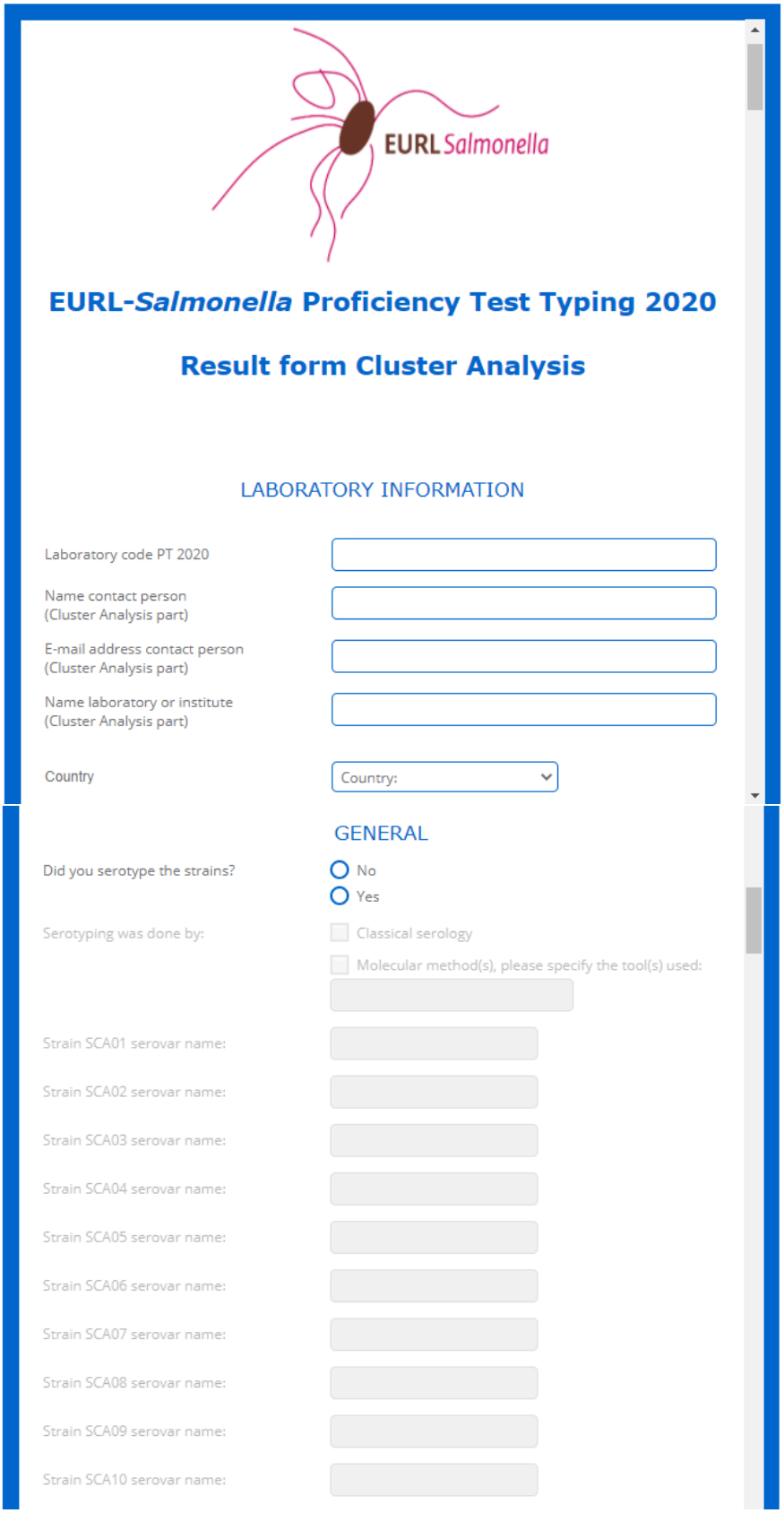
Preview of the on-line Result form Cluster Analysis EURL-*Salmonella* Proficiency Test Typing 2020



EURL-*Salmonella* Proficiency Test Typing 2020

Result form Cluster Analysis

LABORATORY INFORMATION

Laboratory code PT 2020

Name contact person (Cluster Analysis part)

E-mail address contact person (Cluster Analysis part)

Name laboratory or institute (Cluster Analysis part)

Country

Country:

GENERAL

Did you serotype the strains?

