Table S1: Primers used for this study

|  |  |  |  |
| --- | --- | --- | --- |
|  | Target/purpose | Primer Sequence (Fwd-Rev; 5'-3') | Reference |
| IMP | Screening of MBL | CATGGTTTGGTGGTTCTTGT-ATAATTTGGCGGACTTTGGC | ([Patzer et al. 2009](#_ENREF_10)). |
| VIM | Screening of MBL | CACTTCTCGCGGAGATTGAA-GTGCTTTGACAACGTTCGCT | ([Patzer et al. 2009](#_ENREF_10)). |
| SIM | Screening of MBL | TACAAGGGATTCGGCATCG-TAATGGCCTGTTCCCATGTG | ([Patzer et al. 2009](#_ENREF_10)). |
| SPM | Screening of MBL | CTGCTTGGATTCATGGGCGC-CCTTTTCCGCGACCTTGATC | ([Toleman et al. 2002](#_ENREF_16)) |
| GIM | Screening of MBL | AACTTCCAACTTTGCCATGC-TCGACACACCTTGGTCTGAA | ([Patzer et al. 2009](#_ENREF_10)) |
| NDM | Screening of MBL | GGTTTGGCGATCTGGTTTTC-CGGAATGGCTCATCACGATC | ([Yong et al. 2009](#_ENREF_20)) |
| AIM | Screening of MBL | ATGAAACGTCGCTTCACCCTGCTG-TCAAGGCCGCGCGCCGCTGG | ([Leiros et al. 2012](#_ENREF_8)) |
| KHM | Screening of MBL | GGTATGCGCTGACGATTCAT-TACCGCATGGCTAAGATTGC | ([Sekiguchi et al. 2008](#_ENREF_14)) |
| KPC | Screening of Carbapenemases | TGTCACTGTATCGCCGTC-CTCAGTGCTCTACAGAAAACC | ([Yangsoon Lee 2014](#_ENREF_19)) |
| SME | Screening of Carbapenemases | AGCGGTTCCCTTTATGCAGT-CGTGATGCTTCCGCAATAGT | ([Queenan et al. 2000](#_ENREF_12)) |
| GES | Screening of Carbapenemases | CTTCATTCACGCACTATTAC-TAACTTGACCGACAGAGG | ([Poirel et al. 2000](#_ENREF_11)) |
| CMY-1 | Screening of AmpC | GGGGCATATGATGAAAAAATCGTTA-CCGGATCCTCAACCGGCCA | ([Bauernfeind et al. 1996](#_ENREF_3)) |
| CMY-2 | Screening of AmpC | AACACACTGATTGCGTCTGA-TCCTGGGCCTCATCGTCAGTTAT | ([Bauernfeind et al. 1996](#_ENREF_3)) |
| DHA-1 | Screening of AmpC | GCAAAGCCAGTATGCGTACG-CAGTTGTTGCGCCCGTTTTA | ([Verdet et al. 2006](#_ENREF_18)) |
| FOX | Screening of AmpC | TAGTCTGGGCCAGCCATTTG-GTAACCGGATTGGCCTGGAA | ([Gonzalez Leiza et al. 1994](#_ENREF_7)) |
| MIR | Screening of AmpC | TGACGACGCGGGTCTTTAAA-TAAATGCCACGTAGCTGCCA | ([Papanicolaou et al. 1990](#_ENREF_9)) |
| ACC-1 | Screening of AmpC | CCTCCGTCAGCTCAGATACA-TTTACTAGGTGCAAGCCAGACA | ([Bauernfeind et al. 1999](#_ENREF_2)) |
| LAT | Screening of AmpC | TGCCGTTATCTACCAGGGGA-TTCGTTCTGCGGAACCGTAA | ([Tzouvelekis et al. 1993](#_ENREF_17)) |
| ACT-1 | Screening of AmpC | CGTTACGCCGCTGATGAAAG-CCAGGGTAAGGCCTTTCCTG | ([Reisbig MD 2002](#_ENREF_13)) |
| ISAba | Screening of Insertion Sequence | CACGAATGCAGAAGTTG-CGACGAATACTATGACAC | ([Chen et al. 2010](#_ENREF_5)). |
| TEM | Screening of ESBL | GACAGTTACCAATGCTTAATC-ATAAAATTCTTGAAGACGAAA | ([C. Kamatchi 2009](#_ENREF_4)) |
| CTX-M14 | Screening of ESBL | CGCTTTGCGATGTGCAG-ACCGCGATATCGTTGGT | ([Dutour et al. 2002](#_ENREF_6)) |
| OXA | Screening of ESBL | CGCAAATGGCACCAGATTCA-TGTATGATTGCTGTTCCAGAT | ([Sugumar et al. 2014](#_ENREF_15)). |
| SHV-full | Screening of ESBL | ATTTGTCGCTTCTTTACTCGC-TTTATGGCGTTACCTTTGACC | ([Ahmed et al. 2013](#_ENREF_1)) |

Table S2: References used to confirm the resistance genes.

|  |  |  |
| --- | --- | --- |
| **Resistant genes** | **Panel strains** | **Reference accession number (GenBank)** |
| DHA-1 | YMC2011/11/B7578, YMC2010/8/B2027, YMC2012/8/C631  | Y16410 |
| CMY-2 | YMC2010/8/B2027 | DQ478727 |
| CTX-M-15 | YMC2011/7/B774, YMC2013/7/B3993, YMC2010/8/B2027 | DQ302097 |
| IMP-1 | YMC2012/8/C631 | AB469046 |
| OXA-1 | YMC2011/7/B774, YMC2011/7/B7207 | J02967 |
| OXA-9 | YMC2013/7/B3993 | JF703130 |
| SHV-11 | YMC2011/7/B774, YMC2010/8/B2027, YMC2011/8/B10311 | X98101 |
| SHV-12 | YMC2013/7/B3993, YMC2011/11/B7578 | AJ920369 |
| SHV-158 | YMC2011/11/B7578 | JX121125 |
| SHV-187 | YMC2011/7/B7207 | LN515533 |
| TEM-1 | YMC2011/7/B774, YMC2013/7/B3993, YMC2011/7/B7207, YMC2010/8/B2027, YMC2012/8/C631, YMC2011/8/B10311  | J01749 |
| aac(6’)-Ib | YMC2013/7/B3993 | M21682 |
| Aac(6’)-IIa | YMC2011/7/B774, YMC2011/7/B7207, YMC2010/8/B2027, YMC2012/8/C631 | M29695 |
| aadA1 | YMC2013/7/B3993 | JQ480156 |
| aadA2 | YMC2011/11/B7578 | JQ364967 |
| armA | YMC2011/11/B7578 | AY220558 |
| strA | YMC2011/7/B774, YMC2013/7/B3993, YMC2011/7/B7207, YMC2011/11/B7578, YMC2010/8/B2027, YMC2012/8/C631 | NC\_003384 |
| strB | YMC2011/7/B774, YMC2013/7/B3993, YMC2011/7/B7207, YMC2011/11/B7578, YMC2010/8/B2027, YMC2012/8/C631 | M96392 |
| QnrB66 | YMC2011/7/B774, YMC2013/7/B3993, YMC2011/7/B7207 | KC580655 |
| QnrB4 | YMC2011/11/B7578, YMC2010/8/B2027 | DQ303921 |
| aac(6’)Ib-cr | YMC2011/7/B774, YMC2013/7/B3993, YMC2011/7/B7207, YMC2010/8/B2027 | DQ303918 |
| oqxA | YMC2013/7/B3993, YMC2011/7/B7207, YMC2011/11/B7578, YMC2011/8/B10311 | EU370913 |
| oqxB | YMC2011/7/B774, YMC2013/7/B3993, YMC2011/7/B7207, YMC2011/11/B7578, YMC2011/8/B10311 | EU370913 |
| catA2 | YMC2010/8/B2027 | X53796 |
| catB3 | YMC2011/7/B774, YMC2011/7/B7207 | AJ009818 |
| tet(A) | YMC2011/7/B774, YMC2011/7/B7207, YMC2011/8/B10311 | AJ517790 |
| dfrA14 | YMC2011/7/B774, YMC2013/7/B3993, YMC2011/7/B7207, YMC2010/8/B2027, YMC2011/8/B10311 | DQ388123 |
| Sul1 | YMC2011/11/B7578, YMC2010/8/B2027, YMC2012/8/C631 | CP002151 |
| Sul2 | YMC2011/7/B774, YMC2013/7/B3993, YMC2011/7/B7207, YMC2012/8/C631 | GQ421466 |

Table S3: Complete list of panel strains and its MIC.

