Raw data delivery note

SciLifeLab Stockholm

February 16, 2015

Project name

N.Street_14_08

UPPNEX project id

b2015052

Flow cell id

BC6L4PANXX

Lane

2

Sequence data directory

/proj/b2015052/INBOX/N.Street_14_08/P1387_110/150115_BC6L4PANXX

Sample

P1387_110 / Pab.M5-10-08.TR0001. Ordered amount: 11.28 million read pairs.

Method

Clustered using cBot and sequenced on HiSeq2500 (HiSeq Control Software 2.2.38/RTA 1.18.61) 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

9.5 million read pairs in lane with PhiX error rate 0.535%. Average quality score 34.99 (91.19% bases >= Q30).

Raw data delivery note

SciLifeLab Stockholm

February 16, 2015

Project name

N.Street_14_08

UPPNEX project id

b2015052

Flow cell id

BC6L4PANXX

Lane

1

Sequence data directory

/proj/b2015052/INBOX/N.Street_14_08/P1387_117/150115_BC6L4PANXX

Sample

P1387_117 / Pab.F4-10-08.TR0001. Ordered amount: 11.28 million read pairs.

Method

Clustered using cBot and sequenced on HiSeq2500 (HiSeq Control Software 2.2.38/RTA 1.18.61) 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

10.2 million read pairs in lane with PhiX error rate 0.55%. Average quality score 35.18 (92.06% bases >= Q30).

Raw data delivery note

SciLifeLab Stockholm

February 16, 2015

Project name

N.Street_14_08

UPPNEX project id

b2015052

Flow cell id

BC6L4PANXX

Lane

2

Sequence data directory

/proj/b2015052/INBOX/N.Street_14_08/P1387_106/150115_BC6L4PANXX

Sample

P1387_106 / Pab.M5-09-12.TR0001. Ordered amount: 11.28 million read pairs.

Method

Clustered using cBot and sequenced on HiSeq2500 (HiSeq Control Software 2.2.38/RTA 1.18.61) 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

11.3 million read pairs in lane with PhiX error rate 0.535%. Average quality score 35.13 (91.85% bases >= Q30).

Raw data delivery note

SciLifeLab Stockholm

February 16, 2015

Project name

N.Street_14_08

UPPNEX project id

b2015052

Flow cell id

BC6L4PANXX

Lane

1

Sequence data directory

/proj/b2015052/INBOX/N.Street_14_08/P1387_104/150115_BC6L4PANXX

Sample

P1387_104 / Pab.M3-09-12.TR0001. Ordered amount: 11.28 million read pairs.

Method

Clustered using cBot and sequenced on HiSeq2500 (HiSeq Control Software 2.2.38/RTA 1.18.61) 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

8.8 million read pairs in lane with PhiX error rate 0.55%. Average quality score 34.73 (89.93% bases >= Q30).

Raw data delivery note

SciLifeLab Stockholm

February 16, 2015

Project name

N.Street_14_08

UPPNEX project id

b2015052

Flow cell id

BC6L4PANXX

Lane

2

Sequence data directory

/proj/b2015052/INBOX/N.Street_14_08/P1387_107/150115_BC6L4PANXX

Sample

P1387_107 / Pab.M2-10-08.TR0001. Ordered amount: 11.28 million read pairs.

Method

Clustered using cBot and sequenced on HiSeq2500 (HiSeq Control Software 2.2.38/RTA 1.18.61) 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

12.6 million read pairs in lane with PhiX error rate 0.535%. Average quality score 34.87 (90.78% bases >= Q30).

Raw data delivery note

SciLifeLab Stockholm

February 16, 2015

Project name

N.Street_14_08

UPPNEX project id

b2015052

Flow cell id

BC6L4PANXX

Lane

1

Sequence data directory

/proj/b2015052/INBOX/N.Street_14_08/P1387_106/150115_BC6L4PANXX

Sample

P1387_106 / Pab.M5-09-12.TR0001. Ordered amount: 11.28 million read pairs.

Method

Clustered using cBot and sequenced on HiSeq2500 (HiSeq Control Software 2.2.38/RTA 1.18.61) 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

11.2 million read pairs in lane with PhiX error rate 0.55%. Average quality score 35.16 (91.99% bases >= Q30).