No

Yes

Serotyping was done by:

Classical serology

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

Strain SCA01 serovar name:

Strain SCA02 serovar name:

Strain SCA03 serovar name:

Strain SCA04 serovar name:

Strain SCA05 serovar name:

Strain SCA06 serovar name:

Strain SCA07 serovar name:

Strain SCA08 serovar name:

Strain SCA09 serovar name:

Strain SCA10 serovar name:

REPORTING PFGE RESULTS

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

-> **Email the PFGE gel image** as *an uncompressed 8-bit gray scale TIFF file* to wilma.jacobs@rivm.nl .
Be sure to include your laboratory code in the name of the .tif file, preferably like: Lab01_PFGE2020.tif

Date of emailing the PGFE gel image: dd/mm/yyyy dd/mm/yyyy

-> Prepare the ZIP (Bionumerics 7) or XML export files (Bionumerics 6 or below), from the analysis in BioNumerics using the pre-configured database as sent to you in week 45.
Include all test strains and reference strains, as well as the TIFF image.
Email these BN analysis data in a ZIP file to wilma.jacobs@rivm.nl . Be sure to rename your zip file to include your laboratory code in the name, preferably like: Lab01_PFGE2020.zip

Date of emailing the BN analysis data: dd/mm/yyyy dd/mm/yyyy

Which method did you use for PFGE?
- ○ Standard Pulsenet Protocol Salmonella PFGE
- ○ Standard Pulsenet Protocol Salmonella PFGE with modifications
- ○ Other:

Please enter the ID of the strains (SCA01 -SCA10, REF SB) in the corresponding position lanes on your gel (XbaI):

Lane 1	
Lane 2	
Lane 3	
Lane 4	
Lane 5	
Lane 6	
Lane 7	
Lane 8	
Lane 9	
Lane 10	
Lane 11	
Lane 12	
Lane 13	
Lane 14	
Lane 15	

How many clusters did you detect by PFGE data analysis?

- 0
- 1
- 2
- 3
- Other, please describe

Please list the ID for the strains included in PFGE cluster 1

Please list the ID for the strains included in PFGE cluster 2

Please list the ID for the strains included in PFGE cluster 3

Any comments on the PFGE part:

REPORTING MLVA RESULTS

Do you want to submit MLVA results?

- Yes
- No

Please list the allele profile per strain, using the format STTR9-STTR5-STTR6-STTR10-STTR3
Peferably expressed as e.g.: 3-14-13-NA-211

Strain SCA01

Strain SCA02

Strain SCA03

Strain SCA04

Strain SCA05

Strain SCA06

Strain SCA07

Strain SCA08

Strain SCA09

Strain SCA10

Please report per strain if [yes or no] a clustering match was found with the Reference outbreak strain in the EURL-*Salmonella* PT Typing 2020:
monophasic *Salmonella* Typhimurium ST34, MLVA type 3-14-13-NA-211.
In the PT Typing 2020 setting, the cluster definition for MLVA is set at no loci with a different number of repeats.

Strain SCA01	○ Yes ○ No
Strain SCA02	○ Yes ○ No
Strain SCA03	○ Yes ○ No
Strain SCA04	○ Yes ○ No
Strain SCA05	○ Yes ○ No
Strain SCA06	○ Yes ○ No
Strain SCA07	○ Yes ○ No
Strain SCA08	○ Yes ○ No
Strain SCA09	○ Yes ○ No
Strain SCA10	○ Yes ○ 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) to wilma.jacobs@rivm.nl, 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 (given by email in week 45).
Be sure to name your files to include your laboratory code and strain code in the name, preferably like: Lab01_SCA01_R1.fastq, Lab01_SCA01_R2.fastq, etc.

