

# Supplement data S1. Full output of three pMLST tool variants displaying the F31/F36 situation (Fig. 1)

## Conda version

## Short-read sequence

### (B0009108\_Illumina.fasta)

pMLST profile: IncF RST

```
Sequence Type: [F31:A4:B1]
*****
Locus      Identity  Coverage  Alignment Length  Allele Length
Gaps      Allele
*****
FIA         100.0      100.0      384              384
0          FIA_4
FIB         100.0      100.0      373              373
0          FIB_1
FIC         -          -          -                -
-          No hit found
FII         100.0      100.0      157              157
0          FII_31!
FII         100.0      100.0      157              157
0          FII_36!
FIIK        -          -          -                -
-          No hit found
FIIS        -          -          -                -
-          No hit found
FIIV        -          -          -                -
-          No hit found
=====
```

Notes: ! alleles with multiple perfect hits found, multiple STs might be found  
! FII: Multiple perfect hits found

Extended Output:

```
# FIA_4
template: CCATGCTGGTTCTAGAGAAGGTGTTGTGACAAATTGCCCTTAACCCGTGTGACAAATTGCC
|||||
query:    CCATGCTGGTTCTAGAGAAGGTGTTGTGACAAATTGCCCTTAACCCGTGTGACAAATTGCC

template: CTCAGAAGAAGCTGTTTTTCGCAAAGTTATCCCTGCTTATTGACTCTTTTTATTAGT
|||||
query:    CTCAGAAGAAGCTGTTTTTCGCAAAGTTATCCCTGCTTATTGACTCTTTTTATTAGT

template: GTGACAATCTAAAAACTTGTACACCTTCACATGGATCTGTCATGGCGGAAACAGCGGTTA
|||||
query:    GTGACAATCTAAAAACTTGTACACCTTCACATGGATCTGTCATGGCGGAAACAGCGGTTA

template: TCAATCACAGAAACGTAAGAAATAGCCCGCGAATCGTCCAGTCAAACGACCTCACTGAGG
|||||
query:    TCAATCACAGAAACGTAAGAAATAGCCCGCGAATCGTCCAGTCAAACGACCTCACTGAGG

template: CGGCATATAGTCTCTCCCGGGATCAAAAACGTATGCTGTATCTGTTGTTGACCAAGATCA
|||||
query:    CGGCATATAGTCTCTCCCGGGATCAAAAACGTATGCTGTATCTGTTGTTGACCAAGATCA

template: GAAAATCTGATGGCACCTTACAGGAACATGACGGTATCTGCGAGATCCATGTTGCTAAAT
|||||
