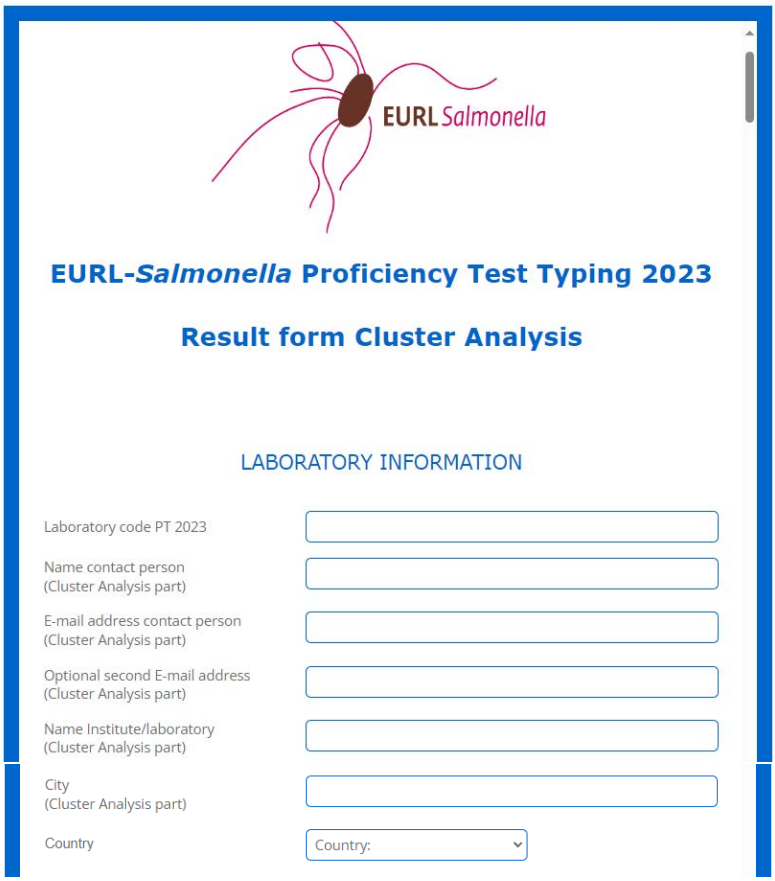
Screenshots of the on-line Result form Cluster Analysis EURL-*Salmonella* Proficiency Test Typing 2023



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 23SCA01 serovar name:

Strain 23SCA02 serovar name:

Strain 23SCA03 serovar name:

Strain 23SCA04 serovar name:

Strain 23SCA05 serovar name:

Strain 23SCA06 serovar name:

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:

Strain 23SCA11 serovar name:

Strain 23SCA12 serovar name:

Strain 23SCA13 serovar name:

Strain 23SCA14 serovar name:

Strain 23SCA15 serovar name:

Strain 23SCA16 serovar name:

REPORTING NGS RESULTS

Do you want to submit NGS results?
- ○ Yes
- ○ No

-> **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: 23SCA01Lab01_R1.fastq, 23SCA01Lab01_R2.fastq, etc.

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

Do you agree that your raw data files (fastq) from the PT Typing 2023, 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-PT2023"?
- ○ Yes
- ○ No
- ○ Other:

-> **Transfer** (optionally, but recommended) **the Md5 checksums**
1): concerning the downloaded files on strains 23SCA11 - 23SCA16 plus 23SCA-REF
2): concerning your uploaded files on strains 23SCA01 - 23SCA06
by uploading the data, for example in .txt or .csv format, to the secure RIVM ftp server.

Date of transferring Md5 checksums: dd/mm/yyyy 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 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.