|  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Strains** | **PIP** | **PIP+TZ** | **CAZ** | **FEP** | **AZT** | **IMI** | **MER** | **CIP** | **CAZ/CLV** | **FOX** | **AMP** | **SAM** |
| **ESBL** | R |  | R | R |  | S | S |  | S | S | R | V |
| YMC2011/7/B774 | 256(R) | 32(I) | 256(R) | 128(R) | 128(R) | 0.25(S) | 0.25(S) | 16(R) | 1(S) | *32(R)* | 256(R) | 64(R) |
| YMC2013/7/B3993  | 256(R) | 128(R) | 256(R) | 64(R) | 128(R) | 0.25(S) | 0.25(S) | 128(R) | 1(S) | *32(R)* | 256(R) | 128(R) |
| YMC2011/7/B7207 | 256(R) | 32(I) | 64(R) | *16(I)* | 128(R) | 0.25(S) | 0.25(S) | 256(R) | 1(S) | *32(R)* | 256(R) | 64(R) |
| YMC2011/11/B7578 | 256(R) | 32(I) | 256(R) | 64(R) | 128(R) | 64(R) | 1(S) | 128(R) | 1(S) | *128(R)* | 256(R) | 64(R) |
| YMC2011/11/B10514 | 256(R) | 32(I) | 256(R) | 64(R) | 128(R) | *2(I)* | 0.25(S) | 32(R) | *128(R)* | *256(R)* | 256(R) | 128(R) |
| YMC2010/08/B4822 | 256(R) | 128(I) | 256(R) | *4(S)* | 128(R) | 0.25(S) | 0.25(S) | 128(R) | *32(R)* | *256(R)* | 256(R) | 128(R) |
| **High level ampc β-lactamase** | R | R | R | S |  | S | S |  | R | *R* | R | R |
| YMC2010/8/B2027 | 256(R) | 128(R) | 256(R) | 2(S) | 128(R) | 0.5(S) | 0.25(S) | 2(I) | 64(R) | 256(R) | 256(R) | 128(R) |
| **Carbapenemase** | R | R | R | R |  | R | R |  | R | R | R | R |
| YMC2012/8/C631 | 256(R) | *8(S)* | 256(R) | 32(R) | 16(I) | 64(R) | 64(R) | 1(S) | 32(R) | 256(R) | 256(R) | 128(R) |
| YMC2010/08/C782 | 256(R) | *8(S)* | 256(R) | *16(I)* | 16(I) | 64(R) | 64(R) | 1(S) | 32(R) | 256(R) | 256(R) | 64(R) |
| YMC2012/09/S50 | 256(R) | *8(S)* | 256(R) | 32(R) | 16(I) | 64(R) | 16(R) | 1(S) | 32(R) | 256(R) | 256(R) | 128(R) |
| YMC2012/09/S50 | 256(R) | 128(R) | 256(R) | *8(S)* | 128(R) | 4(R) | 4(R) | 64(R) | 128(R) | 256(R) | 256(R) | 128(R) |
| YMC2013/03/R1024 | 256(R) | 128(R) | 64(R) | *2(S)* | 0.25(S) | *1(S)* | *2(I)* | 0.5(S) | 32(R) | 256(R) | 256(R) | 128(R) |
| YMC2011/10/B2570 | 256(R) | 128(R) | 256(R) | 32(R) | 16(I) | 4(R) | 4(R) | 4(R) | 64(R) | 256(R) | 256(R) | 128(R) |
| YMC2011/10/B1822 | 256(R) | *2(S)* | 256(R) | 32(R) | 16(I) | 32(R) | 16(R) | 2(I) | 128(R) | 256(R) | 256(R) | 128(R) |
| YMC2013/1/KU2 | 256(R) | *8(S)* | 256(R) | 128(R) | 32(R) | 256(R) | 128(R) | 64(R) | 64(R) | 256(R) | 256(R) | 128(R) |
| YMC2013/1/NDM-506 | 256(R) | 128(R) | 256(R) | 128(R) | 128(R) | 256(R) | 128(R) | 128(R) | 128(R) | 256(R) | 256(R) | 128(R) |
| YMC2014/3/MP14 | 256(R) | 128(R) | 64(R) | 32(R) | 128(R) | 32(R) | 32(R) | 64(R) | 128(R) | 64(R) | 256(R) | 128(R) |
| **High level acquired penicillinase** | R |  | S | S |  | S | S |  | S | S | R | R |
| YMC2011/8/B10311 | 256(R) | 4(S) | 2(S) | 4(S) | 2(S) | 0.5(S) | *2(I)* | 0.5(S) | 2(S) | 8(S) | 256(R) | 128(R) |
| **Wild type** | I | S | S | S |  | S | S |  | S | S | R | S |
| YMC2013/12/R3191 | 4(S) | 1(S) | 0.5(S) | 0.03(S) | 0.25(S) | 0.25(S) | 0.25(S) | 0.12(S) | 0.5(S) | 2(S) | 64(R) | *16(I)* |

Note: Note: MLST, Multilocus sequence typing; R, Resistant; I, Intermediate; S, susceptible; V, Variable; PIP, Piperacillin; PIP/TZ, Piperacillin/Tazobactam; CAZ,ceftazidime; FEP, cefepime; AZT, Aztreonam; IMI, Imipenem; MER, Meropenem; CIP, Ciprofloxacin, CAZ/CLV, ceftazidime/clavulanate; FOX, cefoxitin; AMP, Ampicillin; SAM, Ampicillin/Sulbactam.

Table S4: Raw sequence data from Ion Torrent PGM Sequencer of the panel strains.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Strains** | **Bases** | **≥Q20bases** | **Reads** | **Mean read length** |
| **ESBL** |  |  |  |  |
| YMC2011/7/B774  | 155,676,588 | 130,371,915 | 720,463 | 216 |
| YMC2013/7/B3993  | 205,100,384 | 172,553,864 | 911,427 | 225 |
| YMC2011/7/B7207  | 180,282,790 | 154,674,935 | 890,939 | 202 |
| YMC2011/11/B7578 | 182,887,905 | 151,370,906 | 721,072 | 254 |
| **High level Ampc** **β-lactamase**  |  |  |  |  |
| YMC2010/8/B2027  | 248,533,006 | 207,231,256 | 1,125,343 | 221 |
| **Carbapenemase** |  |  |  |  |
| YMC2012/8/C631 | 210,002,265 | 174,711,461 |

|  |  |
| --- | --- |
|  | 977,292  |

 | 215 |
| **High level acquired penicillinase**  |  |  |  |  |
| YMC2011/8/B10311  | 157,618,861 | 137,135,462 |

|  |  |
| --- | --- |
|  | 780,323  |

 | 202 |

\*all the units are in base-pairs.

Table S5: Subsystem information for the panel strains.

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Strains | Cofactors, Vitamins, Prosthetic Groups, Pigments | Cell Wall and Capsule | Virulence, Disease and Defense | Potassium metabolism | Phages, Prophages, Transposable elements, Plasmids | Membrane Transport | Iron acquisition and metabolism | RNA Metabolism | Nucleosides and Nucleotides | Protein Metabolism | Cell Division and Cell Cycle | Motility and Chemotaxis | Regulation and Cell signaling | Secondary Metabolism | DNA Metabolism | Fatty Acids, Lipids, and Isoprenoids | Nitrogen Metabolism | Dormancy and Sporulation | Respiration | Stress Response | Metabolism of Aromatic Compounds | Amino Acids and Derivatives | Sulfur Metabolism | Phosphorus Metabolism | Carbohydrates |
| **ESBL** |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| YMC2011/7/B774  | 323 | 206 | 148 | 36 | 32 | 262 | 67 | 228 | 145 | 268 | 41 | 9 | 155 | 5 | 168 | 134 | 47 | 5 | 183 | 182 | 78 | 507 | 77 | 64 | 858 |
| YMC2013/7/B3993  | 328 | 218 | 146 | 34 | 69 | 365 | 68 | 224 | 143 | 296 | 45 | 9 | 165 | 5 | 173 | 132 | 47 | 5 | 178 | 178 | 79 | 518 | 76 | 62 | 883 |
| YMC2011/7/B7207  | 326 | 209 | 128 | 34 | 64 | 209 | 67 | 222 | 143 | 301 | 37 | 11 | 151 | 5 | 146 | 126 | 47 | 5 | 176 | 176 | 79 | 520 | 75 | 62 | 840 |
| YMC2011/11/B7578 | 327 | 207 | 129 | 35 | 65 | 253 | 69 | 224 | 141 | 280 | 43 | 8 | 162 | 5 | 110 | 140 | 47 | 5 | 181 | 180 | 78 | 517 | 76 | 62 | 875 |
| **High level Ampc β-lactamase**  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| YMC2010/8/B2027  | 337 | 229 | 153 | 46 | 42 | 289 | 68 | 230 | 144 | 314 | 47 | 10 | 171 | 18 | 204 | 131 | 50 | 6 | 195 | 197 | 78 | 520 | 78 | 62 | 850 |
| **Carbapenemase** |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| YMC2012/8/C631 | 325 | 200 | 139 | 37 | 47 | 366 | 69 | 229 | 141 | 296 | 44 | 9 | 155 | 5 | 176 | 128 | 47 | 6 | 180 | 175 | 79 | 500 | 77 | 60 | 819 |
| **High level acquired penicillinase**  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| YMC2011/8/B10311  | 329 | 207 | 150 | 34 | 46 | 227 | 77 | 226 | 144 | 300 | 41 | 11 | 165 | 5 | 144 | 128 | 46 | 5 | 177 | 178 | 79 | 520 | 76 | 62 | 868 |

Table S6: Mutations in OmpK36 gene in YMC2011/7/B7207, YMC2011/8/B10311 and YMC2011/7/B774.

|  |
| --- |
| Ser88-Gly |
| Ser90-Asp |
| Asp91-Lys |
| Gly181-Del |
| Ala183-Del |
| Leu184-Del |
| Ser185-Asp |
| Pro186-Met |
| Thr192-Gly |
| Leu194-Glu |
| Tyr201-Phe |
| Leu205-Val |
| Tyr210-Trp |
| Leu225-Thr |
| Gly226-Asp |
| Lys231-Del |
| Ala233-Val |
| Asn239-Asp |
| Thr258-Ser |
| Arg309-Add |
| 350His-Arg |

Figure S1: The SDS-Page image of the panel strains representing the porins.



Figure S2: Nucleotide alignment of OmpK 35 gene of panel strain: OmpK-35 gene of YMC2013/7/B3993 and OmpK-35\_YMC2012/8/C631 has been interrupted by insertion of transposon elements (Highlighted in yellow). Arrows indicate the start codon, RBS, -10, -35 and transcription regulators.

