



EURL-Salmonella Proficiency Test Typing 2024

Result form Cluster Analysis

LABORATORY INFORMATION

Laboratory code PT 2024 *	<input type="text"/>
Name contact person (Cluster Analysis part) *	<input type="text"/>
E-mail address contact person (Cluster Analysis part) *	<input type="text"/>
Optional second E-mail address (Cluster Analysis part)	<input type="text"/>
Name Institute/laboratory (Cluster Analysis part) *	<input type="text"/>
City (Cluster Analysis part) *	<input type="text"/>
Country *	Country: <input type="text"/>

GENERAL

Did you serotype the 'wet' strains? *

No
 Yes

Serotyping was done by:

Classical serology
 Molecular method(s), please specify the tool(s) used:

Please report the serovar name without indicating any kind of "S." or "Salmonella", to facilitate the overall evaluation of all participants' results.

Strain 24SCA01 serovar name:	<input type="text"/>
Strain 24SCA02 serovar name:	<input type="text"/>
Strain 24SCA03 serovar name:	<input type="text"/>
Strain 24SCA04 serovar name:	<input type="text"/>
Strain 24SCA05 serovar name:	<input type="text"/>
Strain 24SCA06 serovar name:	<input type="text"/>

Did you serotype the 'dry' strains? *

No
 Yes

Please report the serovar name without indicating any kind of "S." or "Salmonella", to facilitate the overall evaluation of all participants' results.

Please specify the tool(s) used:	<input type="text"/>
Strain 24SCA11 serovar name:	<input type="text"/>
Strain 24SCA12 serovar name:	<input type="text"/>
Strain 24SCA13 serovar name:	<input type="text"/>

Strain 24SCA14 serovar name:

Strain 24SCA15 serovar name:


Strain 24SCA16 serovar name:

REPORTING NGS RESULTS

-> **Transfer the raw reads** (compressed fastq-files) by uploading the files to the secure RIVM ftp server.

Please contact wilma.jacobs@rivm.nl by email if you need further help on the use of the ftp server (details also given by email in week 45) or on other means of transferring the data.

Be sure to name your files including your laboratory code and strain code in the name, preferably like: 24SCA01Lab01_R1.fastq, 24SCA01Lab01_R2.fastq, etc.

Date of transferring the WGS fastq files: *  dd/mm/yyyy

Do you agree that your raw data files (fastq) from the PT Typing 2024, anonymously re-coded, may also be used for additional research purposes or training?
*

Yes

No

Other:

Did you check your md5sum values for all 14 compressed fastq files that you downloaded from the secure RIVM ftp server with the values in the file "ALLmd5" of PT2024?
*


Yes

No

Other:

-> **Transfer** (optionally, but recommended) **the Md5 checksums**

1): concerning the downloaded files on strains 24SCA11 - 24SCA16 plus 24SCA-REF
2): concerning your uploaded files on strains 24SCA01 - 24SCA06
by uploading the data, preferably in .txt or .csv format, to the secure RIVM ftp server.

Date of transferring Md5 checksums:  dd/mm/yyyy

-> **Transfer the distance matrix** by uploading the file

(preferably in .xls or .csv format) to the secure RIVM ftp server.

Be sure to name the file including your laboratory code, preferably like: Lab01_Distance_Matrix.xls

Date of transferring the distance matrix: *  dd/mm/yyyy

BACKGROUND INFORMATION METHODS/QC

DNA extraction was performed: * In-house

Outsourced

Library preparation was performed: *

In-house

Outsourced

Sequencing was performed: *

In-house

Outsourced

WGS platform used: *

Illumina HiSeq

Illumina MiSeq

Illumina NextSeq

Illumina NovaSeq

Ion Torrent PGM

Ion Proton

Other:

Please list (up to a maximum of 10) your main criteria that were used to evaluate the quality of the sequence data. If applicable, also include the tool(s) used and the threshold per criterium.

Criterion 1: 

Criterion 1, specification of "Other":

Tool(s) used for criterium 1:

Threshold used for criterium 1:

Criterion 2:



Criterion 2, specification of "Other":

Tool(s) used for criterium 2:

Threshold used for criterium 2:

Criterium 3:

Criterium 3, specification of "Other":

Tool(s) used for criterium 3:

Threshold used for criterium 3:

Criterium 4:

Criterium 4, specification of "Other":

Tool(s) used for criterium 4:

Threshold used for criterium 4:

Criterium 5:

Criterium 5, specification of "Other":

Tool(s) used for criterium 5:

Threshold used for criterium 5:

Criterium 6:

Criterium 6, specification of "Other":

Tool(s) used for criterium 6:

Threshold used for criterium 6:

Criterium 7:

Tool(s) used for criterium 7:

Threshold used for criterium 7:

Criterium 8:

Tool(s) used for criterium 8:

Threshold used for criterium 8:

Criterium 9:

Tool(s) used for criterium 9:

Threshold used for criterium 9:

Criterium 10:

Tool(s) used for criterium 10:

Threshold used for criterium 10:

Please select the analysis used for the NGS data *

cgMLST-based
 wgMLST-based
 SNP-based - assembly-based
 SNP-based - reference-based
 Other:

If you would like to add results performed with a second or even third analysis on the NGS data, please contact wilma.jacobs@rivm.nl by email to receive a second (and third) Lab code for separate result submissions.