Raw data delivery note

SciLifeLab Stockholm

February 16, 2015

Project name

N.Street_14_08

UPPNEX project id

b2015052

Flow cell id

BC6L4PANXX

Lane

1

Sequence data directory

/proj/b2015052/INBOX/N.Street_14_08/P1387_122/150115_BC6L4PANXX

Sample

P1387_122 / Pab.F3-09-12.TR0001. Ordered amount: 11.28 million read pairs.

Method

Clustered using cBot and sequenced on HiSeq2500 (HiSeq Control Software 2.2.38/RTA 1.18.61) 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

10.7 million read pairs in lane with PhiX error rate 0.55%. Average quality score 35.30 (92.64% bases >= Q30).

Raw data delivery note

SciLifeLab Stockholm

February 16, 2015

Project name

N.Street_14_08

UPPNEX project id

b2015052

Flow cell id

BC6L4PANXX

Lane

2

Sequence data directory

/proj/b2015052/INBOX/N.Street_14_08/P1387_113/150115_BC6L4PANXX

Sample

P1387_113 / Pab.F1-09-12.TR0001. Ordered amount: 11.28 million read pairs.

Method

Clustered using cBot and sequenced on HiSeq2500 (HiSeq Control Software 2.2.38/RTA 1.18.61) 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

9.8 million read pairs in lane with PhiX error rate 0.535%. Average quality score 34.81 (90.18% bases >= Q30).

Raw data delivery note

SciLifeLab Stockholm

February 16, 2015

Project name

N.Street_14_08

UPPNEX project id

b2015052

Flow cell id

BC6L4PANXX

Lane

1

Sequence data directory

/proj/b2015052/INBOX/N.Street_14_08/P1387_109/150115_BC6L4PANXX

Sample

P1387_109 / Pab.M3-10-08.TR0001. Ordered amount: 11.28 million read pairs.

Method

Clustered using cBot and sequenced on HiSeq2500 (HiSeq Control Software 2.2.38/RTA 1.18.61) 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

9.1 million read pairs in lane with PhiX error rate 0.55%. Average quality score 35.16 (92.02% bases >= Q30).

Raw data delivery note

SciLifeLab Stockholm

February 16, 2015

Project name

N.Street_14_08

UPPNEX project id

b2015052

Flow cell id

BC6L4PANXX

Lane

1

Sequence data directory

/proj/b2015052/INBOX/N.Street_14_08/P1387_102/150115_BC6L4PANXX

Sample

P1387_102 / Pab.M1-10-08.TR0001. Ordered amount: 11.28 million read pairs.

Method

Clustered using cBot and sequenced on HiSeq2500 (HiSeq Control Software 2.2.38/RTA 1.18.61) 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

10.9 million read pairs in lane with PhiX error rate 0.55%. Average quality score 34.88 (90.72% bases >= Q30).

Raw data delivery note

SciLifeLab Stockholm

February 16, 2015

Project name

N.Street_14_08

UPPNEX project id

b2015052

Flow cell id

BC6L4PANXX

Lane

2

Sequence data directory

/proj/b2015052/INBOX/N.Street_14_08/P1387_109/150115_BC6L4PANXX

Sample

P1387_109 / Pab.M3-10-08.TR0001. Ordered amount: 11.28 million read pairs.

Method

Clustered using cBot and sequenced on HiSeq2500 (HiSeq Control Software 2.2.38/RTA 1.18.61) 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

9.2 million read pairs in lane with PhiX error rate 0.535%. Average quality score 35.13 (91.88% bases >= Q30).

Raw data delivery note

SciLifeLab Stockholm

February 16, 2015

Project name

N.Street_14_08

UPPNEX project id

b2015052

Flow cell id

BC6L4PANXX

Lane

1

Sequence data directory

/proj/b2015052/INBOX/N.Street_14_08/P1387_119/150115_BC6L4PANXX

Sample

P1387_119 / Pab.V4-10-08.TR0001. Ordered amount: 11.28 million read pairs.

Method

Clustered using cBot and sequenced on HiSeq2500 (HiSeq Control Software 2.2.38/RTA 1.18.61) 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

8.1 million read pairs in lane with PhiX error rate 0.55%. Average quality score 35.11 (91.64% bases >= Q30).

Raw data delivery note

SciLifeLab Stockholm

February 16, 2015

Project name

N.Street_14_08

UPPNEX project id

b2015052

Flow cell id

BC6L4PANXX

Lane

1

Sequence data directory

/proj/b2015052/INBOX/N.Street_14_08/P1387_118/150115_BC6L4PANXX

Sample

P1387_118 / Pab.F5-09-12.TR0001. Ordered amount: 11.28 million read pairs.