1 -------------------------------------GTGTAACGCTTACTGATG---AC OmpK-35\_YMC2013/7/B3993

1 AACAGATTACAACCGTCGCTCGATAGCGGAAACGGCGATGTACCGGGTAAAACAGCTGTT OmpK-35\_YMC2012/8/C631

1 -----GTT------------------------ACGCACTGTTTCGGTGCATCCTGGTGAT OmpK-35\_YMC2011/7/B774

1 -----GTT------------------------ACGCACTGTTTCGGTGCATCCTGGTGAT OmpK-35\_YMC2010/8/B2027

1 -----GTT------------------------ACGCACTGTTTCGGTGCATCCTGGTGAT OmpK-35\_YMC2011/11/B7578

1 -----GTT------------------------ACGCACTGTTTCGGTGCATCCTGGTGAT OmpK-35\_YMC2011/7/B7207

1 -----GTT------------------------ACGCACTGTTTCGGTGCATCCTGGTGAT OmpK-35\_YMC2011/8/B10311

 \*\*\* \*\* \*

21 GTGCAG----TTTTCCCTTCAGAC---------GTGACTCATACATCGGCCAGCCGTCCG OmpK-35\_YMC2013/7/B3993

61 CGGGGGTTCACTGACGCTGC--------GTGACTACGATGGTCAGGTTGCGGAGGCTATG OmpK-35\_YMC2012/8/C631

32 GTTGATCGCACTTTATGTTCATAACAGAGCAAAATGGCTGATAAATTTGCTCATTTTTTG OmpK-35\_YMC2011/7/B774

32 GTAGATCGCACTTTATGTTCATAACTGAGCAAAACCGCTGATAAATTTGCTCATTTTTTG OmpK-35\_YMC2010/8/B2027

32 GTAGATCGCACTTTATGTTCATAACTGAGCAAAACCGCTGATAAATTTGCTCATTTTTTG OmpK-35\_YMC2011/11/B7578

32 GTAGATCGCACTTTATGTTCATAACTCAGCAAAACCGCTGATAAATTTGCTCATTTTTTG OmpK-35\_YMC2011/7/B7207

32 GCAGATCGCACTTTATGTTCATAACTGAGCAAAACCGCTGATAAATTTGCTCATTTTTTG OmpK-35\_YMC2011/8/B10311

 \* \* \* \* \* \*\* \* \*

68 TCATCCATACCACCACGTCAAAAACTGACAGCAGGCTCAGAAGACGCTCCAGTGTGGCCA OmpK-35\_YMC2013/7/B3993

113 GCCCTGGTACGAGCGCTGAACAAAATGACGAAAGC---AGGTATGCCT-GAAAGCGTGCG OmpK-35\_YMC2012/8/C631

92 ACCTTTACCCGCACATCTTGCAA--AGACA--------GAGACTGAATAAAAAGAATACG OmpK-35\_YMC2011/7/B774

92 ACCTTTACCCGCACATCTTGCAA--AGACA--------GAGACTGAATAAAAAGAATACG OmpK-35\_YMC2010/8/B2027

92 ACCTTTACCCGCACATCTTGCAA--AGACA--------GAGACTGAATAAAAAGAATACG OmpK-35\_YMC2011/11/B7578

92 ACCTTTACCCGCACATCTTGCAA--AGACA--------GAGACTGAATAAAAAGAATACG OmpK-35\_YMC2011/7/B7207

92 ACCTTTACCCGCACATCTTGCAA--AGACA--------GAGACTGAATAAAAAGAATACG OmpK-35\_YMC2011/8/B10311

 \* \* \* \*\* \*\*\* \* \* \* \*

128 TAGTGCGTTCACCGAAAACGTGGGCTACCACCG-CCCTGCGTATCCTGTCATACGCGTAA OmpK-35\_YMC2013/7/B3993

169 TATTACCTGAAAACACAACCCGCTACGGG------GGAGACTTACCTGAAATCTGATTTA OmpK-35\_YMC2012/8/C631

142 AATTCAATACACAAAATGAACGAATTGCCGCTTAGCCAAATTAATCATAAATAATTCATA OmpK-35\_YMC2011/7/B774

142 AATTCAATACACAAAATGAACGAATTGCCGCTTAGCCAAATTAATCATAAATAATTCATA OmpK-35\_YMC2010/8/B2027

142 AATTCAATACACAAAATGAACGAATTGCCGCTTAGCCAAATTAATCATAAATAATTCATA OmpK-35\_YMC2011/11/B7578

142 AATTCAATACACAAAATGAACGAATTGCCGCTTAGCCAAATTAATCATAAATAATTCATA OmpK-35\_YMC2011/7/B7207

142 AATTCAATACACAAAATGAACGAATTGCCGCTTAGCCAAATTAATCATAAATAATTCATA OmpK-35\_YMC2011/8/B10311

 \* \* \* \* \* \* \* \* \*\* \*

187 AACAGCCAGCGCTGACGTGATTTT----GCACCGACGTAGCCCCATTGCTCGTCCATCTC OmpK-35\_YMC2013/7/B3993

223 TTCAACAAAGCCTGAACGAGTTCGT----------------------------------- OmpK-35\_YMC2012/8/C631

202 TAGATAGATAAGTAATGGCGTTTGCCCTTATCCGGTGGAACGGAATTT------------ OmpK-35\_YMC2011/7/B774

202 TAGATAGATAAGTAATGGCGTTTGCCCTTATCCGGTGGAACGGAATTT------------ OmpK-35\_YMC2010/8/B2027

202 TAGATAGATAAGTAATGGCGTTTGCCCTTATCCGGTGGAACGGAATTT------------ OmpK-35\_YMC2011/11/B7578

202 TAGATAGATAAGTAATGGCGTTTTCCCTTATCCGGTGGAACGGAATTT------------ OmpK-35\_YMC2011/7/B7207

202 TAGATAGATAAGTAATGGCGTTTGCCCTTATCCGGTGGAACGGAATTT------------ OmpK-35\_YMC2011/8/B10311

 IHF \* \* \* \*\*

243 CGCACAGACAATGACATCACTGCCCGGCTGTATCCGGGAGGTTACTGACTGCGGCCTGAG OmpK-35\_YMC2013/7/B3993

248 -------GCAATTCATTCAGGGCTTCTGAATCTCCCCACAGTATAAAACCTGCATTGTTC OmpK-35\_YMC2012/8/C631

250 -------TGATTAAGTTCACAAAGTTCCGTTAAATACACATTTAGTTACATGATTTTTCG OmpK-35\_YMC2011/7/B774

250 -------TGATTAAGTTCACAAAGTTCCGTTAAATACACATTTAGTTACATGATTTTTCG OmpK-35\_YMC2010/8/B2027

250 -------TGATTAAGTTCACAAAGTTCCGTTAAATACACATTTAGTTACATGATTTTTCG OmpK-35\_YMC2011/11/B7578

250 -------TGATTAAGTTCACAAAGTTCCGTTAAATACACATTTAGTTACATGATTTTTCG OmpK-35\_YMC2011/7/B7207

250 -------TGATTAAGTTCACAAAGTTCCGTTAAATACACATTTAATTACATGATTTTTCG OmpK-35\_YMC2011/8/B10311

 \* \* \*\*\* \* F1 \* \*\* F3

303 TTTTTTAAATGGCGCAAAATGGTGTTGAGGCCCACGCCCATTAGTCGTGCGGTGGCACGG OmpK-35\_YMC2013/7/B3993

301 GGCGTTAACTCGTATCGAAGCATGAGATCAATCATCCTGTTGTTTCAGTCGAAGGAAAGT OmpK-35\_YMC2012/8/C631

303 TTTTGTTACTCATATGAGATATTCGTAG-----------CATTTTCCGGCTAGCGAAACG OmpK-35\_YMC2011/7/B774

303 TTTTGTTACTCATATGAGATATTCGTAG-----------CATTTTCCGGCTAGCGAAACG OmpK-35\_YMC2010/8/B2027

303 TTTTGTTACTCATATGAGATATTCGTAG-----------CATTTTCCGGCTAGCGAAACG OmpK-35\_YMC2011/11/B7578

303 TTTTGTTACTCATATGAGATATTCGTAG-----------CATTTTCCGGCTAGCGAAACG OmpK-35\_YMC2011/7/B7207

303 TTTTGTTACTCATATGAGATATTCGTAG-----------CATTTTCCGGCTAGCGAAACG OmpK-35\_YMC2011/8/B10311

 \* \* \* \* \* F4 \*\* \*-35 \* \*

363 CAACCGA----------CGCCGTTCATAGCCATATCAATGATTTTCTGGTGTGTACCGGG OmpK-35\_YMC2013/7/B3993

361 CTATCAGCAAAGAGAATCTGAGATCAAAGTGGA---------CATTTTAATTGAGCCGGA OmpK-35\_YMC2012/8/C631

352 TTGTCGCGGATGGAAAGATGCCTTCAGACACCAAACTCTCATCAATGGTTCTGTAAGTTT OmpK-35\_YMC2011/7/B774

352 TTGTCGCGGATGGAAAGATGCCTTCAGACACCAAACTCTCATCAATGGTTCTGTAAGTTT OmpK-35\_YMC2010/8/B2027

352 TTGTCGCGGATGGAAAGATGCCTTCAGACACCAAACTCTCATCAATGGTTCTGTAAGTTT OmpK-35\_YMC2011/11/B7578

352 TTGTCGCGGATGGAAAGATGCCTTCAGACACCAAACTCTCATCAATGGTTCTGTAAGTTT OmpK-35\_YMC2011/7/B7207

352 TTGTCGCGGATGGAAAGATGCCTTCAGACACCAAACTCTCATCAATGGTTCTGTAAGTTT OmpK-35\_YMC2011/8/B10311

 \* -10 \*\*\* \* \*\*

413 CTGAGAAGCGGCATAAGTGAAGGTGAGCTGC------CATGTTTTACGGCAGTGAGAGCA OmpK-35\_YMC2013/7/B3993

412 TAAAGGACATTTCAATTGAGCTTTGACAGCACGTGTTCATATAAAAAATATTAATGAGGG OmpK-35\_YMC2012/8/C631

412 TTATTGACAGAACTTATTGACGGCAGTGGCACGTGTTCATATAAAAAATATTAATGAGGG OmpK-35\_YMC2011/7/B774

412 TTATTGACAGAACTTATTGACGGCAGTGGCACGTGTTCATATAAAAAATATTAATGAGGG OmpK-35\_YMC2010/8/B2027

412 TTATTGACAGAACTTTTTGACGGCAGTGGCACGTGTTCATATAAAAAATATTAATGAGGG OmpK-35\_YMC2011/11/B7578

412 TTATTGACAGAACTTATTGACGGCAGTGGCACGTGTTCATATAAAAAATATTAATGAGGG OmpK-35\_YMC2011/7/B7207

412 TTATTGACAGAACTTATTGACGGCAGTGGCACGTGTTCATATAAAAAATATTAATGAGGG OmpK-35\_YMC2011/8/B10311

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 RBS

467 GAGATAACGTTGATGCCCGGCAGTACTTTTGCCATTACGCATCACGCCTTCAGTAGCGGA OmpK-35\_YMC2013/7/B3993

472 TAATAAATAATGATGAAGCGCAATATTCTGGCAGTGGTGATCCCTGCCCTGCTGGTAGCC OmpK-35\_YMC2012/8/C631

472 TAATAAATAATGATGAAGCGCAATATTCTTGCAGTGGTGATCCCTGCCCTGCTGGTAGCC OmpK-35\_YMC2011/7/B774

472 TAATAAATAATGATGAAGCGCAATATTCTGGCAGTGGTGATCCCTGCCCTGCTGGTAGCC OmpK-35\_YMC2010/8/B2027

472 TAATAAATAATGATGAAGCGCAATATTCTGGCAGTGGTGATCCCTGCCCTGCTGGTAGCC OmpK-35\_YMC2011/11/B7578

