**Supplementary 1**

**Analyzed EBOLA RNA-Seq Dataset Description**

**Input datasets and 16S database**

The datasets with the Illumina reads of the samples from the current outbreak published in [4] were retrieved from the SRA. For each sample listed in the Supplementary Table S2 of the article [4] the Experiment sample (SRS) information and links to its SRA experiments (SRX) and runs (SRR) were retrieved using the NCBI Batch Entrez platform (<http://www.ncbi.nlm.nih.gov/sites/batchentrez>).

**RNA-Seq illumina datasets used in this study**

EM095B:

ftp://ftp-trace.ncbi.nlm.nih.gov/sra/sra-instant/reads/ByRun/sra/SRR/SRR155/SRR1553416/SRR1553416.sra

EM095:

ftp://ftp-trace.ncbi.nlm.nih.gov/sra/sra-instant/reads/ByRun/sra/SRR/SRR155/SRR1553417/SRR1553417.sra

EM096:

ftp://ftp-trace.ncbi.nlm.nih.gov/sra/sra-instant/reads/ByRun/sra/SRR/SRR155/SRR1553418/SRR1553418.sra

EM096:

ftp://ftp-trace.ncbi.nlm.nih.gov/sra/sra-instant/reads/ByRun/sra/SRR/SRR155/SRR1553419/SRR1553419.sra

EM098:

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EM104:

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EM104:

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EM106:

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EM106:

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EM110:

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EM110:

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EM111:

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EM112:

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EM115:

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EM115:

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EM119:

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EM124.2:

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EM124.3:

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G3810.2:

ftp://ftp-trace.ncbi.nlm.nih.gov/sra/sra-instant/reads/ByRun/sra/SRR/SRR155/SRR1553550/SRR1553550.sra

G3814:

ftp://ftp-trace.ncbi.nlm.nih.gov/sra/sra-instant/reads/ByRun/sra/SRR/SRR155/SRR1553551/SRR1553551.sra

G3814:

ftp://ftp-trace.ncbi.nlm.nih.gov/sra/sra-instant/reads/ByRun/sra/SRR/SRR155/SRR1553552/SRR1553552.sra

G3816:

ftp://ftp-trace.ncbi.nlm.nih.gov/sra/sra-instant/reads/ByRun/sra/SRR/SRR155/SRR1553553/SRR1553553.sra

G3816:

ftp://ftp-trace.ncbi.nlm.nih.gov/sra/sra-instant/reads/ByRun/sra/SRR/SRR155/SRR1553554/SRR1553554.sra

G3817:

ftp://ftp-trace.ncbi.nlm.nih.gov/sra/sra-instant/reads/ByRun/sra/SRR/SRR155/SRR1553555/SRR1553555.sra

G3817:

ftp://ftp-trace.ncbi.nlm.nih.gov/sra/sra-instant/reads/ByRun/sra/SRR/SRR155/SRR1553556/SRR1553556.sra

G3818:

ftp://ftp-trace.ncbi.nlm.nih.gov/sra/sra-instant/reads/ByRun/sra/SRR/SRR155/SRR1553557/SRR1553557.sra

G3818:

ftp://ftp-trace.ncbi.nlm.nih.gov/sra/sra-instant/reads/ByRun/sra/SRR/SRR155/SRR1553558/SRR1553558.sra

G3819:

ftp://ftp-trace.ncbi.nlm.nih.gov/sra/sra-instant/reads/ByRun/sra/SRR/SRR155/SRR1553559/SRR1553559.sra

G3819:

ftp://ftp-trace.ncbi.nlm.nih.gov/sra/sra-instant/reads/ByRun/sra/SRR/SRR155/SRR1553560/SRR1553560.sra

G3820:

ftp://ftp-trace.ncbi.nlm.nih.gov/sra/sra-instant/reads/ByRun/sra/SRR/SRR155/SRR1553561/SRR1553561.sra

G3820:

ftp://ftp-trace.ncbi.nlm.nih.gov/sra/sra-instant/reads/ByRun/sra/SRR/SRR155/SRR1553562/SRR1553562.sra

G3821:

ftp://ftp-trace.ncbi.nlm.nih.gov/sra/sra-instant/reads/ByRun/sra/SRR/SRR155/SRR1553563/SRR1553563.sra

G3821:

ftp://ftp-trace.ncbi.nlm.nih.gov/sra/sra-instant/reads/ByRun/sra/SRR/SRR155/SRR1553564/SRR1553564.sra

G3822:

ftp://ftp-trace.ncbi.nlm.nih.gov/sra/sra-instant/reads/ByRun/sra/SRR/SRR155/SRR1553565/SRR1553565.sra

G3822:

ftp://ftp-trace.ncbi.nlm.nih.gov/sra/sra-instant/reads/ByRun/sra/SRR/SRR155/SRR1553566/SRR1553566.sra

G3823:

ftp://ftp-trace.ncbi.nlm.nih.gov/sra/sra-instant/reads/ByRun/sra/SRR/SRR155/SRR1553567/SRR1553567.sra

