

S1

SeqSero

O antigen prediction: O-8

H1 antigen prediction(fliC): r

H2 antigen prediction(fljB): 1,5

Predicted antigenic profile: 8:r:1,5

Predicted serotype(s): Hindmarsh or Bovismorbificans*

*The predicted serotypes share the same general formula: 8:r:1,5

The serotype(s) is/are the only serotype(s) with the indicated antigenic profile currently recognized in the Kauffmann White Scheme. New serotypes can emerge and the possibility exists that this antigenic profile may emerge in a different subspecies. Identification of strains to the subspecies level should accompany serotype determination; the same antigenic profile in different subspecies is considered different serotypes.

SeqSero2

O antigen prediction: -

H1 antigen prediction(fliC): r

H2 antigen prediction(fljB): 1,5

Predicted subspecies: I

Predicted antigenic profile: -:r:1,5

Predicted serotype: I -:r:1,5

Note: O antigen was not detected. This result may be due to a rough strain that has deleted the rfb region. For raw reads input, the k-mer workflow is sometimes more sensitive than the microassembly workflow in detecting O antigen. Caution should be used with this approach because the k-mer result may be due to low levels of contamination.

S2

SeqSero

O antigen prediction: O-50

H1 antigen prediction(fliC): r

H2 antigen prediction(fljB): 1,5

Predicted antigenic profile: 50:r:1,5

Predicted serotype(s): N/A (The predicted antigenic profile does not exist in the White-Kauffmann-Le Minor scheme)*

*Raw reads, in general, work better than genome assemblies. Proper de novo assembly of serotype determinants using short reads is sometimes challenging.

SeqSero2

O antigen prediction: 8

H1 antigen prediction(fliC): r

H2 antigen prediction(fljB): 1,5

Predicted subspecies: I

Predicted antigenic profile: 8:r:1,5

Predicted serotype: Bovismorbificans

Note:

S3

SeqSero

O antigen prediction: O-?

H1 antigen prediction(fliC): -

H2 antigen prediction(fljB): -

Predicted antigenic profile: ?:-:-

Predicted serotype(s): N/A (The predicted antigenic profile does not exist in the White-Kauffmann-Le Minor scheme)

SeqSero2

O antigen prediction: -

H1 antigen prediction(fliC): r

H2 antigen prediction(fljB): 1,5

Predicted subspecies: I

Predicted antigenic profile: -:r:1,5

Predicted serotype: I -:r:1,5

Note: O antigen was not detected. This result may be due to a rough strain that has deleted the rfb region. For raw reads input, the k-mer workflow is sometimes more sensitive than the microassembly workflow in detecting O antigen. Caution should be used with this approach because the k-mer result may be due to low levels of contamination.

S6

SeqSero

O antigen prediction: O-?

H1 antigen prediction(fliC): -

H2 antigen prediction(fljB): -

Predicted antigenic profile: ?:-:-

Predicted serotype(s): N/A (The predicted antigenic profile does not exist in the White-Kauffmann-Le Minor scheme)

SeqSero2

O antigen prediction: -

H1 antigen prediction(fliC): r

H2 antigen prediction(fljB): 1,5

Predicted subspecies: I

Predicted antigenic profile: -:r:1,5

Predicted serotype: I -:r:1,5

Note: O antigen was not detected. This result may be due to a rough strain that has deleted the rfb region. For raw reads input, the k-mer workflow is sometimes more sensitive than the

microassembly workflow in detecting O antigen. Caution should be used with this approach because the k-mer result may be due to low levels of contamination.