query:    GAAAATCTGATGGCACCTTACAGGAACATGACGGTATCTGCGAGATCCATGTTGCTAAAT

template: ATGCTGAAATATTTCGGATTGACCT
|||||
query:    ATGCTGAAATATTTCGGATTGACCT

# FII_31
template: CAAAAACCCCGATAACCTTCACCAGGTTTGGCGACTAAGAGAAGATTACCGGGGCCCACT
|||||
query:    CAAAAACCCCGATAACCTTCACCAGGTTTGGCGACTAAGAGAAGATTACCGGGGCCCACT

template: TAAACCGTATAGCCAACAATTACGCTATGCGGGGAGTATAGTTATATGCCCGGAAAAGTT
|||||
query:    TAAACCGTATAGCCAACAATTACGCTATGCGGGGAGTATAGTTATATGCCCGGAAAAGTT

template: CAAGACTTCTTTCTGTGCTCACTCCTTCTGCGCATTG
|||||
query:    CAAGACTTCTTTCTGTGCTCACTCCTTCTGCGCATTG

# FII_36
template: CAAAAACCCCGATAATCTTCACCAGGTTTGGCGACTAAGAGAAGATTACCGGGGCCCACT
|||||
query:    CAAAAACCCCGATAATCTTCACCAGGTTTGGCGACTAAGAGAAGATTACCGGGGCCCACT

template: TAAACCGTATAGCCAACAATTACGCTATGCGGGGAGTATAGTTATATGCCCGGAAAAGTT
|||||
query:    TAAACCGTATAGCCAACAATTACGCTATGCGGGGAGTATAGTTATATGCCCGGAAAAGTT

template: CAAGACTTCTTTCTGTGCTCACTCCTTCTGCGCATTG
|||||
query:    CAAGACTTCTTTCTGTGCTCACTCCTTCTGCGCATTG
```

```
# FIB_1
template: ATTCAGACATCAAAAAACTGTTTCGGCGAGGTGGATAAGTCTCCGGTGAGCTGGTGACAC
|||||
query:    ATTCAGACATCAAAAAACTGTTTCGGCGAGGTGGATAAGTCTCCGGTGAGCTGGTGACAC

template: TGACACCAAACAATAACAACACCGTACAACCTGTGGCGCTGATGCGTCTGGGCGTTTTTG
|||||
query:    TGACACCAAACAATAACAACACCGTACAACCTGTGGCGCTGATGCGTCTGGGCGTTTTTG

template: TACCGACCCCTTAAATCACTGAAGAACAGTAAAAAAATACACTGTCACGTACTGATGCCA
|||||
query:    TACCGACCCCTTAAATCACTGAAGAACAGTAAAAAAATACACTGTCACGTACTGATGCCA

template: CGGAAGAGCTGACACGCTCTTTCCTTGGCCCGTCTGAGGGATTTCGATAAGGTTGAGATCA
|||||
query:    CGGAAGAGCTGACACGCTCTTTCCTTGGCCCGTCTGAGGGATTTCGATAAGGTTGAGATCA

template: CCGGCCCCCGCCTGGATATGGATAATGATTTCAAGACCTGGGTGGGGATCATTCATTCCCT
|||||
query:    CCGGCCCCCGCCTGGATATGGATAATGATTTCAAGACCTGGGTGGGGATCATTCATTCCCT

template: TTGCCCCCATAAACGTGATTGGTGACAAAGTTGAAGTGCCTTTTGTGAGTTTGCAAAAC
|||||
query:    TTGCCCCCATAAACGTGATTGGTGACAAAGTTGAAGTGCCTTTTGTGAGTTTGCAAAAC

template: TGTGTGGTATACC
|||||
query:    TGTGTGGTATACC
```