472 TAATAAATAATGATGAAGCGCAATATTCTGGCAGTGGTGATCCCTGCCCTGCTGGTAGCC OmpK-35\_YMC2011/7/B7207

472 TAATAAATAATGATGAAGCGCAATATTCTGGCAGTGGTGATCCCTGCCGTGCTGGTAGCC OmpK-35\_YMC2011/8/B10311

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 Start

527 ACAGGAGGGACAGCAGACGGAGACTGAAGCCACGGGAGCACCTCAAAAACACCATTATAC OmpK-35\_YMC2013/7/B3993

532 GGT------GCAGCCAACGCTGCAGAAATCTATAACAAAAACGGCA-ACAAACTGGACTT OmpK-35\_YMC2012/8/C631

532 GGT------GCAGCCAACGCTGCAGAAATCTATAACAAAAACGGCA-ACAAACTGGACTT OmpK-35\_YMC2011/7/B774

532 GGT------GCAGCCAACGCTGCAGAAATCTATAACAAAAACGGCA-ACAAACTGGACTT OmpK-35\_YMC2010/8/B2027

532 GG-------GCAGCCAACGCTGCAGAAATCTATAACAAAAACGGCA-ACAAACTGGACTT OmpK-35\_YMC2011/11/B7578

532 GGT------GCAGCCAACGCTGCAGAAATCTATAACAAAAACGGCA-ACAAACTGGACTT OmpK-35\_YMC2011/7/B7207

532 GGT------GCAGCCAACGCTGCAGAAATCTATAACAAAAACGGCA-ACAAACTGGACTT OmpK-35\_YMC2011/8/B10311

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587 ACTAAATCAGCAAGTTGGTAGCATCACCTGGACCACCAATGGCGACACCAGCAGCGACGA OmpK-35\_YMC2013/7/B3993

585 CTATGGAAAAATGGTCGGCGAGCACGTCTGGACCACCAATGGCGACACCAGCAGCGACGA OmpK-35\_YMC2012/8/C631

585 CTATGGAAAAATGGTCGGCGAGCACGTCTGGACCACCAATGGCGACACCAGTAGCGACGA OmpK-35\_YMC2011/7/B774

585 CTATGGAAAAATGGTCGGCGAGCACGTCTGGACCACCAATGGCGACACCAGCAGCGACGA OmpK-35\_YMC2010/8/B2027

584 CTATGGAAAAATGGTCGGCGAGCACGTCTGGACCACCAATGGCGACACCAGCAGCGACGA OmpK-35\_YMC2011/11/B7578

585 CTATGGAAAAATGGTCGGCGAGCACGTCTGGACCACCAATGGCGACACCAGCAGCGACGA OmpK-35\_YMC2011/7/B7207

585 CTATGGAAAAATGGTCGGCGAGCACGTCTGGACCACCAATGGCGACACCAGCAGCGACGA OmpK-35\_YMC2011/8/B10311

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647 TACCACCTATGCCCGTATCGGCCTGAAAGGCGAAACTCAGATCAACGATCAGCTGATCGG OmpK-35\_YMC2013/7/B3993

645 TACCACCTATGCCCGTATCGGCCTGAAAGGCGAAACTCAGATCAACGATCAGCTGATCGG OmpK-35\_YMC2012/8/C631

645 TACCACCTATGCCCGTATCGGCCTGAAAGGCGAAACTCAGATCAACGATCAGCTGATCGG OmpK-35\_YMC2011/7/B774

645 TACCACCTATGCCCGTATCGGCCG-----GCGAAACTCAGATCAACGATCAGCTGATCGG OmpK-35\_YMC2010/8/B2027

644 TACCACCTATGCCCGTATCGGCCTGAAAGGCGAAACTCAGATCAACGATCAGCTGATCGG OmpK-35\_YMC2011/11/B7578

645 TACCACCTATGCCCGTATCGGCCTGAAAGGCGAAACTCAGATCAACGATCAGCTGATCGG OmpK-35\_YMC2011/7/B7207

645 TACCACCTATGCCCGTATCGGCCTGAAAGGCGAAACTCAGATCAACGATCAGCTGATCGG OmpK-35\_YMC2011/8/B10311

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707 CTACGGCCAGTGGGAATACAACATGGACGCGTCCAATGTTGAAGGTTCCCAGACCACAAA OmpK-35\_YMC2013/7/B3993

705 CTACGGCCAGTGGGAATACAACATGGACGCGTCCAATGTTGAAGGTTCCCAGACCACAAA OmpK-35\_YMC2012/8/C631

705 CTACGGCCAGTGGGAATACAACATGGACGCGTCCAATGTTGAAGGTTCCCAGACCACAAA OmpK-35\_YMC2011/7/B774

700 CTACGGCCAGTGGGAATACAACATGGACGCGTCCAATGTTGAAGGTTCCCAGACCACAAA OmpK-35\_YMC2010/8/B2027

704 CTACGGCCAGTGGGAATACAACATGGACGCGTCCAATGTTGAAGGTTCCCAGACCACAAA OmpK-35\_YMC2011/11/B7578

705 CTACGGCCAGTGGGAATACAACATGGACGCGTCCAATGTTGAAGGTTCCCAGACCACAAA OmpK-35\_YMC2011/7/B7207

705 CTACGGCCAGTGGGAATACAACATGGACGCGTCCAATGTTGAAGGTTCCCAGACCACAAA OmpK-35\_YMC2011/8/B10311

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767 AACCCGTCTAGCGTTCGCAGGCCTGAAAGCGGGCGAATACGGTTCATTCGACTATGGCCG OmpK-35\_YMC2013/7/B3993

765 AACCCGTCTGGCGTTCGCGGGCCTGAAAGCGGGCGAATACGGTTCATTCGACTATGGCCG OmpK-35\_YMC2012/8/C631

765 AACCCGTCTGGCGTTCGCGGGCCTGAAAGCGGGCGAATACGGTTCATTCGACTATGGCCG OmpK-35\_YMC2011/7/B774

760 AACCCGTCTGGCGTTCGCGGGCCTGAAAGCGGGCGAATACGGTTCATTCGACTATGGCCG OmpK-35\_YMC2010/8/B2027

764 AACCCGTCTAGCGTTCGCAGGCCTGAAAGCGGGCGAATACGGTTCATTCGACTATGGCCG OmpK-35\_YMC2011/11/B7578

765 AACCCGTCTGGCGTTCGCAGGCCTGAAAGCGGGCGAATACGGTTCATTCGACTATGGCCG OmpK-35\_YMC2011/7/B7207

765 AACCCGTCTGGCGTTCGCAGGCCTGAAAGCGGGCGAATACGGTTCATTCGACTATGGCCG OmpK-35\_YMC2011/8/B10311

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827 TAACTACGGCGCGATCTACGACGTCGAAGCGGCAACCGATATGCTGGTTGAATGGGGCGG OmpK-35\_YMC2013/7/B3993

825 TAACTACGGCGCGATCTACGACGTCGAAGCGGCAACCGATATGCTGGTTGAATGGGGCGG OmpK-35\_YMC2012/8/C631

825 TAACTACGGCGCGATCTACGACGTCGAAGCGGCAACCGATATGCTGGTTGAATGGGGCGG OmpK-35\_YMC2011/7/B774

820 TAACTACGGCGCGATCTACGACGTCGAAGCGGCAACCGATATGCTGGTTGAATGGGGCGG OmpK-35\_YMC2010/8/B2027

824 TAACTACGGCGCGATCTACGACGTCGAAGCGGCAACCGATATGCTGGTTGAATGGGGCGG OmpK-35\_YMC2011/11/B7578

824 TAACTATGGCGCGATCTACGACGTCGAAGCGGCAACCGATATGCTGGTTGAATGGGGCGG OmpK-35\_YMC2011/7/B7207

825 TAACTACGGCGCGATCTACGACGTCGAAGCGGCAACCGATATGCTGGTTGAATGGGGCGG OmpK-35\_YMC2011/8/B10311

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887 TGACGGCTGGAACTATACCGACAACTACATGACCGGTCGTACCAACGGCGTCGCAACCTA OmpK-35\_YMC2013/7/B3993

885 TGACGGCTGGAACTACACCGACAACTACATGACCGGTCGTACCAACGGCGTCGCAACCTA OmpK-35\_YMC2012/8/C631

885 TGACGGCTGGAACTACACCGACAACTACATGACCGGTCGTACCAACGGCGTCGCAACCTA OmpK-35\_YMC2011/7/B774

880 TGACGGCTGGAACTACACCGACAACTACATGACCGGTCGTACCAACGGCGTCGCAACCTA OmpK-35\_YMC2010/8/B2027

884 TGACGGCTGGAACTATACCGACAACTACATGACCGGTCGTACCAACGGCGTCGCAACCTA OmpK-35\_YMC2011/11/B7578

885 TGACGGCTGGAACTACACCGACAACTACATGACCGGTCGTACCAACGGCGTCGCAACCTA OmpK-35\_YMC2011/7/B7207

885 TGACGGCTGGAACTATACCGACAACTACATGACCGGTCGTACCAACGGCGTCGCAACCTA OmpK-35\_YMC2011/8/B10311

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947 CCGTAACTCCGACTTCTTCGGTCTGGTTGACGGTCTGAGCTTCGCGCTGCAGTACCAGGG OmpK-35\_YMC2013/7/B3993

945 CCGTAACTCCGACTTCTTCGGTCTGGTTGACGGTCTGAGCTTCGCGCTGCAGTACCAGGG OmpK-35\_YMC2012/8/C631

945 CCGTAACTCCGACTTCTTCGGTCTGGTTGACGGTCTGAGCTTCGCGCTGCAGTACCAGGG OmpK-35\_YMC2011/7/B774

940 CCGTAACTCCGACTTCTTCGGTCTGGTTGACGGTCTGAGCTTCGCGCTGCAGTACCAGGG OmpK-35\_YMC2010/8/B2027

944 CCGTAACTCCGACTTCTTCGGTCTGGTTGACGGTCTGAGCTTCGCGCTGCAGTACCAGGG OmpK-35\_YMC2011/11/B7578

945 CCGTAACTCTGACTTCTTCGGTCTGGTTGACGGTCTGAGCTTCGCGCTGCAGTACCAGGG OmpK-35\_YMC2011/7/B7207

945 CCGTAACTCCGACTTCTTCGGTCTGGTTGACGGTCTGAGCTTCGCGCTGCAGTACCAGGG OmpK-35\_YMC2011/8/B10311

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1007 TAAAAA OmpK-35\_YMC2013/7/B3993

1005 TAAAAA OmpK-35\_YMC2012/8/C631

1005 TAAAAA OmpK-35\_YMC2011/7/B774

1000 TAAAAA OmpK-35\_YMC2010/8/B2027

1004 TAAAAA OmpK-35\_YMC2011/11/B7578

1005 TAAAAA OmpK-35\_YMC2011/7/B7207

1005 TAAAAA OmpK-35\_YMC2011/8/B10311

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Figure S3: Nucleotide alignment of OmpK 36 gene of panel strain: Multiple point mutations detected in YMC2011/7/B7207, YMC2011/8/B10311 and YMC2011/7/B774 (listed in table S3). OmpK 36 gene of YMC2012/8/C631 has been interrupted due to the IS element insertion (highlighted in yellow). Arrows indicate the start codon, RBS, -10, -35 and transcription regulators.