Method

Clustered using cBot and sequenced on HiSeq2500 (HiSeq Control Software 2.2.38/RTA 1.18.61) 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

10.8 million read pairs in lane with PhiX error rate 0.55%. Average quality score 35.09 (91.59% bases >= Q30).

Raw data delivery note

SciLifeLab Stockholm

February 16, 2015

Project name

N.Street_14_08

UPPNEX project id

b2015052

Flow cell id

BC6L4PANXX

Lane

2

Sequence data directory

/proj/b2015052/INBOX/N.Street_14_08/P1387_103/150115_BC6L4PANXX

Sample

P1387_103 / Pab.M2-09-12.TR0001. Ordered amount: 11.28 million read pairs.

Method

Clustered using cBot and sequenced on HiSeq2500 (HiSeq Control Software 2.2.38/RTA 1.18.61) 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

10.1 million read pairs in lane with PhiX error rate 0.535%. Average quality score 34.95 (90.94% bases >= Q30).

Raw data delivery note

SciLifeLab Stockholm

February 16, 2015

Project name

N.Street_14_08

UPPNEX project id

b2015052

Flow cell id

BC6L4PANXX

Lane

1

Sequence data directory

/proj/b2015052/INBOX/N.Street_14_08/P1387_123/150115_BC6L4PANXX

Sample

P1387_123 / Pab.V3-10-08.TR0001. Ordered amount: 11.28 million read pairs.

Method

Clustered using cBot and sequenced on HiSeq2500 (HiSeq Control Software 2.2.38/RTA 1.18.61) 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

14.1 million read pairs in lane with PhiX error rate 0.55%. Average quality score 35.03 (91.36% bases >= Q30).

Raw data delivery note

SciLifeLab Stockholm

February 16, 2015

Project name

N.Street_14_08

UPPNEX project id

b2015052

Flow cell id

BC6L4PANXX

Lane

2

Sequence data directory

/proj/b2015052/INBOX/N.Street_14_08/P1387_111/150115_BC6L4PANXX

Sample

P1387_111 / Pab.F2-10-08.TR0001. Ordered amount: 11.28 million read pairs.

Method

Clustered using cBot and sequenced on HiSeq2500 (HiSeq Control Software 2.2.38/RTA 1.18.61) 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

9.3 million read pairs in lane with PhiX error rate 0.535%. Average quality score 34.98 (91.11% bases >= Q30).

Raw data delivery note

SciLifeLab Stockholm

February 16, 2015

Project name

N.Street_14_08

UPPNEX project id

b2015052

Flow cell id

BC6L4PANXX

Lane

1

Sequence data directory

/proj/b2015052/INBOX/N.Street_14_08/P1387_110/150115_BC6L4PANXX

Sample

P1387_110 / Pab.M5-10-08.TR0001. Ordered amount: 11.28 million read pairs.

Method

Clustered using cBot and sequenced on HiSeq2500 (HiSeq Control Software 2.2.38/RTA 1.18.61) 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

9.5 million read pairs in lane with PhiX error rate 0.55%. Average quality score 35.03 (91.35% bases >= Q30).

Raw data delivery note

SciLifeLab Stockholm

February 16, 2015

Project name

N.Street_14_08

UPPNEX project id

b2015052

Flow cell id

BC6L4PANXX

Lane

2

Sequence data directory

/proj/b2015052/INBOX/N.Street_14_08/P1387_102/150115_BC6L4PANXX

Sample

P1387_102 / Pab.M1-10-08.TR0001. Ordered amount: 11.28 million read pairs.

Method

Clustered using cBot and sequenced on HiSeq2500 (HiSeq Control Software 2.2.38/RTA 1.18.61) 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

11.0 million read pairs in lane with PhiX error rate 0.535%. Average quality score 34.83 (90.53% bases >= Q30).

Raw data delivery note

SciLifeLab Stockholm

February 16, 2015

Project name

N.Street_14_08

UPPNEX project id

b2015052

Flow cell id

BC6L4PANXX

Lane

2

Sequence data directory

/proj/b2015052/INBOX/N.Street_14_08/P1387_114/150115_BC6L4PANXX

Sample

P1387_114 / Pab.F4-09-12.TR0001. Ordered amount: 11.28 million read pairs.

