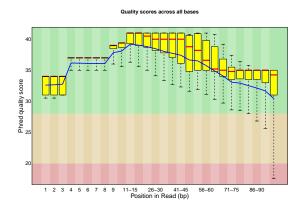
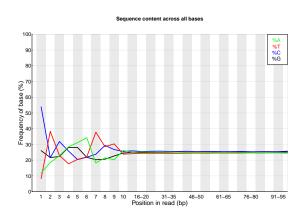
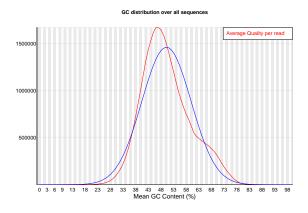
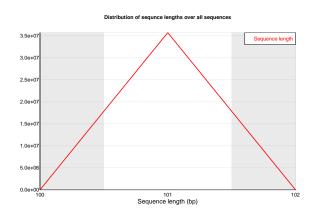
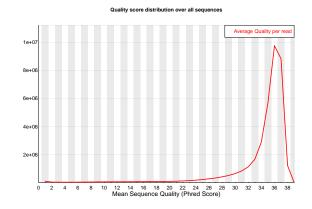
Sample $692_LIB4477_LDI3730$ Multiple files

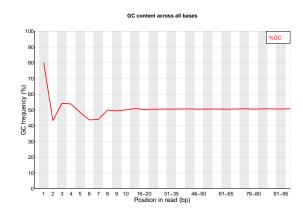


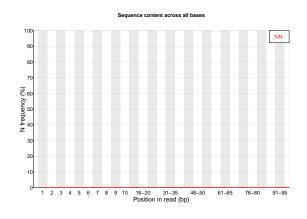


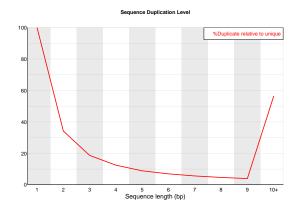












Sample 692_LIB4477_LDI3730 Multiple files

Summary

Filename Multiple files

File type Conventional base calls
Encoding Sanger / Illumina 1.9

Total sequences 3550.0006855

 $\begin{array}{ll} {\rm Filtered\ sequences} & 0 \\ {\rm Sequence\ length} & 101 \\ {\rm \%GC} & 72 \end{array}$

Analysis properties

 $\label{eq:reconstruction} Run \ folder \\ \hspace{2cm} /net/tgac-ngs-qc/vol/qc/130724_SN790_0263_BC1D68ACXX/PAP$

Cassava version 1.8.2

Chemistry version TRUSEQ_SBS_V3

Type of experiment dna Instrument SN790

Run 130724_SN790_0263_BC1D68ACXX

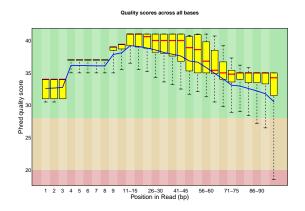
Lane 8

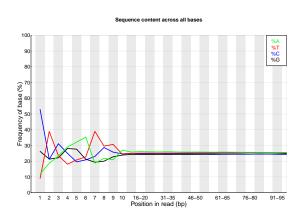
Sample name 692_LIB4477_LDI3730

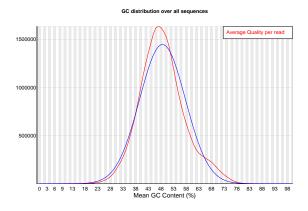
Barcode TGACCA Pair 1 2

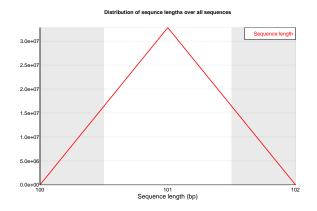
Reference ecoli phix_174 xanthomonas_campestris

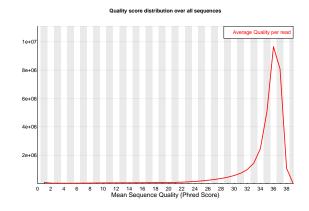
Overrepresented sequences

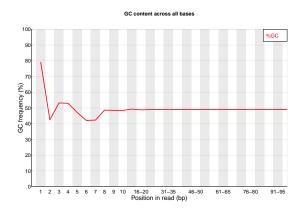


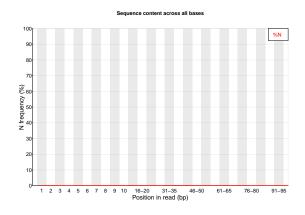


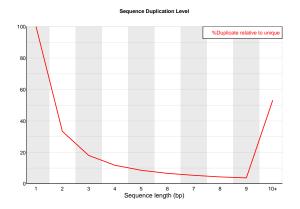












Sample 692_LIB4478_LDI3731 Multiple files

Summary

Filename Multiple files

File type Conventional base calls Encoding Sanger / Illumina 1.9

Total sequences 32825076 Filtered sequences 0 Sequence length 101 %GC 49.000

Analysis properties

 $\label{eq:rundown} Run\ folder \\ \hspace{2cm} /net/tgac-ngs-qc/vol/qc/130724_SN790_0263_BC1D68ACXX/PAP$