1 AATTAAAGTTGTGTAAAGAAGGGTAAAAAAAACCGGATGCGAGGCATCCGGTTGAAATAG OmpK-36\_YMC2011/7/B7207

1 AATTAAAGTTGTGTAAAGAAGGGTAAAAAAAACCGGATGCGAGGCATCCGGTTGAAATAG OmpK-36\_YMC2011/8/B10311

1 AATTAAAGTTGTGTAAAGAAGGGTAAAAAAAACCGGATGCGAGGCATCCGGTTGAAATAG OmpK-36\_YMC2011/7/B774

1 AATTAAAGTTGTGTAAAGAAGGGTAAAAAAAACCGGATGCGAGGCATCCGGTTGAAATAG OmpK-36\_YMC2012/8/C631

1 AATTAAAGTTGTGTAAAGAAGGGTAAAAAAAACCGGATGCGAGGCATCCGGTTGAAATAG OmpK-36\_YMC2010/8/B2027

1 AATTAAAGTTGTGTAAAGAAGGGTAAAAAAAACCGGATGCGAGGCATCCGGTTGAAATAG OmpK-36\_YMC2011/11/B7578

1 AATTAAAGTTGTGTAAAGAAGGGTAAAAAAAACCGGATGCGAGGCATCCGGTTGAAATAG OmpK-36\_YMC2013/7/B3993

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61 GGGTAAACAGACATTCAGAACTGAATGACGGTAATAAATAAAGTTAATGATGATAGCGAC OmpK-36\_YMC2011/7/B7207

61 GGGTAAACAGACATTCAGAACTGAATGACGGTAATAAATAAAGTTAATGATGATAGCGAC OmpK-36\_YMC2011/8/B10311

61 GGGTAAACAGACATTCAGAACTGAATGACGGTAATAAATAAAGTTAATGATGATAGCGAC OmpK-36\_YMC2011/7/B774

61 GGGTAAACAGACATTCAGAACTGAATGACGGTAATAAATAAAGTTAATGATGATAGCGAC OmpK-36\_YMC2012/8/C631

61 GGGTAAACAGACATTCAGAACTGAATGACGGTAATAAATAAAGTTAATGATGATAGCGAC OmpK-36\_YMC2010/8/B2027

61 GGGTAAACAGACATTCAGAACTGAATGACGGTAATAAATAAAGTTAATGATGATAGCGAC OmpK-36\_YMC2011/11/B7578

61 GGGTAAACAGACATTCAGAACTGAATGACGGTAATAAATAAAGTTAATGATGATAGCGAC OmpK-36\_YMC2013/7/B3993

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121 TCTTATTTTAGCCACCAATGATCATTTTGTTTTACCATTCAGTGCTATAGATATGCTGTC OmpK-36\_YMC2011/7/B7207

121 TCTTATTTTAGCCACCAATGATCATTTTGTTTTACCATTCAGTGCTATAGATATGCTGTC OmpK-36\_YMC2011/8/B10311

121 TCTTATTTTAGCCACCAATGATCATTTTGTTTTACCATTCAGTGCTATAGATATGCTGTC OmpK-36\_YMC2011/7/B774

121 TCTTATTTTAGCCACCAATGATCATTTTGTTTTACCATTCAGTGCTATAGATATGTTGTT OmpK-36\_YMC2012/8/C631

121 TCTTATTTTAGCCACCAATGATCATTTTGTTTTACCATTCAGTGCTATAGATATGTTGTT OmpK-36\_YMC2010/8/B2027

121 TCTTATTTTAGCCACCAATGATCATTTTGTTTTACCATTCAGTGCTATAGATATGCTGTC OmpK-36\_YMC2011/11/B7578

121 TCTTATTTTAGCCACCAATGATCATTTTGTTTTACCATTCAGTGCTATAGATATGCTGTC OmpK-36\_YMC2013/7/B3993

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181 GTCTATCACTTTGATTATAAAAGGTTAAATATTTTTTTTGATGATTAGTGCGTATTTCCC OmpK-36\_YMC2011/7/B7207