Method

Clustered using cBot and sequenced on HiSeq2500 (HiSeq Control Software 2.2.38/RTA 1.18.61) 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

11.0 million read pairs in lane with PhiX error rate 0.535%. Average quality score 35.18 (92.10% bases >= Q30).

Raw data delivery note

SciLifeLab Stockholm

February 16, 2015

Project name

N.Street_14_08

UPPNEX project id

b2015052

Flow cell id

BC6L4PANXX

Lane

1

Sequence data directory

/proj/b2015052/INBOX/N.Street_14_08/P1387_121/150115_BC6L4PANXX

Sample

P1387_121 / Pab.F5-10-08.TR0001. Ordered amount: 11.28 million read pairs.

Method

Clustered using cBot and sequenced on HiSeq2500 (HiSeq Control Software 2.2.38/RTA 1.18.61) 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

11.2 million read pairs in lane with PhiX error rate 0.55%. Average quality score 34.94 (90.73% bases >= Q30).

Raw data delivery note

SciLifeLab Stockholm

February 16, 2015

Project name

N.Street_14_08

UPPNEX project id

b2015052

Flow cell id

BC6L4PANXX

Lane

2

Sequence data directory

/proj/b2015052/INBOX/N.Street_14_08/P1387_119/150115_BC6L4PANXX

Sample

P1387_119 / Pab.V4-10-08.TR0001. Ordered amount: 11.28 million read pairs.

Method

Clustered using cBot and sequenced on HiSeq2500 (HiSeq Control Software 2.2.38/RTA 1.18.61) 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

8.3 million read pairs in lane with PhiX error rate 0.535%. Average quality score 35.08 (91.54% bases >= Q30).

Raw data delivery note

SciLifeLab Stockholm

February 16, 2015

Project name

N.Street_14_08

UPPNEX project id

b2015052

Flow cell id

BC6L4PANXX

Lane

1

Sequence data directory

/proj/b2015052/INBOX/N.Street_14_08/P1387_116/150115_BC6L4PANXX

Sample

P1387_116 / Pab.F2-09-12.TR0001. Ordered amount: 11.28 million read pairs.

Method

Clustered using cBot and sequenced on HiSeq2500 (HiSeq Control Software 2.2.38/RTA 1.18.61) 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

11.3 million read pairs in lane with PhiX error rate 0.55%. Average quality score 35.01 (91.31% bases >= Q30).

Raw data delivery note

SciLifeLab Stockholm

February 16, 2015

Project name

N.Street_14_08

UPPNEX project id

b2015052

Flow cell id

BC6L4PANXX

Lane

2

Sequence data directory

/proj/b2015052/INBOX/N.Street_14_08/P1387_112/150115_BC6L4PANXX

Sample

P1387_112 / Pab.F3-10-08.TR0001. Ordered amount: 11.28 million read pairs.

Method

Clustered using cBot and sequenced on HiSeq2500 (HiSeq Control Software 2.2.38/RTA 1.18.61) 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

11.1 million read pairs in lane with PhiX error rate 0.535%. Average quality score 34.84 (90.40% bases >= Q30).

Raw data delivery note

SciLifeLab Stockholm

February 16, 2015

Project name

N.Street_14_08

UPPNEX project id

b2015052

Flow cell id

BC6L4PANXX

Lane

1

Sequence data directory

/proj/b2015052/INBOX/N.Street_14_08/P1387_107/150115_BC6L4PANXX

Sample

P1387_107 / Pab.M2-10-08.TR0001. Ordered amount: 11.28 million read pairs.

Method

Clustered using cBot and sequenced on HiSeq2500 (HiSeq Control Software 2.2.38/RTA 1.18.61) 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

12.6 million read pairs in lane with PhiX error rate 0.55%. Average quality score 34.91 (90.89% bases >= Q30).

Raw data delivery note

SciLifeLab Stockholm

February 16, 2015

Project name

N.Street_14_08

UPPNEX project id

b2015052

Flow cell id

BC6L4PANXX

Lane

2

Sequence data directory

/proj/b2015052/INBOX/N.Street_14_08/P1387_122/150115_BC6L4PANXX

Sample

P1387_122 / Pab.F3-09-12.TR0001. Ordered amount: 11.28 million read pairs.

Method

Clustered using cBot and sequenced on HiSeq2500 (HiSeq Control Software 2.2.38/RTA 1.18.61) 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

10.8 million read pairs in lane with PhiX error rate 0.535%. Average quality score 35.27 (92.53% bases >= Q30).