Cassava version 1.8.2

Chemistry version TRUSEQ_SBS_V3

Type of experiment dna Instrument SN790

Run 130724_SN790_0263_BC1D68ACXX

Lane 8

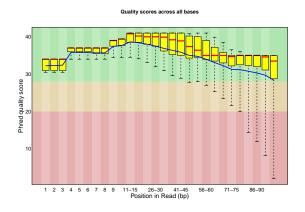
Sample name 692_LIB4478_LDI3731

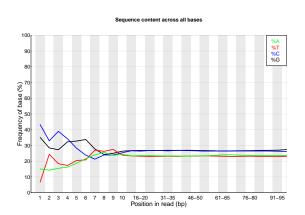
Barcode CAGATC Pair 1 2

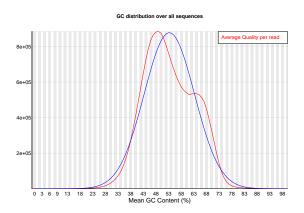
Reference ecoli phix_174 xanthomonas_campestris

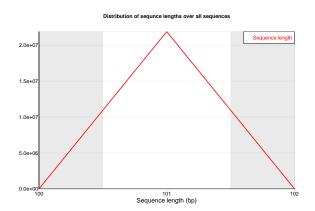
Overrepresented sequences

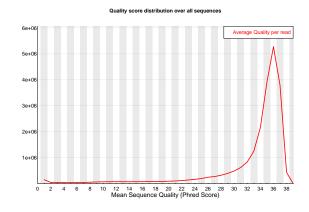
$\begin{array}{c} \mathbf{Sample} \ \mathbf{692_LIB4479_LDI3732} \\ \mathbf{Multiple} \ \mathbf{files} \end{array}$

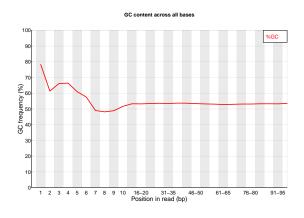


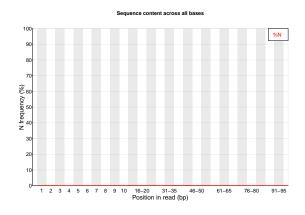


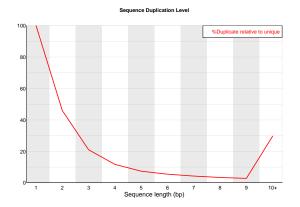












Sample 692_LIB4479_LDI3732 Multiple files

Summary

Filename Multiple files

File type Conventional base calls Encoding Sanger / Illumina 1.9

 $\begin{array}{ll} {\rm Total\ sequences} & 21889996 \\ {\rm Filtered\ sequences} & 0 \\ {\rm Sequence\ length} & 101 \\ {\rm \%GC} & 53.000 \\ \end{array}$

Analysis properties

 $\label{eq:constraint} Run \ folder \\ \hspace{2cm} /net/tgac-ngs-qc/vol/qc/130724_SN790_0263_BC1D68ACXX/PAP$

Cassava version 1.8.2

 $Chemistry\ version \qquad TRUSEQ_SBS_V3$

Type of experiment dna Instrument SN790

Run 130724_SN790_0263_BC1D68ACXX

Lane 8

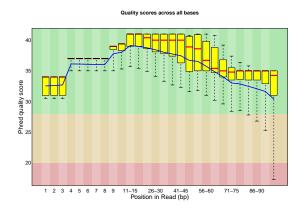
Sample name 692_LIB4479_LDI3732

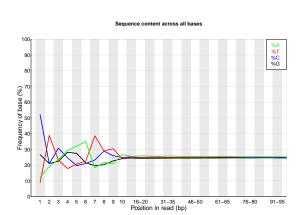
Barcode CCGTCC Pair 1 2

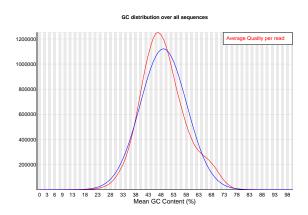
Reference ecoli phix_174 xanthomonas_campestris

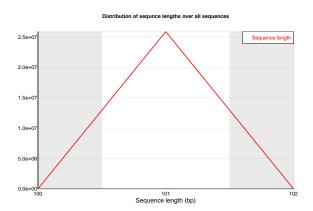
Overrepresented sequences

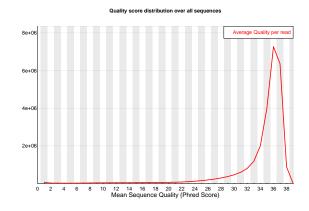
GATCGGAAGAGCACACGTCTGAACTCCAGTCACCCGTCCCGATCT AGATCGGAAGAGCACACGTCTGAACTCCAGTCACCCGTCCCGATC AGATCGGAAGAGCGTCGTGTAGGGAAAGAGTGTAGATCTCGGTGG TruSeq Adapter Index 7 (97% over 36bp) TruSeq Adapter Index 7 (97% over 36bp) Illumina Single End PCR Primer 1 (100% over 50bp)

