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| **File** | **Description** | **Link** |
| **Additional Figures, Tables and Data.zip** | A package of all the following data | <http://wrap.warwick.ac.uk/85593/113/Additional%20Figures%2C%20Tables%20and%20Data.zip> |
| **Additional Figure 4.pdf** | **Ancestral reconstruction 1**  Maximum likelihood phylogeny and geographical origins derived from 61,451 non-repetitive core SNPs within the Para C Lineage plus Birkenhead | <http://wrap.warwick.ac.uk/85593/18/Additional%20Figure%204.pdf> |
| **Additional Table 9.pdf** | **Ancestral reconstruction 2**  Geographic inference of the sources of clades within the Para C Lineage | <http://wrap.warwick.ac.uk/85593/30/Additional%20Table%209.pdf> |
| **Additional Figure 1.pdf** | **Concoct 1**  Single core gene (SCG) frequencies in the 76 Concoct clusters generated after binning contigs | <http://wrap.warwick.ac.uk/85593/15/Additional%20Figure%201.pdf> |
| **Additional Table 1.pdf** | **Concoct 2**  Statistics after clustering all metagenomes with MEGAHIT | <http://wrap.warwick.ac.uk/85593/22/Additional%20Table%201.pdf> |
| **Additional Table 2.pdf** | **Concoct 3**  Taxonomic assignments for 11 metagenome assembled genomes (MAGs) | <http://wrap.warwick.ac.uk/85593/23/Additional%20Table%202.pdf> |
| **Additional Table 3.pdf** | **Concoct 4**  Single-stranded deamination rates for Ragna, human DNA and 11 MAGs | <http://wrap.warwick.ac.uk/85593/24/Additional%20Table%203.pdf> |
| **Additional Table 4.pdf** | **Concoct 5**  Genomic coverage of 11 MAGs by source and sequencing library | <http://wrap.warwick.ac.uk/85593/25/Additional%20Table%204.pdf> |
| **Additional Data 01.xlsx** | **Concoct 6**  Bacterial taxa found by Kraken in SK152 metagenomes at ≥ 0.02% frequency. | <http://wrap.warwick.ac.uk/85593/2/Additional%20Data%2001.xlsx> |
| **Additional Data 02.zip** | **Concoct 7**  Eleven MAGs Contigs. | <http://wrap.warwick.ac.uk/85593/3/Additional%20Data%2002.zip> |
| **Additional Data 03.zip** | **Concoct 8**  Alignments and phylogenies of SCGs across the Tree of Life. | <http://wrap.warwick.ac.uk/85593/4/Additional%20Data%2003.zip> |
| **Additional Figure 3.pdf** | **Date estimation 1**  Date randomization tests for the temporal signal in multiple replicate data sets that were analysed by Beast | <http://wrap.warwick.ac.uk/85593/17/Additional%20Figure%203.pdf> |
| **Additional Figure 5.pdf** | **Date estimation 2**  Linear regression plots (TempEst [37]) of root-to-tip genetic distances to the MRCA of two sets of modern genomes plus Ragna (red), Tepos-14 and Tepos-35 (green) [19] versus their dates of sampling. | <http://wrap.warwick.ac.uk/85593/19/Additional%20figure%205.pdf> |
| **Additional Table 8.pdf** | **Date estimation 3**  Comparison of MRCA dating estimates by Beast using ancient plus modern, and only modern strains | <http://wrap.warwick.ac.uk/85593/29/Additional%20Table%208.pdf> |
| **Additional Data 14.zip** | **Date estimation 4**  Raw Maximum Clade Credibility trees as well as a summary of the mutation rates from BEAST inferences. | <http://wrap.warwick.ac.uk/85593/14/Additional%20Data%2014.zip> |
| **Additional Figure 2.pdf** | **ParaC Pan-genome 1**  Gain and loss of genomic islands shown on a maximum-likelihood radial phylogeny derived from 61,451 non-repetitive core SNPs within the Para C Lineage plus Birkenhead | <http://wrap.warwick.ac.uk/85593/16/Additional%20Figure%202.pdf> |
