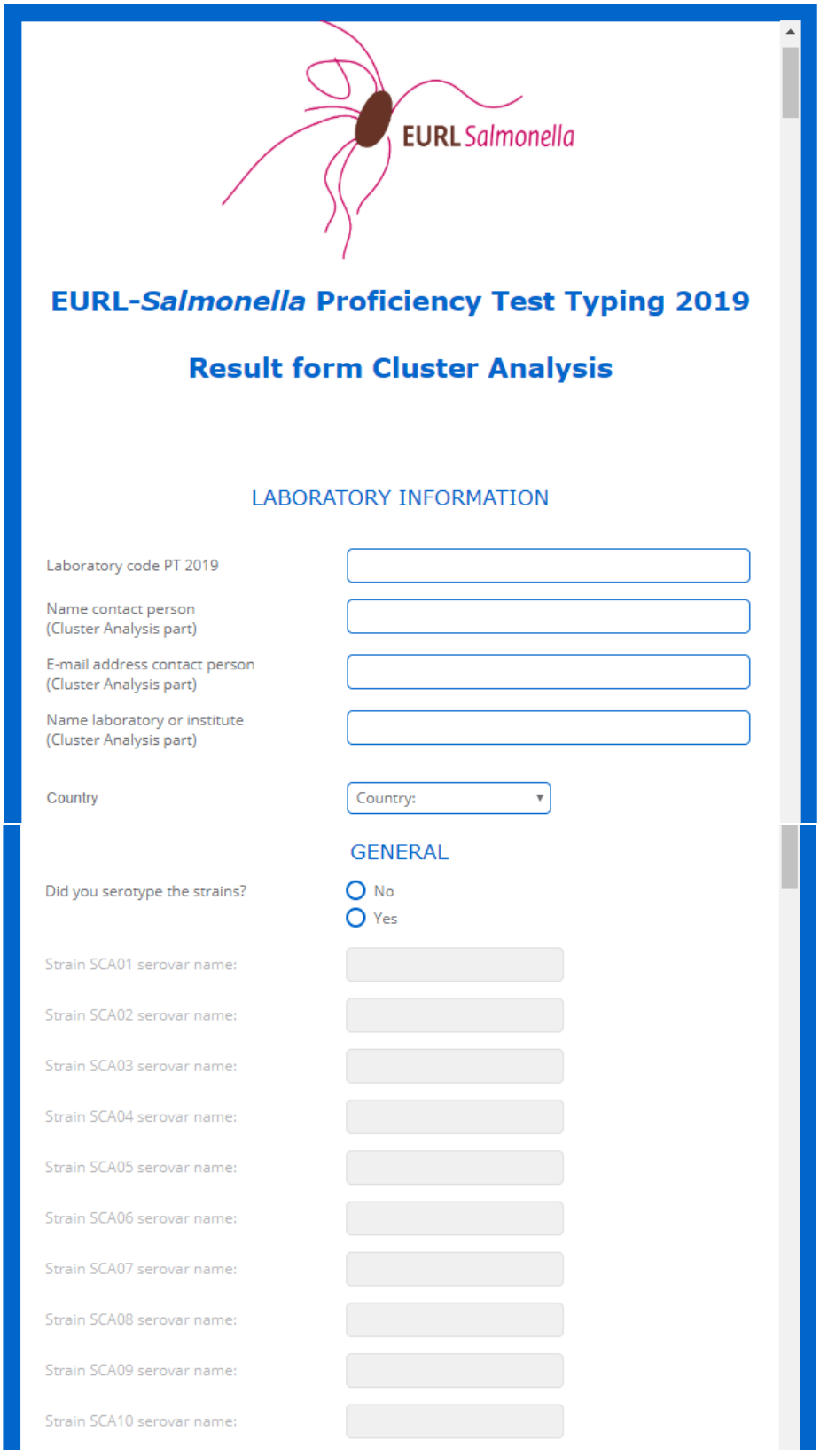
Preview of the on-line Result form Cluster Analysis
EURL-*Salmonella* Proficiency Test Typing 2019



REPORTING PFGE RESULTS

Do you want to submit PFGE results?

- [x] 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_PFGE2019.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, *including 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_PFGE2019.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 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

Please list the total number of bands per strain (> 33kb):

Strain SCA01

Strain SCA02

Strain SCA03

Strain SCA04

Strain SCA05

Strain SCA06

Strain SCA07

Strain SCA08

Strain SCA09

Strain SCA10

REPORTING MLVA RESULTS

Do you want to submit MLVA results?

- ☑ Yes
- ○ No

Please enter the reference to the MLVA scheme that was used:

Please list the loci in the scheme used

Locus 1:

Locus 2:

Locus 3:

Locus 4:

Locus 5:

Please list the allele profile per strain, using the format Locus 1-Locus 2-Locus 3-Locus 4-Locus 5 (expressed as e.g.: 02-09-07-03-02 or 03-12-10-00-211)

Strain SCA01

Strain SCA02

Strain SCA03

Strain SCA04

Strain SCA05

Strain SCA06

Strain SCA07

Strain SCA08

Strain SCA09

Strain SCA10

How many clusters did you detect by MLVA data analysis?

- 0
- 1
- 2
- 3
- Other

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

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

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

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 (mutiple sessions may be required) or by uploading the files to the RIVM ftp server. Please contact wilma.jacobs@rivm.nl by email for further instructions on the use of the ftp server.
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: 11/11/2019 dd/mm/yyyy

-> **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

DNA extraction, library preparation and sequencing was performed:

- In-house
- Outsourced
- Other:

WGS platform used:

- Illumina Mi-Seq
- Illumina NextSeq
- Illumina HiSeq
- Ion Torrent PGM
- Ion Proton
- Ion Torrent S5
- PacBio
- 454
- MinION
- Other:

Please list (up to a maximum of 10) main **quantitative** criteria that were used to evaluate the quality of the sequence data, including the threshold used.
(e.g. coverage, N50, number of contigs, etc.)