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

Do you agree that your raw data files (fastq) from the PT Typing 2020, 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 to include your laboratory code, preferably like: Lab01_Distance_Matrix.xls

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

If applicable, please enter the md5sum value for the fastq files of the Reference strain that you downloaded from the secure RIVM ftp server.

md5sum value 20SCA_REF_R1.fq:

md5sum value 20SCA_REF_R2.fq:

DNA extraction, library preparation and sequencing was performed:
- ○ In-house
- ○ Outsourced
- ○ Other:

WGS platform used:
- ○ Illumina MiSeq
- ○ Illumina NextSeq
- ○ Illumina HiSeq
- ○ 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. (e.g. contamination, serotype, coverage, N50, number of contigs, etc.)

Criterium 1:

Tool(s) used for criterium 1:

Threshold used for criterium 1:

Criterium 2:

Tool(s) used for criterium 2:

Threshold used for criterium 2:

Criterium 3:

Tool(s) used for criterium 3:

Threshold used for criterium 3:

Criterium 4:

Tool(s) used for criterium 4:

Threshold used for criterium 4:

Criterium 5:

Tool(s) used for criterium 5:

Threshold used for criterium 5:

Criterium 6:

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 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.

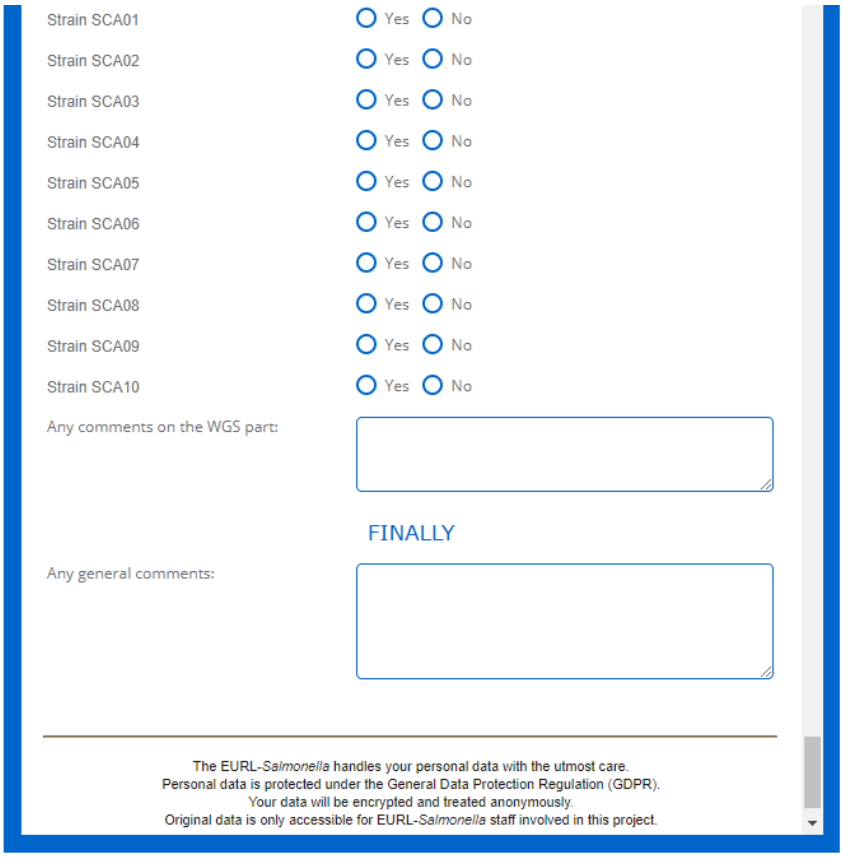
Please select the tool(s) used for analysis:

- ☐ 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] a clustering match was found with the Reference outbreak strain in the EURL-*Salmonella* PT Typing 2020:
20SCA_REF_R1.fq
20SCA_REF_R2.fq
(monophasic *Salmonella* Typhimurium ST34, MLVA type 3-14-13-NA-211)
In the PT Typing 2020 setting, the cluster definition for WGS is set at maximum 6 allelic differences from the reference sequence.


Strain SCA01 Yes No
Strain SCA02 Yes No
Strain SCA03 Yes No
Strain SCA04 Yes No
Strain SCA05 Yes No
Strain SCA06 Yes No
Strain SCA07 Yes No
Strain SCA08 Yes No
Strain SCA09 Yes No
Strain SCA10 Yes No
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.