181 GTCTATCAATTTGATTATAAAAGGTTAAATATTTTTTTTGATGATTAGTGCGTATTTCCC OmpK-36\_YMC2011/8/B10311

181 GTCTATCACTTTGATTATAAAAGGTTAAATATTTTTTTTGATGATTAGTGCGTATTTCCC OmpK-36\_YMC2011/7/B774

181 GTCTATCAATTTGATTATAAAAGGTTAAATATTTTTTTTGATGATTAGTGCGTATTTCCC OmpK-36\_YMC2012/8/C631

181 GTCTATCAATTTGATTATAAAAGGTTAAATATTTTTTTTGATGATTAGTGCGTATTTCCC OmpK-36\_YMC2010/8/B2027

181 GTCTATCGCTTTGATTATAAAAGGTTAAATATTTTTTTTGATGATTAGTGCGTATTTCCC OmpK-36\_YMC2011/11/B7578

181 GTCTATCGCTTTGATTATAAAAGGTTAAATATTTTTTTTGATGATTAGTGCGTATTTCCC OmpK-36\_YMC2013/7/B3993

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 IHF

241 TGACCATTTTGCGGTGAAAAAAGTTCCGCTGAATTTACAAATTGAAACATCTTGTGGGAA OmpK-36\_YMC2011/7/B7207

241 TGACCATTTTGCGGTGAAAAAAGTTCCGCTGAATTTACAAATTGAAACATCTTGTGGGAA OmpK-36\_YMC2011/8/B10311

241 TGACCATTTTGCGGTGAAAAAAGTTCCGCTGAATTTACAAATTGAAACATCTTGTGGGAA OmpK-36\_YMC2011/7/B774

241 TGACCATTTTGCGGTAAAAAAAGTTCCGCTAAATTTACAAATTGAAACATCTTGTGGGAA OmpK-36\_YMC2012/8/C631

241 TGACCATTTTGCGGTAAAAAAAGTTCCGCTAAATTTACAAATTGAAACATCTTGTGGGAA OmpK-36\_YMC2010/8/B2027

241 TGACCATTTTGCGGTGAAAAAAGTTCCGCTAAATTTACAAATTGAAACATCTTGTGGGAA OmpK-36\_YMC2011/11/B7578

241 TGACCATTTTGCGGTGAAAAAAGTTCCGCTAAATTTACAAATTGAAACATCTTGTGGGAA OmpK-36\_YMC2013/7/B3993

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 C1

301 CTTTGAAACATCTTAGAAGTTTTAGTATCATATTCTTGTTGGATTATTCTGCATTTTGCA OmpK-36\_YMC2011/7/B7207

301 CTTTGAAACATCTTAGAAGTTTTAGTATCATATTCTTGTTGGATTATTCTGCATTTTGCA OmpK-36\_YMC2011/8/B10311

301 CTTTGAAACATCTTAGAAGTTTTAGTATCATATTCTTGTTGGATTATTCTGCATTTTGCA OmpK-36\_YMC2011/7/B774

301 CTTTGAAACATCTTAGAAGTTTTAGTATCATATTCTTGTTGGATTATTCTGCATTTTGCA OmpK-36\_YMC2012/8/C631

301 CTTTGAAACATCTTAGAAGTTTTAGTATCATATTCTTGTTGGATTATTCTGCATTTTGCA OmpK-36\_YMC2010/8/B2027

301 CTTTGAAACATCTTAGAAGTTTTAGTATCATATTCTTGTTGGATTATTCTGCATTTTGCA OmpK-36\_YMC2010/8/B2027

301 CTTTGAAACATCTTAGAAGTTTTAGTATCATATTCTTGTTGGATTATTCTGCATTTTGCA OmpK-36\_YMC2013/7/B3993

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 C2 C3 -35

361 GCACAATGAAATAGCCGACTGATTAGAAGGGTAATCAGTAAGCAGTGGCATAATAAAAGG OmpK-36\_YMC2011/7/B7207

361 GCACAATGAAATAGCCGACTGATTAGAAGGGTAATCAGTAAGCAGTGGCATAATAAAAGG OmpK-36\_YMC2011/8/B10311

361 GCACAATGAAATAGCCGACTGATTAGAAGGGTAATCAGTAAGCAGTGGCATAATAAAAGG OmpK-36\_YMC2011/7/B774

361 GCACAATGAAATAGCCGACTGATTAGAAGGGTAATCAGTAAGCAGTGGCATAATAAAAGG OmpK-36\_YMC2012/8/C631

361 GCACAATGAAATAGCCGACTGATTAGAAGGGTAATCAGTAAGCAGTGGCATAATAAAAGG OmpK-36\_YMC2010/8/B2027

361 GCACAATGAAATAGCCGACTGATTAGAAGGGTAATCAGTAAGCAGTGGCATAATAAAAGG OmpK-36\_YMC2011/11/B7578

361 GCACTATGAAATAGCCGACTGATTAGAAGGGTAATCAGTAAGCAGTGGCATAATAAAAGG OmpK-36\_YMC2013/7/B3993

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 -10

421 CATATAACAAACAGAGGGTTAATAACATGAAAGTTAAAGTACTGTCCCTCCTGGTACCGG OmpK-36\_YMC2011/7/B7207

421 CATATAACAAACAGAGGGTTAATAACATGAAAGTTAAAGTACTGTCCCTCCTGGTACCGG OmpK-36\_YMC2011/8/B10311

421 CATATAACAAACAGAGGGTTAATAACATGAAAGTTAAAGTACTGTCCCTCTTGGTACCGG OmpK-36\_YMC2011/7/B774

421 CATATAACAAACAGAGGGTTAATAACATGAAAGTTAAAGTACTGTCCCTCCTGGTACCGG OmpK-36\_YMC2012/8/C631

421 CATATAACAAACAGAGGGTTAATAACATGAAAGTTAAAGTACTGTCCCTCCTGGTACCGG OmpK-36\_YMC2010/8/B2027

421 CATATAACAAACAGAGGGTTAATAACATGAAAGTTAAAGTACTGTCCCTCCTGGTACCGG OmpK-36\_YMC2011/11/B7578

421 CATATAACAAACAGAGGGTTAATAACATGAAAGTTAAAGTACTGTCCCTCCTGGTACCGG OmpK-36\_YMC2013/7/B3993

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 RBS Start

481 CTCTGCTGGTAGCAGGCGCAGCAAATGCGGCTGAAATTTATAACAAAGACGGCAACAAAT OmpK-36\_YMC2011/7/B7207

481 CTCTGCTGGTAGCAGGCGCAGCAAATGCGGCTGAAATTTATAACAAAGACGGCAACAAAT OmpK-36\_YMC2011/8/B10311

481 CTCTGCTGGTAGCAGGCGCAGCAAATGCGGCTGAAATTTATAACAAAGACGGCAACAAAT OmpK-36\_YMC2011/7/B774

481 CTCTGCTGGTAGCAGGCGCAGCAAATGCGGCTGAAATTTATAACAAAGACGGCAACAAAT OmpK-36\_YMC2012/8/C631

481 CTCTGCTGGTAGCAGGCGCAGCAAATGCGGCTGAAATTTATAACAAAGACGGCAACAAAT OmpK-36\_YMC2010/8/B2027

481 CTCTGCTGGTAGCAGGCGCAGCAAATGCGGCTGAAATTTATAACAAAGACGGCAACAAAT OmpK-36\_YMC2011/11/B7578

481 CTCTGCTGGTAGCAGGCGCAGCAAATGCGGCTGAAATTTATAACAAAGACGGCAACAAAT OmpK-36\_YMC2013/7/B3993

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541 TAGACCTGTACGGTAAAATTGACGGTCTGCACTACTTCTCTGACGACAAGAG-------- OmpK-36\_YMC2011/7/B7207

541 TAGACCTGTACGGTAAAATTGACGGTCTGCACTACTTCTCTGACGACAAGAG-------- OmpK-36\_YMC2011/8/B10311

541 TAGACCTGTATGGTAAAATTGACGGTCTGCACTACTTCTCTGACGACAAGAG-------- OmpK-36\_YMC2011/7/B774

541 TAGACCTGTACGGTAAAATTGACGGTCTGCACTACTTCTCTGACGACAAGAGCGTCGACG OmpK-36\_YMC2012/8/C631

541 TAGACCTGTACGGTAAAATTGACGGTCTGCACTACTTCTCTGACGACAAGAG-------- OmpK-36\_YMC2010/8/B2027

541 TAGACCTGTACGGTAAAATTGACGGTCTGCACTACTTCTCTGACGACAAGAG-------- OmpK-36\_YMC2011/11/B7578

541 TAGACCTGTACGGTAAAATTGACGGTCTGCACTACTTCTCTGACGACAAGAG-------- OmpK-36\_YMC2013/7/B3993

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593 ------------------------CGTCGACGGCGACCAGACCTACATGCGTGTAGGCGT OmpK-36\_YMC2011/7/B7207

593 ------------------------CGTCGACGGCGACCAGACCTACATGCGTGTAGGCGT OmpK-36\_YMC2011/8/B10311

593 ------------------------CGTCGACGGCGACCAGACCTACATGCGTGTAGGCGT OmpK-36\_YMC2011/7/B774

601 GCGACCATTCTCTGACGACAAGAGCGTCGACGGCGACCAGACCTACATGCGTGTAGGCGT OmpK-36\_YMC2012/8/C631

593 ------------------------CGTCGACGGCGACCAGACCTACATGCGTGTAGGCGT OmpK-36\_YMC2010/8/B2027

593 ------------------------CGTCGACGGCGACCAGACCTACATGCGTGTAGGCGT OmpK-36\_YMC2011/11/B7578

593 ------------------------CGTCGACGGCGACCAGACCTACATGCGTGTAGGCGT OmpK-36\_YMC2013/7/B3993

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629 GAAAGGCGAAACCCAGATCAACGACCAGCTGACCGGTTACGGCCAGTGGGAATACAACGT OmpK-36\_YMC2011/7/B7207

629 GAAAGGCGAAACCCAGATCAACGACCAGCTGACCGGTTACGGCCAGTGGGAATACAACGT OmpK-36\_YMC2011/8/B10311

629 GAAAGGCGAAACCCAGATCAACGACCAGCTGACCGGTTACGGCCAGTGGGAATACAACGT OmpK-36\_YMC2011/7/B774

661 GAAAGGCGAAACCCAGATCAACGACCAGCTGACCGGTTACGGCCAGTGGGAATACAACGT OmpK-36\_YMC2012/8/C631

629 GAAAGGCGAAACCCAGATCAACGACCAGCTGACCGGTTACGGCCAGTGGGAATACAACGT OmpK-36\_YMC2010/8/B2027

629 GAAAGGCGAAACCCAGATCAACGACCAGCTGACCGGTTACGGCCAGTGGGAATACAACGT OmpK-36\_YMC2011/11/B7578

629 GAAAGGCGAAACCCAGATCAACGACCAGCTGACCGGTTACGGCCAGTGGGAATACAACGT OmpK-36\_YMC2013/7/B3993

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689 TCAGGCGAACAACGTTGAAGGTACTGACAAGTAGTCCTGGACTCGTCTGGCATTCGCGGG OmpK-36\_YMC2011/8/B10311

689 TCAGGCGAACAACACTGAAAGCTCCAGCGATCAGGCATGGACTCGTCTGGCATTCGCAGG OmpK-36\_YMC2011/7/B774

721 TCAGGCGAACAACACTGAAAGCTCCAGCGATCAGGCATGGACTCGTCTGGCATTCGCAGG OmpK-36\_YMC2012/8/C631

689 TCAGGCGAACAACACTGAAAGCTCCAGCGATCAGGCATGGACTCGTCTGGCATTCGCAGG OmpK-36\_YMC2010/8/B2027

689 TCAGGCGAACAACACTGAAAGCTCCAGCGATCAGGCATGGACTCGTCTGGCATTCGCAGG OmpK-36\_YMC2011/11/B7578

689 TCAGGCGAACAACACTGAAAGCTCCAGCGATCAGGCATGGACTCGTCTGGCATTCGCAGG OmpK-36\_YMC2013/7/B3993

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789 TCTGAAATTCGGCGACGCGGGTTCTTTCGACTACGGTCGTAACTACGGCGTTGTTTACGA OmpK-36\_YMC2011/7/B7207

749 TCTGAAATTCGGCGACGCGGGTTCTTTCGACTACGGTCGTAACTACGGCGTTGTTTACGA OmpK-36\_YMC2011/8/B10311

749 CCTGAAATTTGGCGACGCGGGCTCTTTCGACTACGGTCGTAACTACGGCGTAGTATACGA OmpK-36\_YMC2011/7/B774

781 CCTGAAATTTGGCGACGCGGGCTCTTTCGACTACGGTCGTAACTACGGCGTAGTATACGA OmpK-36\_YMC2012/8/C631

749 CCTGAAATTTGGCGACGCGGGCTCTTTCGACTACGGTCGTAACTACGGCGTAGTATACGA OmpK-36\_YMC2010/8/B2027

749 CCTGAAATTTGGCGACGCGGGCTCTTTCGACTACGGTCGTAACTACGGCGTAGTATACGA OmpK-36\_YMC2011/11/B7578

749 CCTGAAATTTGGCGACGCGGGCTCTTTCGACTACGGTCGTAACTACGGCGTAGTATACGA OmpK-36\_YMC2013/7/B3993

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809 CGTAACGTCCTGGACCGACGTTCTGCCGGAATTCGGCGGCGACACCTACGGTTCTGACAA OmpK-36\_YMC2011/7/B774

841 CGTAACGTCCTGGACCGACGTTCTGCCGGAATTCGGCGGCGACACCTACGGTTCTGACAA OmpK-36\_YMC2012/8/C631

809 CGTAACGTCCTGGACCGACGTTCTGCCGGAATTCGGCGGCGACACCTACGGTTCTGACAA OmpK-36\_YMC2010/8/B2027

809 CGTAACGTCCTGGACCGACGTTCTGCCGGAATTCGGCGGCGACACCTACGGTTCTGACAA OmpK-36\_YMC2011/11/B7578

809 CGTAACGTCCTGGACCGACGTTCTGCCGGAATTCGGCGGCGACACCTACGGTTCTGACAA OmpK-36\_YMC2013/7/B3993

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869 CTTCCTGCAGTCCCGTGCTAACGGCGTTGCAACCTATCGTAACTCTGACTTCTTCGGTCT OmpK-36\_YMC2011/8/B10311

869 CTTCCTGCAGTCCCGTGCTAACGGCGTTGCAACCTACCGTAACTCTGATTTCTTCGGTCT OmpK-36\_YMC2011/7/B774

901 CTTCCTGCAGTCCCGTGCTAACGGCGTTGCAACCTACCGTAACTCTGATTTCTTCGGTCT OmpK-36\_YMC2012/8/C631

869 CTTCCTGCAGTCCCGTGCTAACGGCGTTGCAACCTACCGTAACTCTGATTTCTTCGGTCT OmpK-36\_YMC2010/8/B2027

869 CTTCCTGCAGTCCCGTGCTAACGGCGTTGCAACCTACCGTAACTCTGATTTCTTCGGTCT OmpK-36\_YMC2011/11/B7578

869 CTTCCTGCAGTCCCGTGCTAACGGCGTTGCAACCTACCGTAACTCTGATTTCTTCGGTCT OmpK-36\_YMC2013/7/B3993

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929 GGTTGACGGCCTGAACTTTGCCCTGCAGTACCAAGGTAAAAACGGCAGCGTCAGCGGCGA OmpK-36\_YMC2011/8/B10311