Quantitative criterium 1:

Threshold used for quantitative criterium 1:

Quantitative criterium 2:

Threshold used for quantitative criterium 2:

Quantitative criterium 3:

Threshold used for quantitative criterium 3:

Quantitative criterium 4:

Threshold used for quantitative criterium 4:

Quantitative criterium 5:

Threshold used for quantitative criterium 5:

Quantitative criterium 6:

Threshold used for quantitative criterium 6:

Quantitative criterium 7:

Threshold used for quantitative criterium 7:

Quantitative criterium 8:

Threshold used for quantitative criterium 8:

Quantitative criterium 9:

Threshold used for quantitative criterium 9:

Quantitative criterium 10:

Threshold used for quantitative criterium 10:

Please list (up to a maximum of 10) main **qualitative** criteria that were used to evaluate the quality of the sequence data, including the threshold if relevant.
(e.g. contamination, confirmation of genus, etc.)

Qualitative criterium 1:

If relevant, threshold used for qualitative criterium 1:

Qualitative criterium 2:

If relevant, threshold used for qualitative criterium 2:

Qualitative criterium 3:

If relevant, threshold used for qualitative criterium 3:

Qualitative criterium 4:

If relevant, threshold used for qualitative criterium 4:

Qualitative criterium 5:

If relevant, threshold used for qualitative criterium 5:

Qualitative criterium 6:

If relevant, threshold used for qualitative criterium 6:

Qualitative criterium 7:

If relevant, threshold used for qualitative criterium 7:

Qualitative criterium 8:

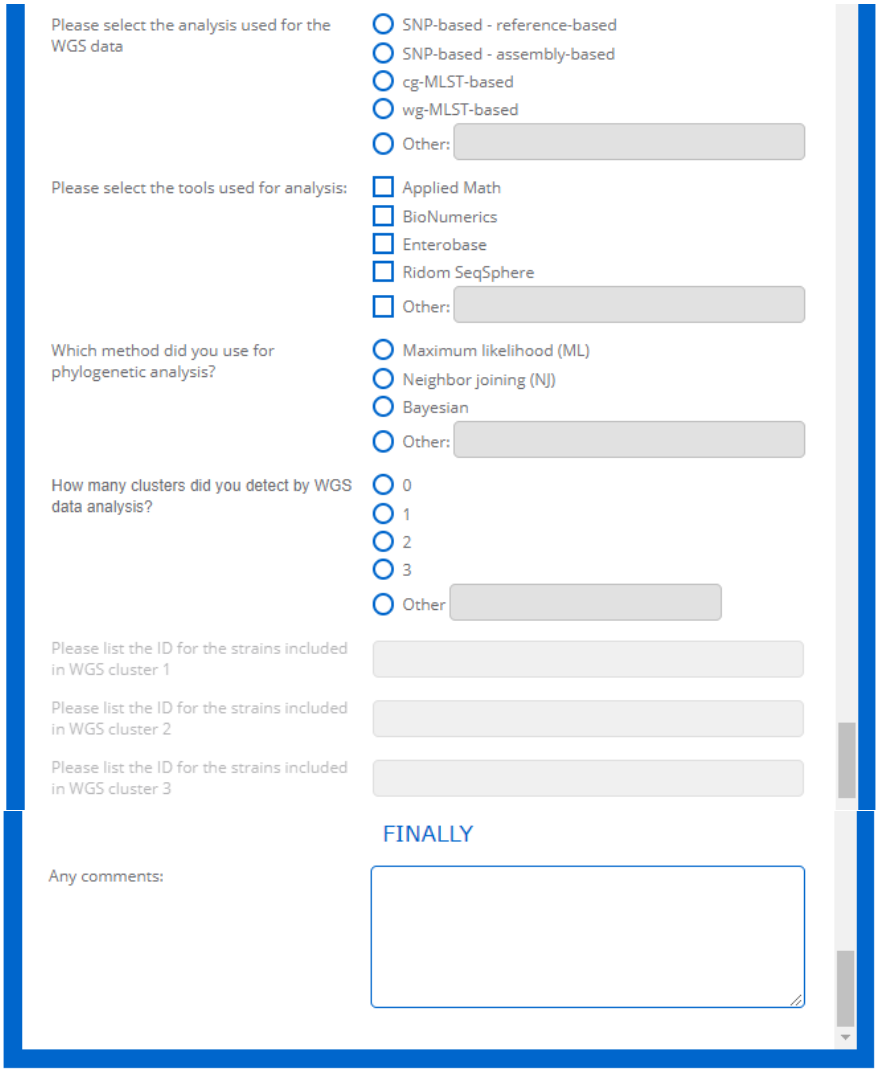
If relevant, threshold used for qualitative criterium 8:

Qualitative criterium 9:

If relevant, threshold used for qualitative criterium 9:

Qualitative criterium 10:

If relevant, threshold used for qualitative 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:
Please select the tools used for analysis:
Applied Math
BioNumerics
Enterobase
Ridom SeqSphere
Other:
Which method did you use for phylogenetic analysis?
Maximum likelihood (ML)
Neighbor joining (NJ)
Bayesian
Other:
How many clusters did you detect by WGS data analysis?
0
1
2
3
Other
Please list the ID for the strains included in WGS cluster 1
Please list the ID for the strains included in WGS cluster 2
Please list the ID for the strains included in WGS cluster 3
FINALLY
Any comments: