

Raw data delivery note

SciLifeLab Stockholm

July 18, 2015

Project name

T.Backhaus_15_01

UPPNEX project id

b2014338

Flow cell id

AC6U4VANXX

Lane

8

Sequence data directory

/proj/b2014338/INBOX/T.Backhaus_15_01/P2201_121/150702_AC6U4VANXX

Sample

P2201_121 / 0,004C AgNP. Ordered amount: 2.925 million read pairs.

Method

Clustered using cBot and sequenced on HiSeq2500 (HiSeq Control Software 2.2.58/RTA 1.18.64) with a 2x126 setup in RapidHighOutput mode. Bcl to Fastq conversion was performed using bcl2Fastq v1.8.3 from the CASAVA software suite. The quality scale is Sanger / phred33 / Illumina 1.8+.

Results

6.7 million read pairs in lane with PhiX error rate 0.455%. Average quality score 34.10 (87.64% bases \geq Q30).

Raw data delivery note

SciLifeLab Stockholm

July 18, 2015

Project name

T.Backhaus_15_01

UPPNEX project id

b2014338

Flow cell id

AC6U4VANXX

Lane

8

Sequence data directory

/proj/b2014338/INBOX/T.Backhaus_15_01/P2201_122/150702_AC6U4VANXX

Sample

P2201_122 / 0,04C AgNP. Ordered amount: 2.925 million read pairs.

Method

Clustered using cBot and sequenced on HiSeq2500 (HiSeq Control Software 2.2.58/RTA 1.18.64) with a 2x126 setup in RapidHighOutput mode. Bcl to Fastq conversion was performed using bcl2Fastq v1.8.3 from the CASAVA software suite. The quality scale is Sanger / phred33 / Illumina 1.8+.

Results

6.5 million read pairs in lane with PhiX error rate 0.455%. Average quality score 34.62 (90.24% bases \geq Q30).

Raw data delivery note

SciLifeLab Stockholm

July 18, 2015

Project name

T.Backhaus_15_01

UPPNEX project id

b2014338

Flow cell id

AC6U4VANXX

Lane

8

Sequence data directory

/proj/b2014338/INBOX/T.Backhaus_15_01/P2201_119/150702_AC6U4VANXX

Sample

P2201_119 / 0,12B AgNP. Ordered amount: 2.925 million read pairs.

Method

Clustered using cBot and sequenced on HiSeq2500 (HiSeq Control Software 2.2.58/RTA 1.18.64) with a 2x126 setup in RapidHighOutput mode. Bcl to Fastq conversion was performed using bcl2Fastq v1.8.3 from the CASAVA software suite. The quality scale is Sanger / phred33 / Illumina 1.8+.

Results

7.2 million read pairs in lane with PhiX error rate 0.455%. Average quality score 34.42 (89.23% bases \geq Q30).

Raw data delivery note

SciLifeLab Stockholm

July 18, 2015

Project name

T.Backhaus_15_01

UPPNEX project id

b2014338

Flow cell id

AC6U4VANXX

Lane

8

Sequence data directory

/proj/b2014338/INBOX/T.Backhaus_15_01/P2201_105/150702_AC6U4VANXX

Sample

P2201_105 / 0,001B Ag+. Ordered amount: 2.925 million read pairs.

Method

Clustered using cBot and sequenced on HiSeq2500 (HiSeq Control Software 2.2.58/RTA 1.18.64) with a 2x126 setup in RapidHighOutput mode. Bcl to Fastq conversion was performed using bcl2Fastq v1.8.3 from the CASAVA software suite. The quality scale is Sanger / phred33 / Illumina 1.8+.

Results

5.8 million read pairs in lane with PhiX error rate 0.455%. Average quality score 34.18 (87.99% bases \geq Q30).

Raw data delivery note

SciLifeLab Stockholm

July 18, 2015

Project name

T.Backhaus_15_01

UPPNEX project id

b2014338

Flow cell id

AC6U4VANXX

Lane

8

Sequence data directory

/proj/b2014338/INBOX/T.Backhaus_15_01/P2201_124/150702_AC6U4VANXX

Sample

P2201_124 / ctrlF AgNP. Ordered amount: 2.925 million read pairs.

Method

Clustered using cBot and sequenced on HiSeq2500 (HiSeq Control Software 2.2.58/RTA 1.18.64) with a 2x126 setup in RapidHighOutput mode. Bcl to Fastq conversion was performed using bcl2Fastq v1.8.3 from the CASAVA software suite. The quality scale is Sanger / phred33 / Illumina 1.8+.

Results

7.4 million read pairs in lane with PhiX error rate 0.455%. Average quality score 34.57 (89.96% bases \geq Q30).

Raw data delivery note

SciLifeLab Stockholm

July 18, 2015

Project name

T.Backhaus_15_01

UPPNEX project id

b2014338

Flow cell id

AC6U4VANXX

Lane

8

Sequence data directory

/proj/b2014338/INBOX/T.Backhaus_15_01/P2201_116/150702_AC6U4VANXX

Sample

P2201_116 / ctrlA AgNP. Ordered amount: 2.925 million read pairs.

Method

Clustered using cBot and sequenced on HiSeq2500 (HiSeq Control Software 2.2.58/RTA 1.18.64) with a 2x126 setup in RapidHighOutput mode. Bcl to Fastq conversion was performed using bcl2Fastq v1.8.3 from the CASAVA software suite. The quality scale is Sanger / phred33 / Illumina 1.8+.

Results

8.9 million read pairs in lane with PhiX error rate 0.455%. Average quality score 34.53 (89.81% bases \geq Q30).

Raw data delivery note

SciLifeLab Stockholm

July 18, 2015

Project name

T.Backhaus_15_01

UPPNEX project id

b2014338

Flow cell id

AC6U4VANXX

Lane

8

Sequence data directory

/proj/b2014338/INBOX/T.Backhaus_15_01/P2201_114/150702_AC6U4VANXX

Sample

P2201_114 / 0,04A AgNP. Ordered amount: 2.925 million read pairs.

Method

Clustered using cBot and sequenced on HiSeq2500 (HiSeq Control Software 2.2.58/RTA 1.18.64) with a 2x126 setup in RapidHighOutput mode. Bcl to Fastq conversion was performed using bcl2Fastq v1.8.3 from the CASAVA software suite. The quality scale is Sanger / phred33 / Illumina 1.8+.

Results

6.4 million read pairs in lane with PhiX error rate 0.455%. Average quality score 34.48 (89.58% bases \geq Q30).

Raw data delivery note

SciLifeLab Stockholm

July 18, 2015

Project name

T.Backhaus_15_01

UPPNEX project id

b2014338

Flow cell id

AC6U4VANXX

Lane

8

Sequence data directory

/proj/b2014338/INBOX/T.Backhaus_15_01/P2201_107/150702_AC6U4VANXX

Sample

P2201_107 / 0,04B Ag+. Ordered amount: 2.925 million read pairs.

Method

Clustered using cBot and sequenced on HiSeq2500 (HiSeq Control Software 2.2.58/RTA 1.18.64) with a 2x126 setup in RapidHighOutput mode. Bcl to Fastq conversion was performed using bcl2Fastq v1.8.3 from the CASAVA software suite. The quality scale is Sanger / phred33 / Illumina 1.8+.

Results

7.2 million read pairs in lane with PhiX error rate 0.455%. Average quality score 34.23 (88.21% bases \geq Q30).

Raw data delivery note

SciLifeLab Stockholm

July 18, 2015

Project name

T.Backhaus_15_01

UPPNEX project id

b2014338

Flow cell id

AC6U4VANXX

Lane

8

Sequence data directory

/proj/b2014338/INBOX/T.Backhaus_15_01/P2201_104/150702_AC6U4VANXX

Sample

P2201_104 / ctrlB Ag+. Ordered amount: 2.925 million read pairs.

Method

Clustered using cBot and sequenced on HiSeq2500 (HiSeq Control Software 2.2.58/RTA 1.18.64) with a 2x126 setup in RapidHighOutput mode. Bcl to Fastq conversion was performed using bcl2Fastq v1.8.3 from the CASAVA software suite. The quality scale is Sanger / phred33 / Illumina 1.8+.

Results

6.5 million read pairs in lane with PhiX error rate 0.455%. Average quality score 34.01 (87.45% bases \geq Q30).

Raw data delivery note

SciLifeLab Stockholm

July 18, 2015

Project name

T.Backhaus_15_01

UPPNEX project id

b2014338

Flow cell id

AC6U4VANXX

Lane

8

Sequence data directory

/proj/b2014338/INBOX/T.Backhaus_15_01/P2201_111/150702_AC6U4VANXX

Sample

P2201_111 / 0,04c Ag+. Ordered amount: 2.925 million read pairs.

Method

Clustered using cBot and sequenced on HiSeq2500 (HiSeq Control Software 2.2.58/RTA 1.18.64) with a 2x126 setup in RapidHighOutput mode. Bcl to Fastq conversion was performed using bcl2Fastq v1.8.3 from the CASAVA software suite. The quality scale is Sanger / phred33 / Illumina 1.8+.

Results

6.1 million read pairs in lane with PhiX error rate 0.455%. Average quality score 34.28 (88.59% bases \geq Q30).

Raw data delivery note

SciLifeLab Stockholm

July 18, 2015

Project name

T.Backhaus_15_01

UPPNEX project id

b2014338

Flow cell id

AC6U4VANXX

Lane

8

Sequence data directory

/proj/b2014338/INBOX/T.Backhaus_15_01/P2201_102/150702_AC6U4VANXX

Sample

P2201_102 / 0,01A Ag+. Ordered amount: 2.925 million read pairs.

Method

Clustered using cBot and sequenced on HiSeq2500 (HiSeq Control Software 2.2.58/RTA 1.18.64) with a 2x126 setup in RapidHighOutput mode. Bcl to Fastq conversion was performed using bcl2Fastq v1.8.3 from the CASAVA software suite. The quality scale is Sanger / phred33 / Illumina 1.8+.

Results

6.2 million read pairs in lane with PhiX error rate 0.455%. Average quality score 34.38 (89.00% bases \geq Q30).

Raw data delivery note

SciLifeLab Stockholm

July 18, 2015

Project name

T.Backhaus_15_01

UPPNEX project id

b2014338

Flow cell id

AC6U4VANXX

Lane

8

Sequence data directory

/proj/b2014338/INBOX/T.Backhaus_15_01/P2201_109/150702_AC6U4VANXX

Sample

P2201_109 / 0,001c Ag+. Ordered amount: 2.925 million read pairs.

Method

Clustered using cBot and sequenced on HiSeq2500 (HiSeq Control Software 2.2.58/RTA 1.18.64) with a 2x126 setup in RapidHighOutput mode. Bcl to Fastq conversion was performed using bcl2Fastq v1.8.3 from the CASAVA software suite. The quality scale is Sanger / phred33 / Illumina 1.8+.

Results

5.9 million read pairs in lane with PhiX error rate 0.455%. Average quality score 34.52 (89.72% bases \geq Q30).

Raw data delivery note

SciLifeLab Stockholm

July 18, 2015

Project name

T.Backhaus_15_01

UPPNEX project id

b2014338

Flow cell id

AC6U4VANXX

Lane

8

Sequence data directory

/proj/b2014338/INBOX/T.Backhaus_15_01/P2201_123/150702_AC6U4VANXX

Sample

P2201_123 / 0,12C AgNP. Ordered amount: 2.925 million read pairs.

Method

Clustered using cBot and sequenced on HiSeq2500 (HiSeq Control Software 2.2.58/RTA 1.18.64) with a 2x126 setup in RapidHighOutput mode. Bcl to Fastq conversion was performed using bcl2Fastq v1.8.3 from the CASAVA software suite. The quality scale is Sanger / phred33 / Illumina 1.8+.

Results

7.9 million read pairs in lane with PhiX error rate 0.455%. Average quality score 34.39 (89.14% bases \geq Q30).

Raw data delivery note

SciLifeLab Stockholm

July 18, 2015

Project name

T.Backhaus_15_01

UPPNEX project id

b2014338

Flow cell id

AC6U4VANXX

Lane

8

Sequence data directory

/proj/b2014338/INBOX/T.Backhaus_15_01/P2201_103/150702_AC6U4VANXX

Sample

P2201_103 / 0,04A Ag+. Ordered amount: 2.925 million read pairs.

Method

Clustered using cBot and sequenced on HiSeq2500 (HiSeq Control Software 2.2.58/RTA 1.18.64) with a 2x126 setup in RapidHighOutput mode. Bcl to Fastq conversion was performed using bcl2Fastq v1.8.3 from the CASAVA software suite. The quality scale is Sanger / phred33 / Illumina 1.8+.

Results

6.3 million read pairs in lane with PhiX error rate 0.455%. Average quality score 34.37 (89.04% bases \geq Q30).

Raw data delivery note

SciLifeLab Stockholm

July 18, 2015

Project name

T.Backhaus_15_01

UPPNEX project id

b2014338

Flow cell id

AC6U4VANXX

Lane

8

Sequence data directory

/proj/b2014338/INBOX/T.Backhaus_15_01/P2201_108/150702_AC6U4VANXX

Sample

P2201_108 / ctrlID Ag+. Ordered amount: 2.925 million read pairs.

Method

Clustered using cBot and sequenced on HiSeq2500 (HiSeq Control Software 2.2.58/RTA 1.18.64) with a 2x126 setup in RapidHighOutput mode. Bcl to Fastq conversion was performed using bcl2Fastq v1.8.3 from the CASAVA software suite. The quality scale is Sanger / phred33 / Illumina 1.8+.

Results

6.8 million read pairs in lane with PhiX error rate 0.455%. Average quality score 34.41 (89.35% bases \geq Q30).

Raw data delivery note

SciLifeLab Stockholm

July 18, 2015

Project name

T.Backhaus_15_01

UPPNEX project id

b2014338

Flow cell id

AC6U4VANXX

Lane

8

Sequence data directory

/proj/b2014338/INBOX/T.Backhaus_15_01/P2201_112/150702_AC6U4VANXX

Sample

P2201_112 / ctrlC Ag+. Ordered amount: 2.925 million read pairs.

Method

Clustered using cBot and sequenced on HiSeq2500 (HiSeq Control Software 2.2.58/RTA 1.18.64) with a 2x126 setup in RapidHighOutput mode. Bcl to Fastq conversion was performed using bcl2Fastq v1.8.3 from the CASAVA software suite. The quality scale is Sanger / phred33 / Illumina 1.8+.

Results

6.7 million read pairs in lane with PhiX error rate 0.455%. Average quality score 34.02 (87.52% bases \geq Q30).

Raw data delivery note

SciLifeLab Stockholm

July 18, 2015

Project name

T.Backhaus_15_01

UPPNEX project id

b2014338

Flow cell id

AC6U4VANXX

Lane

8

Sequence data directory

/proj/b2014338/INBOX/T.Backhaus_15_01/P2201_117/150702_AC6U4VANXX

Sample

P2201_117 / 0,004B AgNP. Ordered amount: 2.925 million read pairs.

Method

Clustered using cBot and sequenced on HiSeq2500 (HiSeq Control Software 2.2.58/RTA 1.18.64) with a 2x126 setup in RapidHighOutput mode. Bcl to Fastq conversion was performed using bcl2Fastq v1.8.3 from the CASAVA software suite. The quality scale is Sanger / phred33 / Illumina 1.8+.

Results

6.5 million read pairs in lane with PhiX error rate 0.455%. Average quality score 34.61 (90.13% bases \geq Q30).

Raw data delivery note

SciLifeLab Stockholm

July 18, 2015

Project name

T.Backhaus_15_01

UPPNEX project id

b2014338

Flow cell id

AC6U4VANXX

Lane

8

Sequence data directory

/proj/b2014338/INBOX/T.Backhaus_15_01/P2201_101/150702_AC6U4VANXX

Sample

P2201_101 / 0,001A Ag+. Ordered amount: 2.925 million read pairs.

Method

Clustered using cBot and sequenced on HiSeq2500 (HiSeq Control Software 2.2.58/RTA 1.18.64) with a 2x126 setup in RapidHighOutput mode. Bcl to Fastq conversion was performed using bcl2Fastq v1.8.3 from the CASAVA software suite. The quality scale is Sanger / phred33 / Illumina 1.8+.

Results

7.6 million read pairs in lane with PhiX error rate 0.455%. Average quality score 34.14 (88.04% bases \geq Q30).

Raw data delivery note

SciLifeLab Stockholm

July 18, 2015

Project name

T.Backhaus_15_01

UPPNEX project id

b2014338

Flow cell id

AC6U4VANXX

Lane

8

Sequence data directory

/proj/b2014338/INBOX/T.Backhaus_15_01/P2201_106/150702_AC6U4VANXX

Sample

P2201_106 / 0,01B Ag+. Ordered amount: 2.925 million read pairs.

Method

Clustered using cBot and sequenced on HiSeq2500 (HiSeq Control Software 2.2.58/RTA 1.18.64) with a 2x126 setup in RapidHighOutput mode. Bcl to Fastq conversion was performed using bcl2Fastq v1.8.3 from the CASAVA software suite. The quality scale is Sanger / phred33 / Illumina 1.8+.

Results

6.6 million read pairs in lane with PhiX error rate 0.455%. Average quality score 34.42 (89.36% bases \geq Q30).

Raw data delivery note

SciLifeLab Stockholm

July 18, 2015

Project name

T.Backhaus_15_01

UPPNEX project id

b2014338

Flow cell id

AC6U4VANXX

Lane

8

Sequence data directory

/proj/b2014338/INBOX/T.Backhaus_15_01/P2201_118/150702_AC6U4VANXX

Sample

P2201_118 / 0,04B AgNP. Ordered amount: 2.925 million read pairs.

Method

Clustered using cBot and sequenced on HiSeq2500 (HiSeq Control Software 2.2.58/RTA 1.18.64) with a 2x126 setup in RapidHighOutput mode. Bcl to Fastq conversion was performed using bcl2Fastq v1.8.3 from the CASAVA software suite. The quality scale is Sanger / phred33 / Illumina 1.8+.

Results

5.7 million read pairs in lane with PhiX error rate 0.455%. Average quality score 34.49 (89.47% bases \geq Q30).

Raw data delivery note

SciLifeLab Stockholm

July 18, 2015

Project name

T.Backhaus_15_01

UPPNEX project id

b2014338

Flow cell id

AC6U4VANXX

Lane

8

Sequence data directory

/proj/b2014338/INBOX/T.Backhaus_15_01/P2201_113/150702_AC6U4VANXX

Sample

P2201_113 / 0,004A AgNP. Ordered amount: 2.925 million read pairs.

Method

Clustered using cBot and sequenced on HiSeq2500 (HiSeq Control Software 2.2.58/RTA 1.18.64) with a 2x126 setup in RapidHighOutput mode. Bcl to Fastq conversion was performed using bcl2Fastq v1.8.3 from the CASAVA software suite. The quality scale is Sanger / phred33 / Illumina 1.8+.

Results

5.8 million read pairs in lane with PhiX error rate 0.455%. Average quality score 34.13 (87.76% bases \geq Q30).

Raw data delivery note

SciLifeLab Stockholm

July 18, 2015

Project name

T.Backhaus_15_01

UPPNEX project id

b2014338

Flow cell id

AC6U4VANXX

Lane

8

Sequence data directory

/proj/b2014338/INBOX/T.Backhaus_15_01/P2201_110/150702_AC6U4VANXX

Sample

P2201_110 / 0,01c Ag+. Ordered amount: 2.925 million read pairs.

Method

Clustered using cBot and sequenced on HiSeq2500 (HiSeq Control Software 2.2.58/RTA 1.18.64) with a 2x126 setup in RapidHighOutput mode. Bcl to Fastq conversion was performed using bcl2Fastq v1.8.3 from the CASAVA software suite. The quality scale is Sanger / phred33 / Illumina 1.8+.

Results

6.7 million read pairs in lane with PhiX error rate 0.455%. Average quality score 34.31 (88.69% bases \geq Q30).

Raw data delivery note

SciLifeLab Stockholm

July 18, 2015

Project name

T.Backhaus_15_01

UPPNEX project id

b2014338

Flow cell id

AC6U4VANXX

Lane

8

Sequence data directory

/proj/b2014338/INBOX/T.Backhaus_15_01/P2201_120/150702_AC6U4VANXX

Sample

P2201_120 / ctrlE AgNP. Ordered amount: 2.925 million read pairs.

Method

Clustered using cBot and sequenced on HiSeq2500 (HiSeq Control Software 2.2.58/RTA 1.18.64) with a 2x126 setup in RapidHighOutput mode. Bcl to Fastq conversion was performed using bcl2Fastq v1.8.3 from the CASAVA software suite. The quality scale is Sanger / phred33 / Illumina 1.8+.

Results

7.1 million read pairs in lane with PhiX error rate 0.455%. Average quality score 34.07 (87.72% bases \geq Q30).

Raw data delivery note

SciLifeLab Stockholm

July 18, 2015

Project name

T.Backhaus_15_01

UPPNEX project id

b2014338

Flow cell id

AC6U4VANXX

Lane

8

Sequence data directory

/proj/b2014338/INBOX/T.Backhaus_15_01/P2201_115/150702_AC6U4VANXX

Sample

P2201_115 / 0,12A AgNP. Ordered amount: 2.925 million read pairs.

Method

Clustered using cBot and sequenced on HiSeq2500 (HiSeq Control Software 2.2.58/RTA 1.18.64) with a 2x126 setup in RapidHighOutput mode. Bcl to Fastq conversion was performed using bcl2Fastq v1.8.3 from the CASAVA software suite. The quality scale is Sanger / phred33 / Illumina 1.8+.

Results

6.7 million read pairs in lane with PhiX error rate 0.455%. Average quality score 34.21 (88.35% bases \geq Q30).