G3823:

ftp://ftp-trace.ncbi.nlm.nih.gov/sra/sra-instant/reads/ByRun/sra/SRR/SRR155/SRR1553568/SRR1553568.sra

G3825.1:

ftp://ftp-trace.ncbi.nlm.nih.gov/sra/sra-instant/reads/ByRun/sra/SRR/SRR155/SRR1553569/SRR1553569.sra

G3825.1:

ftp://ftp-trace.ncbi.nlm.nih.gov/sra/sra-instant/reads/ByRun/sra/SRR/SRR155/SRR1553570/SRR1553570.sra

G3825.2:

ftp://ftp-trace.ncbi.nlm.nih.gov/sra/sra-instant/reads/ByRun/sra/SRR/SRR155/SRR1553571/SRR1553571.sra

G3825.2:

ftp://ftp-trace.ncbi.nlm.nih.gov/sra/sra-instant/reads/ByRun/sra/SRR/SRR155/SRR1553572/SRR1553572.sra

G3826:

ftp://ftp-trace.ncbi.nlm.nih.gov/sra/sra-instant/reads/ByRun/sra/SRR/SRR155/SRR1553573/SRR1553573.sra

G3826:

ftp://ftp-trace.ncbi.nlm.nih.gov/sra/sra-instant/reads/ByRun/sra/SRR/SRR155/SRR1553574/SRR1553574.sra

G3827:

ftp://ftp-trace.ncbi.nlm.nih.gov/sra/sra-instant/reads/ByRun/sra/SRR/SRR155/SRR1553575/SRR1553575.sra

G3827:

ftp://ftp-trace.ncbi.nlm.nih.gov/sra/sra-instant/reads/ByRun/sra/SRR/SRR155/SRR1553576/SRR1553576.sra

G3829:

ftp://ftp-trace.ncbi.nlm.nih.gov/sra/sra-instant/reads/ByRun/sra/SRR/SRR155/SRR1553577/SRR1553577.sra

G3829:

ftp://ftp-trace.ncbi.nlm.nih.gov/sra/sra-instant/reads/ByRun/sra/SRR/SRR155/SRR1553578/SRR1553578.sra

G3831:

ftp://ftp-trace.ncbi.nlm.nih.gov/sra/sra-instant/reads/ByRun/sra/SRR/SRR155/SRR1553579/SRR1553579.sra

G3831:

ftp://ftp-trace.ncbi.nlm.nih.gov/sra/sra-instant/reads/ByRun/sra/SRR/SRR155/SRR1553580/SRR1553580.sra

G3834:

ftp://ftp-trace.ncbi.nlm.nih.gov/sra/sra-instant/reads/ByRun/sra/SRR/SRR155/SRR1553581/SRR1553581.sra

G3834:

ftp://ftp-trace.ncbi.nlm.nih.gov/sra/sra-instant/reads/ByRun/sra/SRR/SRR155/SRR1553582/SRR1553582.sra

G3838:

ftp://ftp-trace.ncbi.nlm.nih.gov/sra/sra-instant/reads/ByRun/sra/SRR/SRR155/SRR1553583/SRR1553583.sra

G3838:

ftp://ftp-trace.ncbi.nlm.nih.gov/sra/sra-instant/reads/ByRun/sra/SRR/SRR155/SRR1553584/SRR1553584.sra

G3840:

ftp://ftp-trace.ncbi.nlm.nih.gov/sra/sra-instant/reads/ByRun/sra/SRR/SRR155/SRR1553585/SRR1553585.sra

G3840:

ftp://ftp-trace.ncbi.nlm.nih.gov/sra/sra-instant/reads/ByRun/sra/SRR/SRR155/SRR1553586/SRR1553586.sra

G3841:

ftp://ftp-trace.ncbi.nlm.nih.gov/sra/sra-instant/reads/ByRun/sra/SRR/SRR155/SRR1553587/SRR1553587.sra

G3841:

ftp://ftp-trace.ncbi.nlm.nih.gov/sra/sra-instant/reads/ByRun/sra/SRR/SRR155/SRR1553588/SRR1553588.sra

G3845:

ftp://ftp-trace.ncbi.nlm.nih.gov/sra/sra-instant/reads/ByRun/sra/SRR/SRR155/SRR1553589/SRR1553589.sra

G3845:

ftp://ftp-trace.ncbi.nlm.nih.gov/sra/sra-instant/reads/ByRun/sra/SRR/SRR155/SRR1553590/SRR1553590.sra

G3846:

ftp://ftp-trace.ncbi.nlm.nih.gov/sra/sra-instant/reads/ByRun/sra/SRR/SRR155/SRR1553591/SRR1553591.sra

G3846:

ftp://ftp-trace.ncbi.nlm.nih.gov/sra/sra-instant/reads/ByRun/sra/SRR/SRR155/SRR1553592/SRR1553592.sra