Raw data delivery note

SciLifeLab Stockholm

February 16, 2015

Project name

N.Street_14_08

UPPNEX project id

b2015052

Flow cell id

BC6L4PANXX

Lane

2

Sequence data directory

/proj/b2015052/INBOX/N.Street_14_08/P1387_118/150115_BC6L4PANXX

Sample

P1387_118 / Pab.F5-09-12.TR0001. Ordered amount: 11.28 million read pairs.

Method

Clustered using cBot and sequenced on HiSeq2500 (HiSeq Control Software 2.2.38/RTA 1.18.61) 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

10.9 million read pairs in lane with PhiX error rate 0.535%. Average quality score 35.05 (91.44% bases >= Q30).

Raw data delivery note

SciLifeLab Stockholm

February 16, 2015

Project name

N.Street_14_08

UPPNEX project id

b2015052

Flow cell id

BC6L4PANXX

Lane

2

Sequence data directory

/proj/b2015052/INBOX/N.Street_14_08/P1387_101/150115_BC6L4PANXX

Sample

P1387_101 / Pab.M1-09-12.TR0001. Ordered amount: 11.28 million read pairs.

Method

Clustered using cBot and sequenced on HiSeq2500 (HiSeq Control Software 2.2.38/RTA 1.18.61) 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

9.7 million read pairs in lane with PhiX error rate 0.535%. Average quality score 35.06 (91.58% bases >= Q30).

Raw data delivery note

SciLifeLab Stockholm

February 16, 2015

Project name

N.Street_14_08

UPPNEX project id

b2015052

Flow cell id

BC6L4PANXX

Lane

2

Sequence data directory

/proj/b2015052/INBOX/N.Street_14_08/P1387_121/150115_BC6L4PANXX

Sample

P1387_121 / Pab.F5-10-08.TR0001. Ordered amount: 11.28 million read pairs.

Method

Clustered using cBot and sequenced on HiSeq2500 (HiSeq Control Software 2.2.38/RTA 1.18.61) 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

11.5 million read pairs in lane with PhiX error rate 0.535%. Average quality score 34.93 (90.73% bases >= Q30).

Raw data delivery note

SciLifeLab Stockholm

February 16, 2015

Project name

N.Street_14_08

UPPNEX project id

b2015052

Flow cell id

BC6L4PANXX

Lane

2

Sequence data directory

/proj/b2015052/INBOX/N.Street_14_08/P1387_104/150115_BC6L4PANXX

Sample

P1387_104 / Pab.M3-09-12.TR0001. Ordered amount: 11.28 million read pairs.

Method

Clustered using cBot and sequenced on HiSeq2500 (HiSeq Control Software 2.2.38/RTA 1.18.61) 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 0.535%. Average quality score 34.69 (89.84% bases >= Q30).

Raw data delivery note

SciLifeLab Stockholm

February 16, 2015

Project name

N.Street_14_08

UPPNEX project id

b2015052

Flow cell id

BC6L4PANXX

Lane

1

Sequence data directory

/proj/b2015052/INBOX/N.Street_14_08/P1387_125/150115_BC6L4PANXX

Sample

P1387_125 / Pab.V1-10-08.TR0001. Ordered amount: 11.28 million read pairs.

Method

Clustered using cBot and sequenced on HiSeq2500 (HiSeq Control Software 2.2.38/RTA 1.18.61) 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

9.5 million read pairs in lane with PhiX error rate 0.55%. Average quality score 35.17 (92.00% bases >= Q30).

Raw data delivery note

SciLifeLab Stockholm

February 16, 2015

Project name

N.Street_14_08

UPPNEX project id

b2015052

Flow cell id

BC6L4PANXX

Lane

1

Sequence data directory

/proj/b2015052/INBOX/N.Street_14_08/P1387_111/150115_BC6L4PANXX

Sample

P1387_111 / Pab.F2-10-08.TR0001. Ordered amount: 11.28 million read pairs.

Method

Clustered using cBot and sequenced on HiSeq2500 (HiSeq Control Software 2.2.38/RTA 1.18.61) 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

9.1 million read pairs in lane with PhiX error rate 0.55%. Average quality score 35.02 (91.22% bases >= Q30).