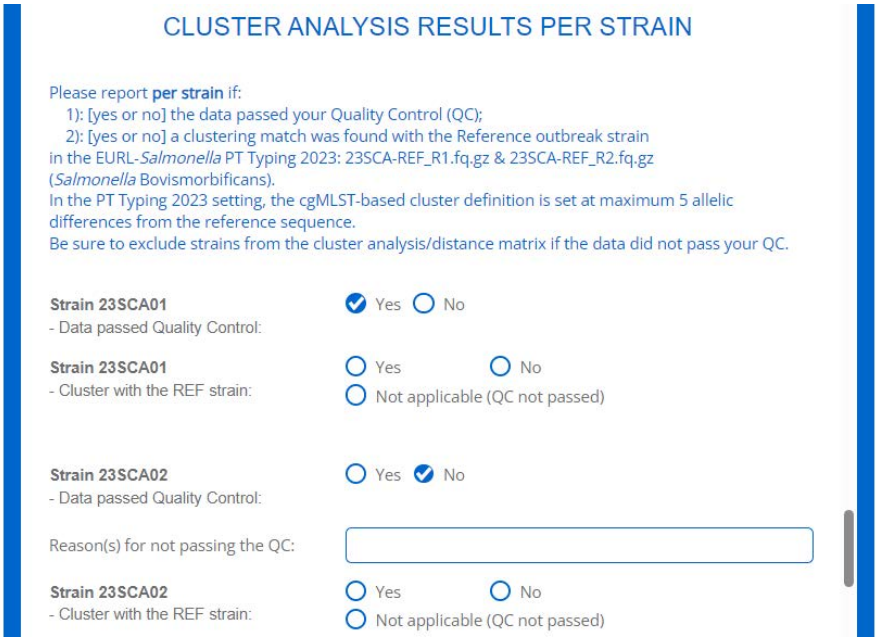
Criterium 1:	Contamination
Criterium 1, specification of "Other":	
Tool(s) used for criterium 1:	
Threshold used for criterium 1:	
Criterium 2:	Coverage
Criterium 2, specification of "Other":	
Tool(s) used for criterium 2:	
Threshold used for criterium 2:	
Criterium 3:	Other, please specify below
Criterium 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 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 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 2023: 23SCA-REF_R1.fq.gz & 23SCA-REF_R2.fq.gz (*Salmonella* Bovismorbificans).
In the PT Typing 2023 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 23SCA01
- Data passed Quality Control: (●) Yes ( ) No

Strain 23SCA01
- Cluster with the REF strain: ( ) Yes ( ) No ( ) Not applicable (QC not passed)

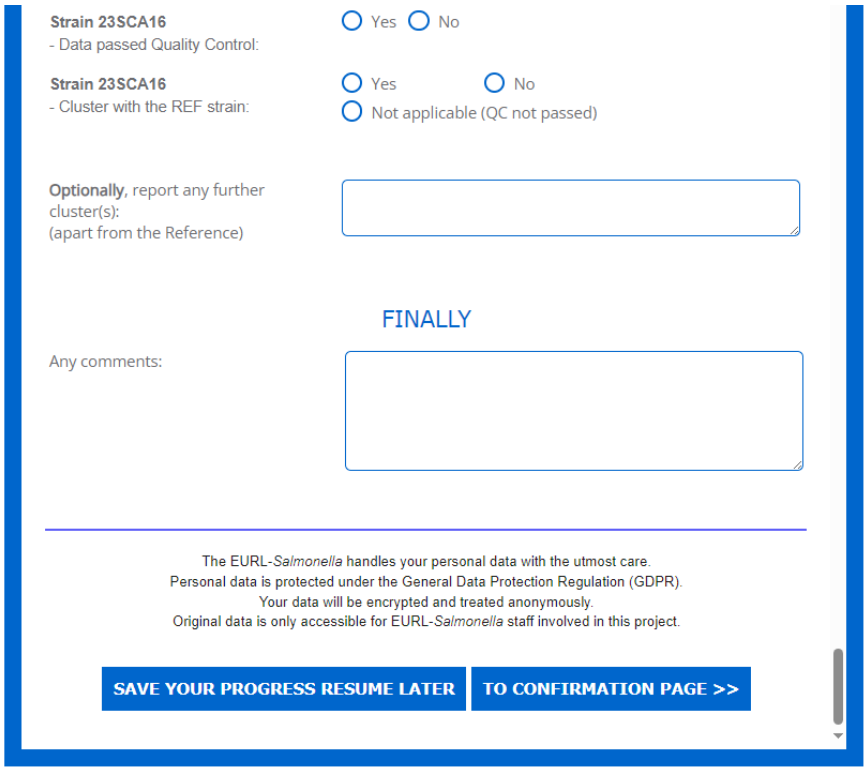
Strain 23SCA02
- Data passed Quality Control: ( ) Yes (●) No

Reason(s) for not passing the QC:

Strain 23SCA02
- Cluster with the REF strain: ( ) Yes ( ) No ( ) Not applicable (QC not passed)

-> Strains 23SCA03, 23SCA04, 23SCA05, 23SCA06

23SCA11, 23SCA12, 23SCA13, 23SCA14, 23SCA15 ->



Strain 23SCA16
- Data passed Quality Control: ( ) Yes ( ) No

Strain 23SCA16
- Cluster with the REF strain: ( ) Yes ( ) No ( ) Not applicable (QC not passed)

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

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.

SAVE YOUR PROGRESS RESUME LATER | TO CONFIRMATION PAGE >>