Please select the tool(s) used for analysis:

BioNumerics
 Enterobase
 Ridom SeqSphere
 Other:

Which method did you use for cluster analysis? *

Maximum likelihood (ML)
 Minimum Spanning Tree (MST)
 Neighbor joining (NJ)

Bayesian

Other:

Cluster cut-off used in your SNP-based analysis:

CLUSTER ANALYSIS RESULTS PER STRAIN

Please report **per strain** if:

1): [yes or no] the data passed your Quality Control (QC);

2): [yes or no] a clustering match was found with the Reference outbreak strain in the EURL-*Salmonella* PT Typing 2024: 24SCA-REF_R1.fq.gz & 24SCA-REF_R2.fq.gz (*Salmonella* Infantis).

In the PT Typing 2024 setting, the cgMLST-based cluster definition is set at maximum 5 allelic differences from the reference sequence.

Be sure to exclude strains from the cluster analysis/distance matrix if the data did not pass your QC.

Strain 24SCA01

- Data passed Quality Control: *

Yes No

Reason(s) for not passing the QC: *

Strain 24SCA01

- Cluster with the REF strain: *

Yes No
 Not applicable (QC not passed)

Strain 24SCA02

- Data passed Quality Control: *

Yes No

Strain 24SCA02

- Cluster with the REF strain: *

Yes No
 Not applicable (QC not passed)

Strain 24SCA03

- Data passed Quality Control: *

Yes No

Strain 24SCA03

- Cluster with the REF strain: *

Yes No
 Not applicable (QC not passed)

Strain 24SCA04

- Data passed Quality Control: *

Yes No

Strain 24SCA04

- Cluster with the REF strain: *

Yes No
 Not applicable (QC not passed)

Strain 24SCA05

- Data passed Quality Control: *

Yes No

Strain 24SCA05

- Cluster with the REF strain: *

Yes No
 Not applicable (QC not passed)

Strain 24SCA06

- Data passed Quality Control: *

Yes No

Strain 24SCA06

- Cluster with the REF strain: *

Yes No
 Not applicable (QC not passed)

Strain 24SCA11

- Data passed Quality Control: *

Yes No

Strain 24SCA11

- Cluster with the REF strain: *

Yes No
 Not applicable (QC not passed)

Strain 24SCA12

- Data passed Quality Control: *

Yes No

Strain 24SCA12

- Cluster with the REF strain: *

Yes No
 Not applicable (QC not passed)

Strain 24SCA13

- Data passed Quality Control: *

Yes No

Strain 24SCA13

- Cluster with the REF strain: *

Yes No
 Not applicable (QC not passed)

Strain 24SCA14

- Data passed Quality Control: *

Yes No

Strain 24SCA14

- Cluster with the REF strain: *

- Yes No
 Not applicable (QC not passed)

Strain 24SCA15

- Data passed Quality Control: *

- Yes No

Strain 24SCA15

- Cluster with the REF strain: *

- Yes No
 Not applicable (QC not passed)

Strain 24SCA16

- Data passed Quality Control: *

- Yes No

Strain 24SCA16

- Cluster with the REF strain: *

- Yes No
 Not applicable (QC not passed)

Optionally, report any further cluster(s):
(apart from the Reference)

Optionally, did your NGS analysis include
identification of AMR markers?

- yes
 no

Tool(s) used for identification of AMR
markers:

AMR markers identified for strain 24SCA01:

AMR markers identified for strain 24SCA02:

AMR markers identified for strain 24SCA03:

AMR markers identified for strain 24SCA04:

AMR markers identified for strain 24SCA05:

AMR markers identified for strain 24SCA06:

AMR markers identified for strain 24SCA11:

AMR markers identified for strain 24SCA12:

AMR markers identified for strain 24SCA13:

AMR markers identified for strain 24SCA14:

AMR markers identified for strain 24SCA15:

AMR markers identified for strain 24SCA16:

FINALLY

Any comments:

The EURL-*Salmonella* handles your personal data with the utmost care.
Personal data is protected under the General Data Protection Regulation (GDPR).
Your data will be encrypted and treated anonymously.
Original data is only accessible for EURL-*Salmonella* staff involved in this project.

* = Input is required