Raw data delivery note

SciLifeLab Stockholm

February 16, 2015

Project name

N.Street_14_08

UPPNEX project id

b2015052

Flow cell id

BC6L4PANXX

Lane

1

Sequence data directory

/proj/b2015052/INBOX/N.Street_14_08/P1387_120/150115_BC6L4PANXX

Sample

P1387_120 / Pab.V5-10-08.TR0001. Ordered amount: 11.28 million read pairs.

Method

Clustered using cBot and sequenced on HiSeq2500 (HiSeq Control Software 2.2.38/RTA 1.18.61) 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

9.7 million read pairs in lane with PhiX error rate 0.55%. Average quality score 34.90 (90.64% bases >= Q30).

Raw data delivery note

SciLifeLab Stockholm

February 16, 2015

Project name

N.Street_14_08

UPPNEX project id

b2015052

Flow cell id

BC6L4PANXX

Lane

1

Sequence data directory

/proj/b2015052/INBOX/N.Street_14_08/P1387_108/150115_BC6L4PANXX

Sample

P1387_108 / Pab.M4-10-08.TR0001. Ordered amount: 11.28 million read pairs.

Method

Clustered using cBot and sequenced on HiSeq2500 (HiSeq Control Software 2.2.38/RTA 1.18.61) 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

9.4 million read pairs in lane with PhiX error rate 0.55%. Average quality score 34.98 (91.19% bases >= Q30).

Raw data delivery note

SciLifeLab Stockholm

February 16, 2015

Project name

N.Street_14_08

UPPNEX project id

b2015052

Flow cell id

BC6L4PANXX

Lane

2

Sequence data directory

/proj/b2015052/INBOX/N.Street_14_08/P1387_116/150115_BC6L4PANXX

Sample

P1387_116 / Pab.F2-09-12.TR0001. Ordered amount: 11.28 million read pairs.

Method

Clustered using cBot and sequenced on HiSeq2500 (HiSeq Control Software 2.2.38/RTA 1.18.61) 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

11.4 million read pairs in lane with PhiX error rate 0.535%. Average quality score 34.98 (91.19% bases >= Q30).

Raw data delivery note

SciLifeLab Stockholm

February 16, 2015

Project name

N.Street_14_08

UPPNEX project id

b2015052

Flow cell id

BC6L4PANXX

Lane

1

Sequence data directory

/proj/b2015052/INBOX/N.Street_14_08/P1387_105/150115_BC6L4PANXX

Sample

P1387_105 / Pab.M4-09-12.TR0001. Ordered amount: 11.28 million read pairs.

Method

Clustered using cBot and sequenced on HiSeq2500 (HiSeq Control Software 2.2.38/RTA 1.18.61) 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

10.1 million read pairs in lane with PhiX error rate 0.55%. Average quality score 34.80 (90.06% bases >= Q30).

Raw data delivery note

SciLifeLab Stockholm

February 16, 2015

Project name

N.Street_14_08

UPPNEX project id

b2015052

Flow cell id

BC6L4PANXX

Lane

1

Sequence data directory

/proj/b2015052/INBOX/N.Street_14_08/P1387_114/150115_BC6L4PANXX

Sample

P1387_114 / Pab.F4-09-12.TR0001. Ordered amount: 11.28 million read pairs.

Method

Clustered using cBot and sequenced on HiSeq2500 (HiSeq Control Software 2.2.38/RTA 1.18.61) 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

10.9 million read pairs in lane with PhiX error rate 0.55%. Average quality score 35.22 (92.24% bases >= Q30).

Raw data delivery note

SciLifeLab Stockholm

February 16, 2015

Project name

N.Street_14_08

UPPNEX project id

b2015052

Flow cell id

BC6L4PANXX

Lane

2

Sequence data directory

/proj/b2015052/INBOX/N.Street_14_08/P1387_125/150115_BC6L4PANXX

Sample

P1387_125 / Pab.V1-10-08.TR0001. Ordered amount: 11.28 million read pairs.

Method

Clustered using cBot and sequenced on HiSeq2500 (HiSeq Control Software 2.2.38/RTA 1.18.61) 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

9.7 million read pairs in lane with PhiX error rate 0.535%. Average quality score 35.13 (91.87% bases >= Q30).

Raw data delivery note

SciLifeLab Stockholm

February 16, 2015

Project name

N.Street_14_08

UPPNEX project id

b2015052

Flow cell id

BC6L4PANXX

Lane

2

Sequence data directory

/proj/b2015052/INBOX/N.Street_14_08/P1387_117/150115_BC6L4PANXX

Sample

P1387_117 / Pab.F4-10-08.TR0001. Ordered amount: 11.28 million read pairs.