## Conda version

## Long-read sequence

### (B0009108\_F31-F36\_A4\_B1\_minion.fasta)

pMLST profile: IncF RST

```
Sequence Type: [F36:A4:B58]
*****
Locus      Identity      Coverage      Alignment Length      Allele
Length     Gaps      Allele
*****
FIA         100.0         100.0         384                 384
0          FIA_4
FIB         100.0         92.22520107238606  344                 373
0          FIB_58?
FIC         -             -             -                 -
-          No hit found
FII         100.0         100.0         157                 157
0          FII_36!
FII         100.0         100.0         157                 157
0          FII_31!
FIIK        -             -             -                 -
-          No hit found
FIIS        -             -             -                 -
-          No hit found
FIIY        -             -             -                 -
-          No hit found
*****
```

Notes: !? alleles with multiple perfect hits found, multiple STs might be found  
? FIB: Uncertain hit, ST can not be trusted.  
! FII: Multiple perfect hits found

Extended Output:

```
# FIA_4
template: CCATGCTGGTTCTAGAGAAGGTGTTGTGACAAATTGCCCTTAACCGTGTGACAAATTGCC
|||||
query:    CCATGCTGGTTCTAGAGAAGGTGTTGTGACAAATTGCCCTTAACCGTGTGACAAATTGCC

template: CTCAGAAGAAGCTGTTTTTCGCAAAGTTATCCCTGCTTATTGACTCTTTTTATTATTAGT
|||||
query:    CTCAGAAGAAGCTGTTTTTCGCAAAGTTATCCCTGCTTATTGACTCTTTTTATTATTAGT

template: GTGACAATCTAAAAACTTGTACACTTCACATGGATCTGTCATGGCGGAAACAGCGGTTA
|||||
query:    GTGACAATCTAAAAACTTGTACACTTCACATGGATCTGTCATGGCGGAAACAGCGGTTA

template: TCAATCACAAGAAACGTAAAAATAGCCCGCGAATCGTCCAGTCAAACGACCTCACTGAGG
|||||
query:    TCAATCACAAGAAACGTAAAAATAGCCCGCGAATCGTCCAGTCAAACGACCTCACTGAGG

template: CGGCATATAGTCTCTCCCGGGATCAAAAACGTATGCTGTATCTGTTGTTGACCAGATCA
|||||
query:    CGGCATATAGTCTCTCCCGGGATCAAAAACGTATGCTGTATCTGTTGTTGACCAGATCA

template: GAAAATCTGATGGCACCCCTACAGGAACATGACGGTATCTGCGAGATCCATGTTGCTAAAT