G3848:

ftp://ftp-trace.ncbi.nlm.nih.gov/sra/sra-instant/reads/ByRun/sra/SRR/SRR155/SRR1553593/SRR1553593.sra

G3848:

ftp://ftp-trace.ncbi.nlm.nih.gov/sra/sra-instant/reads/ByRun/sra/SRR/SRR155/SRR1553594/SRR1553594.sra

G3850:

ftp://ftp-trace.ncbi.nlm.nih.gov/sra/sra-instant/reads/ByRun/sra/SRR/SRR155/SRR1553595/SRR1553595.sra

G3850:

ftp://ftp-trace.ncbi.nlm.nih.gov/sra/sra-instant/reads/ByRun/sra/SRR/SRR155/SRR1553596/SRR1553596.sra

G3851:

ftp://ftp-trace.ncbi.nlm.nih.gov/sra/sra-instant/reads/ByRun/sra/SRR/SRR155/SRR1553597/SRR1553597.sra

G3851:

ftp://ftp-trace.ncbi.nlm.nih.gov/sra/sra-instant/reads/ByRun/sra/SRR/SRR155/SRR1553598/SRR1553598.sra

G3856.1:

ftp://ftp-trace.ncbi.nlm.nih.gov/sra/sra-instant/reads/ByRun/sra/SRR/SRR155/SRR1553599/SRR1553599.sra

G3856.1:

ftp://ftp-trace.ncbi.nlm.nih.gov/sra/sra-instant/reads/ByRun/sra/SRR/SRR155/SRR1553600/SRR1553600.sra

G3856.3:

ftp://ftp-trace.ncbi.nlm.nih.gov/sra/sra-instant/reads/ByRun/sra/SRR/SRR155/SRR1553601/SRR1553601.sra

G3856.3:

ftp://ftp-trace.ncbi.nlm.nih.gov/sra/sra-instant/reads/ByRun/sra/SRR/SRR155/SRR1553602/SRR1553602.sra

G3857:

ftp://ftp-trace.ncbi.nlm.nih.gov/sra/sra-instant/reads/ByRun/sra/SRR/SRR155/SRR1553603/SRR1553603.sra

G3857:

ftp://ftp-trace.ncbi.nlm.nih.gov/sra/sra-instant/reads/ByRun/sra/SRR/SRR155/SRR1553604/SRR1553604.sra

NM042.1:

ftp://ftp-trace.ncbi.nlm.nih.gov/sra/sra-instant/reads/ByRun/sra/SRR/SRR155/SRR1553605/SRR1553605.sra

NM042.1:

ftp://ftp-trace.ncbi.nlm.nih.gov/sra/sra-instant/reads/ByRun/sra/SRR/SRR155/SRR1553606/SRR1553606.sra

NM042.2:

ftp://ftp-trace.ncbi.nlm.nih.gov/sra/sra-instant/reads/ByRun/sra/SRR/SRR155/SRR1553607/SRR1553607.sra

NM042.2:

ftp://ftp-trace.ncbi.nlm.nih.gov/sra/sra-instant/reads/ByRun/sra/SRR/SRR155/SRR1553608/SRR1553608.sra

NM042.3:

ftp://ftp-trace.ncbi.nlm.nih.gov/sra/sra-instant/reads/ByRun/sra/SRR/SRR155/SRR1553609/SRR1553609.sra

NM042.3:

ftp://ftp-trace.ncbi.nlm.nih.gov/sra/sra-instant/reads/ByRun/sra/SRR/SRR155/SRR1553610/SRR1553610.sra

**Download of the sequences**

The dataset for the whole sequencing project (Project ID: SRP045416) was downloaded from this URL ftp://ftp-trace.ncbi.nlm.nih.gov/sra/sra-instant/reads/ByStudy/sra/SRP/SRP045/SRP045416/. Then, for each sample two FASTQ files were generated:

* File called SampleName.fastq: which contains all reads (reverse and forward) of all the SRA runs for such sample
* File called Samplename.rc.fastq: which contains the reverse complement sequences of the sequences of the fileSampleName.fastq(version 2.4.1 for CentOS Linux64)

Firstly, the FASTQ files containing the forward and reverse reads from the .sra files were generated with the SRA toolkit version 2.4.1 for CentOS Linux64 (Cite Sequence Read Archive Submissions Staff. Using the SRA Toolkit to convert .sra files into other formats. In: SRA Knowledge Base [Internet]. Bethesda (MD): National Center for Biotechnology Information (US); 2011-. Available from: <http://www.ncbi.nlm.nih.gov/books/NBK158900/>) as follows

fastq-dump --split-files --readids ./input/run.sra

Secondly, the forward and reverse files were merged in a single file and the reverse complement of this file was generated with the FastX toolkit (<http://hannonlab.cshl.edu/fastx_toolkit/>) (Version 0.0.13 for Linux 64bit) as follows

fastx\_reverse\_complement -Q 33 -i ./output/run.fastq -o ./output/run.rc.fastq

This way the files needed for the analysis were obtained.