




Preview of the on-line Result form Cluster Analysis EURL-*Salmonella* Proficiency Test Typing 2022


EURL-*Salmonella* Proficiency Test Typing 2022
Result form Cluster Analysis

LABORATORY INFORMATION

Laboratory code PT 2022	<input type="text"/>
Name contact person (Cluster Analysis part)	<input type="text"/>
E-mail address contact person (Cluster Analysis part)	<input type="text"/>
Name laboratory or institute (Cluster Analysis part)	<input type="text"/>
Country	Country: <input type="text"/>

GENERAL

Did you serotype the 'wet' strains?	<input type="radio"/> No <input type="radio"/> Yes
Serotyping was done by:	<input type="checkbox"/> Classical serology <input type="checkbox"/> Molecular method(s), please specify the tool(s) used: <input type="text"/>
Strain 22SCA01 serovar name:	<input type="text"/>
Strain 22SCA02 serovar name:	<input type="text"/>
Strain 22SCA03 serovar name:	<input type="text"/>
Strain 22SCA04 serovar name:	<input type="text"/>
Strain 22SCA05 serovar name:	<input type="text"/>
Strain 22SCA06 serovar name:	<input type="text"/>
Did you serotype the 'dry' strains?	<input type="radio"/> No <input type="radio"/> Yes
Please specify the tool(s) used:	<input type="text"/>
Strain 22SCA11 serovar name:	<input type="text"/>
Strain 22SCA12 serovar name:	<input type="text"/>
Strain 22SCA13 serovar name:	<input type="text"/>
Strain 22SCA14 serovar name:	<input type="text"/>
Strain 22SCA15 serovar name:	<input type="text"/>
Strain 22SCA16 serovar name:	<input type="text"/>



REPORTING MLVA RESULTS

Do you want to submit MLVA results? Yes
 No

Please list the allele profile per strain, using the format SENTR7-SENTR5-SENTR6-SENTR4-SE-3
Preferably expressed as e.g.: 3-10-6-3-1

Strain 22SCA01	<input type="text"/>
Strain 22SCA02	<input type="text"/>
Strain 22SCA03	<input type="text"/>
Strain 22SCA04	<input type="text"/>
Strain 22SCA05	<input type="text"/>
Strain 22SCA06	<input type="text"/>

Please report per strain if [yes or no] a clustering match was found with the Reference outbreak strain in the EURL-*Salmonella* PT Typing 2022: *Salmonella* Enteritidis ST11, MLVA type 3-10-6-3-1.
In the PT Typing 2022 setting, the cluster definition for MLVA is set at no loci with a different number of repeats.

Strain 22SCA01	<input type="radio"/> Yes	<input type="radio"/> No
Strain 22SCA02	<input type="radio"/> Yes	<input type="radio"/> No
Strain 22SCA03	<input type="radio"/> Yes	<input type="radio"/> No
Strain 22SCA04	<input type="radio"/> Yes	<input type="radio"/> No
Strain 22SCA05	<input type="radio"/> Yes	<input type="radio"/> No
Strain 22SCA06	<input type="radio"/> Yes	<input type="radio"/> No

Any comments on the MLVA part:



REPORTING WGS RESULTS

Do you want to submit WGS results? Yes
 No

-> **Transfer the raw reads** (fastq-files), either by using wetransfer.com (multiple sessions may be required) or by uploading the files to the secure RIVM ftp server.
Please contact wilma.jacobs@rivm.nl by email if you need further instructions on the use of the ftp server (also given by email in week 45).

Be sure to name your files including your laboratory code and strain code in the name, preferably like: 22SCA01Lab01_R1.fastq, 22SCA01Lab01_R2.fastq, etc.

Date of sending the WGS fastq files: dd/mm/yyyy

Do you agree that your raw data files (fastq) from the PT Typing 2022, anonymously re-coded, may also be used for additional research purposes or training? Yes
 No
 Other:

-> **Email the distance matrix** (preferably as an .xls or .csv file) to wilma.jacobs@rivm.nl
Be sure to name the file including your laboratory code, preferably like: Lab01_Distance_Matrix.xls

Date of emailing the distance matrix: dd/mm/yyyy

Did you check the md5sum values for all 14 compressed fastq files that you downloaded from the secure RIVM ftp server? Yes
 No
 Other:

Please copy/paste your md5sum output for all your strains:

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
 Ion Torrent S5
 PacBio
 454
 MinION
 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.

Criterium 1:

Criterium 1, specification of "Other":

Tool(s) used for criterium 1:

Threshold used for criterium 1:

Criterium 2:

Criterium 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 9 ->

Criterium 10:

Tool(s) used for criterium 10:

Threshold used for criterium 10:

Please select the analysis used for the WGS data

- SNP-based - reference-based
- SNP-based - assembly-based
- cg-MLST-based
- wg-MLST-based
- Other:

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



Please report **per strain** if:
[yes or no] the data passed your Quality Control (QC);
[yes or no] a clustering match was found with the Reference outbreak strain in the EURL-*Salmonella* PT Typing 2022: 22SCA-REF_R1.fq.gz & 22SCA-REF_R2.fq.gz (*Salmonella* Enteritidis ST11, MLVA type 3-10-6-3-1).
In the PT Typing 2022 setting, the cgMLST-based cluster definition is set at maximum 6 allelic differences from the reference sequence.

Strain 22SCA01 Yes No
- Data passed Quality Control:

Reason(s) for not passing the QC:

Strain 22SCA01 Yes No
- Cluster with the REF strain: Not applicable (QC not passed)

Strain 22SCA02 Yes No
- Data passed Quality Control:

Reason(s) for not passing the QC:

Strain 22SCA02 Yes No
- Cluster with the REF strain: Not applicable (QC not passed)

-> Strains 22SCA03, 22SCA04, 22SCA05, 22SCA06

22SCA11, 22SCA12, 22SCA13, 22SCA14, 22SCA15 ->

Strain 22SCA16 Yes No
- Data passed Quality Control:

Reason(s) for not passing the QC:

Strain 22SCA16 Yes No
- Cluster with the REF strain: Not applicable (QC not passed)

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

Any comments on the WGS part:

FINALLY

Any general 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.