|||||
query:    GAAAATCTGATGGCACCCCTACAGGAACATGACGGTATCTGCGAGATCCATGTTGCTAAAT

template: ATGCTGAAATATTTCGGATTGACCT
|||||
query:    ATGCTGAAATATTTCGGATTGACCT

# FIB_58
template: ATTCAGACATAAAAAAACTGTTCCGCGAGGTGGATAAGTCCTCCGGTGAGCTGGTGACAC
|||||
query:    -----GTGGATAAGTCCTCCGGTGAGCTGGTGACAC

template: TGACACCAACAATAACAACACCGTACAACCTGTGGCGCTGATGCGTCTGGGCGTTTTTG
|||||
query:    TGACACCAACAATAACAACACCGTACAACCTGTGGCGCTGATGCGTCTGGGCGTTTTTG

template: TACCGACCCCTTAAATCACTGAAGAACAGTAAAAAAATACACTGTCACGTACTGATGCCA
|||||
query:    TACCGACCCCTTAAATCACTGAAGAACAGTAAAAAAATACACTGTCACGTACTGATGCCA

template: CGGAAGAGCTGACACGTCCTTCCCTGGCCCGTGTGAGGGATTGATAAGGTTGAGATCA
|||||
query:    CGGAAGAGCTGACACGTCCTTCCCTGGCCCGTGTGAGGGATTGATAAGGTTGAGATCA

template: CCGGCCCCCGCCTGGATATGGATAATGATTTCAAGACCTGGGTGGGGATCATTATTCCCT
|||||
query:    CCGGCCCCCGCCTGGATATGGATAATGATTTCAAGACCTGGGTGGGGATCATTATTCCCT

template: TTGCCCCCATAACGTGATTGTTGACAAAGTTGAACTGCCTTTTGTGAGTTTGCAAAAC
|||||
query:    TTGCCCCCATAACGTGATTGTTGACAAAGTTGAACTGCCTTTTGTGAGTTTGCAAAAC

template: TGTGTGGTATACC
|||||
query:    TGTGTGGTATACC
```

```
# FII_36
template: CAAAAACCCCGATAATCTTCACCAGGTTTGGCGACTAAGAGAAGATTACCGGGGCCCACT
|||||
query:    CAAAAACCCCGATAATCTTCACCAGGTTTGGCGACTAAGAGAAGATTACCGGGGCCCACT

template: TAAACCGTATAGCCAACAATTGAGCTATGCGGGGAGTATAGTTATATGCCCGGAAAAAGTT
|||||
query:    TAAACCGTATAGCCAACAATTGAGCTATGCGGGGAGTATAGTTATATGCCCGGAAAAAGTT

template: CAAGACTTCTTTCTGTGCTCACTCCTTCTGCGCATTG
|||||
query:    CAAGACTTCTTTCTGTGCTCACTCCTTCTGCGCATTG

# FII_31
template: CAAAAACCCCGATAACCTTCACCAGGTTTGGCGACTAAGAGAAGATTACCGGGGCCCACT
|||||
query:    CAAAAACCCCGATAACCTTCACCAGGTTTGGCGACTAAGAGAAGATTACCGGGGCCCACT

template: TAAACCGTATAGCCAACAATTGAGCTATGCGGGGAGTATAGTTATATGCCCGGAAAAAGTT
|||||
query:    TAAACCGTATAGCCAACAATTGAGCTATGCGGGGAGTATAGTTATATGCCCGGAAAAAGTT

template: CAAGACTTCTTTCTGTGCTCACTCCTTCTGCGCATTG
|||||
query:    CAAGACTTCTTTCTGTGCTCACTCCTTCTGCGCATTG
```