929 GGTTGACGGCCTGAACTTTGCTCTGCAGTATCAGGGTAAAAACGGCAGCGTCAGCGGCGA OmpK-36\_YMC2011/7/B774

961 GGTTGACGGCCTGAACTTTGCTCTGCAGTATCAGGGTAAAAACGGCAGCGTCAGCGGCGA OmpK-36\_YMC2012/8/C631

929 GGTTGACGGCCTGAACTTTGCTCTGCAGTATCAGGGTAAAAACGGCAGCGTCAGCGGCGA OmpK-36\_YMC2010/8/B2027

929 GGTTGACGGCCTGAACTTTGCTCTGCAGTATCAGGGTAAAAACGGCAGCGTCAGCGGCGA OmpK-36\_YMC2011/11/B7578

929 GGTTGACGGCCTGAACTTTGCTCTGCAGTATCAGGGTAAAAACGGCAGCGTCAGCGGCGA OmpK-36\_YMC2013/7/B3993

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989 AGACATGA---------CCAACAACGGTCGTGGCGCTCAGAAACAGAACGGCGACGGCTT OmpK-36\_YMC2011/8/B10311

989 AGGCGCGA---------CCAACAACGGTCGTGGTTGGAGCAAACAGAACGGCGACGGCTT OmpK-36\_YMC2011/7/B774

1021 AGGCGCTCTGTCTCCTACCAACAACGGTCGTACCGCCTTGAAACAGAACGGCGACGGTTA OmpK-36\_YMC2012/8/C631

989 AGGCGCTCTGTCTCCTACCAACAACGGTCGTACCGCCTTGAAACAGAACGGCGACGGTTA OmpK-36\_YMC2010/8/B2027

989 AGGCGCTCTGTCTCCTACCAACAACGGTCGTACCGCCTTGAAACAGAACGGCGACGGTTA OmpK-36\_YMC2011/11/B7578

989 AGGCGCTCTGTCTCCTACCAACAACGGTCGTACCGCCTTGAAACAGAACGGCGACGGTTA OmpK-36\_YMC2013/7/B3993

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1040 CGGCACCTCCGTAACTTATGATATCTGGGACGGCATCAGCGCTGGTTTCGCTTACTCCCA OmpK-36\_YMC2011/8/B10311

1040 CGGCACCTCTCTGACCTACGATATTTGGGATGGCATCAGCGCTGGTTTCGCGTACTCGCA OmpK-36\_YMC2011/7/B774

1081 CGGTACTTCTCTGACCTATGACATCTATGATGGCATCAGCGCTGGTTTCGCATACTCTAA OmpK-36\_YMC2012/8/C631

1049 CGGTACTTCTCTGACCTATGACATCTATGATGGCATCAGCGCTGGTTTCGCATACTCTAA OmpK-36\_YMC2010/8/B2027

1049 CGGTACTTCTCTGACCTATGACATCTATGATGGCATCAGCGCTGGTTTCGCATACTCTAA OmpK-36\_YMC2011/11/B7578

1049 CGGTACTTCTCTGACCTATGACATCTATGATGGCATCAGCGCTGGTTTCGCATACTCTAA OmpK-36\_YMC2013/7/B3993

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1100 CTCTAAACGTACTGATGACCAGAAC---AACCTGGTACTGGGTCGTGGTGACGACGCTGA OmpK-36\_YMC2011/8/B10311

1100 CTCCAAACGTACCGACGAGCAGAATAGTGTTCCGGCACTGGGTCGTGGCGACAACGCTGA OmpK-36\_YMC2011/7/B774

1141 CTCCAAACGTCTTGGCGACCAGAACAGCAAGCTGGCACTGGGTCGTGGCGACAACGCTGA OmpK-36\_YMC2012/8/C631

1109 CTCCAAACGTCTTGGCGACCAGAACAGCAAGCTGGCACTGGGTCGTGGCGACAACGCTGA OmpK-36\_YMC2010/8/B2027

1109 CTCCAAACGTCTTGGCGACCAGAACAGCAAGCTGGCACTGGGTCGTGGCGACAACGCTGA OmpK-36\_YMC2011/11/B7578

1109 CTCCAAACGTCTTGGCGACCAGAACAGCAAGCTGGCACTGGGTCGTGGCGACAACGCTGA OmpK-36\_YMC2013/7/B3993

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1157 AACCTATACCGGTGGTCTGAAATACGACGCCAACAACATCTACCTGGCCTCTCAGTACAC OmpK-36\_YMC2011/8/B10311

1160 AACCTACACCGGTGGTCTGAAATACGACGCCAACAACATCTACCTGGCCTCTCAGTACAC OmpK-36\_YMC2011/7/B774

1201 AACCTACACCGGCGGTCTGAAATACGACGCGAACAACATCTACCTGGCCACTCAGTACAC OmpK-36\_YMC2012/8/C631

1169 AACCTACACCGGCGGTCTGAAATACGACGCGAACAACATCTACCTGGCCACTCAGTACAC OmpK-36\_YMC2010/8/B2027

1169 AACCTACACCGGCGGTCTGAAATACGACGCGAACAACATCTACCTGGCCACTCAGTACAC OmpK-36\_YMC2011/11/B7578

1169 AACCTACACCGGCGGTCTGAAATACGACGCGAACAACATCTACCTGGCCACTCAGTACAC OmpK-36\_YMC2013/7/B3993

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1220 CCAGACCTACAACGCAACTCGCGCCGGTTCCCTGGGCTTTGCAAACAAAGCGCAGAACTT OmpK-36\_YMC2011/7/B774

1261 CCAGACCTACAACGCGACCCGCGCCGGTTCCCTGGGCTTTGCTAACAAAGCGCAGAACTT OmpK-36\_YMC2012/8/C631

1229 CCAGACCTACAACGCGACCCGCGCCGGTTCCCTGGGCTTTGCTAACAAAGCGCAGAACTT OmpK-36\_YMC2010/8/B2027

1229 CCAGACCTACAACGCGACCCGCGCCGGTTCCCTGGGCTTTGCTAACAAAGCGCAGAACTT OmpK-36\_YMC2011/11/B7578

1229 CCAGACCTACAACGCGACCCGCGCCGGTTCCCTGGGCTTTGCTAACAAAGCGCAGAACTT OmpK-36\_YMC2013/7/B3993

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1277 CGAAGTGGTTGCTCAGTACCAGTTCGACTTCGGTCTGCGTCCGTCTGTGGCTTACCTGCA OmpK-36\_YMC2011/8/B10311

1280 CGAAGTGGTTGCTCAGTACCAGTTCGACTTCGGTCTGCGTCCGTCTGTGGCTTACCTGCA OmpK-36\_YMC2011/7/B774

1321 CGAAGTGGTTGCTCAGTACCAGTTCGACTTCGGTCTGCGTCCGTCCGTGGCTTACCTGCA OmpK-36\_YMC2012/8/C631

1289 CGAAGTGGTTGCTCAGTACCAGTTCGACTTCGGTCTGCGTCCGTCCGTGGCTTACCTGCA OmpK-36\_YMC2010/8/B2027

1289 CGAAGTGGTTGCTCAGTACCAGTTCGACTTCGGTCTGCGTCCGTCCGTGGCTTACCTGCA OmpK-36\_YMC2011/11/B7578

1289 CGAAGTGGTTGCTCAGTACCAGTTCGACTTCGGTCTGCGTCCGTCCGTGGCTTACCTGCA OmpK-36\_YMC2013/7/B3993

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1337 GTCTAAAGGTAAGGATCTGGAGCGCGGCTACGGCGACCAGGACATCCTGAAATATGTTGA OmpK-36\_YMC2011/8/B10311

1340 GTCTAAAGGTAAGGATCTGGAGCGCGGCTACGGCGACCAGGACATCCTGAAATATGTTGA OmpK-36\_YMC2011/7/B774

1438 GTCTAAAGGTAAGGATCTGGAAG---GCTACGGCGACCAGGACATCCTGAAATATGTTGA OmpK-36\_YMC2012/8/C631

1406 GTCTAAAGGTAAGGATCTGGAAG---GCTACGGCGACCAGGACATCCTGAAATATGTTGA OmpK-36\_YMC2010/8/B2027

1406 GTCTAAAGGTAAGGATCTGGAAG---GCTACGGCGACTAGGACATCCTGAAATATGTTGA OmpK-36\_YMC2011/11/B7578

1406 GTCTAAAGGTAAGGATCTGGAAG---GCTACGGCGACCAGGACATCCTGAAATATGTTGA OmpK-36\_YMC2013/7/B3993

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1397 CGTTGGCGCGACCTACTACTTCAACAAAAACATGTCCACCTATGTTGACTACAAAATCAA OmpK-36\_YMC2011/7/B7207

1397 CGTTGGCGCGACCTACTACTTCAACAAAAACATGTCCACCTATGTTGACTACAAAATCAA OmpK-36\_YMC2011/8/B10311

1400 CGTTGGCGCGACCTACTACTTCAACAAAAACATGTCCACCTATGTTGACTACAAAATCAA OmpK-36\_YMC2011/7/B774

1438 CGTTGGCGCGACCTACTACTTCAACAAAAACATGTCCACCTATGTTGACTACAAAATCAA OmpK-36\_YMC2012/8/C631

1406 CGTTGGCGCGACCTACTACTTCAACAAAAACATGTCCACCTATGTTGACTACAAAATCAA OmpK-36\_YMC2010/8/B2027

1406 CGTTGGCGCGACCTACTACTTCAACAAAAACATGTCCACCTATGTTGACTACAAAATCAA OmpK-36\_YMC2011/11/B7578

1406 CGTTGGCGCGACCTACTACTTCAACAAAAACATGTCCACCTATGTTGACTACAAAATCAA OmpK-36\_YMC2013/7/B3993

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1457 CCTGCTGGACGACAACAGCTTCACCCGCAACGCCGGTATCTCTACCGACGACGTGGTTGC OmpK-36\_YMC2011/7/B7207

