wall ribonucleases G and E3. Putative pilus subunit proteins |
| 31 | 6,425 | 48.76 | - | - | + | 1. ParB-like protein2. Plasmid recombination protein3. Hypothetical protein4. RNA polymerase sigma factor sigma-70 family5. Sigma-70 region 4 domain-containing protein |
| 32 | 5,410 | 38.30 | - | - | + | 1. RNA-directed DNA polymerase2. SNF2 family protein3. Group II intron reverse transcriptase/maturase |
| 33 | 3,516 | 27.67 | - | - | - | 1. Glycine hydroxymethyltransferase2. Hypothetical protein3. Signal Transduction Histidine Kinase (STHK) with GAF sensor |
| 34 | 16,831 | 37.28 | - | - | - | 1. DeoR family transcriptional regulator2. Rhamnulokinase3. Arabinose isomerase4. L-fuculose phosphate aldolase5. Sugar ABC superfamily ATP binding cassette transporter, sugar-binding protein6. Sugar ABC superfamily ATP binding cassette transporter, permease protein7. Sugar ABC superfamily ATP binding cassette transporter, membrane protein8. Possible alpha-L-fucosidase9. Alpha-N-acetylgalactosaminidase10. 6-phosphate glucose kinase11. Hypothetical protein |
| 35 | 2,862 | 28.83 | - | - | - | 1. Hypothetical protein2. Putative abortive phage resistance protein |

**Table S3**. Region of difference (RDs) identified in ST104 (ID24525) (continued)

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| **RDs** | **Size (bp)** | **% GC content** | **ST1** | **ST7** | **ST25** | **Product** |
| **P1/7****BM407****GZ1****ID26154** | **SC84****98HAH33****05ZYH33** | **89-1591** |
| 36 | 5,185 | 40.46 | - | - | - | 1. Similar to beta-lactam resistance factor / aminoacyltransferase femB (FemAB superfamily)2. Similar to serine/alanine adding enzyme (FemAB superfamily)3. Putative peptidoglycan branched peptide synthesis protein MurM (FemAB superfamily)4. Putative HTH-type transcriptional activator mta / transcriptional regulator5. Hypothetical protein (UPF0158 superfamily)6. SWIM zinc finger [Streptococcus criceti HS-6] |
| 37 | 1,783 | 43.86 | - | - | - | 1. Resolvase, N-terminal domain protein |
| 38 | 15,517 | 32.20 | - | - | - | 1. Hypothetical protein2. Tn5252 transposon protein3. Relaxase4. Lantibiotic leader peptide processing serine protease5. Nisin biosynthesis regulatory protein NisR6. Nisin biosynthesis sensor protein NisK7. Antibiotic ABC superfamily ATP binding cassette transporter8. NsuE protein / lantibiotic protection ABC transporter permease9. Antibiotic ABC superfamily ATP binding cassette transporter permease protein10. Nisin immunity protein11. Phage integrase family site-specific recombinase |
| 39 | 7,453 | 40.41 | - | - | - | 1. LPXTG cell wall surface protein2. Cell wall surface anchor family protein or collagen adhesin3. Glutaredoxin 24. Transcriptional regulator5. Stress response-related Clp ATPase |
| 40 | 807 | 43.87 | - | - | + | 1. Cytidyltransferase-related domain protein |
| 41 | 1,486 | 39.17 | - | - | - | 1. Hypothetical protein |
| 42 | 1,135 | 37.89 | - | - | + | 1. Hypothetical protein2. Cytidine/deoxycytidylate deaminase family protein |

**Table S3**. Region of difference (RDs) identified in ST104 (ID24525) (continued)

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| **RDs** | **Size (bp)** | **% GC content** | **ST1** | **ST7** | **ST25** | **Product** |
| **P1/7****BM407****GZ1****ID26154** | **SC84****98HAH33****05ZYH33** | **89-1591** |
| 43 | 4,109 | 37.11 | - | - | - | 1. Similar to phosphotransferase system protein2. Phosphotransferase system cellobiose-specific component IIA3. UbiC transcription regulator-associated or GntR family transcriptional regulator4. PEP phosphonomutase family protein5. PTS lactose/cellobiose IIC component |
| 44 | 1,417 | 39.73 | - | - | + | 1. Transposase IS3/IS911 family protein2. Integrase catalytic region |
| 45 | 3,835 | 33.12 | - | - | + | 1. Hypothetical protein2. ABC transporter related protein |
| 46 | 877 | 48.23 | - | - | + | 1. Putative transcriptional regulator, PucR family |
| 47 | 9,298 | 38.80 | - | - | +  | 1. Tyrosine recombinase xerC / phage integrase family integrase/recombinase2. DNA binding domain protein, excisionase family3. hypothetical protein4. DEAD/DEAH box helicase-like protein |
| 48 | 35,119 | 41.41 | - | - | +  | 1. SH3 type-5 domain protein2. Phage holin, LL-H family3. Phage minor structural protein4. Phage protein5. Putative phage tail protein6. Phage structural protein7. Terminase8. Protein of unknown function DUF14839. HNH endonuclease10. Protein of unknown function DUF137211. Single-strand binding protein12. Protein of unknown function DUF135113. Phage recombination protein Bet14. Phage antirepressor protein15. Putative phage repressor16. Transcriptional modulator of MazE/toxin, MazF17. Integrase family protein18. Hypothetical protein |
| 49 | 6,472 | 33.48 | - | - | + | 1. Protein of unknown function DUF9552. Putative transcriptional regulator3. Hypothetical protein |

**Table S3**. Region of difference (RDs) identified in ST104 (ID24525) (continued)

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| **RDs** | **Size (bp)** | **% GC content** | **ST1** | **ST7** | **ST25** | **Product** |
| **P1/7****BM407****GZ1****ID26154** | **SC84****98HAH33****05ZYH33** | **89-1591** |  |
| 50 | 1,000 | 30.30 | - | - | - | 1. ABC-type transporter like-protein |
| 51 | 2,995 | 26.41 | - | - | - | 1. Hypothetical protein |
| 52 | 5, 275 | 38.86 | - | - | - | 1. Muramidase-released like protein (MRP-like protein) |
| 53 | 1,456 | 36.54 | - | - | + | 1. Translation initiation factor 2 GTPase |
| 54 | 1,756 | 40.49 | - | - | + | 1. ABC transporter related protein2. Protein of unknown function DUF214 |
| 55 | 1,246 | 41.09 | - | - | - | 1. Putative membrane protein2. Cro/CI family transcriptional regulator |
| 56 | 1,693 | 28.17 | - | - | + | 1. Hypothetical protein |
| 57 | 6,976 | 36.10 | - | - | - | 1. Replication protein2. Similar to hypothetical protein pSpnP1\_p13. Similar to hypothetical protein pSpnP1\_p64. Hypothetical protein |
| 58 | 1,412 | 39.24 | - | - | + | 1. Transposase IS3/IS911 family protein2. Integrase catalytic region |