**Supplementary File 1. Software used by TORMES pipeline.**

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| --- | --- | --- | --- |
|  | **Software** | **Link** | **Publication** |
|  | PRINSEQ | http://prinseq.sourceforge.net/ | Schmieder and Edwards, 2011 |
|  | Trimmomatic | http://www.usadellab.org/cms/?page=trimmomatic | Bolger et al., 2014  |
|  | Kraken | https://ccb.jhu.edu/software/kraken/ | Wood and Salzberg, 2014  |
|  | SPAdes | http://cab.spbu.ru/software/spades/ | Bankevich et al., 2012  |
|  | QUAST | http://quast.sourceforge.net/quast | Gurevich et al., 2013  |
|  | progressiveMauve | http://darlinglab.org/mauve/mauve.html | Darling et al., 2010  |
|  | Prokka | https://github.com/tseemann/prokka | Seeman, 2014  |
|  | Roary | https://sanger-pathogens.github.io/Roary/ | Page et al., 2015  |
|  | FastTree | http://meta.microbesonline.org/fasttree/ | Price et al., 2009  |
|  | roary2svg.pl | https://github.com/sanger-pathogens/Roary/blob/master/contrib/roary2svg/roary2svg.pl |  |
|  | mlst | https://github.com/tseemann/mlst |  |
|  | ABRicate | https://github.com/tseemann/abricate |  |
|  | BLAST | ftp://ftp.ncbi.nlm.nih.gov/blast/executables/blast+/LATEST/ | Zhang et al., 2000  |
|  | GNU Parallel | https://www.gnu.org/software/parallel/ | Tange, 2014  |
| **Enabled using -g/--genera option** | Serotypefinder | https://bitbucket.org/genomicepidemiology/serotypefinder | Joensen et al., 2015  |
| SISTR | https://lfz.corefacility.ca/sistr-app/ | Yoshida et al., 2016  |
| FimTyper | https://bitbucket.org/genomicepidemiology/fimtyper/overview |  |
|  | R | https://cran.r-project.org/ | R Development Core Team, 2008  |
| **R packages** | ggplot2 | https://cran.r-project.org/web/packages/ggplot2/index.html | Wickham, 2009  |
| ggtree | https://bioconductor.org/packages/release/bioc/html/ggtree.html | Yu et al., 2017  |
| knitr | https://cran.r-project.org/web/packages/knitr/index.html | Xie, 2018  |
| plotly | https://cran.r-project.org/web/packages/plotly/index.html | Sievert et al., 2017  |
| RColorBrewer | https://cran.r-project.org/web/packages/RColorBrewer/index.html | Neuwirth et al., 2014  |
| reshape2 | https://cran.r-project.org/web/packages/reshape2/index.html | Wickham, 2007  |
| rmarkdown | https://cran.r-project.org/web/packages/rmarkdown/index.html | Allaire et al., 2016  |

**Supplementary File 2. Case study samples, *Salmonella* isolation, DNA extraction, library preparation and sequencing.**

As part of the European research project PROMISE (www.promise-net.eu), 200 food samples were confiscated by the border authorities at the International Bilbao Airport, Spain (www.aeropuertodebilbao.net) from the luggage of passengers arriving from 22 non-EU countries during April, May and June 2013 (Rodríguez-Lázaro et al., 2015). Ten food products (five cheeses, three meat products and two poultry products) were positive for *Salmonella* spp. DNA from pure *Salmonella* spp. cultures was extracted and sequenced on a MiSeq platform (Illumina) after library preparation as previously described (Hernández et al., 2015). The Whole Genome Shotgun project has been deposited at the DDBJ/ENA/GenBank under the submission BioProject PRJNA507086 and accessions numbers: SGBG00000000, SGBH00000000, SGBI00000000, SGBJ00000000, SGBK00000000, SGBL00000000, SGBM00000000, SGBN00000000, SGBO00000000, SGBP00000000,

**Supplementary File 3. Source, sequencing stats and typing of case study *Salmonella* spp.**

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Isolate** | **Source** | **Numebr of reads** | **Number of contigs** | **Genome length (bp)** | **Average contig length (bp)** | **N50** | **GC content (%)** | **Sequencing depth** | **Identified specie** | **Percent specie identification** | **Sequence Type (ST)** | **Serovar** | **Serogroup** |
| MS0495 | Cheese (Georgia) | 587544 | 41 | 4650624 | 640249 | 308791 | 52.26 | 32X | Salmonella enterica | 98.25 | 4 | Montevideo | C1 |
| MS0496 | Cheese (Bolivia) | 888038 | 107 | 4763977 | 336019 | 136467 | 52.15 | 47X | Salmonella enterica | 94.2 | 279 | I 4,[5],12:d:- | B |
| MS0497 | Cheese (Moldova) | 622536 | 91 | 4643658 | 438202 | 128141 | 52.29 | 34X | Salmonella enterica | 98.25 | 4 | Montevideo | C1 |
| MS0498 | Meat (Peru) | 673312 | 154 | 4757288 | 225116 | 83927 | 52.17 | 36X | Salmonella enterica | 94.55 | 279 | I 4,[5],12:d:- | B |
| MS0499 | Cheese (Peru) | 828090 | 115 | 4760115 | 414408 | 99676 | 52.16 | 42X | Salmonella enterica | 94.54 | 279 | I 4,[5],12:d:- | B |
| MS0500 | Poultry (Eq. Guinea) | 793160 | 64 | 4652143 | 439190 | 174151 | 52.15 | 43X | Salmonella enterica | 97.47 | 11 | Enteritidis | D1 |
| MS0501 | Poultry (Eq. Guinea) | 666626 | 178 | 4560864 | 209922 | 65339 | 52.19 | 38X | Salmonella enterica | 98.87 | 23 | Oranienburg | C1 |
| MS0502 | Meat (Bolivia) | 692768 | 73 | 4637517 | 558286 | 204883 | 52.17 | 38X | Salmonella enterica | 97.83 | 64 | Anatum | E1 |
| MS0503 | Meat (Bolivia) | 620020 | 74 | 4634553 | 408239 | 198288 | 52.17 | 34X | Salmonella enterica | 97.96 | 64 | Anatum | E1 |
| MS0504 | Cheese (Bolivia) | 542482 | 188 | 4709098 | 206809 | 52159 | 52.29 | 30X | Salmonella enterica | 97.8 | 45 | Newport | C2-C3 |

**Supplementary File 4. Pangenome comparison based on the presence/absence of genes in each isolated case study *Salmonella enterica*.** Genes present in each isolate are represented in blue. The core genome (genes common in all isolates) represent 62% of all genes found (3,602 out of 5,811 genes). The pangenomic tree was also build on the gene presence/absence.

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