## Docker version

## Short-read sequence

### (B0009108\_illumina.fasta)

pMLST profile: IncF RST

```
Sequence Type: [F31:A4:B1]
*****
Locus      Identity  Coverage  Alignment Length  Allele Length
Gaps      Allele
*****
FIA         100.0      100.0      384                384
0          FIA_4
FIB         100.0      100.0      373                373
0          FIB_1
FIC         -          -          -                  -
-          No hit found
FII         100.0      100.0      157                157
0          FII_31!
FII         100.0      100.0      157                157
0          FII_36!
FIIK        -          -          -                  -
-          No hit found
FIIS        -          -          -                  -
-          No hit found
FIIY        -          -          -                  -
-          No hit found
*****
```

Notes: ! alleles with multiple perfect hits found, multiple STs might be found  
! FII: Multiple perfect hits found

Extended Output:

```
# FII_31
template: CAAAAACCCCGATAACCTTCACCAGGTTTGGCGACTAAGAGAAGATTACCGGGGCCCACT
query: CAAAAACCCCGATAACCTTCACCAGGTTTGGCGACTAAGAGAAGATTACCGGGGCCCACT

template: TAAACCGTATAGCCAACAATTTCAGCTATGCGGGGAGTATAGTTATATGCCCGGAAAAAGTT
query: TAAACCGTATAGCCAACAATTTCAGCTATGCGGGGAGTATAGTTATATGCCCGGAAAAAGTT

template: CAAGACTTCTTTCTGTGCTCACTCCTTCTGCGCATTG
query: CAAGACTTCTTTCTGTGCTCACTCCTTCTGCGCATTG

# FII_36
template: CAAAAACCCCGATAATCTTCACCAGGTTTGGCGACTAAGAGAAGATTACCGGGGCCCACT
query: CAAAAACCCCGATAATCTTCACCAGGTTTGGCGACTAAGAGAAGATTACCGGGGCCCACT

template: TAAACCGTATAGCCAACAATTTCAGCTATGCGGGGAGTATAGTTATATGCCCGGAAAAAGTT
query: TAAACCGTATAGCCAACAATTTCAGCTATGCGGGGAGTATAGTTATATGCCCGGAAAAAGTT

template: CAAGACTTCTTTCTGTGCTCACTCCTTCTGCGCATTG
query: CAAGACTTCTTTCTGTGCTCACTCCTTCTGCGCATTG

# FIB_1
template: ATTCAGACATCAAAAAACTGTTTCGGCGAGGTGGATAAGTCCTCCGGTGAGCTGGTGACAC
query: ATTCAGACATCAAAAAACTGTTTCGGCGAGGTGGATAAGTCCTCCGGTGAGCTGGTGACAC

template: TGACACCAAAACAATAACAACACCGTACAACCTGTGGCGCTGATGCGTCTGGGCGTTTTTG
query: TGACACCAAAACAATAACAACACCGTACAACCTGTGGCGCTGATGCGTCTGGGCGTTTTTG

template: TACCGACCCCTAAATCACTGAAGAACAGTAAAAAAAATACACTGTCACGTACTIONGATGCCA
query: TACCGACCCCTAAATCACTGAAGAACAGTAAAAAAAATACACTGTCACGTACTIONGATGCCA

template: CGGAAGAGCTGACACGCTTTCCCTGGCCCGTGTGAGGATTGCGATAAGGTTGAGATCA
query: CGGAAGAGCTGACACGCTTTCCCTGGCCCGTGTGAGGATTGCGATAAGGTTGAGATCA

template: CCGGCCCCCGCCTGGATATGGATAATGATTTCAAGACCTGGGTGGGGATCATTATTCCT
query: CCGGCCCCCGCCTGGATATGGATAATGATTTCAAGACCTGGGTGGGGATCATTATTCCT

template: TTGCCCGCCATAACGCTGATTGGTGACAAAGTTGAACTGCCTTTTGTGAGTTTGCAAAAC
query: TTGCCCGCCATAACGCTGATTGGTGACAAAGTTGAACTGCCTTTTGTGAGTTTGCAAAAC

template: TGTGTGGTATACC
query: TGTGTGGTATACC
```

```
# FIA_4
template: CCATGCTGGTTCTAGAGAAGGTGTTGTGACAAATTGCCCTTAACCCCTGTGACAAATTGCC
query: CCATGCTGGTTCTAGAGAAGGTGTTGTGACAAATTGCCCTTAACCCCTGTGACAAATTGCC

template: CTCAGAAGAAGCTGTTTTTCGCAAAGTTATCCCTGCTTATTGACTCTTTTTTATTAGT
query: CTCAGAAGAAGCTGTTTTTCGCAAAGTTATCCCTGCTTATTGACTCTTTTTTATTAGT

template: GTGACAATCTAAAAACTTGTACACTTCACATGGATCTGTCATGGCGGAAACAGCGGTTA
query: GTGACAATCTAAAAACTTGTACACTTCACATGGATCTGTCATGGCGGAAACAGCGGTTA

template: TCAATCACAAGAAACGTAAGAAATAGCCCGCGAATCGTCCAGTCAAACGACCTCACTGAGG
query: TCAATCACAAGAAACGTAAGAAATAGCCCGCGAATCGTCCAGTCAAACGACCTCACTGAGG

template: CGGCATATAGTCTCTCCCGGGATCAAAAACGATGCTGTATCTGTTCGTTGACCAGATCA
query: CGGCATATAGTCTCTCCCGGGATCAAAAACGATGCTGTATCTGTTCGTTGACCAGATCA

template: GAAAACTGATGGCACCCCTACAGGAACATGACGGTATCTGCGAGATCCATGTTGCTAAAT
query: GAAAACTGATGGCACCCCTACAGGAACATGACGGTATCTGCGAGATCCATGTTGCTAAAT

template: ATGCTGAAATATTCGGATTGACCT
query: ATGCTGAAATATTCGGATTGACCT
```

## Long-read sequence

pMLST profile: IncF RST

Notes: ?! alleles with multiple perfect hits found, multiple STs might be found  
! FII: Multiple perfect hits found  
? FIB: Uncertain hit, ST can not be trusted.

Extended Output:

```
# FII_36
template: CAAAAACCCGATAATCTTCACAGGTTTGGCGACTAAGAGAAGATTACCGGGGCCACT
          CAAAAACCCGATAATCTTCACAGGTTTGGCGACTAAGAGAAGATTACCGGGGCCACT
query:    CAAAAACCCGATAATCTTCACAGGTTTGGCGACTAAGAGAAGATTACCGGGGCCACT
```

```
template: TAAACCGTATAGCCAACAATTCAGCTATGCGGGGAGTATAGTTATATGCCCGGAAAAGTT
          |||
query:    TAAACCGTATAGCCAACAATTCAGCTATGCGGGGAGTATAGTTATATGCCCGGAAAAGTT
```

```
template: CAAGACTTCTTTCTGTGCTCACTCCTTCTGCGCATTG
          |||||||||||||||||||||||||||||||||||
query:    CAAGACTTCTTTCTGTGCTCACTCCTTCTGCGCATTG
```

```
# FII_31
template: CAAAAACCCGATAACCTTCACCAAGTTTGGCGACTAAGAGAAGATTACCGGGGGCCACT
          CAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
query:     CAAAAACCCGATAACCTTCACCAAGTTTGGCGACTAAGAGAAGATTACCGGGGGCCACT
```

```
template: TAAACCGTATAGCCAACAATTACAGCTATGCGGGGAGTATAGTTATATGCCCGGAAAAGTT
          |||
query:    TAAACCGTATAGCCAACAATTACAGCTATGCGGGGAGTATAGTTATATGCCCGGAAAAGTT
```

```
template: CAAGACTTCTTTCTGTGCTCACTCCTTCTGCGCATTG
          |||
query:     CAAGACTTCTTTCTGTGCTCACTCCTTCTGCGCATTG
```

```
# FIB_1
template: ATTCAGACATCAAAAACTGTTCCGGCAGAGTGGATAAGTCCTCCGGTGAGCTGGTGACAC
query: -----GTGGATAAGTCCTCCGGTGAGCTGGTGACAC
```

```
template: TGACACCAAACAATAACAACACCGTACAACCTGTGGCGCTGATGCGTCTGGGCGTTTTTG
          |||
query:    TGACACCAAACAATAACAACACCGTACAACCTGTGGCGCTGATGCGTCTGGGCGTTTTTG
```

```
template: TACCAGACCCTTAAATCACTGAAGAACAGTAAAAAAAATACACTGTCACGTACTGATGCCA
          |||
query:     TACCAGACCCTTAAATCACTGAAGAACAGTAAAAAAAATACACTGTCACGTACTGATGCCA
```

```
template: CGGAAGAGCTGACACGTCTTTCCCTGGCCCGTGCTGAGGGATTTCGATAAGGTTGAGATCA
          |||
query:     CGGAAGAGCTGACACGTCTTTCCCTGGCCCGTGCTGAGGGATTTCGATAAGGTTGAGATCA
```

```
template: CCGGCCCGCCTGGATATGGATAATGATTTCAGACCTGGGTGGGGATCATTCAATCCT
          |||
query:    CCGGCCCGCCTGGATATGGATAATGATTTCAGACCTGGGTGGGGATCATTCAATCCT
```

```
template: TTGCCCGCCATAACGTGATTGGTGACAAAGTTGAACTGCCTTTTGTGTGAGTTTGCAAAAC
          |||
query:    TTGCCCGCCATAACGTGATTGGTGACAAAGTTGAACTGCCTTTTGTGTGAGTTTGCAAAAC
```

```
template: TGTGTGGTATACC
          |||||
query:    TGTGTGGTATACC
```

```
# FIA_4
template: CCATGCTGGTTC TAGAGAAGGTGTTGTGACAAATTGCCCTTAACCGTGTGACAAATTGCC
          |||
query:    CCATGCTGGTTC TAGAGAAGGTGTTGTGACAAATTGCCCTTAACCGTGTGACAAATTGCC
```

```
template: CTCAGAAGAAGCTGTTTTTCGCAAAGTTATCCCTGCTTATTGACTCTTTTTTATTAGT
          |||||
query:    CTCAGAAGAAGCTGTTTTTCGCAAAGTTATCCCTGCTTATTGACTCTTTTTTATTAGT
```

```

template: GTGACAATCTAAAAACTTGTCACTTCACATGGATCTGTCATGGCGGAAACAGCGGTTA
          |||
query:     GTGACAATCTAAAAACTTGTCACTTCACATGGATCTGTCATGGCGGAAACAGCGGTTA

```

```
template: TCAATCACAAGAAACGTAAAAATAGCCCGCGAATCGTCCAGTCAAACGACCTCACTGAGG
          |||
query:    TCAATCACAAGAAACGTAAAAATAGCCCGCGAATCGTCCAGTCAAACGACCTCACTGAGG
```

```
template: CGGCATATAGTCTCTCCGGGATCAAAACGTATGCTGTATCTGTTGTTGACCAGATCA
          |||||
query:     CGGCATATAGTCTCTCCGGGATCAAAACGTATGCTGTATCTGTTGTTGACCAGATCA
```

```
template: GAAATCTGATGGCACCCCTACAGGAACATGACGGTATCTGCGAGATCCATGTTGCTAAAT
          |||
query:    GAAATCTGATGGCACCCCTACAGGAACATGACGGTATCTGCGAGATCCATGTTGCTAAAT
```

```

template: ATGCTGAAATATTCGGATTGACCT
           |||
query:     ATGCTGAAATATTCGGATTGACCT

```

## CGE web version

### Short-read sequence

(B0009108\_Illumina.fasta)

#### 1st run

pMLST profile: *IncF RST*

Sequence Type: *[F31:A4:B1]*

| Locus | Identity          | Coverage | Alignment Length | Allele Length | Gaps | Allele       |
|-------|-------------------|----------|------------------|---------------|------|--------------|
| FIA   | 100.0             | 100.0    | 384              | 384           | 0    | FIA_4        |
| FIB   | 100.0             | 100.0    | 373              | 373           | 0    | FIB_1        |
| FIC   | 98.61111111111111 | 72.0     | 144              | 200           | 0    | FIC_37*      |
| FII   | 100.0             | 100.0    | 157              | 157           | 0    | FII_31!      |
| FII   | 100.0             | 100.0    | 157              | 157           | 0    | FII_36!      |
| FIIK  |                   |          |                  |               |      | No hit found |
| FIIS  |                   |          |                  |               |      | No hit found |
| FIY   |                   |          |                  |               |      | No hit found |

Notes: \*?! alleles with multiple perfect hits found, multiple STs might be found

?\* FIC: *Imperfect hit, ST can not be trusted!*

! FII: *Multiple perfect hits found*

#### 2nd run

pMLST profile: *IncF RST*

Sequence Type: *[F36:A4:B1]*

| Locus | Identity          | Coverage | Alignment Length | Allele Length | Gaps | Allele       |
|-------|-------------------|----------|------------------|---------------|------|--------------|
| FIA   | 100.0             | 100.0    | 384              | 384           | 0    | FIA_4        |
| FIB   | 100.0             | 100.0    | 373              | 373           | 0    | FIB_1        |
| FIC   | 98.61111111111111 | 72.0     | 144              | 200           | 0    | FIC_37*      |
| FII   | 100.0             | 100.0    | 157              | 157           | 0    | FII_36!      |
| FII   | 100.0             | 100.0    | 157              | 157           | 0    | FII_31!      |
| FIIK  |                   |          |                  |               |      | No hit found |
| FIIS  |                   |          |                  |               |      | No hit found |
| FIY   |                   |          |                  |               |      | No hit found |

Notes: \*? alleles with less than 100% identity and 100% coverages found

! FII: *Multiple perfect hits found*

?\* FIC: *Imperfect hit, ST can not be trusted!*

## CGE web version

### Long-read sequence

(B0009108\_F31-F36\_A4\_B1\_minion.fasta)

pMLST profile: *IncF RST*

Sequence Type: *[F36:A4:B58]*

| Locus | Identity          | Coverage          | Alignment Length | Allele Length | Gaps | Allele       |
|-------|-------------------|-------------------|------------------|---------------|------|--------------|
| FIA   | 100.0             | 100.0             | 384              | 384           | 0    | FIA_4        |
| FIB   | 100.0             | 92.22520107238606 | 344              | 373           | 0    | FIB_58?      |
| FIC   | 98.61111111111111 | 72.0              | 144              | 200           | 0    | FIC_3?*      |
| FII   | 100.0             | 100.0             | 157              | 157           | 0    | FII_36!      |
| FII   | 100.0             | 100.0             | 157              | 157           | 0    | FII_31!      |
| FIIK  |                   |                   |                  |               |      | No hit found |
| FIIS  |                   |                   |                  |               |      | No hit found |
| FIIY  |                   |                   |                  |               |      | No hit found |

Notes: !?\* alleles with multiple perfect hits found, multiple STs might be found

? **FIB:** *Uncertain hit, ST can not be trusted.*

?\* **FIC:** *Imperfect hit, ST can not be trusted!*

! **FII:** *Multiple perfect hits found*