| **Additional Table 6.pdf** | **ParaC Pan-genome 2**  Summary statistics for pan-genomic contents of Ragna plus 219 modern genomes of the Para C Lineage | <http://wrap.warwick.ac.uk/85593/27/Additional%20Table%206.pdf> |
| **Additional Table 7.pdf** | **ParaC Pan-genome 3**  Gene gain/loss events and numbers of pseudogenes by sub-lineage | <http://wrap.warwick.ac.uk/85593/28/Additional%20Table%207.pdf> |
| **Additional Data 10.xlsx** | **ParaC Pan-genome 4**  The pan-genome of the Para C Lineage based on 6,665 single copy genes from 220 genomes. | <http://wrap.warwick.ac.uk/85593/10/Additional%20Data%2010.xlsx> |
| **Additional Data 11.zip** | **ParaC Pan-genome 5**  Sequences, original gene names and annotations of the reference sequences for 6,665 pan genes in the Para C Lineage. | <http://wrap.warwick.ac.uk/85593/11/Additional%20Data%2011.zip> |
| **Additional Data 12.xlsx** | **ParaC Pan-genome 6**  Pseudogenes associated with sub-lineages and clades of the Para C Lineage. | <http://wrap.warwick.ac.uk/85593/12/Additional%20Data%2012.xlsx> |
| **Additional Data 13.xlsx** | **ParaC Pan-genome 7**  Genomic islands and plasmids. | <http://wrap.warwick.ac.uk/85593/13/Additional%20Data%2013.xlsx> |
| **Additional Data 15.zip** | **ParaC Pan-genome 8**  Data and script for extracting rate of gene gain/loss and pseudogenes from the branches of an ML tree. See readme.txt for instructions. | <http://wrap.warwick.ac.uk/85593/112/Additional%20Data%2015.zip> |
| **Additional Table 5.pdf** | **ParaC genome SNPs 1**  Numbers of mutational and recombinational SNPs per clade within the Para C Lineage plus Birkenhead | <http://wrap.warwick.ac.uk/85593/26/Additional%20Table%205.pdf> |
| **Additional Data 08.xlsx** | **ParaC genome SNPs 2**  SNPs in the core genome of the Para C Lineage plus Birkenhead. | <http://wrap.warwick.ac.uk/85593/8/Additional%20Data%2008.xlsx> |
| **Additional Data 09.nex** | **ParaC genome SNPs 3**  Maximum likelihood phylogeny and inferred geographical origins based on 61,451 non-repetitive core SNPs from the Para C Lineage plus Birkenhead. | <http://wrap.warwick.ac.uk/85593/9/Additional%20Data%2009.nex> |
| **Additional Figure 7.pdf** | **ParaC genome SNPs 4**  Venn diagram of substitutions scored as recombinational by RecHMM, ClonalFrameML and Gubbins. | <http://wrap.warwick.ac.uk/85593/9/Additional%20Figure%207.pdf> |
| **Additional Data 04.xlsx** | ***Salmonella* supertree 1**  Metadata for 2,964 representative genomes in Salmonella enterica subsp. I. | <http://wrap.warwick.ac.uk/85593/5/Additional%20Data%2004.xlsx> |
| **Additional Data 05.nex** | ***Salmonella* supertree 2**  A species tree (ASTRID) based on 3,002 core gene trees from 2,964 representative genomes from *S. enterica* subsp. I. | <http://wrap.warwick.ac.uk/85593/6/Additional%20Data%2005.nex> |
| **Additional Data 06.nex** | ***Salmonella* supertree 3**  A RAxML maximum likelihood phylogeny based on a 2.8 Mbp concatenate of 3,002 core genes from 2,964 representative genomes from *S. enterica* subsp. I | <http://wrap.warwick.ac.uk/85593/7/Additional%20Data%2006.nex> |
| **Additional Figure 6.pdf** | **Workflow**  Workflow to reconstruct the Ragna genome | <http://wrap.warwick.ac.uk/85593/20/Additional%20Figure%206.pdf> |