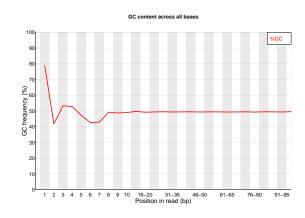


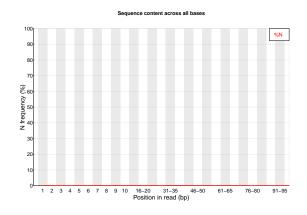


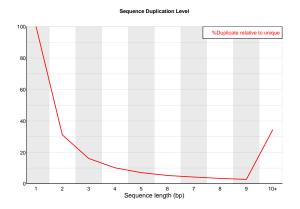












Sample 692_LIB4480_LDI3733 Multiple files

Summary

Filename Multiple files

File type Conventional base calls Encoding Sanger / Illumina 1.9

 $\begin{array}{ll} {\rm Total\ sequences} & 25878697 \\ {\rm Filtered\ sequences} & 0 \\ {\rm Sequence\ length} & 101 \\ {\rm \%GC} & 49.000 \\ \end{array}$

Analysis properties

 $\label{eq:rundown} Run\ folder \\ \hspace{2cm} /net/tgac-ngs-qc/vol/qc/130724_SN790_0263_BC1D68ACXX/PAP$

Cassava version 1.8.2

Chemistry version TRUSEQ_SBS_V3

Type of experiment dna Instrument SN790

Run 130724_SN790_0263_BC1D68ACXX

Lane 8

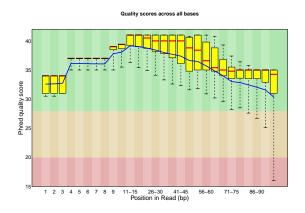
Sample name 692_LIB4480_LDI3733

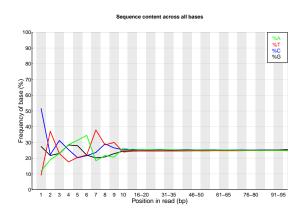
Barcode GTCCGC Pair 1 2

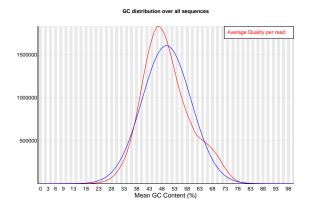
Reference ecoli phix_174 xanthomonas_campestris

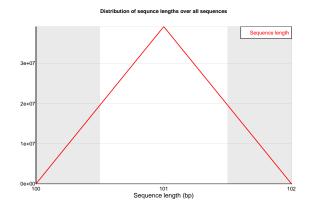
Overrepresented sequences

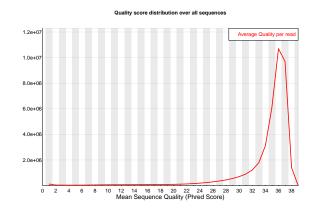
Sample $692_LIB4481_LDI3734$ Multiple files

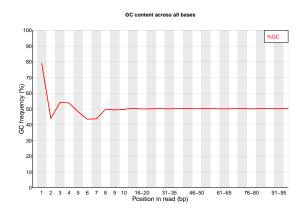


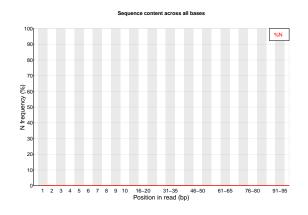


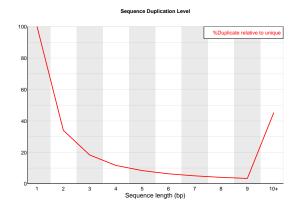












Sample 692_LIB4481_LDI3734 Multiple files

Summary

Filename Multiple files

File type Conventional base calls Encoding Sanger / Illumina 1.9

Analysis properties

 $\label{eq:run folder} {\it Run folder} \qquad /{\rm net/tgac\text{-}ngs\text{-}qc/vol/qc/130724\text{-}SN790\text{-}0263\text{-}BC1D68ACXX/PAP}$

Cassava version 1.8.2

Chemistry version TRUSEQ_SBS_V3

Type of experiment dna Instrument SN790

Run 130724_SN790_0263_BC1D68ACXX

Lane 8

 $Sample \ name \\ 692_LIB4481_LDI3734$

Barcode GTGAAA Pair 1 2

Reference ecoli phix_174 xanthomonas_campestris

Overrepresented sequences