Method

Clustered using cBot and sequenced on HiSeq2500 (HiSeq Control Software 2.2.38/RTA 1.18.61) 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

10.3 million read pairs in lane with PhiX error rate 0.535%. Average quality score 35.14 (91.90% bases >= Q30).

Raw data delivery note

SciLifeLab Stockholm

February 16, 2015

Project name

N.Street_14_08

UPPNEX project id

b2015052

Flow cell id

BC6L4PANXX

Lane

1

Sequence data directory

/proj/b2015052/INBOX/N.Street_14_08/P1387_101/150115_BC6L4PANXX

Sample

P1387_101 / Pab.M1-09-12.TR0001. Ordered amount: 11.28 million read pairs.

Method

Clustered using cBot and sequenced on HiSeq2500 (HiSeq Control Software 2.2.38/RTA 1.18.61) 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

9.6 million read pairs in lane with PhiX error rate 0.55%. Average quality score 35.10 (91.74% bases >= Q30).

Raw data delivery note

SciLifeLab Stockholm

February 16, 2015

Project name

N.Street_14_08

UPPNEX project id

b2015052

Flow cell id

BC6L4PANXX

Lane

2

Sequence data directory

/proj/b2015052/INBOX/N.Street_14_08/P1387_123/150115_BC6L4PANXX

Sample

P1387_123 / Pab.V3-10-08.TR0001. Ordered amount: 11.28 million read pairs.

Method

Clustered using cBot and sequenced on HiSeq2500 (HiSeq Control Software 2.2.38/RTA 1.18.61) 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

14.2 million read pairs in lane with PhiX error rate 0.535%. Average quality score 35.00 (91.26% bases >= Q30).

Raw data delivery note

SciLifeLab Stockholm

February 16, 2015

Project name

N.Street_14_08

UPPNEX project id

b2015052

Flow cell id

BC6L4PANXX

Lane

2

Sequence data directory

/proj/b2015052/INBOX/N.Street_14_08/P1387_105/150115_BC6L4PANXX

Sample

P1387_105 / Pab.M4-09-12.TR0001. Ordered amount: 11.28 million read pairs.

Method

Clustered using cBot and sequenced on HiSeq2500 (HiSeq Control Software 2.2.38/RTA 1.18.61) 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

10.3 million read pairs in lane with PhiX error rate 0.535%. Average quality score 34.77 (90.02% bases >= Q30).

Raw data delivery note

SciLifeLab Stockholm

February 16, 2015

Project name

N.Street_14_08

UPPNEX project id

b2015052

Flow cell id

BC6L4PANXX

Lane

2

Sequence data directory

/proj/b2015052/INBOX/N.Street_14_08/P1387_115/150115_BC6L4PANXX

Sample

P1387_115 / Pab.F1-10-08.TR0001. Ordered amount: 11.28 million read pairs.

Method

Clustered using cBot and sequenced on HiSeq2500 (HiSeq Control Software 2.2.38/RTA 1.18.61) 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

12.6 million read pairs in lane with PhiX error rate 0.535%. Average quality score 34.95 (91.09% bases >= Q30).

Raw data delivery note

SciLifeLab Stockholm

February 16, 2015

Project name

N.Street_14_08

UPPNEX project id

b2015052

Flow cell id

BC6L4PANXX

Lane

1

Sequence data directory

/proj/b2015052/INBOX/N.Street_14_08/P1387_115/150115_BC6L4PANXX

Sample

P1387_115 / Pab.F1-10-08.TR0001. Ordered amount: 11.28 million read pairs.

Method

Clustered using cBot and sequenced on HiSeq2500 (HiSeq Control Software 2.2.38/RTA 1.18.61) 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

12.5 million read pairs in lane with PhiX error rate 0.55%. Average quality score 34.99 (91.19% bases >= Q30).

Raw data delivery note

SciLifeLab Stockholm

February 16, 2015

Project name

N.Street_14_08

UPPNEX project id

b2015052

Flow cell id

BC6L4PANXX

Lane

1

Sequence data directory

/proj/b2015052/INBOX/N.Street_14_08/P1387_124/150115_BC6L4PANXX

Sample

P1387_124 / Pab.V2-10-08.TR0001. Ordered amount: 11.28 million read pairs.