1457 CCTGCTGGACGACAACAGCTTCACCCGCAACGCCGGTATCTCTACCGACGACGTGGTTGC OmpK-36\_YMC2011/8/B10311

1460 CCTGCTGGACGACAACAGCTTCACCCGCAACGCCGGTATCTCTACCGACGACGTGGTTGC OmpK-36\_YMC2011/7/B774

1498 CCTGCTGGACGACAACAGCTTCACCCGCAACGCCGGTATCTCTACCGACGACGTGGTTGC OmpK-36\_YMC2012/8/C631

1466 CCTGCTGGACGACAACAGCTTCACCCGCAACGCCGGTATCTCTACCGACGACGTGGTTGC OmpK-36\_YMC2010/8/B2027

1466 CCTGCTGGACGACAATAGCTTCACCCACAACGCCGGTATCTCTACCGACGACGTGGTTGC OmpK-36\_YMC2011/11/B7578

1466 CCTGCTGGACGACAATAGCTTCACCCACAACGCCGGTATCTCTACCGACGACGTGGTTGC OmpK-36\_YMC2013/7/B3993

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1417 ACTGGGCCTGGTTTACCAGTTCTAA OmpK-36\_YMC2011/8/B10311

1520 ACTGGGCCTGGTTTACCAGTTCTAA OmpK-36\_YMC2011/7/B774

1558 ACTGGGCCTGGTTTACCAGTTCTAA OmpK-36\_YMC2012/8/C631

1526 ACTGGGCCTGGTTTACCAGTTCTAA OmpK-36\_YMC2010/8/B2027

1526 ACTGGGCCTGGTTTACCAGTTCTAA OmpK-36\_YMC2011/11/B7578

1526 ACTGGGCCTGGTTTACCAGTTCTAA OmpK-36\_YMC2013/7/B3993

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Figure S4: Amino acid alignment of SHV-11, SHV-12, SHV-187 and SHV-158 of Panel strains along with the reference sequences: Clustal 0 (1.2.3) multiple sequence alignment of SHV genes. SHV-12\_AJ920369, SHV-187\_LN515533, SHV-158\_JX121125 and SHV-11\_X98101 are the reference sequences. Polymorphism are highlighted in grey.

1 MRYIRLCIISLLATLPLAVHASPQPLEQIKQSESQLSGRVGMIEMDLASGRTLTAWRADE SHV-12\_AJ920369

1 MRYIRLCIISLLATLPLAVHASPQPLEQIKQSESQLSGRVGMIEMDLASGRTLTAWRADE SHV-12\_YMC2011/11/B7578

1 MRYIRLCIISLLATLPLAVHASPQPLEQIKQSESQLSGRVGMIEMDLASGRTLTAWRADE SHV-12\_YMC2013/7/B3993\_1

1 MRYIRLCIISLLATLPLAVHASPQPLEQIKQSESQLSGRVGMIEMDLASGRTLTAWRADE SHV-12\_YMC2013/7/B3993\_2

1 KRYIRLCIISLLATLPLAVHASPQPLEQIKLSESQLSGRVGMIEMDLASGRTLTAWRADE SHV-187\_LN515533

1 KRYIRLCIISLLATLPLAVHASPQPLEQIKLSESQLSGRVGMIEMDLASGRTLTAWRADE SHV-187\_YMC2011/7/B7207

1 MRYIRLCIISLLATLPLAVHASPQPLEQIKQSESQLSGRVGMIEMDLASGRTLAAWRADE SHV-158\_JX121125

1 MRYIRLCIISLLATLPLAVHASPQPLEQIKQSESQLSGRVGMIEMDLASGRTLAAWRADE SHV-158\_YMC2011/11/B7578

1 MRYIRLCIISLLATLPLAVHASPQPLEQIKQSESQLSGRVGMIEMDLASGRTLTAWRADE SHV-11\_X98101

1 MRYIRLCIISLLATLPLAVHASPQPLEQIKQSESQLSGRVGMIEMDLASGRTLTAWRADE SHV-11\_YMC2011/7/B774

1 MRYIRLCIISLLATLPLAVHASPQPLEQIKQSESQLSGRVGMIEMDLASGRTLTAWRADE SHV-11\_YMC2011/8/B10311

1 MRYIRLCIISLLATLPLAVHASPQPLEQIKQSESQLSGRVGMIEMDLASGRTLTAWRADE SHV-11\_YMC2010/8/B2027

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61 RFPMMSTFKVVLCGAVLARVDAGDEQLERKIHYRQQDLVDYSPVSEKHLADGMTVGELCA SHV-12\_YMC2011/11/B7578

61 RFPMMSTFKVVLCGAVLARVDAGDEQLERKIHYRQQDLVDYSPVSEKHLADGMTVGELCA SHV-12\_YMC2013/7/B3993\_1

61 RFPMMSTFKVVLCGAVLARVDAGDEQLERKIHYRQQDLVDYSPVSEKHLADGMTVGELCA SHV-12\_YMC2013/7/B3993\_2

61 RFPMMSTFKVVLCGAVLARVDAGDEQLERKIHYRQQDLVDYSPVSEKHLADGMTVGELCA SHV-187\_LN515533

61 RFPMMSTFKVVLCGAVLARVDAGDEQLERKIHYRQQDLVDYSPVSEKHLADGMTVGELCA SHV-187\_YMC2011/7/B7207

61 RFPMMSTFKVVLCGAVLARVDAGDEQLERKIHYRQQDLVDYSPVSEKHLADGMTVGELCA SHV-158\_JX121125

61 RFPMMSTFKVVLCGAVLARVDAGDEQLERKIHYRQQDLVDYSPVSEKHLADGMTVGELCA SHV-158\_YMC2011/11/B7578

61 RFPMMSTFKVVLCGAVLARVDAGDEQLERKIHYRQQDLVDYSPVSEKHLADGMTVGELCA SHV-11\_X98101

61 RFPMMSTFKVVLCGAVLARVDAGDEQLERKIHYRQQDLVDYSPVSEKHLADGMTVGELCA SHV-11\_YMC2011/7/B774

61 RFPMMSTFKVVLCGAVLARVDAGDEQLERKIHYRQQDLVDYSPVSEKHLADGMTVGELCA SHV-11\_YMC2011/8/B10311

61 RFPMMSTFKVVLCGAVLARVDAGDEQLERKIHYRQQDLVDYSPVSEKHLADGMTVGELCA SHV-11\_YMC2010/8/B2027

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121 AAITMSDNSAANLLLATVGGPAGLTAFLRQIGDNVTRLDRWETELNEALPGDARDTTTPA SHV-12\_YMC2013/7/B3993\_1

121 AAITMSDNSAANLLLATVGGPAGLTAFLRQIGDNVTRLDRWETELNEALPGDARDTTTPA SHV-12\_YMC2013/7/B3993\_2

121 AAITMSDNSAANLLLATVGGPAGLTAFLRQIGDNVTRLDRWETELNEALPGDARDTTTPA SHV-187\_LN515533

121 AAITMSDNSAANLLLATVGGPAGLTAFLRQIGDNVTRLDRWETELNEALPGDARDTTTPA SHV-187\_YMC2011/7/B7207

121 AAITMSDNSAANLLLATVGGPAGLTAFLRQIGDNVTRLDRWETELNEALPGDARDTTTPA SHV-158\_JX121125

121 AAITMSDNSAANLLLATVGGPAGLTAFLRQIGDNVTRLDRWETELNEALPGDARDTTTPA SHV-158\_YMC2011/11/B7578

121 AAITMSDNSAANLLLATVGGPAGLTAFLRQIGDNVTRLDRWETELNEALPGDARDTTTPA SHV-11\_X98101

121 AAITMSDNSAANLLLATVGGPAGLTAFLRQIGDNVTRLDRWETELNEALPGDARDTTTPA SHV-11\_YMC2011/7/B774

121 AAITMSDNSAANLLLATVGGPAGLTAFLRQIGDNVTRLDRWETELNEALPGDARDTTTPA SHV-11\_YMC2011/8/B10311

121 AAITMSDNSAANLLLATVGGPAGLTAFLRQIGDNVTRLDRWETELNEALPGDARDTTTPA SHV-11\_YMC2010/8/B2027

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181 SMAATLRKLLTSQRLSARSQRQLLQWMVDDRVAGPLIRSVLPAGWFIADKTGASKRGARG SHV-12\_YMC2011/11/B7578

181 SMAATLRKLLTSQRLSARSQRQLLQWMVDDRVAGPLIRSVLPAGWFIADKTGASKRGARG SHV-12\_YMC2013/7/B3993\_1

181 SMAATLRKLLTSQRLSARSQRQLLQWMVDDRVAGPLIRSVLPAGWFIADKTGASKRGARG SHV-12\_YMC2013/7/B3993\_2

181 SMAATLRKLLTSQRLSARSQRQLLQWMVDDRVAGPLIRSVLPAGWFIADKTGAGERGARG SHV-187\_LN515533

181 SMAATLRKLLTSQRLSARSQRQLLQWMVDDRVAGPLIRSVLPAGWFIADKTGAGERGARG SHV-187\_YMC2011/7/B7207

181 SMAATLRKLLTSQRLSARSQRQLLQWMVDDRVAGPLIRSVLPAGWFIADKTGAGERGARG SHV-158\_JX121125

181 SMAATLRKLLTSQRLSARSQRQLLQWMVDDRVAGPLIRSVLPAGWFIADKTGAGERGARG 158\_YMC2011/11/B7578

181 SMAATLRKLLTSQRLSARSQRQLLQWMVDDRVAGPLIRSVLPAGWFIADKTGAGERGARG SHV-11\_X98101

181 SMAATLRKLLTSQRLSARSQRQLLQWMVDDRVAGPLIRSVLPAGWFIADKTGAGERGARG SHV-11\_YMC2011/7/B774

181 SMAATLRKLLTSQRLSARSQRQLLQWMVDDRVAGPLIRSVLPAGWFIADKTGAGERGARG SHV-11\_YMC2011/8/B10311

181 SMAATLRKLLTSQRLSARSQRQLLQWMVDDRVAGPLIRSVLPAGWFIADKTGAGERGARG SHV-11\_YMC2010/8/B2027

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241 IVALLGPNNKAERIVVIYLRDTPASMAERNQQIAGIGAALIEHWQR SHV-11\_YMC2010/8/B2027

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