Method

Clustered using cBot and sequenced on HiSeq2500 (HiSeq Control Software 2.2.38/RTA 1.18.61) 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

9.5 million read pairs in lane with PhiX error rate 0.55%. Average quality score 35.07 (91.54% bases >= Q30).

Raw data delivery note

SciLifeLab Stockholm

February 16, 2015

Project name

N.Street_14_08

UPPNEX project id

b2015052

Flow cell id

BC6L4PANXX

Lane

2

Sequence data directory

/proj/b2015052/INBOX/N.Street_14_08/P1387_120/150115_BC6L4PANXX

Sample

P1387_120 / Pab.V5-10-08.TR0001. Ordered amount: 11.28 million read pairs.

Method

Clustered using cBot and sequenced on HiSeq2500 (HiSeq Control Software 2.2.38/RTA 1.18.61) 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

9.9 million read pairs in lane with PhiX error rate 0.535%. Average quality score 34.87 (90.56% bases >= Q30).

Raw data delivery note

SciLifeLab Stockholm

February 16, 2015

Project name

N.Street_14_08

UPPNEX project id

b2015052

Flow cell id

BC6L4PANXX

Lane

1

Sequence data directory

/proj/b2015052/INBOX/N.Street_14_08/P1387_112/150115_BC6L4PANXX

Sample

P1387_112 / Pab.F3-10-08.TR0001. Ordered amount: 11.28 million read pairs.

Method

Clustered using cBot and sequenced on HiSeq2500 (HiSeq Control Software 2.2.38/RTA 1.18.61) 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

11.0 million read pairs in lane with PhiX error rate 0.55%. Average quality score 34.86 (90.48% bases >= Q30).

Raw data delivery note

SciLifeLab Stockholm

February 16, 2015

Project name

N.Street_14_08

UPPNEX project id

b2015052

Flow cell id

BC6L4PANXX

Lane

1

Sequence data directory

/proj/b2015052/INBOX/N.Street_14_08/P1387_103/150115_BC6L4PANXX

Sample

P1387_103 / Pab.M2-09-12.TR0001. Ordered amount: 11.28 million read pairs.

Method

Clustered using cBot and sequenced on HiSeq2500 (HiSeq Control Software 2.2.38/RTA 1.18.61) 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

9.9 million read pairs in lane with PhiX error rate 0.55%. Average quality score 34.98 (91.05% bases >= Q30).

Raw data delivery note

SciLifeLab Stockholm

February 16, 2015

Project name

N.Street_14_08

UPPNEX project id

b2015052

Flow cell id

BC6L4PANXX

Lane

1

Sequence data directory

/proj/b2015052/INBOX/N.Street_14_08/P1387_113/150115_BC6L4PANXX

Sample

P1387_113 / Pab.F1-09-12.TR0001. Ordered amount: 11.28 million read pairs.

Method

Clustered using cBot and sequenced on HiSeq2500 (HiSeq Control Software 2.2.38/RTA 1.18.61) 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

9.6 million read pairs in lane with PhiX error rate 0.55%. Average quality score 34.83 (90.21% bases >= Q30).

Raw data delivery note

SciLifeLab Stockholm

February 16, 2015

Project name

N.Street_14_08

UPPNEX project id

b2015052

Flow cell id

BC6L4PANXX

Lane

2

Sequence data directory

/proj/b2015052/INBOX/N.Street_14_08/P1387_124/150115_BC6L4PANXX

Sample

P1387_124 / Pab.V2-10-08.TR0001. Ordered amount: 11.28 million read pairs.

Method

Clustered using cBot and sequenced on HiSeq2500 (HiSeq Control Software 2.2.38/RTA 1.18.61) 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

9.6 million read pairs in lane with PhiX error rate 0.535%. Average quality score 35.03 (91.42% bases >= Q30).

Raw data delivery note

SciLifeLab Stockholm

February 16, 2015

Project name

N.Street_14_08

UPPNEX project id

b2015052

Flow cell id

BC6L4PANXX

Lane

2

Sequence data directory

/proj/b2015052/INBOX/N.Street_14_08/P1387_108/150115_BC6L4PANXX

Sample

P1387_108 / Pab.M4-10-08.TR0001. Ordered amount: 11.28 million read pairs.

Method

Clustered using cBot and sequenced on HiSeq2500 (HiSeq Control Software 2.2.38/RTA 1.18.61) 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

9.4 million read pairs in lane with PhiX error rate 0.535%. Average quality score 34.95 (91.09% bases >= Q30).